The role of the environment in eco-evolutionary feedback dynamics

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Effect of Dispersal Network Structure on the Eco-Evolutionary Dynamics of Network Coexistence

Summary of the dissertation

In my thesis, I studied the effect of environmental changes such as the induction of abiotic stress and spatial structure in the link between evolution and ecology with the aim to develop an understanding when and how often ecological and evolutionary dynamics interplay to affect the fate of natural populations.

The first chapter is a conceptual work discussing the processes through which abiotic stress can enhance or impede the link between evolution and ecology. Here I synthesize the knowledge from the fields of evolutionary biology and ecology to discuss the potential processes through which abiotic stress can affect the link between evolution and ecology. I identify gaps in our knowledge and propose further experimental and theoretical directions that need to be investigated. This chapter has been an important driver for my thesis.

In the second chapter, I follow one of the experimental directions that I propose in my first chapter. Based on the experimental model system, with the alga *Chlorella variabilis* as a host and the virus *PBCV-1*, I combined a mathematical and an experimental approach to test if abiotic stress can break the link between resistance evolution and ecology through changes in the strength of the host resistance-growth trade-off and host mortality rate. I use an experimental approach to verify the predictions of my mathematical model that an abiotic stressor could break the link between evolution and ecology by increasing the strength of the trade-off between host resistance and growth rate and increasing host mortality. This chapter underlines the importance of combining mathematical

modelling approaches with experimental evolution. It is also a significant step in developing a predictive understanding of when and how eco-evolutionary dynamics might occur in nature.

In the third chapter, I extend the mathematical model of chapter two that describes the host-virus community and I add a predator for the host as an additional consumer for the algal host. My motivation is to investigate the role of another environmental factor such as spatial structure for eco-evolutionary feedback dynamics. Already in the first chapter I highlight the potential of dispersal to affect the link between evolution and ecology and thus eco-evolutionary feedback dynamics. In my chapter III, I model the eco-evolutionary dynamics of the three species first in one patch and then I extend it to more complex spatial scales of eight patches that are connected by dispersal. This chapter shows that when there is spatial homogeneity, dispersal network structure has no significant effect on the species eco-evolutionary dynamics as well as on species coexistence. In addition, I test the effect of dispersal network structure in the absence of eco-evolutionary dynamics (i.e., only ecological dynamics) and I find that the species specific interactions play a more important role for species coexistence compare to dispersal network structure. This chapter is an important the first step towards testing more realistic cases and predictions from metapopulation theory.

Zusammenfassung der Dissertation

In meiner Doktorarbeit untersuchte ich die Auswirkung von Umweltveränderungen wie abiotischem Stress und räumlicher Struktur auf das Verhältnis zwischen Evolution und Ökologie. Mein Ziel ist es, ein Verständnis dafür zu entwickeln, in welchem Umfang ökologische und evolutionäre Dynamik zusammenwirken, um natürliche Populationen zu beeinflussen.

Das erste Kapitel dient als konzeptionelle Arbeit, welche die Dynamik zwischen abiotischem Stress, Ökologie und Evolution behandelt. Dort verbinde ich Grundlagen der Evolutionsbiologie und Ökologie, um die potentiellen Prozesse zu diskutieren, durch welche abiotischer Stress auf das Verhältnis von Evolution und Ökologie einwirken kann. Ich zeige Lücken auf und schlage weitere Richtungen für experimentelle und theoretische Untersuchungen vor. Dieses Kapitel stellt die grundlegende Motivation für diese Doktorarbeit dar.

Im zweiten Kapitel verfolge ich eine der experimentellen Untersuchungen, die ich im ersten Kapitel aufgezeigt habe. Basierend auf einem Modellsystem, bestehend aus der Alge *Chlorella variabilis* als Wirt und dem Virus *PBCV-1*, kombinierte ich einen mathematischen und einen experimentellen Ansatz. Damit möchte ich testen, ob abiotischer Stress die Verbindung zwischen Resistenz-Evolution und Ökologie stören kann, durch Veränderungen in Form von einem Tradeoff zwischen Resistenz und Wachstumsrate des Wirts und der Sterberate des Wirts. Zusätzlich wende ich einen experimentellen Ansatz an, um die Vorhersagen des mathematischen Modells zu verifizieren. Dieses Kapitel zeigt,

wie wichtig es ist, mathematische Modelle mit experimenteller Evolution zu kombinieren und ist ein erster Schritt, um ein vorhersagendes Verständnis davon zu entwickeln, wo und in welchem Umfang öko-evolutionäre Dynamiken in der Natur vorkommen.

Im dritten Kapitel erweitere ich das mathematische Modell aus dem zweiten Kapitel, welches die Wirts-Virus-Gemeinschaft beschreibt und füge einen Fressfeind des Wirts hinzu. Das Ziel ist es, die Rolle eines weiteren Umweltfaktors, nämlich räumlicher Struktur, in der öko-evolutionären Feedback-Dynamik zu untersuchen. Bereits im ersten Kapitel wurde die potentielle Auswirkung von räumlicher Ausbreitung auf die Verbindung von Evolution und Ökologie und damit öko-evolutionäre Feedfack-Dynamik hervorgehoben. Im dritten Kapitel wird nun die öko-evolutionäre Dynamik der drei Spezies in einem Gebiet modelliert und dann erweitert auf einen komplexeren räumlichen Fall mit acht Gebieten, die durch Migration verbunden sind. Dieses Kapitel zeigt, dass wenn räumliche Homogenität vorliegt, kein signifikanter Einfluss des Ausbreitungsnetzwerks auf die öko-evolutionäre Dynamik der Spezies und deren Koexistenz besteht. Zusätzlich teste ich die Auswirkung der Struktur des Ausbreitungsnetzwerkes in Abwesenheit von öko-evolutionärer Dynamik und finde, dass die spezifischen Interaktionen der Spezies eine wichtigere Rolle in der Koexistenz der Spezies haben, als die Struktur des Ausbreitungsnetzwerkes. Dieses Kapitel ist der erste Schritt, um Bedingungen zu testen, die den natürlichen Habitaten entsprechen und damit Vorhersagen der Metapopulationstheorie zu überprüfen.

General Introduction

The idea that evolution can be rapid enough to act on similar timescales to those of ecology has unified the fields of evolutionary biology and ecology, creating the synthetic field of eco-evolutionary dynamics. David Pimentel in early 60s and Brian Charlesworth in the late 70s were the first to report this concept. The first experimental evidence was published long after, at the beginning of this century, and provided proof of the concept (Yoshida *et al.* 2003; Hairston *et al.* 2005; Bassar *et al.* 2010; Becks *et al.* 2010). Since then, the scientific community has realized the importance of using an eco-evolutionary approach in research to answer in-depth questions related to adaptation, speciation and the maintenance and origins of biodiversity, species coexistence, species interactions, evolution of sex, cancer and cooperation (Pelletier *et al.* 2009; Post & Palkovacs 2009; Quigley *et al.* 2012; Hendry 2013; Cortez 2016; Haafke *et al.* 2016). As a more general illustration of the importance of eco-evolutionary dynamics, a search of the ISI Web of Science was performed using the terms “eco-evolutionary dynamics” and “eco-evolutionary feedback” and more than 100 articles were found from 2017, which is 5x higher to the number of publications published in 2010 (Figure 1).

The central dogma of eco-evolutionary dynamics is eco-evolutionary feedback dynamics, where evolution alters the ecological dynamics which then, in turn, shape the course of subsequent evolution. To date, the few studies which have dealt with this topic show that consideration of eco-evolutionary feedback dynamics allows a better understanding of, and more accurate predictions for, processes such as adaptation, species coexistence and community dynamics

(Becks et al. 2010; Matthews et al. 2016; Brunner et al. 2017). Despite the importance of eco-evolutionary feedback dynamics, the role of environmental changes in determining how often evolution and ecology interact to affect the fate of natural processes, is not yet understood. Fussmann *et al.* 2007 highlighted the importance of this topic very little has been reported so far (Rudman *et al.* 2017).

Chapter One:

Selection by multiple stressors and eco-evolutionary dynamics

In the first chapter of my thesis I take a first step in addressing this question by demonstrating that an environmental change as common as the introduction of an abiotic stressor, i.e., a factor that leads to a sharp reduction in fitness, can either promote or impede eco-evolutionary feedback dynamics by controlling whether phenotypic variation has an impact on the ecological dynamics. Abiotic stress can affect both ecological and evolutionary dynamics, but how it can affect their interplay, and especially the link between evolution and ecology, has not been studied. I have combined knowledge from evolutionary biology, ecology and population genetics to address conceptually how abiotic stress can break the link between evolution and ecology. To obtain a better (mechanistic) understanding, I use a conceptual predator-prey model where the prey can rapidly evolve anti-predator defences and stress resistance. I discuss the potential processes through which abiotic stress may decouple or enhance the link between the adaptive evolution of anti-predator defences and the predator-prey population dynamics. Furthermore, I developed various scenarios, thus providing a diagnostic for the predator-prey population dynamics. Finally, I have identified gaps in current knowledge and suggested future experiments to provide a mechanistic

understanding of, and develop a predictive capability for, community responses to abiotic stress.

Chapter Two:

Abiotic Stress can Break the Link Between Rapid Evolution and Ecology

One important outcome from Chapter one was the fact that abiotic stress can break the link between evolutionary and ecological change through changes in the strength of a trade-off. I extended a mathematical model for the alga-virus experimental model system developed by Frickel *et al.* (2016) to test this hypothesis. Based on numerical simulations the model predicted that the likelihood of the products of alga-host evolution being maintained in the population and having an impact on the population dynamics of the system decreases with an increase in additional host mortality introduced by an abiotic stressor as well as with an increase in the cost of the host's resistance.

Based on the outcome of the model, two experimental treatments were designed: one treatment under benign conditions and one under stressful conditions. The experimental data verified the mathematical predictions, where the likelihood of the link between evolution and ecology to break to increase with the increasing the resistance-growth rate and the mortality of the alga. The study is an important step in developing a predictive understanding of when and how eco-evolutionary dynamics occur in nature. More empirical and theoretical data are required for different model systems under various environmental conditions in order to achieve a deeper and mechanistic understanding of the interplay between ecology and evolution in nature.

Chapter Three:

Effect of Dispersal Network Structure on the Eco-Evolutionary Dynamics of Network Coexistence

The aim of the third chapter was to investigate the role of another environmental factor such as the spatial structure, for eco-evolutionary feedback dynamics. In the first chapter, I highlighted the potential of dispersal to affect the link between evolution and ecology and thus eco-evolutionary feedback dynamics. So far, most of the research has been focused on the role of eco-evolutionary dynamics in isolated populations (Toju *et al.* 2017). In chapter three, I modelled the eco-evolutionary dynamics of an experimental system with three interacting species in one patch and then extended to more complex spatial scales of eight patches. The three species include the alga-host *Chlorella variabilis*, its virus *PBCV-1*, and a host-predator the rotifer *Brachionus calyciflorus.* In the model algae and virus coevolve while the rotifers do not evolve. To describe the interaction between the host alga and the virus we applied a modified gene-for-gene interaction without costs for the virus. The modified gene for gene interactions assumes that a viral mutant, $\boldsymbol{P_j}$ can infect a host mutant $\boldsymbol{C_i}$ only if $i \leq j$. In our model, we assume five types of alga-host mutants and four types of viral mutants.

The results indicate that when there is spatial homogeneity, the dispersal network structure has no significant effect on the eco-evolutionary dynamics or on species coexistence. In addition, the effect of the dispersal network structure in the absence of eco-evolutionary dynamics (i.e., only ecological dynamics of the focal species, the host) was tested, and I found that specific interactions of the different algal types with the virus played an important role in species coexistence and that the dispersal network structure had no effect on their transient dynamics. The

results represent a first step towards answering exciting questions such as the role of the dispersal network structure for eco-evolutionary feedback dynamics when there is spatial heterogeneity among the patches, when there is asymmetric dispersal among the patches, when different species disperse asymmetrically or when there is stochastic extinction or viability of the species in some patches, and the role of evolutionary cold- and hot-spots in networks.

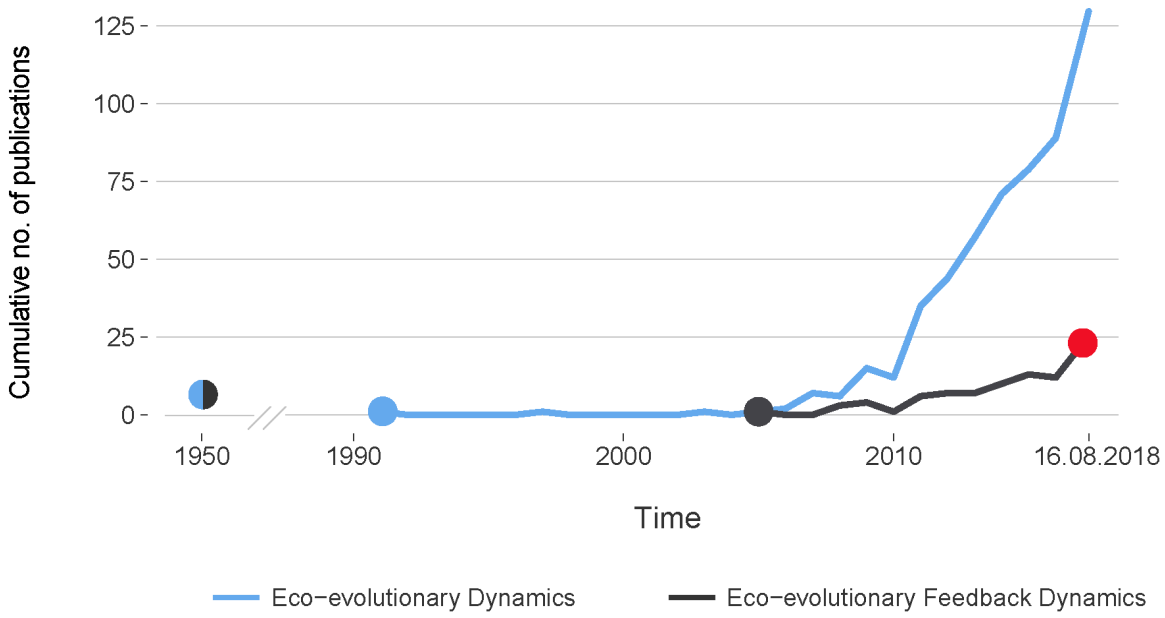

Figure 1: Cumulative number of publications over the years with the term “eco-evolutionary dynamics” (blue) and “eco-evolutionary feedback dynamics” (black). The red dot indicates the time point of the current thesis and the attempt to answer fundamental questions in the field. The half-blue half-black circle indicates the first conceptual studies related to eco-evolutionary dynamics.

Research Aims

Chapter One

In this chapter, I conceptually investigate how abiotic stress affects eco-evolutionary feedback dynamics by decoupling or enhancing the link between adaptive evolution and ecological dynamics. I review empirical and theoretical evidence, identify gaps in our knowledge and suggest future studies.

Chapter Two

I combined mechanistic modelling of eco-evolutionary feedback dynamics with experimental evolution to test predictions about the role of abiotic stress in breaking the link between adaptive evolution and ecological dynamics in the system. I used the host-virus system, *Chlorella variabilis-PBCV-I,* which offers an excellent opportunity to study eco-evolutionary feedback dynamics over multiple generations.

Chapter Three

In this chapter, I use a mathematical model to extend the alga-virus system by adding a host predator. I investigate how the predator alters the eco-evolutionary dynamics of the host-virus system in a single patch and in networks with various structures. I investigate the role of the dispersal network structure in the presence and the absence of eco-evolutionary dynamics in the system.

CHAPTER ONE

Manuscript

Selection by multiple stressors and eco-evolutionary dynamics

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Summary

1. We review and synthesize evidence from the fields of ecology, evolutionary biology and population genetics to investigate how the presence of abiotic stress can affect the interplay between evolution and ecology on ecological timescales.

2. To obtain a better mechanistic understanding under which conditions and how an abiotic stressor can influence eco-evolutionary dynamics, we use a conceptual predator-prey model where the prey can rapidly evolve anti-predator defences and stress resistance.

3. We discuss potential processes through which an abiotic stressor may decouple or enhance the link between rapid adaptive evolution of anti-predator defences and the predator-prey population dynamics.

4. Overall, we identify important gaps in our current knowledge and suggest future experiments and directions to develop an understanding for the role of eco-evolutionary dynamics in more complex ecological and evolutionary scenarios.

Keywords: eco-evolutionary dynamics, predator-prey, adaptive genetic variation, trade-off, migration, epistasis, pleiotropy

Main text

When adaptive evolution of ecologically important traits is rapid, i.e. within a dozen generations, the evolutionary change can have an impact on the ecological change in the same or in other interacting species (Charlesworth, 1971; Pimentel, 1968). This concept represents the central dogma of eco-evolutionary dynamics. Building on early mathematical models (e.g., Abrams & Matsuda, 1997), recent studies suggest that eco-evolutionary dynamic processes are prevalent in both laboratory and natural populations. For example, the rapid evolution of resistance and infectivity drove the population dynamics of an alga-virus system, where host population sizes increased when they evolved resistance and decreased when the virus produced counter-adaptations (Frickel, Feulner, Karakoc, & Becks, 2018; Frickel, Sieber, & Becks, 2016). Guppies (*Poecilia reticulata*) rapidly evolved different life-history strategies under different levels of predation, which further affected the interactions with their predators (Post & Palkovacs, 2009; Reznick, 1982) and whole-ecosystem processes (Bassar et al., 2010). When curly-tailed lizards (*Leiocephalus carinatus*) were introduced into the Bahamas, their prey (the brown anoles *Anolis sergrei*) fled onto trees. This response contributed to the rapid selection of longer limbs in the brown lizards and to an increase in their population size (Steinberg et al., 2014). These and other studies underline the importance of using an eco–evolutionary approach in understanding the dynamics of populations and species interactions (Andrade-Domínguez, Salazar, Del Carmen Vargas-Lagunas, Kolter, & Encarnación, 2014; Brunner, Anaya-Rojas, Matthews, & Eizaguirre, 2017; Matthews, Aebischer, Sullam, Lundsgaard-Hansen, & Seehausen, 2016).

A significant challenge in the field of community ecology is to predict how environmental changes alter the size of populations and species interactions, particularly in response to abiotic stressors, i.e., an abiotic factor that leads to a sharp reduction in fitness in populations (Alberto et al., 2013; Macnair, 1997; Moya-Larano et al., 2012); examples for environmental changes include water pollution, increases in temperature and salinity, ocean acidification or heavy metal pollution like copper and have been reviewed elsewhere. Predicting when and how populations react to abiotic stressors might allow the development of measures to preserve communities and ecosystem functions. The ecological response to abiotic stress can affect the interactions between rapid evolution and ecological change since the link from ecology to evolution in eco-evolutionary dynamics is (mainly) driven through changes in selection (Fig. 1). Processes that lead to differences in selection in the presence of (multiple) stressors can thus have dramatic influences on the eco-evolutionary dynamics. Additionally, changes in the environment caused by the presence of an abiotic stressor can directly affect evolutionary changes in a population in different ways (Fig. 1), which can determine their impact on demographic changes in populations. It is therefore important to understand when and how eco-evolutionary dynamics are altered by the presence of an abiotic stressor. However, to the best of knowledge, there are no studies investigating the role of such stressors in the context of eco-evolutionary dynamics. Thus we use here thought experiments and not existing data, but when is possible we provide examples of relevant studies.

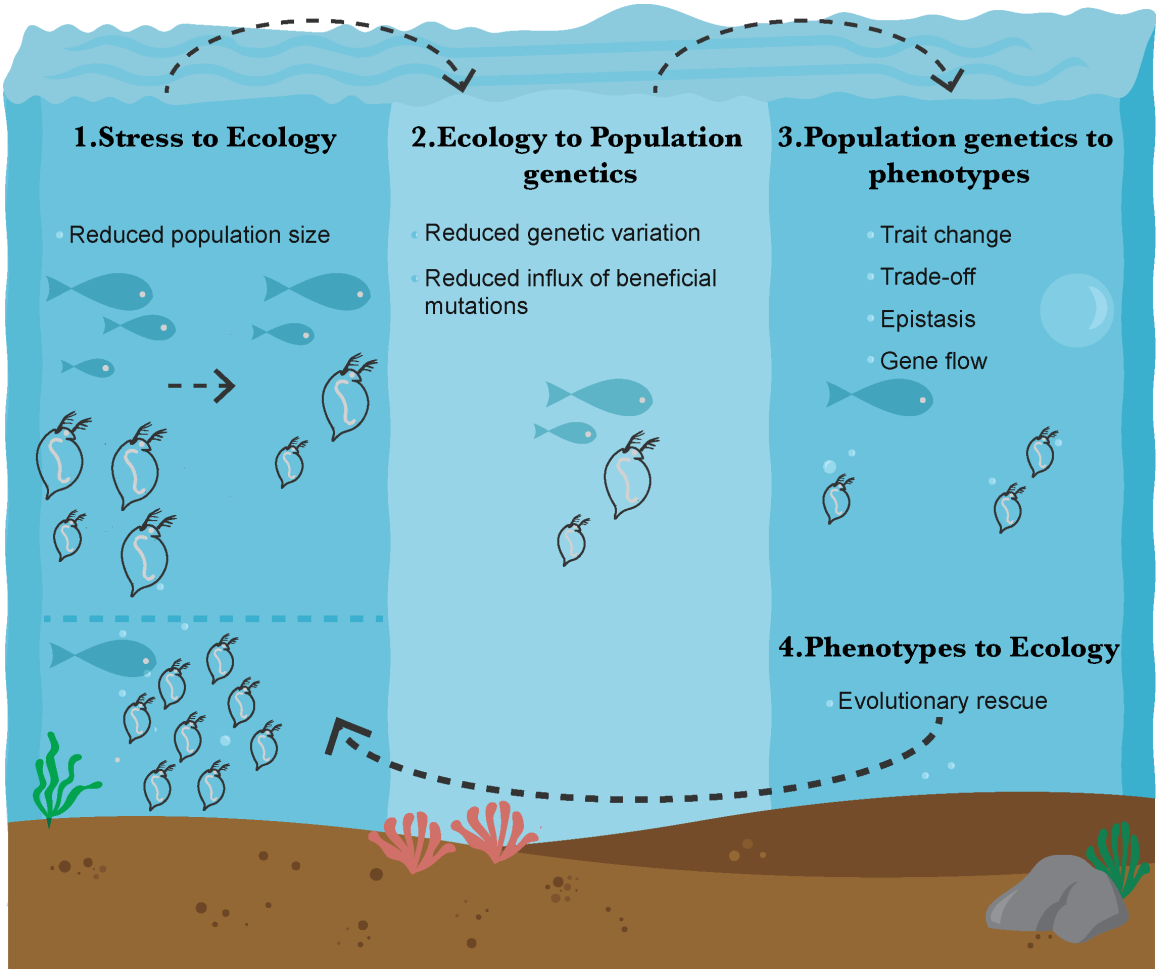

Figure 1: Conceptual figure of the role of an abiotic stressor in the evolution of anti-predator defence and the consequences for eco-evolutionary dynamics. 1) **Stress to Ecology:** an abiotic stress reduces the population size of a Daphina species in the presence of a fish predator. 2) **Ecology to Population genetics:** the reduction in population size decreases the standing genetic variation as well as the influx of beneficial mutations and thus the pace and/or probability of the anti-predatory defence to evolve. When defence evolution is slow, there is a high probability that the Daphnia population goes extinct 3) **Population genetics to Phenotype:** the evolutionary outcome in the Daphnia population (e.g. defence through smaller body size like in Daphnia melanica (Miner, De Meester, Pfrender, Lampert, & Hairston, 2012) can be further influenced in the presence of an abiotic stressor through effects of trade-offs, epistasis and gene flow. 4) **Phenotype to Ecology:** When defence evolves the population size will increase again.

To begin building such understanding, we develop here general predictions for the link between evolutionary and ecological change in the presence and absence of an abiotic stressor. We focus on predator-prey interactions as an example, as these are commonplace in nature and many examples of eco-evolutionary dynamics stem from predator-prey interactions, e.g., models (Abrams & Matsuda, 1997; Huang, Traulsen, Werner, Hiltunen, & Becks, 2017; Laura E. Jones & Ellner, 2007) bacteria-protozoa (Hiltunen & Becks, 2014; Hiltunen, Kaitala, Laakso, & Becks, 2017), algae-rotifers (Hairston, Ellner, Geber, Yoshida, & Fox, 2005; L. E. Jones et al., 2009; Yoshida, Jones, Ellner, Fussmann, & Hairston, 2003), fish-fish predation (Bassar et al., 2010; Reznick, 1982; Travis et al., 2014) fish-zooplankton predation (Post & Palkovacs, 2009; Walsh & Post, 2011). We assume different scenarios, where the prey population can evolve anti-predatory defences with or without costs (trade-off), as well as resistance to the abiotic stressor. For the sake of simplicity, we assume that the predator does not evolve (i.e., there is no counter-adaptation to the prey defence or the abiotic stressor). Specifically, we will provide examples of how abiotic stress can alter anti-predator defence evolution for the prey (i.e., pace of evolution and fitness effects) and thus impact the ecological dynamics of predator and prey, i.e. the link from evolution to ecology. We compare eco-evolutionary dynamics in the absence of the abiotic stressor to cases where the abiotic stressor is present. We explore the consequences of the stressor on standing genetic variation in the prey, and how trade-offs between traits, genetic correlations (i.e., pleiotropy) and epistatic interactions among mutations, mutation rates and gene flow affect the role of the stressor for the eco-evolutionary dynamics. Although we focus on a hypothetical predator-prey system and the scenarios discussed here are not a comprehensive

evaluation, the concepts developed here have broader applications for other evolutionary scenarios and other types of species interactions (e.g., host-parasite, competition or mutualism). The scenarios presented here will contribute to further developing an understanding about which processes are important for the observation of eco-evolutionary dynamics in laboratory experiments with reduced complexity and in larger communities and natural communities.

Eco-Evolutionary Dynamics in a Predator-Prey System

In a classical predator-prey system without evolution (Fig. 2), models suggest three qualitative different outcomes, extinctions, steady state dynamics or cyclic dynamics (Barbosa & Castellanos, 2005; Hörnfeldt, 1978; Krebs et al., 1995; Utida, 1957). All three possibilities have been observed in field and experimental data. The simplest case is that predator and prey populations become extinct when the overall consumption by the predator is greater than the growth of the prey can sustain. When coexisting, predator and prey may show constant population sizes over time (steady-state dynamics) or they may show classical predator-prey cycles with a characteristic quarter-phase lag between the changes in prey and the predator population size.

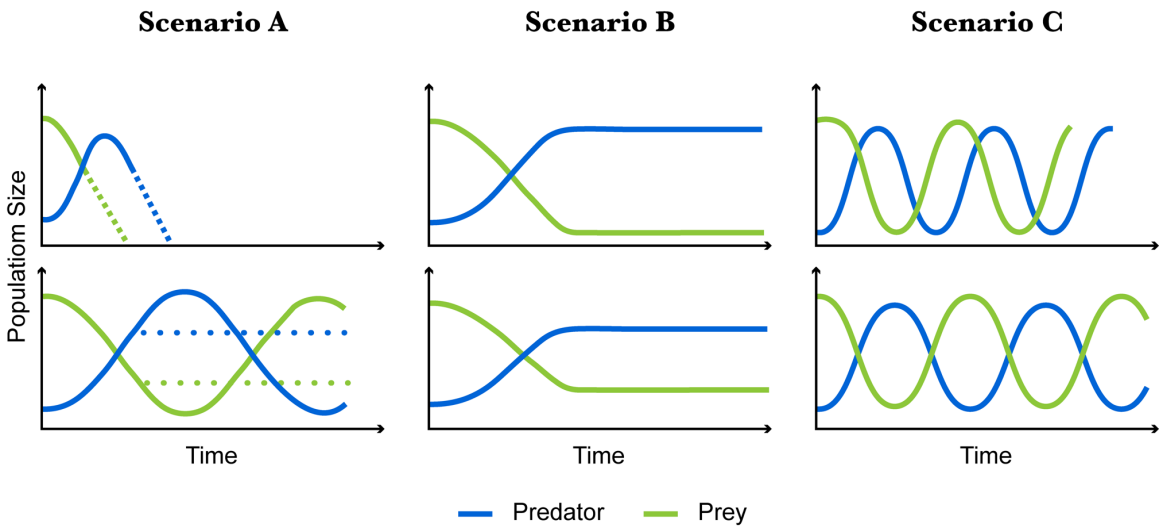

Figure 2: Ecological dynamics (top) and eco-evolutionary dynamics (bottom) in a hypothetical predator-prey system (prey = green, predator = blue). **Scenario A** describes an evolutionary rescue scenario where the prey will go extinct (followed by the predator) without the evolution of an anti-predatory defence trait in the prey population (arrow). In **scenario B**, the prey defence evolution leads to higher prey population but lower predator population sizes. For **scenario C**, we assume that the prey defence comes at the cost of reduced competitiveness and the prey population maintains a polymorphism of defended and undefended prey. The polymorphism can lead to eco-evolutionary feedback dynamics.

The population dynamics of predator and prey might be altered in the presence of an adaptive change in the prey that reduces predator consumption. In the first case, the prey population, and consequently the predator, might be rescued from extinction, and the prey might be able to coexist with the predator (Fig. 2, scenario A). With predator and prey in a steady state, defence evolution in the prey population might lead to changes in the prey and predator population sizes, with higher prey and lower predator densities compared to before the evolutionary change (Fig. 2, scenario B). When the prey defence evolution comes at the cost of reduced growth, this trade-off might lead to similar prey densities but lower predator densities.

The trade-off is also important in the third case, where predator-prey cycles change from a quarter-phase lag to anti-phase cycles, i.e., predator densities are highest when prey densities are lowest and vice versa (Fig. 2, scenario C). The latter case occurs when defence is very costly but efficient, which allows the maintenance of a polymorphism within the prey population over time; low densities in the predator lead to selection for the competitive and less defended prey type (ecology to evolution link), and high predator densities lead to selection for the defended but less competitive prey type (ecology to evolution link). As the predator density depends on the prey density and the fraction of undefended edible prey, the predator density changes along with the changes in the prey population (evolution to ecology link); predator densities decrease when defended prey is abundant, and increases when edible prey is at high densities. These ecological and evolutionary changes occur with some delay and can continue over long time scales. This continues link from ecology to evolution and back is referred to as eco-evolutionary feedback dynamics as defined in Post & Palkovacs (2009). A special

case of eco-evolutionary feedback dynamics is the appearance of cryptic cycles, where the population size of the prey is constant over time while the predator and prey types (defended and undefended) cycle over time (Yoshida et al., 2007). Cryptic dynamics are of special interest, as observations of changes in population sizes could lead to the conclusion that there is no interaction between evolution and ecology (Kinnison, Hairston, & Hendry, 2015; Yoshida et al., 2007).

In all scenarios above, rapid adaptive evolution in the prey has a rapid and significant effect on the ecological dynamics either by rescuing the population from extinction (scenario A), leading to higher population densities (scenario B) or resulting in continuous eco-evolutionary feedback dynamics with characteristic anti-phase cycles of predator and prey (scenario C), or cryptic dynamics. In the following we will discuss cases under which this link between the evolutionary change in the prey and the predator-prey dynamics is altered or broken when the addition of an abiotic stressor affects some aspect of the ecological and/or evolutionary dynamics.

Reduction in adaptive genetic variation

Selection acting on genetic variation can influence population dynamics when changes in gene frequencies translate into changes in phenotypic traits that affect demographic rates. Previous work showed that the impact of rapid evolution on population dynamics does, however, also depend on the range of genetic variation (Becks, Ellner, Jones, & Hairston Nelson G., 2010; Cortez, 2017; Steiner & Masse, 2013), with increasing additive genetic variation leading to a greater probability of altering the population dynamics (Cortez, 2016). Thus, factors or processes that affect genetic variation can have a strong impact on the evolution

to ecology link. It is widely thought that small populations have less additive genetic variance (often estimated through neutral genetic variation and low heterozygosity at marker loci (Frankham, 1996; Willi, Van Buskirk, & Hoffmann, 2006) and thus respond less efficiently to natural selection compared to large populations (Falconer, 2017). To explore this in the context of eco-evolutionary dynamics, we consider a scenario where an abiotic stressor is added to the predator-prey system and reduces prey or predator population size. We discuss the consequences for the pace of adaptive change in the prey population and the link from evolution to ecology, in comparison to the eco-evolutionary dynamics in the absence of the abiotic stressor (Fig. 2).

When the addition of the abiotic stressor affects only the prey, the prey population size will be significantly reduced. When we assume neutrality and additive gene action, the additive genetic variation should be reduced in proportion to the (effective) population size, due to genetic drift, (i.e., the random loss and fixation of alleles in the population) and because selection is more efficient in larger populations (Hill, 1972; KIMURA, 1962). This is particularly important when populations decline because parents have fewer offspring than expected for a population of the same constant size (Otto & Whitlock, 1997). The reduced genetic variation could then lead to an evolutionary constraint and can thus impact on the evolution-to-ecology link of eco-evolutionary dynamics. With the loss of variation in the ecologically relevant trait (here the anti-predatory defence in the prey population), no evolutionary rescue occurs (Scenario A in Fig. 2), and the prey, followed by the predator, will become extinct, densities of both populations will be low (Scenario B in Fig. 2), or they will cycle with a classical quarter-phase shift (Scenario C in Fig. 2). With low genetic variation for the relevant ecological trait

after the introduction of the stressor, the evolutionary response to selection by the predator, and thus the shift in ecology, will be slower.

Counter-intuitively, small population sizes and a reduction in additive genetic variation can also speed up evolutionary responses. The efficacy of selection can be low in large asexual populations where several beneficial mutations compete for fixation (Fogle, Nagle, & Desai, 2008; Maddamsetti, Lenski, & Barrick, 2015; Park & Krug, 2007). As a reduction in additive genetic variation can reduce competition between beneficial mutations, anti-predatory defence evolution and a shift towards anti-phase cycles might occur faster in the presence of an additional stressor.

When the abiotic stressor affects the fitness of the predator but not the prey, we expect its population either to become extinct or to remain at low densities compared to the stressor-free environment. Lower predator population densities will impose weaker selection on the prey. Weak selection for anti-predatory defence, added to the cost of the defence, can prevent the maintenance of the anti-predator defence. As for the case where only the prey is affected by the stressor, we expect consequences for the population dynamics; predator and prey continue cycling with a phase shift of a quarter of a period, but the predator population densities will remain lower and the prey population will achieve higher densities. The extinction of the predator would allow the survival of the prey without the evolution of an anti-predator defence and population sizes to reach the carrying capacity.

These simple examples show that the presence of the abiotic stressor can alter the link from evolution to ecology through slowing down or accelerating evolution by altering additive genetic variation in the prey, by changing the strength

of selection or the relative roles of genetic drift and selection, even though the effect of drift is often assumed to act on longer timescales (but see for example (Otto & Whitlock, 1997). While the role of small and declining population sizes has been studied in other fields, it is rarely considered in studies on eco-evolutionary dynamics outside the context of evolutionary rescue. Studies testing the evolutionary rescue of the same species in different environments could show how changes in adaptive genetic variation in response to a stressor could alter the likelihood and timing of evolutionary rescue. Evolutionary rescue in experimental red flour beetle (*Tribolium castaneum*) populations was, for example, faster in environments with a greater mismatch between a population and its environment than in those with a smaller mismatch (Stewart et al., 2017). The authors of this study also showed that small population sizes resulted in lower standing genetic variation due to inbreeding and/or genetic drift. Similar effects of population sizes and standing genetic variation have been shown in mathematical models, (e.g., Gomulkiewicz & Houle, 2009; Uecker & Hermisson, 2016; Yamamichi & Miner, 2015) and experiments, (e.g., Bell & Gonzalez, 2009; Cameron, Plaistow, Mugabo, Piertney, & Benton, 2014; Carlson, Cunningham, & Westley, 2014; Gonzalez & Bell, 2012; Low-Décarie et al., 2015).

There are only a few studies comparing eco-evolutionary dynamics considering species interactions in different environments. Such studies allow testing for the important interaction between population size and additive genetic variation for the evolution-to-ecology link. In an experimental evolution study following adaptive changes in a bacterial prey population, Hiltunen and co-authors (Hiltunen, Ayan, & Becks, 2015) showed that evolution of anti-predatory defence was significantly delayed in the presence of reduced resources or an abiotic

stressor (salt) that only affected the predator. The slower evolution of defences in the prey population resulted in different predator-prey dynamics.

Other examples include studies focusing on host-parasite interactions in different resource environments (Gómez et al., 2015; Harrison, Laine, Hietala, & Brockhurst, 2013; Lopez Pascua et al., 2014; Lopez-Pascua & Buckling, 2008) or in the presence of antimicrobial substances (Escobar-Páramo *et al.* 2012; Knezevic *et al.* 2013; Coulter *et al.* 2014). While these studies show mostly significant effects on the evolutionary dynamics (e.g. slowing down or accelerating coevolution of host and parasite), these studies do not examine the link from evolution to ecology. Using bacteria-phage communities, a recent study showed that the presence of an abiotic stressor (the antibiotic streptomycin below the minimum inhibitory concentration) could alter the evolution of resistance against phage, which led to the extinction of the phage in the presence of the stressor (Cairns, Becks, Jalasvuori, & Hiltunen, 2016). The authors found, however, no difference in the number of mutations when comparing whole genome information of isolated genotypes between the environments with only one-stressor (phage or antibiotic) and the two-stressor environment (Cairns, Frickel, Jalasvuori, Hiltunen, & Becks, 2017) suggesting that differences in genetic variation did not play a role for the evolution of phage-resistance and the link from evolution to ecology.

Future studies on the role of abiotic stressors in eco-evolutionary dynamics should thus include studies that follow and contrast the genetic variation of interacting populations in the presence and absence of the stressor. Results from genomic analyses, measures of variance in fitness over time as an estimate of genetic and phenotypic variation and tests of heterozygosity should complement data on trait changes and population sizes in response to abiotic stressors.

Although the above discussion concerns simple systems and laboratory experiments with reduced complexity, correlations between reduced genetic variation, slower evolutionary change and consequent changes in or breaking of the link from evolution to ecology should also be observable in natural or larger experimental communities. As we know from several studies that the amount of genetic variation, and thus the evolutionary response, is also driven by factors other than population size, we will discuss some of these factors in the following. The presence of genetic correlations, epistasis, and trade-offs are included in the discussion, but we do not discuss further the mode of selection or the selection strength.

Genetic Architecture

The interactions between different traits under selection can influence the rate of adaptation positively or negatively (Agrawal & Stinchcombe, 2009). The outcome depends on the genetic correlation of the traits, which describes how traits are inherited together and can arise by pleiotropy and/or linkage disequilibrium (Conner & Hartl, 2004; Lande & Arnold, 1983; Worley & Barrett, 2000). Linkage disequilibrium and pleiotropy, as well as their combination, can speed up evolution when positive, but slow down adaptive evolution when their combinations are negative (Barton & Partridge, 2000; Polechová & Barton, 2015)

Pleiotropy defines the condition where single mutations affect the fitness of multiple traits (Caspari, 1952; Dobzhansky & Holz, 1943; Wright, 1968). Pleiotropy can increase the mean fitness of a trait when the covariance is positive and there are no physical or physiological limitations. As an example of a physical limitation, consider how the breathing system restricts the body size of the beetles. Beetles

breathe through trachea allowing oxygen to reach all tissues in the body when distances are short. Under these conditions, an increase in the beetle body size cannot take place without an increase in the breathing system. Experimental studies suggest that positive pleiotropy is common. Mutations that increase the mean fitness of the bacterium *Escherichia coli* in glucose can increase, for example, the mean fitness in other novel resource environments (Ostrowski, Rozen, & Lenski, 2005). In plants, pleiotropy can lead to the rapid evolution of several floral traits and can increase their mean fitness (Smith, 2016). Pleiotropy can also have a negative effect on the mean fitness of other traits when one mutation leads one trait closer to its optimum and another trait away from its optimum. Examples for antagonistic pleiotropy are found in crops, where selection for increased yield has a metabolic cost that inadvertently leads to reduced herbivore defences (Rosenthal & Dirzo, 1997). Linkage disequilibrium refers to the condition where traits are linked more frequently than expected due to drift, selection and assortative mating (Alachiotis & Pavlidis, 2016; Kim & Stephan, 2002).

We use again the example of the conceptual predator-prey model to show how positive pleiotropy and antagonistic pleiotropy between two traits (here stress resistance and anti-predator defence) can affect the pace of the evolution of anti-predator defence and thus eco-evolutionary dynamics (Fig. 2). With strong selection for both traits, a positive pleiotropic mutation will increase the mean fitness of the prey population via the evolution of stress resistance and anti-predator defences at the same time. Under these conditions, we would expect the predator-prey system to move from cycles with a quarter-phase lag towards anti-phase cycles (Fig. 2, Scenario C). When there is antagonistic pleiotropy between

the two traits, the mean fitness of the prey population can increase, either as a result of an increase in the frequency in one of the two traits or by decoupling the trade-off and increasing the frequency of both traits. Empirical evidence shows that decoupling such trade-offs is challenging and typically requires longer time periods than considered here (Losos, 2014; Justin R. Meyer et al., 2012).

Importantly, the strength of selection and the genetic variation present for each trait can influence the outcome of evolutionary change and thus the link from evolution to ecology. When the strength of selection is similar for both traits, the evolutionary response of the population will depend on the amount of genetic variance underlying these traits. Assuming there is a higher genetic variation for the trait related to stress resistance, we expect the evolution towards stress resistance to be faster (optimum P_1, Fig. 3) compared to the evolution of the defence traits (optimum P_2, Fig. 3). In the case where the prey population evolves towards optimum P_1, we do not anticipate the presence of anti-predator prey types and hence we expect no link between the evolutionary change in the prey defence and the predator-prey dynamics. Under these conditions, no evolutionary rescue occurs (Scenario A in Fig. 2), and the prey, followed by the predator, will become extinct, densities of both populations will be low (Scenario B in Fig. 2), or they will cycle with a classical quarter-phase shift (Scenario C in Fig. 2). In contrast, when the population evolves towards optimum P_2 we expect to see the evolution of anti-predatory defences affecting the predator-prey ecological dynamics and the predator-prey system to move from cycles with a quarter-phase lag towards anti-phase cycles (Fig. 2, Scenario C).

So far, several empirical studies have shown that antagonistic pleiotropy and pleiotropy in general are common. However, their role has, as far as we know,

not been investigated in the field of eco-evolutionary dynamics, although it is clear that the genetic architecture of traits determines the rate of evolution of ecologically important traits and thus the link from rapid evolutionary change to ecological dynamics (Saastamoinen et al., 2018). A first step for empirical studies requires the identification of adaptive trait(s) and their genetic basis for example through genome-wide associated studies (GWAS) (Pallares, Harr, Turner, & Tautz, 2014) or linkage studies (Duffy, Turner, & Burch, 2006). Knowing the genetic basis of (two) different adaptive traits, one could control their standing variation either with experimental crosses, artificial selection experiments, (e.g., Jasmin & Zeyl, 2013) or CRISPR techniques (i.e., gene knockouts) and experimentally investigate how multivariate selection can affect the pace of evolution of each one of the traits and the impact of evolution on the ecological dynamics. A possibility for investigating the impact of different levels of linkage disequilibrium on the evolution of adaptive traits and subsequently on the ecological dynamics is to use of asexual and sexual individuals of the same the species. In the absence of recombination, asexual individuals will represent higher linkage disequilibrium compared to their sexual counterparts.

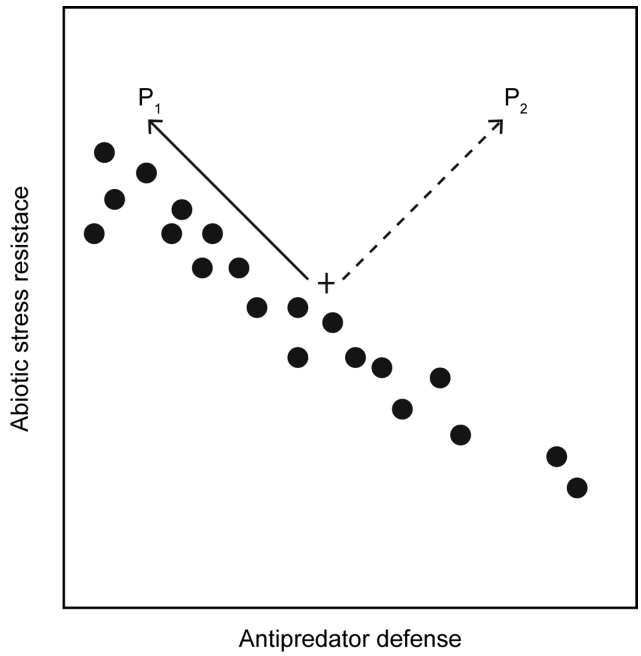

Figure 3: An example of evolutionary constraints caused by a trade-off between the evolution of abiotic stress resistance and anti-predator defence. The points represent trait values and the cross represents the current mean for both traits in the population. The labels P_1 and P_2 represent the evolutionary optima for the two traits. To reach the evolutionary optima P_2, it is required to decouple the trade-off between abiotic stress resistance and anti-predator defence.

Epistatic Interactions

Another genetic interaction that could limit or enhance the evolution to ecology link of eco-evolutionary dynamics is the epistatic interaction among mutations. Two mutations interact epistatically when the contribution to a trait at one site depends on the state of the other site. As for genetic correlations, the interaction can be positive or negative, and the effect of a mutation thus depends on the genetic environment in which it finds itself. Note that this is also true when alleles or mutations are shuffled via genetic mixing or horizontal gene transfer. Positive and negative epistasis has been frequently observed (Breen, Kemena, Vlasov, Notredame, & Kondrashov, 2012; S. Elena & Lenski, 1997; Kouyos, Silander, & Bonhoeffer, 2007; Poon & Chao, 2005; D. Rokyta, Badgett, Molineux, & Bull, 2002; D. R. Rokyta et al., 2011; Sackman & Rokyta, 2018) and recent studies showed that negative interactions can slow down adaptation (Chou, Chiu, Delaney, Segrè, & Marx, 2011; Khan, Dinh, Schneider, Lenski, & Cooper, 2011) as well as modify the probability of adaptation (MacLean, Hall, Perron, & Buckling, 2010).

We explore here the potential role of epistatic interactions in the predator-prey system, assuming that the prey population becomes extinct without adaptation to the presence of the predator (Fig. 2, scenario A). We consider that individual mutations are either beneficial or deleterious and their combined effect on fitness can be either positive or negative. In the case of beneficial mutations for anti-predatory defence and abiotic stress resistance (Fig. 4a), we expect evolutionary rescue in all cases, but rescue will be fastest when the mutations increase each other's effect on fitness, and slowest when they reduce each other's effect on fitness. When one or both mutations are deleterious, negative epistasis

can hinder the evolution of an anti-predatory trait, as the overall effect on fitness can be deleterious. Consequently, there will be no link between evolution and ecology. When the effect of the mutations is additive, the outcome for overall fitness depends on the effect size of the individual mutations. When the effect size of the deleterious mutation is larger than that of the beneficial mutation (as in Fig. 4), no evolutionary rescue will be observed. In the case where the combined effect of two deleterious mutations on fitness is positive, the prey population can be rescued from extinction.

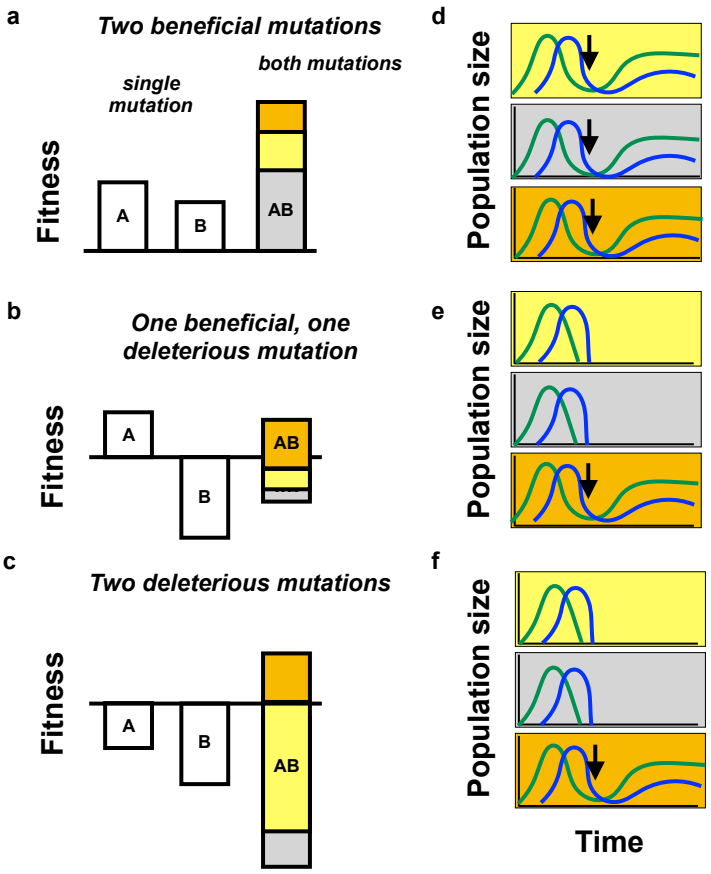

Figure 4: The effects of epistasis on fitness **(a-c)** in a prey population and eco-evolutionary dynamics (here evolutionary rescue, Fig. 2, scenario A) **(d-f)**. **a)** Fitness compared to the wild type (horizontal line) for single mutations providing a benefit related to the presence of the predator (A) and the abiotic stressor (B) when both mutations occur within the same genotype (AB) and they interact additively (yellow), negatively (grey) or positively (orange). **b)** With a beneficial and a deleterious mutation and their combined effect on fitness. **c)** With both mutations being deleterious and their combined effect on fitness. **d-f)** Predicted predator-prey dynamics for the respective scenarios in **a-c.**

This simple example shows that the adaptive potential of a population and the pace of adaptation in the presence of epistatic interactions can have strong effects on eco-evolutionary dynamics. The evolutionary history and adaptive past, i.e., the genetic background in which the new mutation occurs in or an allele is crossed in, could thus have a significant effect on the evolution to ecology link. In an experimental evolution study where the green alga *Chlamydomonas reinhardtii* was exposed to stressful concentrations of different herbicides in different orders, Lagator and co-authors found different outcomes depending on the herbicides used (Lagator, Morgan, Neve, & Colegrave, 2014). For one herbicide they observed that the selection history of other herbicides increased the likelihood of adaptation, probably through antagonistic epistatic interactions between resistance mutations and growth related mutations. Experiments with evolving lineages of the social bacterium *Myxococcus xanthus* in parallel have been used to demonstrate the severe effects of negative epistatic interactions after reintroducing a previously deleted gene related to swarming behaviour (Zee & Velicer, 2017). Another approach for exploring the effect of epistasis between mutations related to the interaction with the predator (or other biotic interaction) and abiotic stressor is the construction of genotypes with pairs of mutations that have previously been identified (e.g. as D. R. Rokyta et al., 2011). Similar approaches could be used in laboratory experiments focusing on species interactions and an abiotic stressor but experiments should measure ecological dynamics in addition to fitness and changes in traits. An alternative approach is combining experimental evolution and sequencing approaches and comparing the dynamics on the population, phenotypes and genome level between environments

with and without an additional stressor. It is, however, important to realize that interactions between mutations are also very specific in terms of their order (Colegrave & Buckling, 2005; S. F. Elena & Lenski, 2003) and a generalization will only be possible with respect to the fact that there is an effect of epistasis and of the sign of the epistatic interactions. This is in particular important as with multiple stressors and adaptation to such stressors, epistatic interactions are probably even more important as the effects will likely differ with an increasing number of loci involved (Østman, Hintze, & Adami, 2012)

Increase in Genetic Variation

Genetic variation within randomly mating and asexual populations is generally increased by mutation and dispersal, and these processes can thus drive adaptive evolution. They have the potential to introduce novel and adaptive alleles and to speed up evolutionary change. Alternatively, these processes can lead to the introduction of maladapted genotypes or alleles, which would limit adaptive evolution and eventually lead to a break of the evolution to ecology link.

Mutation Rates

The general role of DNA mutation rates on adaptive evolution is still unclear (Lynch, 2010) as they fuel sequences with the variability that is essential for adaptive evolution, while at the same time they can reduce fitness, since most mutations have a negative impact (Rainey, 1999; Sniegowski, Gerrish, & Lenski, 1997). The presence of an abiotic stressor can have a direct impact on mutation rates as well as mutation supply through reduced population sizes. Previous empirical studies showed that mutation rates could be elevated under stressful

conditions, leading to gene loss and eventually to the extinction of populations (Bull, Sanjuán, & Wilke, 2007; Chen & Shakhnovich, 2009; Martin & Gandon, 2010). Other studies showed that the presence of an abiotic stressor favours bacteria with an elevated mutation rate because they generate adaptive mutations more rapidly and can exploit the resources of their environment more efficiently (Giraud et al., 2001; Oliver & Mena, 2010). The role of mutation rates and mutation supply in eco-evolutionary dynamics is still unclear, but it should be of high relevance for mutation-limited systems, populations that reproduce mainly asexually and systems with low standing genetic variation.

Assuming that most mutations are deleterious, accumulation of mutations might lead to gene or function loss and is likely to lead to insufficient genetic variation for the selection of anti-predator defences. Under these circumstances, the prey population might become extinct or exhibit a continuous cycle with a phase shift of a quarter of a period (Fig. 2). An increase in the mutation rate of the prey induced by the abiotic stressor may allow the prey population to respond rapidly. The rapid evolution of anti-predatory defences could lead to fast evolutionary rescue or a switch to anti-phase cycles in predator and prey when defence evolution is costly.

Gene Flow

An important factor that can influence genetic variation (and hence adaptation) as well as population dynamics is gene flow. Gene flow occurs when gametes or individuals migrate or disperse from one population to another. In general, gene flow can introduce adaptive mutations into a population and increase the rate of adaptive evolution or can limit adaptive evolution by introducing

maladapted mutations. We illustrate here the effect of gene flow for eco-evolutionary dynamics in the presence of an abiotic stress. We assume two locally adapted populations with the population in patch 1 being locally adapted to the abiotic stressor (predators absent), whereas the population in patch 2 is locally adapted to the predator (abiotic stressor absent). In the latter, we assume the same growth-defence trade-off as described above, so that the populations show anti-phase cycles and continuous eco-evolutionary feedback dynamics in the absence of the abiotic stressor and gene flow (Fig. 2, scenario C). In the case where the fitness of locally adapted individuals in one patch is close to zero but is not zero in the other patch (Fig. 5a), with migration between the two patches, maladapted genotypes will be introduced from one patch into the other. When migration is small compared to selection, there will be little or no effect on the eco-evolutionary dynamics in patch 2 (Fig. 5b top), as the immigrant has no defence but has the same low growth rate (or an even lower growth rate), compared to the defended prey (Ehrlich, Becks, & Gaedke, 2017). With high gene flow, a large fraction of the prey population is maladapted, moving the population in a direction opposite to the selection in the patch. Thus, local adaptation, i.e., the polymorphism across patches, will be lost quickly. In the case of patch 2, the prey population will have a lower level of defence, which could lead to a shift from antiphase cycles towards cycles with a quarter-phase lag.

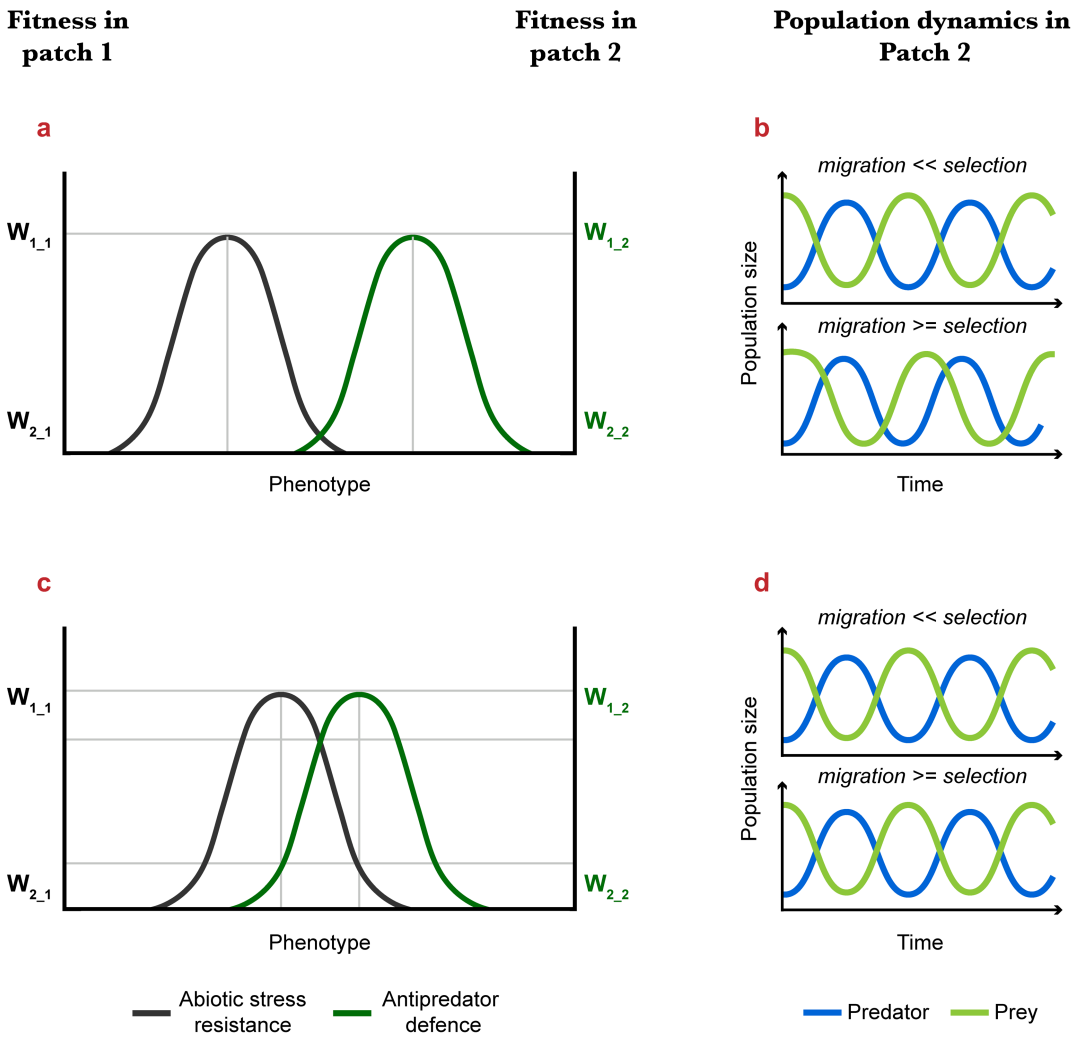

Figure: 5: Fitness of locally adapted populations **(a,c)** and the predator-prey dynamics with gene flow **(b,d)**. Fitness $W_{i,j}$, with i = origin of population (patch 1 or 2), j = current environment (patch 1 or 2). **a)** Hypothetical scenario where a trait is under stabilizing selection for different optima in patch 1 (= adapted to abiotic stress; black curve) and in patch 2 (= adapted to predation; green curve). Patch 1 has no predators, and patch 2 no abiotic stressor. **b)** With low migration rates and thus gene flow from patch 1 to patch 2, (i.e., migration << selection), little or no effect on the population dynamics is expected and thus the link between evolution and ecology is not altered. When migration is strong compared to selection (migration >= selection), the polymorphism in the two patches is lost (= gene swamping) and the population dynamics will not be driven by the defence evolution. **c)** Fitness is maximized in the local patch (W_{1_1} and $W_{2\_2} > 0$) and fitness in the foreign patch is zero (W_{1_2} and $W_{2\_1} = 0$). **d**) We expect little or no effect on the eco-evolutionary dynamics. Vertical and horizontal lines in a,c mark fitness in the respective environments.

It is also possible that the fitness of locally adapted populations is greater than zero in the other environment but still smaller than in their own environment (Fig. 5c). Independently of whether migration is small or large compared to selection, we expect little or no change in the predator-prey dynamics, since the level of defence will be on average still high and the eco-evolutionary feedback dynamics are thus maintained (Fig. 5d). However, this will change when we make different assumptions about local adaptation with respect to the traits involved and their trade-offs. When local adaptation to the stressor confers at the same time some level of defence against the predator (positive pleiotropic effect, see above), invasion from small numbers is possible, provided the defence is cheap compared to the resident defended type. Depending on the trait-fitness relationship in the specific system, the invader will outcompete the defended prey, the undefended prey or both, which will lead to a change in the population dynamics (see Fig. 4 in Ehrlich, Becks, & Gaedke, 2017).

These scenarios show that local adaptation and gene flow can have consequences for eco-evolutionary dynamics when populations are locally adapted to an abiotic stressor or there is interaction with another species. Based on previous work on local adaptation and gene flow (Brockhurst, Buckling, Poullain, & Hochberg, 2007; Lenormand, 2002; Lion & Gandon, 2015; Morgan, Gandon, & Buckling, 2005), on the exact mechanism of local adaptation (pleiotropic effects and trade-offs) and on the timing of invasion (Yamamichi, Yoshida, & Sasaki, 2014) the predictions for the eco-evolutionary dynamics will change.

Defence-Growth Trade-Off

Trade-offs between different traits are important for the maintenance of trait polymorphism within populations and are a key driver for eco-evolutionary dynamics. They can be the result of genetic, energetic or engineering constraints (for the former see the discussion on pleiotropy above). Important examples are trade-offs between anti-consumer traits, e.g., defence against a predator or resistance against a pathogen and traits involved in competitiveness, including predator-prey, (e.g., (Becks, Ellner, Jones, & Hairston, 2012; Becks et al., 2010; Yoshida et al., 2003) and host-parasite, (e.g., Frickel et al., 2016). The role of trade-offs for eco-evolutionary dynamics changes, however, with the trait range (Becks et al., 2010; L. E. Jones et al., 2009) and the costs of the defence (Ehrlich et al., 2017; Huang et al., 2017; J R Meyer, Ellner, Hairston, Jones, & Yoshida, 2006; Yoshida et al., 2007)

The presence of an abiotic stressor for the prey can alter the role and consequences of the trade-off in eco-evolutionary dynamics (Fig. 6). In the simplest case, the reduction in fitness caused by the stressor is the same for all prey types (Fig. 6b). A very strong reduction in fitness might lead to the extinction of the defended prey, since the growth rate, which is already low, is reduced even further. As a consequence, the link between evolution and ecology will be altered and the populations will return to classical predator-prey cycles with the undefended prey only, (i.e., the polymorphism in the prey is not maintained and there is no eco-evolutionary feedback). This is a different mechanism from the one described above in the section on reduction in adaptive genetic variation, as in this case specific alleles or types are removed from the population. When the reduction in fitness is less strong and variation in the prey population is maintained, the

slower growth rates of the defended prey can lead to slower cycles, since the level of defence is the same as without the stressor, but the defence becomes costlier (Fig. 6c).

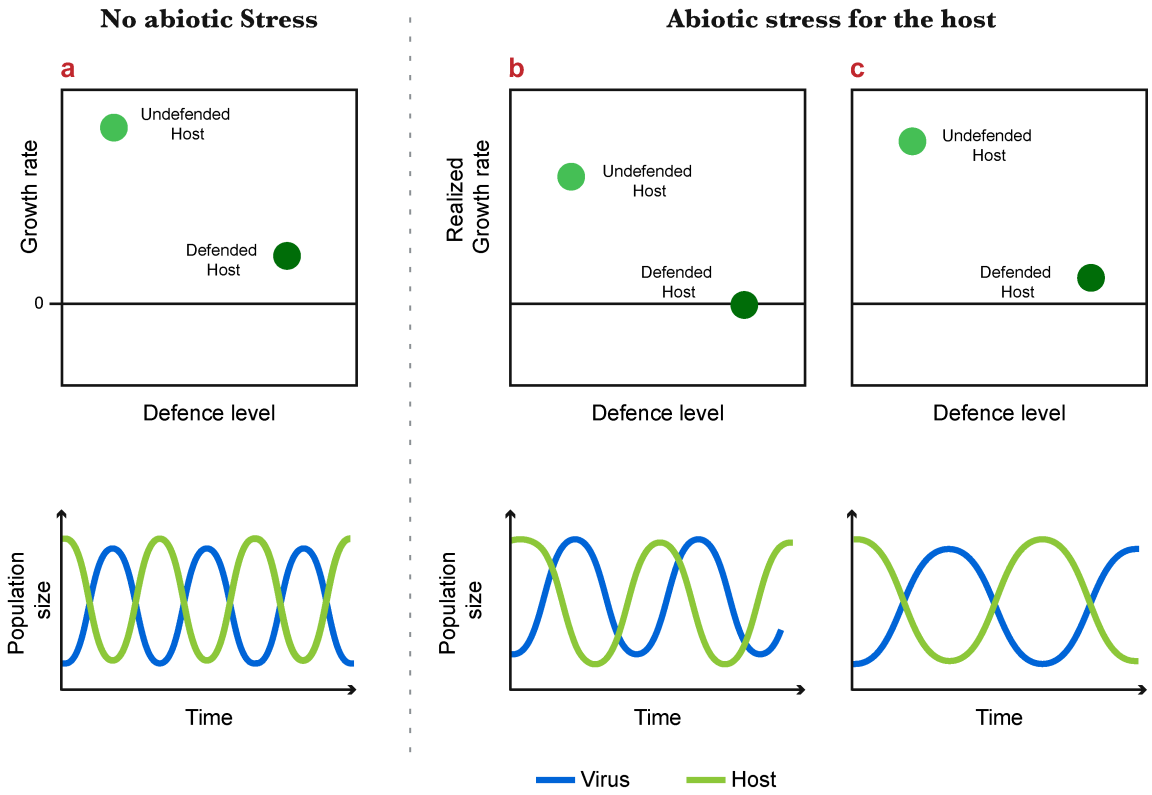

Figure 6: The effect of an abiotic stressor on the eco-evolutionary dynamics in the presence of a defence-growth trade-off for the prey of a predator-prey system (Fig. 2, scenario C). **a)** With a strong trade-off within the prey population, a defended and undefended prey type can coexist with the predator and show characteristic anti-phase cycling (the hallmark of eco-evolutionary feedback dynamics (Hiltunen et al., 2014). **b)** The same genotypes are assumed to be present in the prey population but with an additional abiotic stressor which lowers the growth rates of these prey types in such a way that the realized net-growth rate of the defended prey is zero or below, and hence only undefended prey and the predator will be present and we find classical predator-prey cycles. **c)** When the realized growth rates are affected in such a way that the undefended type has a growth rate that is very close to zero, we expect to find eco-evolutionary dynamics, but the increase in the defended prey will slow down and cycles will be longer.

Again, the presence of the stressor can determine whether we observe eco-evolutionary dynamics. Developing these general predictions and testing them experimentally requires a priori information on the trade-off and its strength. Considering the increasing evidence for the role of trade-offs in eco-evolutionary dynamics, together with experimental approaches that allow the manipulation of the strength of the trade-off in prey populations through manipulation of the diversity within a population (Kasada, Yamamichi, & Yoshida, 2014; J R Meyer et al., 2006), it is possible to test how the strength of the trade-off in combination with different levels of the abiotic stressor can determine the potential and the details of the eco-evolutionary dynamics. These approaches should be extended to larger communities in and tested in the presence and absence of stressors.

Conclusion

In here, we present simplified scenarios where we hypothesize that the presence of an abiotic stressor alters the link between ecological and evolutionary dynamics in a predator-prey system. For almost all the discussed scenarios, we identified conditions where predictions for the eco-evolutionary dynamics based on the stressor-free environment were not valid in the presence of the stressor. This includes cases where the evolution-to-ecology link is broken, i.e., no evolutionary rescue occurs, where the evolutionary change is significantly slowed down or where the stressor has only a small effect on the eco-evolutionary dynamics. Thus, phenotypes driving eco-evolutionary dynamics and the genomic basis of phenotypes with a large impact on population dynamics can be expected to be highly dependent on the environment. This insight is not novel, but it has consequences for the interpretation of the lack of eco-evolutionary dynamics and

the relative contributions of ecological and evolutionary change in ecological dynamics, as well as for experimental design. The scenarios discussed here are not a comprehensive list of potential mechanisms, and we have discussed only the simple case of a predator-prey system. They are, however, general enough to warrant a careful evaluation of eco-evolutionary dynamics in systems with multiple stressors acting at the same time.

AUTHORS CONTRIBUTIONS:

LT, TH, LB conceived the ideas, LT and LB led the writing of the manuscript

REFERENCES

Abrams, P. A., & Matsuda, H. (1997). Prey Adaptation as a Cause of Predator-Prey Cycles. *Evolution*, *51*(6), 1742–1750. doi:10.1111/j.1558-5646.1997.tb05098.x

Agrawal, A. F., & Stinchcombe, J. R. (2009). How much do genetic covariances alter the rate of adaptation? *Proceedings of the Royal Society B: Biological Sciences*, *276*(1659), 1183–1191. doi:10.1098/rspb.2008.1671

Alachiotis, N., & Pavlidis, P. (2016). Scalable linkage-disequilibrium-based selective sweep detection: a performance guide. *GigaScience*, *5*(1), 1–22. doi:10.1186/s13742-016-0114-9

Alberto, F. J., Aitken, S. N., Alía, R., González-Martínez, S. C., Hänninen, H., Kremer, A., … Savolainen, O. (2013). Potential for evolutionary responses to climate change - evidence from tree populations. *Global Change Biology*, *19*(6), 1645–1661. doi:10.1111/gcb.12181

Andrade-Domínguez, A., Salazar, E., Del Carmen Vargas-Lagunas, M., Kolter, R., & Encarnación, S. (2014). Eco-evolutionary feedbacks drive species interactions. *ISME Journal*. doi:10.1038/ismej.2013.208

Barbosa, P., & Castellanos, I. (2005). *Ecology of predator-prey interactions*. Oxford University Press.

Barton, N., & Partridge, L. (2000). Limits to natural selection. *BioEssays*, *22*(12), 1075–1084. doi:10.1002/1521-1878(200012)22:12<1075::AID-BIES5>3.0.CO;2-M

Bassar, R. D., Marshall, M. C., Lopez-Sepulcre, A., Zandona, E., Auer, S. K., Travis, J., Reznick, D. N. (2010). Local adaptation in Trinidadian guppies

alters ecosystem processes. *Proceedings of the National Academy of Sciences*, *107*(8), 3616–3621. doi:10.1073/pnas.0908023107

Becks, L., Ellner, S. P., Jones, L. E., & Hairston, N. G. (2012). The functional genomics of an eco-evolutionary feedback loop: Linking gene expression, trait evolution, and community dynamics. *Ecology Letters*. doi:10.1111/j.1461-0248.2012.01763.x

Becks, L., Ellner, S. P., Jones, L. E., & Hairston Nelson G., J. G. (2010). Reduction of adaptive genetic diversity radically alters eco-evolutionary community dynamics. *Ecology Letters*. doi:10.1111/j.1461-0248.2010.01490.x

Bell, G., & Gonzalez, A. (2009). Evolutionary rescue can prevent extinction following environmental change. *Ecology Letters*, *12*(9), 942–948. doi:10.1111/j.1461-0248.2009.01350.x

Breen, M. S., Kemena, C., Vlasov, P. K., Notredame, C., & Kondrashov, F. A. (2012). Epistasis as the primary factor in molecular evolution. *Nature*, *490*(7421), 535–538. doi:10.1038/nature11510

Brockhurst, M. A., Buckling, A., Poullain, V., & Hochberg, M. E. (2007). The impact of migration from parasite-free patches on antagonistic host-parasite coevolution. *Evolution*. doi:10.1111/j.1558-5646.2007.00087.x

Brunner, F. S., Anaya-Rojas, J. M., Matthews, B., & Eizaguirre, C. (2017). Experimental evidence that parasites drive eco-evolutionary feedbacks. *Proceedings of the National Academy of Sciences*, *114*(14), 3678–3683. doi:10.1073/pnas.1619147114

Bull, J. J., Sanjuán, R., & Wilke, C. O. (2007). Theory of Lethal Mutagenesis for Viruses. *Journal of Virology*, *81*(6), 2930–2939. doi:10.1128/JVI.01624-06

Cairns, J., Becks, L., Jalasvuori, M., & Hiltunen, T. (2016). Sublethal streptomycin concentrations and lytic bacteriophage together promote resistance evolution. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*. doi:10.1038/srep39642

Cairns, J., Frickel, J., Jalasvuori, M., Hiltunen, T., & Becks, L. (2017). Genomic evolution of bacterial populations under coselection by antibiotics and phage. *Molecular Ecology*, *26*(7), 1848–1859. doi:10.1111/mec.13950

Cameron, T. C., Plaistow, S., Mugabo, M., Piertney, S. B., & Benton, T. G. (2014). *Eco-evolutionary dynamics. Experiments in a model system*. *Advances in Ecological Research* (1st ed., Vol. 50). Elsevier Ltd. doi:10.1016/B978-0-12-801374-8.00005-0

Carlson, S. M., Cunningham, C. J., & Westley, P. A. H. (2014). Evolutionary rescue in a changing world. *Trends in Ecology and Evolution*, *29*(9), 521–530. doi:10.1016/j.tree.2014.06.005

Caspari, E. (1952). Pleiotropic Gene Action. *Evolution*, *6*(1), 1–18. doi:10.1111/j.1558-5646.1952.tb02808.x

Charlesworth, B. (1971). Selection in Density-Regulated Populations Author (s): Brian Charlesworth Published by : Wiley on behalf of the Ecological Society of America Stable URL : http://www.jstor.org/stable/1937629 REFERENCES Linked references are available on JSTOR for this a. *Ecology*, *52*(3), 469–474.

Chen, P., & Shakhnovich, E. I. (2009). Lethal Mutagenesis in Viruses and Bacteria. *Genetics*, *183*(2), 639–650. doi:10.1534/genetics.109.106492

Chou, H.-H., Chiu, H.-C., Delaney, N. F., Segrè, D., & Marx, C. J. (2011). Diminishing Returns Epistasis Among Beneficial Mutations Decelerates

Adaptation. *Science*, *332*(6034), 1190–1192. doi:10.1126/science.1203799

Colegrave, N., & Buckling, A. (2005). Microbial experiments on adaptive landscapes. *BioEssays*, *27*(11), 1167–1173. doi:10.1002/bies.20292

Conner, J. K., & Hartl, D. L. (2004). *A Primer of Ecological Genetics*. Sinauer. Retrieved from https://books.google.de/books?id=_aRsQgAACAAJ

Cortez, M. H. (2016). How the Magnitude of Prey Genetic Variation Alters Predator-Prey Eco-Evolutionary Dynamics. *The American Naturalist*, *188*(3), 329–341. doi:10.1086/687393

Cortez, M. H. (2017). Genetic variation determines which feedbacks drive and alter predator-prey eco-evolutionary cycles. doi:10.1002/ecm.1304

Dobzhansky, T., & Holz, A. M. (1943). A Re-Examination of the Problem of Manifold Effects of Genes in Drosophila Melanogaster. *Genetics*, *28*(4), 295–303. Retrieved from http://www.genetics.org/content/28/4/295

Duffy, S., Turner, P. E., & Burch, C. L. (2006). Pleiotropic Costs of Niche Expansion in the RNA Bacteriophage Φ6. *Genetics*, *172*(2), 751–757. doi:10.1534/genetics.105.051136

Ehrlich, E., Becks, L., & Gaedke, U. (2017). Trait–fitness relationships determine how trade-off shapes affect species coexistence. *Ecology*, *98*(12), 3188–3198. doi:10.1002/ecy.2047

Elena, S. F., & Lenski, R. E. (2003). Microbial genetics: Evolution experiments with microorganisms: the dynamics and genetic bases of adaptation. *Nature Reviews Genetics*, *4*(6), 457–469. doi:10.1038/nrg1088

Elena, S., & Lenski, R. (1997). Test of synergistic interactions among deleterious mutations in bacteria. *Nature*, *4762*(1979), 395–398. Retrieved from http://www.nature.com/nature/journal/v390/n6658/abs/390395a0.html

Falconer, D. S. (2017). *Introduction to Quantitative Genetics*. CreateSpace Independent Publishing Platform. Retrieved from https://books.google.de/books?id=KiMntAEACAAJ

Fogle, C. A., Nagle, J. L., & Desai, M. M. (2008). Clonal interference, multiple mutations and adaptation in large asexual populations. *Genetics*, *180*(4), 2163–2173. doi:10.1534/genetics.108.090019

Frankham, R. (1996). Relationship of genetic variation to population size in wildlife. *Conservation Biology*, *10*(6), 1500–1508. doi:10.1046/j.1523-1739.1996.10061500.x

Frickel, J., Feulner, P. G., Karakoc, E., & Becks, L. (2018). Population size changes and selection drive patterns of parallel evolution in a host–virus system. *Nature Communications*, *9*.

Frickel, J., Sieber, M., & Becks, L. (2016). Eco-evolutionary dynamics in a coevolving host-virus system. *Ecology Letters*, *19*(4), 450–459. doi:10.1111/ele.12580

Giraud, A., Matic, I., Tenaillon, O., Clara, A., Radman, M., Fons, M., & Taddei, F. (2001). Costs and Benefits of High Mutation Rates: Adaptive Evolution of Bacteria in the Mouse Gut. *Science*, *291*(5513), 2606–2608. doi:10.1126/science.1056421

Gómez, P., Ashby, B., Buckling, A., Gomez, P., Ashby, B., & Buckling, A. (2015). Population mixing promotes arms race host-parasite coevolution.

Proceedings of the Royal Society B, *282*(1798), 20142297–20142297. doi:10.1098/rspb.2014.2297

Gomulkiewicz, R., & Houle, D. (2009). Demographic and Genetic Constraints on Evolution. *The American Naturalist*, *174*(6), E218–E229. doi:10.1086/645086

Gonzalez, A., & Bell, G. (2012). Evolutionary rescue and adaptation to abrupt environmental change depends upon the history of stress. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *368*(1610), 20120079–20120079. doi:10.1098/rstb.2012.0079

Hairston, N. G., Ellner, S. P., Geber, M. A., Yoshida, T., & Fox, J. A. (2005). Rapid evolution and the convergence of ecological and evolutionary time. *Ecology Letters*, *8*(10), 1114–1127. doi:10.1111/j.1461-0248.2005.00812.x

Harrison, E., Laine, A.-L., Hietala, M., & Brockhurst, M. a. (2013). Rapidly fluctuating environments constrain coevolutionary arms races by impeding selective sweeps. *Proceedings of the Royal Society B*, *280*(1764), 20130937–20130937. doi:10.1098/rspb.2013.0937

Hill, W. G. (1972). Probability of fixation of genes in populations of variable size. *Theoretical Population Biology*, *3*(1), 27–40. doi:10.1016/0040-5809(72)90032-9

Hiltunen, T., Ayan, G. B., & Becks, L. (2015). Environmental fluctuations restrict eco-evolutionary dynamics in predator–prey system. *Proc. R. Soc. B*, *282*(1808), 20150013.

Hiltunen, T., & Becks, L. (2014). Consumer co-evolution as an important component of the eco-evolutionary feedback. *Nature Communications*. doi:10.1038/ncomms6226

Hiltunen, T., Hairston, N. G., Hooker, G., Jones, L. E., Ellner, S. P., & Adler, F. (2014). A newly discovered role of evolution in previously published consumer–resource dynamics. *Ecology Letters*, *17*(8), 915–923. doi:10.1111/ele.12291

Hiltunen, T., Kaitala, V., Laakso, J., & Becks, L. (2017). Evolutionary contribution to coexistence of competitors in microbial food webs. *Proceedings of the Royal Society B: Biological Sciences*. doi:10.1098/rspb.2017.0415

Hörnfeldt, B. (1978). Synchronous Population Fluctuations in Voles, Small Game, Owls, and Tularemia in Northern Sweden. *Oecologia*, *32*(2), 141–152. Retrieved from http://www.jstor.org/stable/4215564

Huang, W., Traulsen, A., Werner, B., Hiltunen, T., & Becks, L. (2017). Dynamical trade-offs arise from antagonistic coevolution and decrease intraspecific diversity. *Nature Communications*. doi:10.1038/s41467-017-01957-8

Jasmin, J.-N., & Zeyl, C. (2013). Evolution of pleiotropic costs in experimental populations. *Journal of Evolutionary Biology*, *26*(6), 1363–1369. doi:10.1111/jeb.12144

Jones, L. E., Becks, L., Ellner, S. P., Hairston, N. G., Yoshida, T., & Fussmann, G. F. (2009). Rapid contemporary evolution and clonal food web dynamics. *Philosophical Transactions of the Royal Society B: Biological Sciences*. doi:10.1098/rstb.2009.0004

Jones, Laura E., & Ellner, S. P. (2007). Effects of rapid prey evolution on predator–prey cycles. *Journal of Mathematical Biology*, *55*(4), 541–573. doi:10.1007/s00285-007-0094-6

Kasada, M., Yamamichi, M., & Yoshida, T. (2014). Form of an evolutionary tradeoff affects eco-evolutionary dynamics in a predator–prey system.

Proceedings of the National Academy of Sciences, *111*(45), 16035–16040. doi:10.1073/pnas.1406357111

Khan, A. I., Dinh, D. M., Schneider, D., Lenski, R. E., & Cooper, T. F. (2011). Negative epistasis between beneficial mutations in an evolving bacterial population. *Science (New York, N.Y.)*, *332*(6034), 1193–6. doi:10.1126/science.1203801

Kim, Y., & Stephan, W. (2002). Detecting a local signature of genetic hitchhiking along a recombining chromosome. *Genetics*, *160*(2), 765–77. Retrieved from http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1461968&tool=pmcentrez&rendertype=abstract

KIMURA, M. (1962). On the probability of fixation of mutant genes in a population. *Genetics*, *47*(391), 713–719. doi:10.1007/BF01418872

Kinnison, M. T., Hairston, N. G., & Hendry, A. P. (2015). Cryptic eco-evolutionary dynamics. *Annals of the New York Academy of Sciences*. doi:10.1111/nyas.12974

Kouyos, R. D., Silander, O. K., & Bonhoeffer, S. (2007). Epistasis between deleterious mutations and the evolution of recombination. *Trends in Ecology & Evolution*, *22*(6), 308–15. doi:10.1016/j.tree.2007.02.014

Krebs, C. J., Boutin, S., Boonstra, R., Sinclair, A. R. E., Smith, J. N. M., Dale, M. R. T., … Turkington, R. (1995). Impact of Food and Predation on the Snowshoe Hare Cycle. *Science*, *269*(5227), 1112–1115. doi:10.1126/science.269.5227.1112

Lagator, M., Morgan, A., Neve, P., & Colegrave, N. (2014). Role of sex and migration in adaptation to sink environments. *Evolution*, *68*(8), 2296–2305. doi:10.1111/evo.12440

Lande, R., & Arnold, S. J. (1983). The Measurement of Selection on Correlated Characters. *Evolution*, *37*(6), 1210–1226. doi:10.2307/2408842

Lenormand, T. (2002). Gene flow and the limits to natural selection. *Trends in Ecology and Evolution*, *17*(4), 183–189. doi:10.1016/S0169-5347(02)02497-7

Lion, S., & Gandon, S. (2015). Evolution of spatially structured host-parasite interactions. *Journal of Evolutionary Biology*, *28*(1), 10–28. doi:10.1111/jeb.12551

Lopez Pascua, L., Hall, A. R., Best, A., Morgan, A. D., Boots, M., & Buckling, A. (2014). Higher resources decrease fluctuating selection during host-parasite coevolution. *Ecology Letters*, *17*(11), 1380–1388. doi:10.1111/ele.12337

Lopez-Pascua, L. D. C., & Buckling, A. (2008). Increasing productivity accelerates host–parasite coevolution. *Journal of Evolutionary Biology*, *21*(3), 853–860. doi:10.1111/j.1420-9101.2008.01501.x

Losos, J. B. (Ed.). (2014). *The Princeton guide to evolution*. Princeton ; Oxford: Princeton University Press.

Low-Décarie, E., Kolber, M., Homme, P., Lofano, A., Dumbrell, A., Gonzalez, A., & Bell, G. (2015). Community rescue in experimental metacommunities. *Proceedings of the National Academy of Sciences*, *112*(46), 14307–14312. doi:10.1073/pnas.1513125112

Lynch, M. (2010). Evolution of the mutation rate. *Trends in Genetics : TIG*, *26*(8), 345–352. doi:10.1016/j.tig.2010.05.003

MacLean, R. C., Hall, A. R., Perron, G. G., & Buckling, A. (2010). The population genetics of antibiotic resistance: integrating molecular mechanisms and treatment contexts. *Nature Reviews Genetics*, *11*(6), 405–414. doi:10.1038/nrg2778

Macnair, M. (1997). The evolution of plants in metal-contaminated environments. *Environmental Stress, Adaptation, and Evolution*. doi:10.1007/978-3-0348-8882-0_1

Maddamsetti, R., Lenski, R. E., & Barrick, J. E. (2015). Adaptation, clonal interference, and frequency-dependent interactions in a long-term evolution experiment with escherichia coli. *Genetics*, *200*(2), 619–631. doi:10.1534/genetics.115.176677

Martin, G., & Gandon, S. (2010). Lethal mutagenesis and evolutionary epidemiology. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *365*(1548), 1953–1963. doi:10.1098/rstb.2010.0058

Matthews, B., Aebischer, T., Sullam, K. E., Lundsgaard-Hansen, B., & Seehausen, O. (2016). Experimental evidence of an eco-evolutionary feedback during adaptive Divergence. *Current Biology*, *26*(4), 483–489. doi:10.1016/j.cub.2015.11.070

Meyer, J R, Ellner, S. P., Hairston, N. G., Jones, L. E., & Yoshida, T. (2006). Prey evolution on the time scale of predator-prey dynamics revealed by allele-specific quantitative PCR. *Proceedings of the National Academy of Sciences of the United States of America*, *103*(28), 10690–10695. doi:DOI 10.1073/pnas.0600434103

Meyer, Justin R., Dobias, D. T., Weitz, J. S., Barrick, J. E., Quick, R. T., & Lenski, R. E. (2012). Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. *Science*, *335*(6067), 428–432. doi:10.1126/science.1214449

Miner, B. E., De Meester, L., Pfrender, M. E., Lampert, W., & Hairston, N. G. (2012). Linking genes to communities and ecosystems: Daphnia as an ecogenomic model. *Proceedings of the Royal Society B: Biological Sciences*, *279*(1735), 1873–1882. doi:10.1098/rspb.2011.2404

Morgan, A. D., Gandon, S., & Buckling, A. (2005). The effect of migration on local adaptation in a coevolving host-parasite system. *Nature*, *437*(7056), 253–256. doi:10.1038/nature03913

Moya-Larano, J., Verdeny-Vilalta, O., Rowntree, J., Melguizo-Ruiz, N., Montserrat, M., & Laiolo, P. (2012). *Climate Change and Eco-Evolutionary Dynamics in Food Webs*. *Advances in Ecological Research*. doi:10.1016/B978-0-12-398315-2.00001-6

Oliver, A., & Mena, A. (2010). Bacterial hypermutation in cystic fibrosis, not only for antibiotic resistance. *Clinical Microbiology and Infection*, *16*(7), 798–808. doi:10.1111/j.1469-0691.2010.03250.x

Østman, B., Hintze, A., & Adami, C. (2012). Impact of epistasis and pleiotropy on evolutionary adaptation. *Proceedings of the Royal Society B: Biological Sciences*, *279*(1727), 247–256. doi:10.1098/rspb.2011.0870

Ostrowski, E. A., Rozen, D. E., & Lenski, R. E. (2005). Pleiotropic Effects of Beneficial Mutations in Escherichia Coli. *Evolution*, *59*(11), 2343–2352. doi:10.1111/j.0014-3820.2005.tb00944.x

Otto, S. P., & Whitlock, M. C. (1997). The probability of fixation in populations of changing size. *Genetics*, *146*(2), 723–733. doi:10.1534/genetics.104.040089

Pallares, L. F., Harr, B., Turner, L. M., & Tautz, D. (2014). Use of a natural hybrid zone for genomewide association mapping of craniofacial traits in the house mouse. *Molecular Ecology*, *23*(23), 5756–5770. doi:10.1111/mec.12968

Park, S.-C., & Krug, J. (2007). Clonal interference in large populations. *Proceedings of the National Academy of Sciences*. doi:10.1073/pnas.0705778104

Pimentel, D. (1968). Population regulation and genetic feedback. *Science*, *159*(1963), 1432–1437. doi:10.1126/science.159.3822.1432

Polechová, J., & Barton, N. H. (2015). Limits to adaptation along environmental gradients. *Proceedings of the National Academy of Sciences*, *112*(20), 6401–6406. doi:10.1073/pnas.1421515112

Poon, A., & Chao, L. (2005). The Rate of Compensatory Mutation in the DNA Bacteriophage φX174. *Genetics*, *170*(3), 989–999. doi:10.1534/genetics.104.039438

Post, D. M., & Palkovacs, E. P. (2009). Eco-evolutionary feedbacks in community and ecosystem ecology: interactions between the ecological theatre and the evolutionary play. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *364*(1523), 1629–1640. doi:10.1098/rstb.2009.0012

Rainey, P. B. (1999). Evolutionary genetics: The economics of mutation. *Current Biology*, *9*(10), R371–R373. doi:10.1016/S0960-9822(99)80230-9

Reznick, D. (1982). The Impact of Predation on Life History Evolution in Trinidadian Guppies: Genetic Basis of Observed Life History Patterns. *Evolution*, *36*(6), 1236. doi:10.2307/2408156

Rokyta, D., Badgett, M. R., Molineux, I. J., & Bull, J. J. (2002). Experimental Genomic Evolution: Extensive Compensation for Loss of DNA Ligase Activity in a Virus. *Molecular Biology and Evolution*, *19*(3), 230–238. doi:10.1093/oxfordjournals.molbev.a004076

Rokyta, D. R., Joyce, P., Caudle, S. B., Miller, C., Beisel, C. J., & Wichman, H. A. (2011). Epistasis between Beneficial Mutations and the Phenotype-to-Fitness Map for a ssDNA Virus. *PLoS Genetics*, *7*(6), e1002075. doi:10.1371/journal.pgen.1002075

Rosenthal, J. P., & Dirzo, R. (1997). Effects of life history, domestication and agronomic selection on plant defence against insects: Evidence from maizes and wild relatives. *Evolutionary Ecology*, *11*(3), 337–355. doi:10.1023/A:1018420504439

Saastamoinen, M., Bocedi, G., Cote, J., Legrand, D., Guillaume, F., Wheat, C. W., Delgado, M. del M. (2018). Genetics of dispersal. *Biological Reviews*, *93*(1), 574–599. doi:10.1111/brv.12356

Sackman, A. M., & Rokyta, D. R. (2018). Additive Phenotypes Underlie Epistasis of Fitness Effects. *Genetics*, *208*(1), 339–348. doi:10.1534/genetics.117.300451

Smith, S. D. (2016). Pleiotropy and the evolution of floral integration. *New Phytologist*, *209*(1), 80–85. doi:10.1111/nph.13583

Sniegowski, P. D., Gerrish, P. J., & Lenski, R. E. (1997). Evolution of high mutation rates in experimental populations of E. coli. *Nature*, *387*(6634), 703–705. doi:10.1038/42701

Steinberg, D. S., Losos, J. B., Schoener, T. W., Spiller, D. A., Kolbe, J. J., & Leal, M. (2014). Predation-associated modulation of movement-based signals by a Bahamian lizard. *Proceedings of the National Academy of Sciences*, *111*(25), 9187–9192. doi:10.1073/pnas.1407190111

Steiner, C. F., & Masse, J. (2013). The stabilizing effects of genetic diversity on predator-prey dynamics. *F1000Research*, (0), 1–14. doi:10.3410/f1000research.2-43.v1

Stewart, G. S., Morris, M. R., Genis, A. B., Szűcs, M., Melbourne, B. A., Tavener, S. J., & Hufbauer, R. A. (2017). The power of evolutionary rescue is constrained by genetic load. *Evolutionary Applications*, *10*(7), 731–741. doi:10.1111/eva.12489

Travis, J., Reznick, D., Bassar, R. D., López-Sepulcre, A., Ferriere, R., & Coulson, T. (2014). *Eco-Evolutionary Dynamics*. *Advances in Ecological Research*. doi:10.1016/B978-0-12-801374-8.00001-3

Uecker, H., & Hermisson, J. (2016). The role of recombination in evolutionary rescue. *Genetics*, *202*(2), 721–732. doi:10.1534/genetics.115.180299

Utida, S. (1957). Cyclic Fluctuations of Population Density Intrinsic to the Host-Parasite System. *Ecology*, *38*(3), 442–449. doi:10.2307/1929888

Walsh, M. R., & Post, D. M. (2011). Interpopulation variation in a fish predator drives evolutionary divergence in prey in lakes. *Proceedings of the Royal Society B: Biological Sciences*, *278*(1718), 2628–2637. doi:10.1098/rspb.2010.2634

Willi, Y., Van Buskirk, J., & Hoffmann, A. A. (2006). Limits to the Adaptive Potential of Small Populations. *Annual Review of Ecology, Evolution, and Systematics*, *37*(1), 433–458. doi:10.1146/annurev.ecolsys.37.091305.110145

Worley, A. C., & Barrett, S. C. (2000). Evolution of floral display in Eichhornia paniculata (Pontederiaceae): direct and correlated responses to selection on flower size and number. *Evolution; International Journal of Organic Evolution*, *54*(5), 1533–1545.

Wright, S. (1968). *Evolution and the Genetics of Populations: Genetic and biometric foundations*. University of Chicago Press.

Yamamichi, M., & Miner, B. E. (2015). Indirect evolutionary rescue: Prey adapts, predator avoids extinction. *Evolutionary Applications*, *8*(8), 787–795. doi:10.1111/eva.12295

Yamamichi, M., Yoshida, T., & Sasaki, A. (2014). Timing and propagule size of invasion determine its success by a time-varying threshold of demographic regime shift. *Ecology*, *95*(8), 2303–2315. doi:10.1890/13-1527.1

Yoshida, T., Ellner, S. P., Jones, L. E., Bohannan, B. J. M., Lenski, R. E., & Hairston, N. G. (2007). Cryptic population dynamics: Rapid evolution masks trophic interactions. *PLoS Biology*, *5*(9), 1868–1879. doi:10.1371/journal.pbio.0050235

Yoshida, T., Jones, L. E., Ellner, S. P., Fussmann, G. F., & Hairston, N. G. (2003). Rapid evolution drives ecological dynamics in a predator-prey system. *Nature*, *424*(6946), 303–6. doi:10.1038/nature01767

Zee, P. C., & Velicer, G. J. (2017). Parallel emergence of negative epistasis across experimental lineages. *Evolution*, *71*(4), 1088–1095. doi:10.1111/evo.13190

CHAPTER TWO

Manuscript

Abiotic stress can break the link from rapid evolution to ecology

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Abstract:

Eco-evolutionary feedback dynamics play an essential role in understanding adaptation, diversity and ecological interactions in nature. However, little is known about conditions that may break eco-evolutionary feedback dynamics by preventing the products of rapid evolution having an impact on the ecological dynamics. Here, we combine modelling and laboratory experiments with a host-virus system to show that the presence and absence of abiotic stress may determine whether we observe eco-evolutionary feedback dynamics or not. Our results show that in benign conditions, the evolution of host resistance carries a fitness cost and is correlated with an increase in host population abundances. However, in the presence of an abiotic stress, the evolution of host resistance is not maintained by increasing the host death rate in addition to the fitness cost of resistance, leading to significantly different population dynamics. Overall, our study shows that eco-evolutionary feedback can be limited by the presence of abiotic stress.

Introduction

The idea of eco-evolutionary dynamics is based on the notion that evolution can be rapid, allowing ecological and evolutionary dynamics to operate on similar timescales[1–3]. The core of eco-evolutionary dynamics is the feedback between ecology and evolution, hereafter eco-evolutionary feedback dynamics. These eco-evolutionary feedback dynamics can occur when selection, mediated by ecological interactions, changes the heritability of trait variation, which in turn alters the ecological dynamics[4,5]. Theoretical models and empirical studies showed that considering eco-evolutionary feedback dynamics allows a better understanding of and more accurate predictions for processes such as adaptation, species coexistence and community dynamics[6–9]. Despite the importance of eco-evolutionary feedback dynamics, it is not yet known how often evolution and ecology interact to affect the fate of natural populations[5,10,11].

A first step to address this is to reveal the conditions that either enhance or break eco-evolutionary feedback dynamics by controlling whether phenotypic trait variation has an impact on the ecological dynamics[12]. Among several ecological factors, abiotic stress, i.e., a factor that leads to a sharp reduction in fitness of a population, is a potential way to break the link between evolution and ecology (see Chapter I). Abiotic stress can affect both ecological and evolutionary conditions[13,14]. So far, most research has been focused on how it affects ecology and evolution independently and not on the link between them, especially the link between evolution and ecology where the traits of phenotypic variation do not have an impact on the ecological dynamics through changes in the population size of the interacting species.

Here, we combine mechanistic modelling of eco-evolutionary dynamics with the experimental evolution in laboratory microcosms, to test predictions for the role of abiotic stress in breaking the feedback between phenotypic trait evolution and ecological interactions. In the present study we use an experimental host-virus model system, with the asexual alga *Chlorella variabilis* as host and the lytic dsDNA virus *PBCV-1* which offers an excellent opportunity to study eco-evolutionary feedback over multiple generations[15–17].

Results and Discussion

First, in order to investigate theoretically various cases under which abiotic stress can affect or break the feedback between phenotypic trait evolution and ecological interaction in the algae-virus system, we constructed a mathematical model. Our mathematical model describes the eco-evolutionary feedback dynamics previously recorded for the alga-virus system. As in the study of Frickel et al. (2016), we designed our mathematical model such that the alga-virus coevolution would increase the alga intraspecific biodiversity and lead to alga types with different levels of resistance. We described the alga-virus interaction by assuming a modified gene-for-gene model with five algal types and four virus types (for details of the mathematical model, see Materials and Methods section). The resistant types of algae were associated with a linear resistance-growth-rate trade-off, with the most resistant type having the lowest growth rate.

We ran up to 100 simulations demonstrating the alga-virus interactions. In each run we simulated 500 days. We initiated each simulation by pseudorandomizing the cost of resistance and thus the form of the resistance-growth-rate trade-off among the alga resistance types, and the alga-host mortality rate. To estimate the impact of the form of the resistance-growth-rate trade-off and host mortality in algal biodiversity and thus the maintenance of the host resistant types in the population, we used the Shannon index for the time period 200-500 in each simulation. We summarized the results for 100 simulations by using an interaction plot showing the combined effect of the cost of the trade-off and host mortality on alga biodiversity. We found that when the cost of resistance is high and host mortality is high, the ancestral type dominates the algal population and there is not eco-evolutionary feedback dynamics. When the cost of resistance is

low and host mortality is low, then all five types are maintained in the population and have an impact in the alga population dynamics and thus eco-evolutionary feedback dynamics takes place. Overall, our numerical simulation predicted that the likelihood of the algal resistant types being maintained in the population and having an impact on the population dynamics of the system decreases with an increase in host death rate as well as with an increase in the fitness cost of the host resistance evolution (Figure 1).

Based on the outcome of our model we designed two experimental treatments: one treatment under benign conditions and one under stressful conditions, varying the host death rate and the form of resistance-growth rate trade-off.

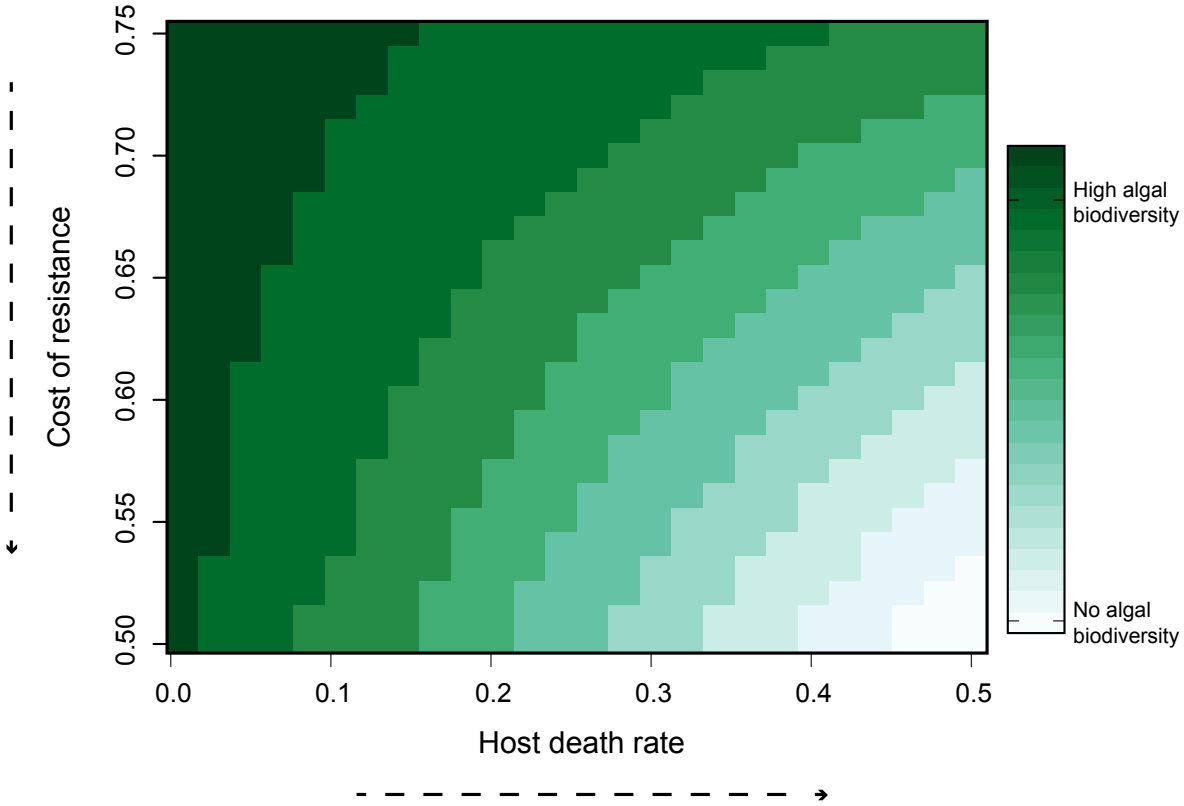

Figure 1: Host biodiversity as a function of host death rate and the cost of host resistance using the mathematical model for our host-virus system. Arrows on the x-axis indicate the direction of increase in host death rate. Arrows on the y-axis indicate the direction of increase in host resistance cost. The colours indicate differences in the biodiversity in the host population with dark green representing the highest host biodiversity and white indicating the absence of host biodiversity (i.e., only the ancestral type was present).

To test our model predictions, we experimentally evolved an isogenic algal population under both treatments, with and without the virus. To set up the benign and stressful treatments for the algal population, we used different concentrations of ammonium chloride (NH_4Cl). Ammonium chloride is the main nitrogen source for algae in the inorganic medium used here, and is required for the synthesis of amino acids[18]. However, in concentrations above 20 mM, NH_4Cl acts as an abiotic stressor by inhibiting the photosynthetic activity of the algae and increasing the death rate in the algal population[19,20]. We used two different concentrations of ammonium chloride: for the benign treatment we used 2.94 mM NH_4Cl (as in the experiments of Frickel et al. 2016) and for the stressful treatment we used 29.4 mM NH_4Cl.

To examine the effect of the different concentrations of NH_4Cl on the fitness of the algal population, one isogenic population of the alga *Chlorella variabilis* was experimentally evolved under benign and stressful treatments with no virus, for 120 days (three independent replicates per treatment). Overall we found significant differences in the algal population dynamics between the two treatments (Figure 2; Generalized Estimating Equations (geeglm) to test the treatment effect: $x^2 = 1.82*10^{30}$, df = 1, $p < 2*10^{-16}$). In the benign treatment, the algal population in all replicates grew and maintained in the densities of ~$5*10^6$ cells/ml, while in the stressful treatment, algal densities declined after day 12 and maintained to a 10-fold lower density of ~$4*10^5$ cells/ml. Our results indicate significant difference in the algal carrying capacity between the two treatments (Figures 2, Figure 3B; ANOVA: F = 1.12, df = 1, p < 0.0001) but no decrease in maximum algal growth rate (Figure 3A; ANOVA: F = 0.03, df = 1, p = 0.97).

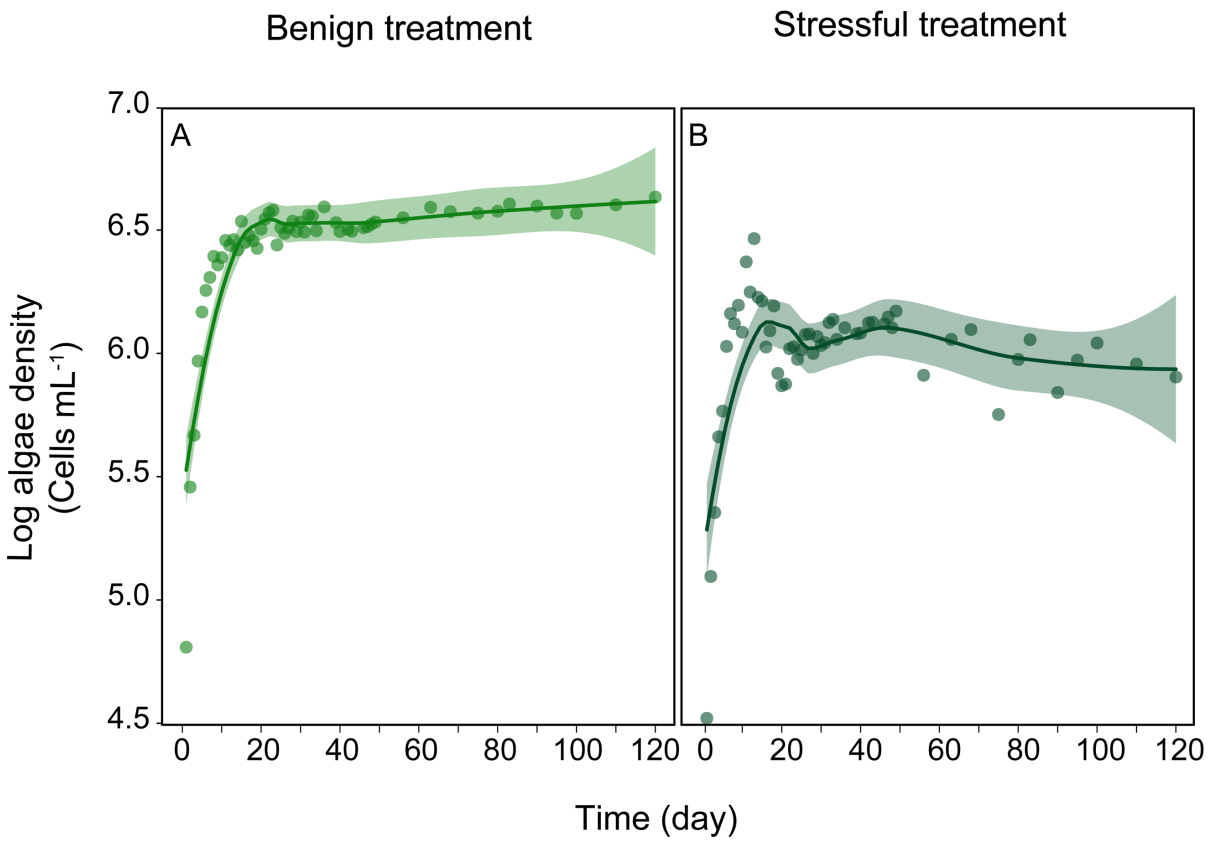

Figure 2: Population densities of the algal host for (A) the benign and (B) the stressful treatment. Overall we observed significant differences in the algal population densities between the two treatments. In both treatments, algal populations grew to high densities, where they stabilized. In the benign treatment, algae stabilized at significantly higher densities compared to the stressful treatment. Dots in the graph represent the raw experimental counts and the line represents the average raw data for three technical replicates smoothed with the R function smooth.spline (A-B). The shaded area around the line describes the standard error of the mean, for statistics see main text.

To test the effects of abiotic stress on the alga-virus coevolution and thus on the alga-virus eco-evolutionary dynamics, the same isogenic algal populations were grown with a purified viral population under the benign and stressful treatments (three independent replicates per treatment). In both treatments, we tracked the coevolutionary and population dynamics of the alga and virus over 120 days.

To track the host-virus coevolutionary dynamics we used time-shift experiments (Gaba & Ebert 2009). Time-shift experiments allow us to quantify algal resistance and virus infectivity from combinations of host clones and virus populations, isolated at different time points over the course of the experiment. Previous studies have reported that coevolutionary dynamics may occur in two different forms: 1) arms-race dynamics (ARD), where directional selection would lead to an increased host resistance and virus infectivity over time and 2) fluctuating selection (FSD) where evolution is driven by negative frequency-dependent selection[21,22]. However, it is not expected that coevolution will always strictly follow one of these two forms.

In the benign treatment, we observed two different patterns of host resistance and parasite infectivity coevolution. The first pattern was observed during days 0-40 and the second during days 50-120. We found that isolated algal-host clones from early time points (days 0, 12, 20, 30 and 40) were resistant against their relative past viral populations and were susceptible to viral populations from future time points (Figure S1A, Figure S2A, Figure S3A; General Linear Model (GLM): $F_{3.794} = 9.15$, $p = 9.57*10^{-5}$, post hoc Tukey test; past-future: $p < 10^{-5}$). These results indicate an increased host resistance and virus infectivity during days 0-40, which potentially stops after this time point. This pattern of

resistance and infectivity suggests that antagonistic algae-virus coevolution occurs via arms-race dynamics, where directional selection leads to an increase in algal resistance and virus infectivity over time.

When we challenged algal clones from later time points (days 50, 60, 70, 90 100 and 120) with viral populations from their relative past and future time points, we found that host resistance and virus infectivity were not uniformly high but fluctuated over time in a way that is more consistent with the pattern of fluctuating selection dynamics. Additionally we did not observe significant differences in susceptibility of the isolated algal-host clones from the later time points when they were challenged against virus population from its relative past and relative future (Figure S1B, Figure S2B, Figure S3B; GLM: $F_{1.23} = 1.45$, $p = 0.195$, post hoc Tukey test; past-future: $p = 0.19$).

Another interesting observation during days 50-120 was the evolution, around day 50, of a general resistant alga host, resistant to all virus populations. The general resistant algal host did not become fixed in the population but coexisted with the clones with less resistance, owing to the resistance-growth-rate trade-off (Figure 7A; Linear Mixed effect Model (LMM): $\chi^2 = 0.36$, $df = 1$, $p = 0.54$). The evolution and maintenance of the general resistant host in all the benign treatment seem to play an important role in the two different coevolutionary dynamics we observed. Before the evolution of general resistant host we observed ARD while after FSD similarly to the study of Frickel et al. (2016).

Strikingly, in the stressful treatment, the algal resistance evolution differed from that in the benign treatment (GLM, $F_{2.43} = 4.27$, $p = 1.94*10^{-5}$). Our data indicate that in the stressful treatment, algal resistance is selected, but not maintained in the population (Figure 5B). Thus, in the stressful treatment, over the

course of the experiment (Figure S4, Figure S5, Figure S6) the host resistance range increased up to a single time point and then decreased again, in a pattern that is closer to that of fluctuating selection dynamics for all three technical replicates.

To further investigate the effect of abiotic stress in the algae-virus coevolutionary dynamics we used network analyses (Figure 4C, Figure 5C)[23,24]. Previous studies on coevolving species showed that network structural analysis could offer an insight into the coevolutionary dynamics between two species. A matrix metric that indicates the network structure is the modularity. In our study, the modularity shows whether a distinct cluster of virus populations can affect a distinct cluster of algal clones[25]. For each replicate in each treatment, we generated a bipartite network with nodes representing host and virus populations at each time point (10 algal clones represent each host population). Our results show that in the benign treatment, the algae-virus network was more modular than in the stressful treatment (Figure 6; t-test: $t = 4.37$, $df = 2.04$, $p = 0.04$). The higher modularity in the network of the benign treatment is an effect of the pattern of arms-race dynamics observed between alga and virus in the first 50 days[25].

To test whether there is a difference in the selection for algal resistance between the two treatments, we calculated the multiplicity of infection in both treatments (MOI) over time. First, we calculated from the time-shift data the proportion of susceptible clones per point and the proportion of infective virions per point. Subsequently, we multiplied the proportions of resistant and infective types by the population sizes of the alga and virus at that time point and calculated their ratios as the MOI. We found no significant differences in the MOI in the two

treatments (Figure S7, ANOVA: F = 1.73, df = 1, p = 0.197) which indicates that there are not differences in selection for alga resistance between treatments.

To determine whether there is a growth-rate cost related to the evolution of resistance and if there is a treatment effect on that, we compared the growth rate of 20 individual general resistant algal clones taken from each treatment to ancestral algal clones. In both treatments, the general resistant clones displayed a growth-rate cost compared to their ancestors, but in the stressful treatment the fitness cost of the general resistant clones was significantly higher (Figure 7A; LMM: $\chi^2 = 0.36$, df = 1, p = 0.54), (Figure 7C; LMM: $\chi^2 = 5.54$, df = 1, p = 0.01). To confirm that the abiotic stress has an effect on the form of the trade-off between resistance and growth rate, we tested clones from the benign treatment in the stressful treatment and vice versa (Figure 7B, Figure 7D). Our results indicate that abiotic stress had a significant effect on the form of the trade-off between resistance and growth rate (Figure 7B, LMM, $\chi^2 = 26.4$, df = 1, $p = 2.76*10^{-7}$). The presence of the abiotic stress changes the form of the trade-off, making it significantly stronger. When we tested clones from the stressful treatment in the benign treatment the strength of the trade-off was less (Figure 7D, LMM, $\chi^2 = 5.24$, df = 1, p = 0.022). This suggests that the abiotic stressor has an impact on the form of the fitness-resistance trade-off. Our results suggest that even though resistance evolves in both treatments, the cost of resistance combined with the additional mortality prevents the spread of the algal resistant types in the stressful treatment, which is in accordance with our model predictions.

If we consider the population dynamics, we see that the lack of resistance evolution results in significant differences in the population dynamics for the two treatments (algae-virus population dynamics in response to treatment; geeglm: x^2

= $2.45*10^{15}$, df = 1, $p < 2*10^{-16}$). In both treatments, the algae grew without the presence of the virus during the first 12 days, and after 12 days, when we inoculated the virus, the alga populations declined drastically. In the benign treatment, up to day 45, the algae and virus populations cycled, subsequently following more stable population dynamics. Conversely, in the stressful treatment, the host and virus populations fluctuated rapidly with low amplitudes. Around day 100, the virus population became extinct in two of the three technical replicates, and the algae reached high densities.

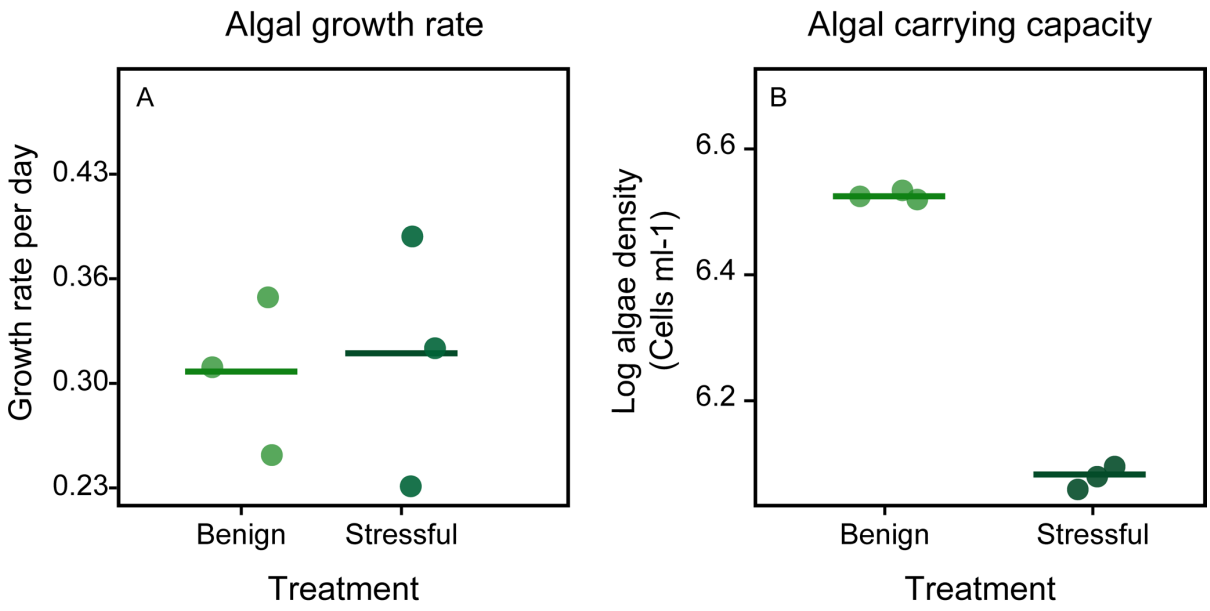

Figure 3: Analysis of the algal host growth rate and carrying capacity when grown for 120 days in the benign and stressful treatments. (A) Panel A shows no significant differences in the algal growth rate between treatments. (B) Panel B indicates significant differences in the algal carrying capacity between the two treatments. Dots represent the experimental counts and the line represents the average data for three independent chemostat replicates. The light green colour indicates the benign treatment while the dark green the stressful treatment.

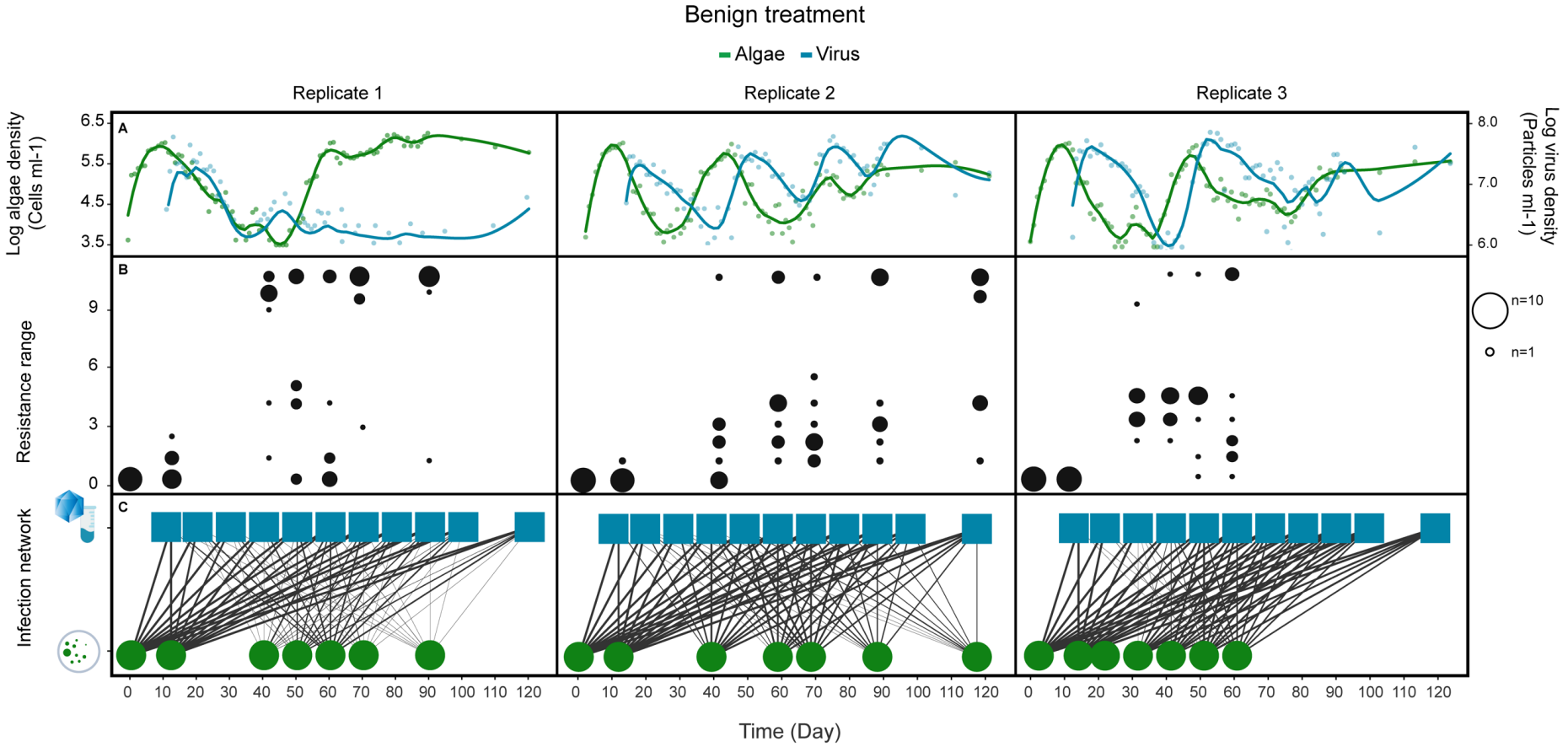

Figure 4: Eco-evolutionary dynamics of the algal-host and its virus in the benign treatment. (A) Host-virus population dynamics in three independent replicates. In all replicates, the algae-virus population dynamics cycled for ~50 days and then stabilized. The dots in the graph represent the raw experimental counts and the line represents the smoothed lines from the R-function smooth.spline. (B) Host range resistance evolution over time in three independent chemostat replicates. To calculate the host resistance range we challenged 10 alga resistant clones with isolated viral populations from different time points. (C) Phenotypic coevolution of alga-virus system based on the virus populations infectivity to the alga colonies. We calculated infectivity in the same way we calculated host resistance range. Phage infectivity is proportional to the width of the edges. Blue squares correspond to the isolated virus populations from the chemostats; green circles correspond to ten alga colonies isolated from the algae-virus chemostats. The absence of a line indicates that all ten alga colonies from that time point are resistant to the virus.

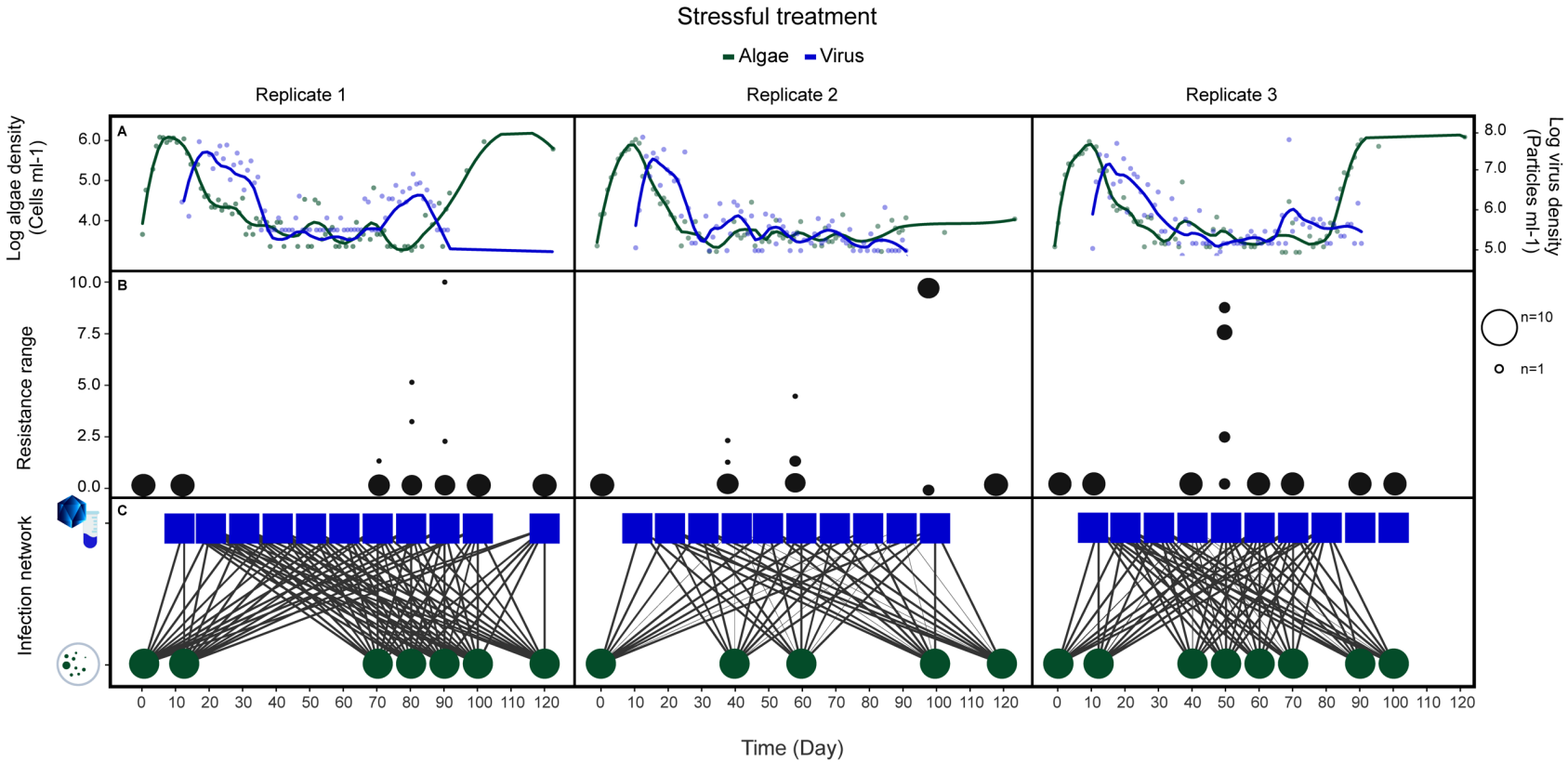

Figure 5: Eco-evolutionary dynamics of the alga-host and its virus in the stressful treatment. (A) Host-virus population dynamics in the stressful treatment for three independent replicates. In the stressful treatment, the host and virus population fluctuated rapidly with low amplitudes. Around day 100, the virus populations reached their lowest points in the second and third technical replicate and became extinct. The latter, allowed the alga population to grow to high densities. The dots in the graph represent the raw experimental counts and the line represents the raw data smoothed with the R function smooth.spline. (B) Host range resistance evolution over time in the three independent chemostat replicates. To calculate the host resistance range, in each time point possible we challenged ten alga clones with isolated viral populations from different time points throughout the experiment. (C) Phenotypic coevolution in the alga-virus system based on the phage infectivity on algal colonies. We calculated infectivity in the same way we calculated the host resistance range. Phage infectivity is proportional to the width of the edges. Blue squares correspond to the isolated virus populations from the chemostats; green circles correspond to ten alga colonies isolated from the algae-virus chemostats. The absence of a line indicates that all ten alga colonies from that time point are resistant to the virus.

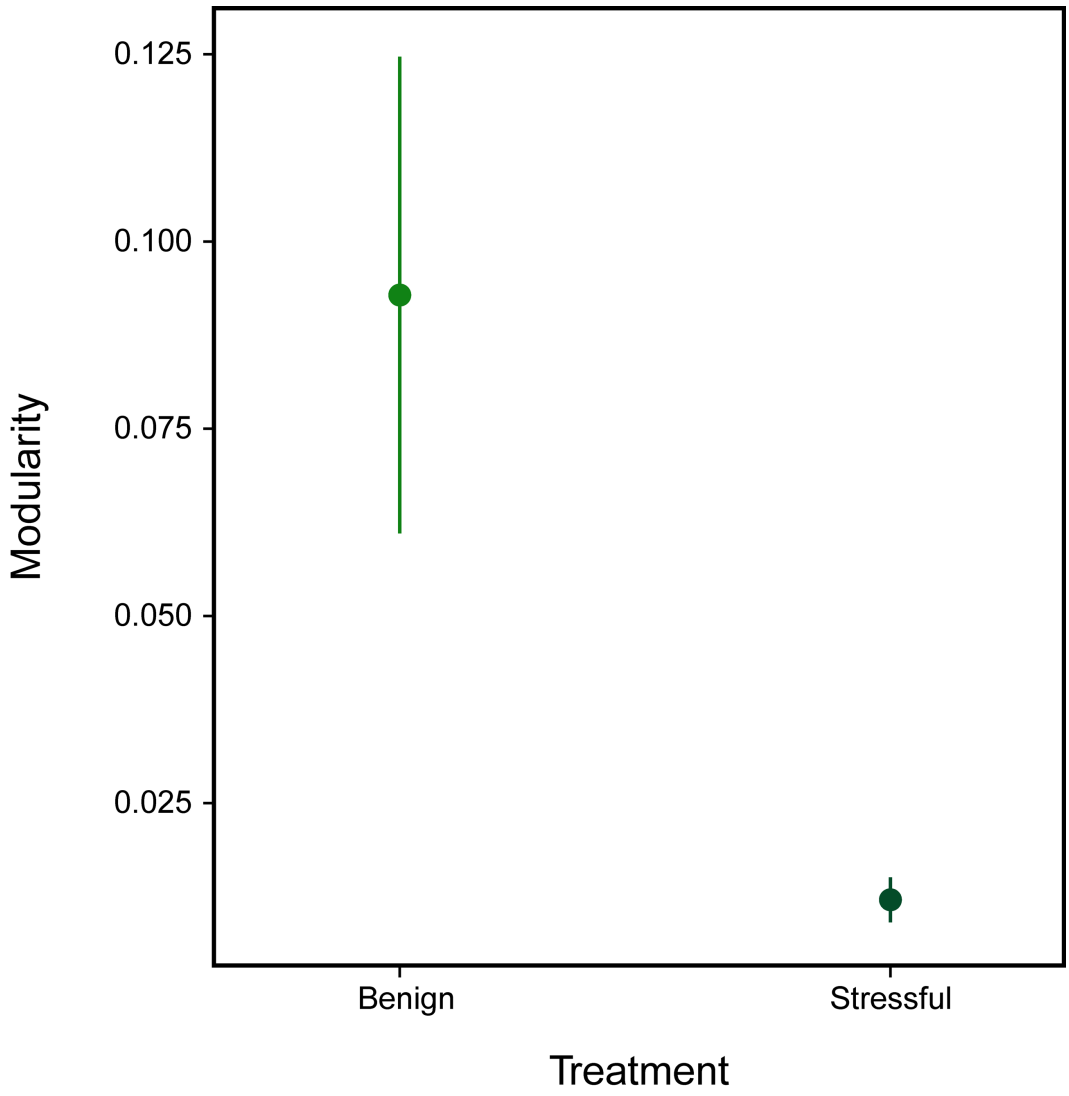

Figure 6: Modularity of host-virus infection networks in the two treatments. Our graph shows that in the benign treatment, the alga-virus network was more modular than in the stressful treatment. The dots represent the mean modularity out of three chemostat replicates and the error bar the standard deviation of the mean. The light green colour indicates the benign treatment while the dark green the stressful treatment.

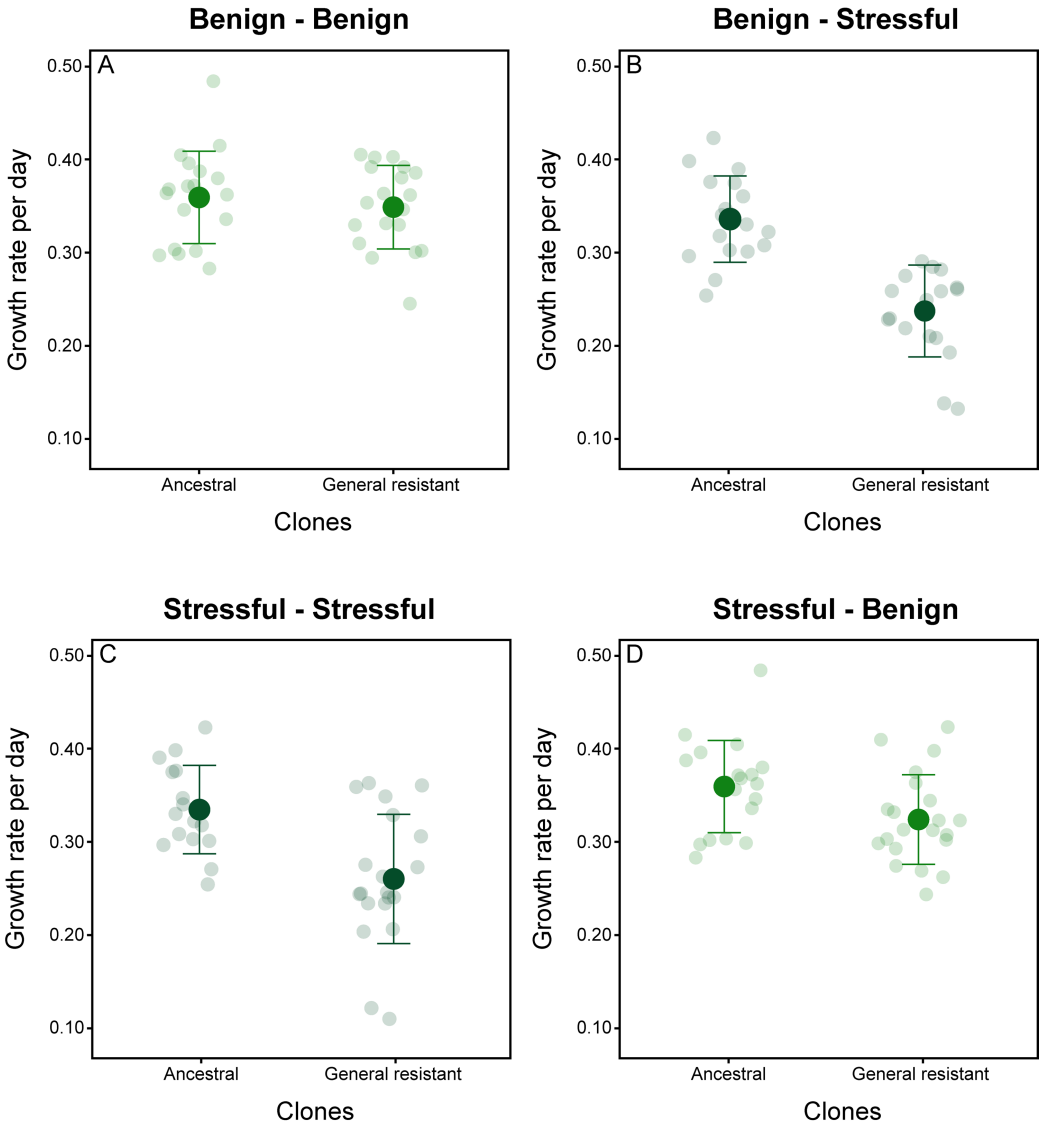

Figure 7: Growth-rate-resistance trade-off in the algal clones and a treatment effect on the form of the trade-off. To test if there is a growth-rate cost associated with the algal resistance in the alga clones, we compared the growth rate of 20 individual general resistant algal clones to 20 ancestral algal clones taken from each treatment in the treatment in which they were initially isolated (A-C). We found that in the stressful treatment, the trade-off between growth rate and resistance is significantly stronger. To investigate further the effect of treatment on the form of the trade-off, we obtained the growth rate of the clones that were isolated from the benign treatment in the stressful treatment and vice versa. We found that the treatment alters the strength of the cost, with the benign treatment being associated with a lower cost and the stressful treatment with a higher cost (B-D). The headers above each panel indicate the treatment from which alga clones were isolated and the treatment where the growth rate was obtained, e.g., panel D, headed stressful-benign indicates that the clones were isolated from the stressful treatment, but tested in the benign treatment conditions. The transparent dots represent the experimental counts. The opaque dots represent the mean out of 20 experimental counts and the error bar the standard deviation of the mean. Light green and dark green indicate the benign and stressful treatments respectively for testing the clones.

Eco-evolutionary feedback dynamics can be essential for species evolution, maintenance of biodiversity and species coexistence, but do they always occur? Based on a mathematical model, we predicted that the likelihood of eco-evolutionary feedback prevailing decreases with an increase in the host death rate, and an increase in the form of the trade-off between host resistance and growth rate. We demonstrated experimentally that in a benign treatment, rapid evolution of resistance affects algal population dynamics over the course of the experiment and thus eco-evolutionary dynamics are maintained. Conversely, in a stressful treatment the high fitness cost of host resistance and the increase host mortality, does not allow the resistant algal types to be maintained in the population and have an effect in the alga-virus population dynamics.

Previous studies demonstrated that heritable trait variation, as well the trade-off among the trait variants, could affect eco-evolutionary feedback dynamics. For instance, Becks *et al.* (2010) showed that the initial presence or absence of genetic variation in the prey affected the amount of genetic variation that was maintained in the prey population, which in turn affected the predator-prey population dynamics. Similarly, *Kasada et al.* (2015) used an experimental predator-prey system to demonstrate that differences in the form of trade-offs between anti-predator defence and competitive ability in the prey population resulted in changes in the clonal frequency of the algal prey, which in turn affected the predator-prey population dynamics. Our study is different from any of the previous studies since it provides the first empirical demonstration that a change in the treatment as common as the induction of an abiotic stressor, can break the eco-evolutionary feedback dynamics in a host-virus system, by preventing the maintenance of resistance evolution in the host population even though they initially evolve.

How does the host resistance evolve under the two treatments? In both treatments there is a similar strong selection for host resistance and therefore host resistance emerges in both cases. However, host resistance is not maintained in the stressful treatment. The presence of the abiotic stress reduces the fitness of all host types, resistant and less resistant ones. At the same time, the cost of resistance results in the host resistant types having even lower growth rates compared to the non-resistant types. As a consequence, the stressful treatment favours the presence of susceptible host types in the population.

Indeed, many other mechanisms could have broken the evolution of host resistance in our experimental study case. Some studies predict that if the host receptors for nutrient transport are the same as those for virus adsorption, then changes in nutrients such as those we see in the stressful treatment may prevent host resistance evolution by not allowing the virus to adsorb[26]. However, phycodnaviruses like the PBCV-1 virus used in our study are not known to use protein receptors[27–29]. In addition, if the higher levels of ammonium chloride in the stressful treatment had an impact on the viral adsorption to the host, this would be reflected in the ratio of virus population to host population for the two treatments, which is not the case (Figure S7).

Abiotic stress is an environmental factor that has been studied for decades, but it has not been investigated how it can affect the eco-evolutionary dynamics of species interaction. Our study shows that a factor as common as abiotic stress can prevent the product of evolution having an impact on the ecological dynamics. Our study is a first step in developing a predictive understanding of when and how eco-evolutionary dynamics occur in nature and affect the fate of natural populations.

Materials and Methods

Chemostat cultures: We ran 18 chemostat cultures in total, at a constant dilution rate of 0.1 d^{-1}, with two different concentrations of ammonium chloride (2.94 mM NH_4Cl for the benign treatment and 29.4 mM NH_4Cl for the stressful treatment) with and without virus. Algae and virus populations were grown in 500-ml glass chemostat bottles, with 400 ml of modified Bold's Basal Medium[15]. We maintained the chemostats at a constant temperature of 20˚C and mixed the culture using magnetic stirring bars. We started all the chemostats from an isogenic clone of the alga *Chlorella variabilis* (strain NC64A). After 12 days, we inoculated nine of the chemostats with purified, concentrated virus, while the other nine served as controls.

Population dynamics: To track the population densities of algae and virus, we sampled all the chemostats daily under sterile conditions. We determined the algal densities using a hemocytometer with an inverted microscope, and the viral densities using a flow cytometer[15].

Time-shift experiments: To test the effects of abiotic stress on the algae-virus coevolutionary dynamics we performed time-shift experiments as described by Frickel and colleagues (2016), with small modifications. In short, every second day we stored alga colonies on agar plates and filtered virus populations at 4˚C. However, in the end we were not able to use all the samples stored, since at many of the time points, the alga colonies did not grow on the plates and the virus population was not detected due to very low population size in the chemostats. We quantified alga resistance and virus infectivity, using the available isolated alga

colonies and virus populations in each technical replicate, as shown in Figure 5B for the benign treatment and in Figure 6B for the stressful treatment. From each time point, we isolated algae by randomly choosing 10 algal colonies and growing them in batch cultures. We transferred the isolated colonies into 96-well plates and diluted them to equal densities by matching the optical density to 0.045 on a Tecan Infinite M200 PRO 680 (Männedorf, Switzerland). We set up four technical replicates of each algal colony to grow with the available virus populations from past, current and future time points and four technical replicates to grow without virus populations. We determined their growth rates initially and after 72 hours, using optical density on a Tecan instrument (Tecan, Infinite M200PRO,680 Männedorf, Switzerland). We identified algal colonies as resistant or susceptible by comparing the mean growth rate plus two standard deviations for the four technical replicates with a virus to the mean growth rate minus two standard deviations for the technical replicates without the virus. If there was an overlap between their two times standard deviations then the clones were scored as resistant.

Data analysis: All data analyses were performed using RStudio[30] (version 1.1.453) and R[31] (version 3.4.3). To check the effect of the treatment in the alga-host population dynamics that grew without virus in three replicated chemostats in each treatment, we used the geeglm function from geepack package[32] (Figure 2). Similarly, we used the geeglm function to test the treatment effect on alga-host virus population dynamics in three replicated chemostats for each treatment (Figure 4A, Figure 5A). For each chemostat replicate, we calculated the resistance range (Figure 4B, Figure 5B) of each host-alga clone by calculating its resistance

to the free virus population from its past, current and future time points. For example, when a host-algal clone was resistant to all 11 free virus populations, then it was awarded a resistance range of 11. Similarly, we calculated the virus infectivity ranges as the proportion of host-alga clones per time point (10 host-alga clones per time point) that could be infected by a particular virus population.

Based on the host-algal resistance data and virus infectivity data we divided each chemostat replicate into two periods: the period up to when a general resistant host was first observed and the period including all later time points. In each period, we calculated for each host-alga clone the proportion of virus populations from the past, current and future time points with which it was infected. If ARD drove the algae-virus coevolutionary dynamics, we would expect that hosts would be highly resistant to the virus populations from the relative past and not resistant to virus populations from the relative future. To test this statistically, we used a generalized linear model (GLM, quasi-binomial errors) with infected proportions of algal clones as a response value to virus populations from past and future time points. On the other hand, if the algae-virus coevolutionary dynamics were driven by FSD, we would expect no significant differences in the proportions of alga clones infected by virus populations from past and future time points.

To test whether there is a correlation between the resistance range and the growth rate, and how this is affected by the treatment conditions, we obtained the growth rates of the 20 individual general resistant clones and 20 individual ancestral clones. We grew each clone in four wells of a 96-well plate without virus for three days, under the treatment condition from which it was isolated and also under the conditions of the other treatment. To test statistically the correlations between growth rate and resistance range we used a linear mixed effect model

(LMM) with the mean growth rate of each clone as a fixed effect and the replicate chemostat as a random effect. To apply the LMM test in the R treatment we used the lme4 package[33]. To study the effect of abiotic stress on the algae-virus coevolutionary dynamics we used time-shift network analyses. For each one of the nine chemostats with virus, we created infection matrices containing the proportions of successful infections in hosts that were challenged by past, contemporary and future virus populations (Figure 4C, Figure 5C). To quantify the differences in the coevolutionary dynamics between the benign and stressful treatment, we calculated the modularity for each chemostat infection matrix using the bipartite package[34]. We then tested for differences in modularity between treatments using t-test. Lastly, to test the treatment effect on the alga growth rate, the alga carrying capacity as well as for the multiplicity of virus infection (MOI) we used an ANOVA test.

Mathematical model: We described the interaction between the algal-host and the virus assuming a modified gene-for-gene interaction without costs for the virus. The modified gene-for-gene model of interactions assumes that a viral mutant P_j can infect a host mutant C_i only if $i \leq j$. In our model, we assume five types of alga-host mutants and four types of viral mutants. Based on the modified gene-for-gene interactions, host mutant C_5 will be generally resistant to all virus types (see Figure 8). An increase in alga resistance is associated with a cost to its growth rate, described by the factor b_c in the function $F_c(N)$. The functional response curve $F_c(N)$ describes the nutrient uptake of the algae. In the current model, $n = NV$ represents the quantity of nitrate (the limiting nutrient) in μmol per chemostat.

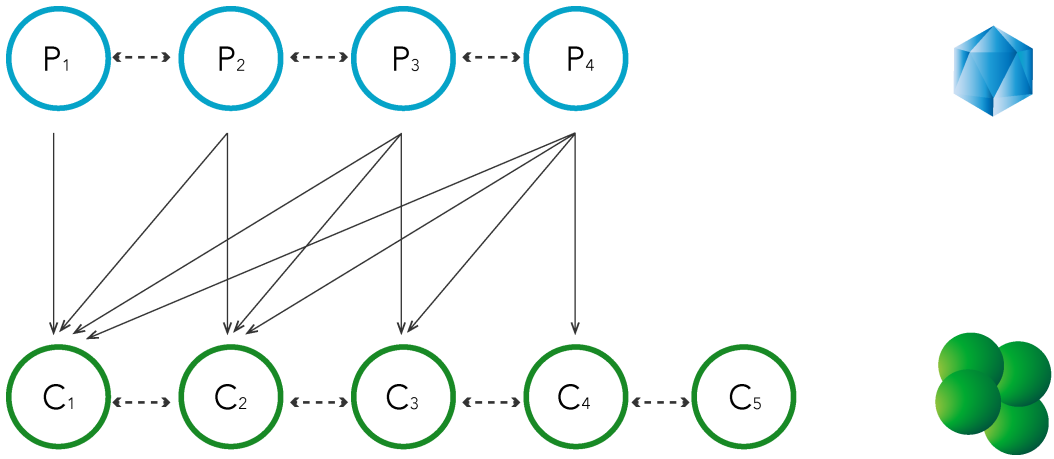

Figure 8: Schematic representation of the modified gene-for-gene model. The modified gene-for-gene interactions assume that a viral mutant P_j can infect a host mutant C_i only if $i \leq j$. In our model, we assume five types of alga-host mutants and four types of viral mutants. Based on the modified gene-for-gene interactions, host mutant *C_5* will be resistant to all virus types.

The alga-virus eco-evolutionary dynamics was modelled using the following three differential equations.

$$\frac{dN}{dt} = D(VNi - N) - \sum_{i=1}^{n=5} F_c\,(N)_i C_i \qquad (1)$$

$$\frac{dC}{dt} = M_c * x_c F_c(N)C - \varphi AC * P - DC \qquad (2)$$

$$\frac{dP}{dt} = M_p b * (\varphi t(A)P * C\,) - (\varphi t(A)P * C) - DP \qquad (3)$$

Where $F_c(N)_i = \frac{\omega_c b_{c_i} N}{\varepsilon_c\,(K_c + N)}$

In addition, b_c = (0.7, 0.68, 0.66, 0.64, 0.62) indicates the growth of the five alga types. The ancestral alga type *C_1*, which is susceptible to all virus types, has the highest growth rate at 0.7, while the general resistant alga type *C_5* has the lowest growth rate at 0.62. Model parameters which are defined in Table 1 are coming from the studies of Fussmann and co-authors[35], Suzuki and co-authors[36].

The values of virus adsorption rate and virus burst size have been adapted to represent our experimental data. Differential equation (ODE) (1) describes changes in nutrients over time. ODE (2) describes changes in the population of the alga-host *Chlorella variabilis* over time. ODE (3) refers to the changes in the population of the virus PBCV-I over time. The sign "*" in the ODE's refers to component wise multiplication.

Matrix A represents the modified gene for gene interaction between algae and virus assuming five types of an algal-host and four types of virus.

$$A = \begin{pmatrix} 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

The alga-host evolves by point mutations with a mutation rate "ε", represented by the matrix "M_c" below.

$$M_c = \begin{pmatrix} 1-\varepsilon & \varepsilon/2 & 0 & 0 & 0 \\ \varepsilon & 1-\varepsilon & \varepsilon/2 & 0 & 0 \\ 0 & \varepsilon/2 & 1-\varepsilon & \varepsilon/2 & 0 \\ 0 & 0 & \varepsilon/2 & 1-\varepsilon & \varepsilon \\ 0 & 0 & 0 & \varepsilon/2 & 1-\varepsilon \end{pmatrix}$$

The virus evolves by point mutations with a mutation rate "ε", represented by the matrix "M_p" below.

$$M_p = \begin{pmatrix} 1-\varepsilon & \varepsilon/2 & 0 & 0 \\ \varepsilon & 1-\varepsilon & \varepsilon/2 & 0 \\ 0 & \varepsilon/2 & 1-\varepsilon & \varepsilon \\ 0 & 0 & \varepsilon/2 & 1-\varepsilon \end{pmatrix}$$

Table 1: Parameter values of the model.

Parameter	Biological Meaning	Value
D	Chemostat volume dilution rate (per day)	0.69
Ni	Inflow resource concentration (μmole N/L)	80
V	Chemostat volume (L)	0.33
K_c	Minimum half-saturation constant for nutrient uptake by Chlorella (μmole N/L)	4.3
b_c	Maximum recruitment rate, Chlorella	3.3
x_c	Conversion efficiency by algae	0.05
ω_c	N content in 10^9 Chlorella cells (μ mole)	20
ε_c	Assimilation efficiency	1
φ	Virus adsorption rate	$9*10^{-2}$
b	Virus burst size	50
ε	Point mutation rates	10^{-3}

REFERENCES

1. Pimentel, D. Population regulation and genetic feedback. *Science* **159,** 1432–1437 (1968).
2. Charlesworth, B. Selection in Density-Regulated Populations. *Ecology* **52,** 469–474 (1971).
3. Hairston, N. G., Ellner, S. P., Geber, M. A., Yoshida, T. & Fox, J. A. Rapid evolution and the convergence of ecological and evolutionary time. *Ecol. Lett.* **8,** 1114–1127 (2005).
4. Post, D. M. & Palkovacs, E. P. Eco-evolutionary feedbacks in community and ecosystem ecology: interactions between the ecological theatre and the evolutionary play. *Philos. Trans. R. Soc. B Biol. Sci.* **364,** 1629–1640 (2009).
5. Koch, H., Frickel, J., Valiadi, M. & Becks, L. Why rapid, adaptive evolution matters for community dynamics. *Front. Ecol. Evol.* **2,** 1–10 (2014).
6. Becks, L., Ellner, S. P., Jones, L. E. & Hairston Nelson G., J. G. Reduction of adaptive genetic diversity radically alters eco-evolutionary community dynamics. *Ecol. Lett.* **13,** 989–997 (2010).
7. Matthews, B., Aebischer, T., Sullam, K. E., Lundsgaard-Hansen, B. & Seehausen, O. Experimental evidence of an eco-evolutionary feedback during adaptive Divergence. *Curr. Biol.* **26,** 483–489 (2016).
8. Brunner, F. S., Anaya-Rojas, J. M., Matthews, B. & Eizaguirre, C. Experimental evidence that parasites drive eco-evolutionary feedbacks. *Proc. Natl. Acad. Sci.* **114,** 3678–3683 (2017).
9. Kasada, M., Yamamichi, M. & Yoshida, T. Form of an evolutionary tradeoff affects eco-evolutionary dynamics in a predator–prey system. *Proc. Natl. Acad. Sci.* **111,** 16035–16040 (2014).

10. Fussmann, G. F., Loreau, M. & Abrams, P. A. Eco-evolutionary dynamics of communities and ecosystems. *Funct. Ecol.* **21**, 465–477 (2007).

11. Rudman, S. M. *et al.* What genomic data can reveal about eco-evolutionary dynamics. *Nat. Ecol. Evol.* **2,** 9–15 (2017).

12. Legrand, D. *et al.* Eco-evolutionary dynamics in fragmented landscapes. *Ecography* **40***,* 1–17 (2016).

13. Hoffmann, A. A. & Hercus, M. J. Treatmental stress as an evolutionary force. *BioScience* **50,** 217–226 (2000).

14. Loeschcke, V., Krebs, R. A., Dahlgaard, J. & Michalak, P. High-temperature stress and the evolution of thermal resistance in Drosophila. in *Treatmental Stress, Adaptation and Evolution.* Birkhäuser Verlag, Basel, 175–190 (1997).

15. Frickel, J., Sieber, M. & Becks, L. Eco-evolutionary dynamics in a coevolving host-virus system. *Ecol. Lett.* **19,** 450–459 (2016).

16. Frickel, J., Theodosiou, L. & Becks, L. Rapid evolution of hosts begets species diversity at the cost of intraspecific diversity. *Proc. Natl. Acad. Sci.* **114,** 11193-11198 (2017).

17. Frickel, J., Feulner, P. G., Karakoc, E. & Becks, L. Population size changes and selection drive patterns of parallel evolution in a host–virus system. *Nat. Commun.* **9,** (2018).

18. Podevin, M., De Francisci, D., Holdt, S. L. & Angelidaki, I. Effect of nitrogen source and acclimatization on specific growth rates of microalgae determined by a high-throughput in vivo microplate autofluorescence method. *J. Appl. Phycol.* **27,** 1415–1423 (2015).

19. Thompson, P. a., Levasseur, M. E. & Harrison, P. J. Light-limited growth on ammonium vs. nitrate: What is the advantage for marine phytoplankton? *Limnol. Oceanogr.* **34,** 1014–1024 (1989).

20. Berg, G. M., Driscoll, S., Hayashi, K., Ross, M. & Kudela, R. Variation in growth rate, carbon assimilation, and photosynthetic efficiency in response to nitrogen source and concentration in phytoplankton isolated from upper San Francisco Bay. *J. Phycol.* **53**, 664–679 (2017).

21. Hall, A. R., Scanlan, P. D., Morgan, A. D. & Buckling, A. Host-parasite coevolutionary arms races give way to fluctuating selection. *Ecol. Lett.* **14,** 635–642 (2011).

22. Lopez Pascua, L. *et al.* Higher resources decrease fluctuating selection during host-parasite coevolution. *Ecol. Lett.* **17,** 1380–1388 (2014).

23. Dormann, C. F. & Strauss, R. A method for detecting modules in quantitative bipartite networks. *Methods Ecol. Evol.* **5,** 90–98 (2014).

24. Larsen, M. L., Wilhelm, S. W. & Lennon, J. T. Nutrient stoichiometry shapes microbial coevolution. *bioRxiv* (2017).

25. Beckett, S. J. & Williams, H. T. P. Coevolutionary diversification creates nested-modular structure in phage-bacteria interaction networks. *Interface Focus* **3,** 20130033 (2013).

26. Menge, D. N. L. & Weitz, J. S. Dangerous nutrients: Evolution of phytoplankton resource uptake subject to virus attack. *J. Theor. Biol.* **257,** 104–115 (2009).

27. Meints, R. H., Burbank, D. E., Van Etten, J. L. & Lamport, D. T. A. Properties of the chlorella receptor for the virus PBCV-11. *Virology* **164,** 15–21 (1988).

28. Van Etten, J. L. & Dunigan, D. D. Chloroviruses: Not your everyday plant virus. *Trends Plant Sci.* **17,** 1–8 (2012).

29. Agarkova, I. *et al.* Dynamic attachment of Chlorovirus PBCV-1 to Chlorella variabilis. *Virology* **466,** 95–102 (2014).

30. Studio, R. RStudio: integrated development treatment for R. *RStudio Inc Boston Mass.* (2012).

31. Team, R. C. R: A language and treatment for statistical computing. (2013).

32. Halekoh, U., Højsgaard, S. & Yan, J. The R Package geepack for Generalized Estimating Equations. *J. Stat. Softw.* **15,** 1–11 (2006).

33. Bates, D., Mächler, M., Bolker, B. & Walker, S. *Fitting Linear Mixed-Effects Models using lme4. J. Stat. Soft.* **67**, 1-48 (2014).

34. Dormann, C. F., Gruber, B. & Fründ, J. Introducing the bipartite package: Analysing ecological networks. *R News* **8,** 8 (2008).

35. Fussmann, G. F. Crossing the Hopf Bifurcation in a Live Predator-Prey System. *Science* **290,** 1358–1360 (2000).

36. Suzuki, K. & Yoshida, T. Non-random spatial coupling induces desynchronization, chaos and multistability in a predator-prey-resource system. *J. Theor. Biol.* **300,** 81–90 (2012).

Supplementary Material

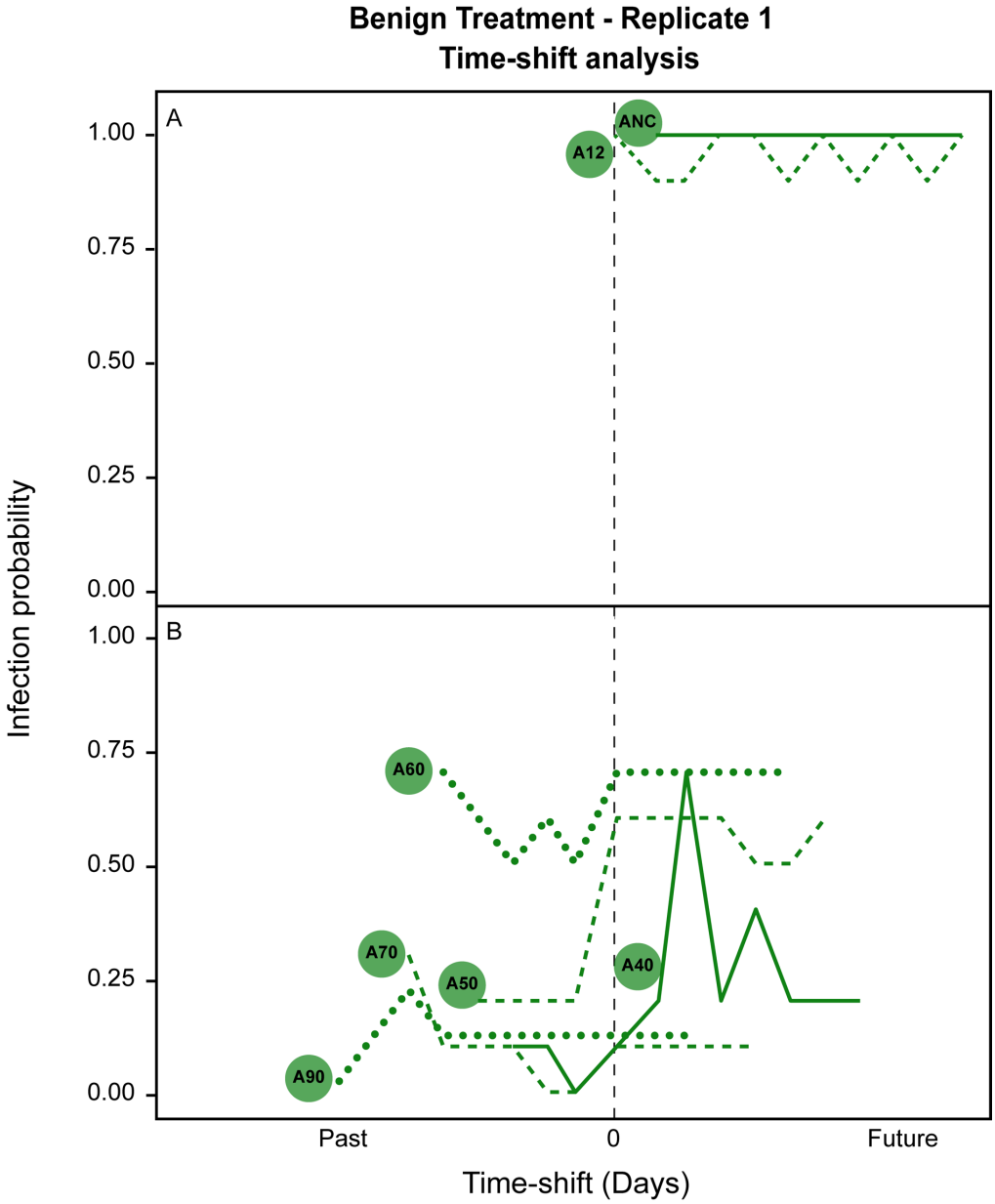

Figure S1: Time-shift analysis of host-virus infectivity over time in the benign treatment-replicate 3. In the centre of the diagram, we placed alga clones and virus populations isolated from the same time point. We placed the interactions between alga clones and their past virus populations on the left of the diagram and interactions between alga clones and their future virus populations on the right of the diagram. Each line matches with the infection probability of ten host-alga clones isolated from specific time points which are indicated by the label in the centre of the green dots. Panel A includes alga clones isolated from the time points "12" and the ancestral alga clones. Panel B includes alga clones isolated from the time points "40,50,60,70,90" over the course of the experiment. In the panel A, when algal clones were challenged with virus populations from past time points their infection probability was still high because no algal resistance evolution had been taken place by that time point. We inoculated the virus at time point "12". Similarly when alga clones from "0,12" time points were challenged with virus populations from future time points their infection probability was high (up to 100%). In the panel B, when alga clones were challenged with virus population from the past, contemporary and future points, we observe fluctuations in the infectivity which is consistent with fluctuating selection dynamics.

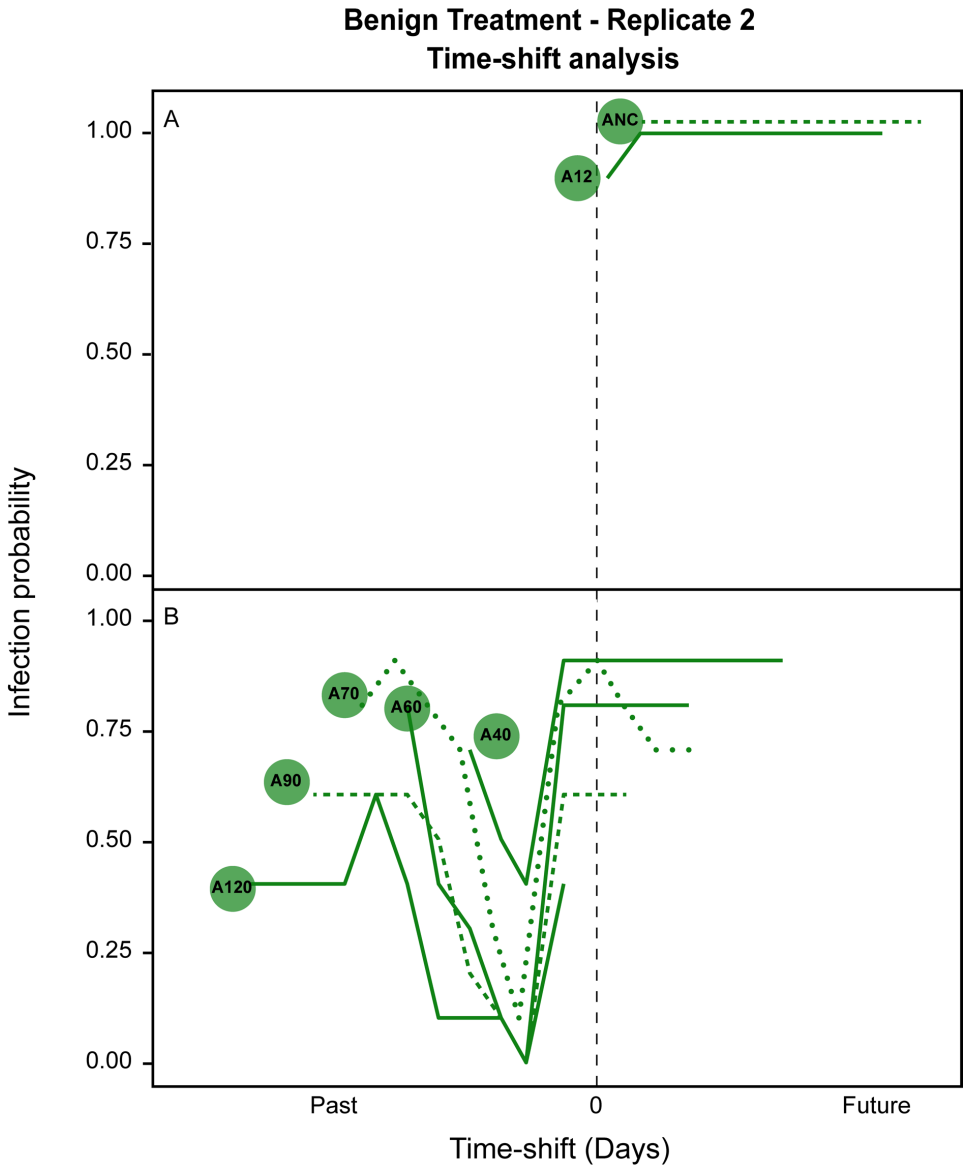

Figure S2: Time-shift analysis of host-virus infectivity over time in the benign treatment-replicate 2. In the centre of the diagram, we placed alga clones and virus populations isolated from the same time point. We placed the interactions between alga clones and their past virus populations on the left of the diagram and interactions between alga clones and their future virus populations on the right of the diagram. Each line matches with the infection probability of ten host-alga clones isolated from specific time points which are indicated by the label in the centre of the green dots. Panel A includes alga clones isolated from the time points "12" and the ancestral alga clones. Panel B includes alga clones isolated from the time points "40,60,70,90.120" over the course of the experiment. In the panel A, when alga clones were challenged with virus populations from past time points their infection probability was still high because no algal resistance evolution had been taken place by that time point. Notably, we inoculated the virus in the alga cultures at time point "12". Similarly when the algal clones from "0,12" time points were challenged with virus populations from future time points their infection probability was high (up to 100%). In the panel B, when alga clones were challenged with virus populations from the past, contemporary and future points, we observe fluctuations in the infectivity which is consistent with fluctuating selection dynamics.

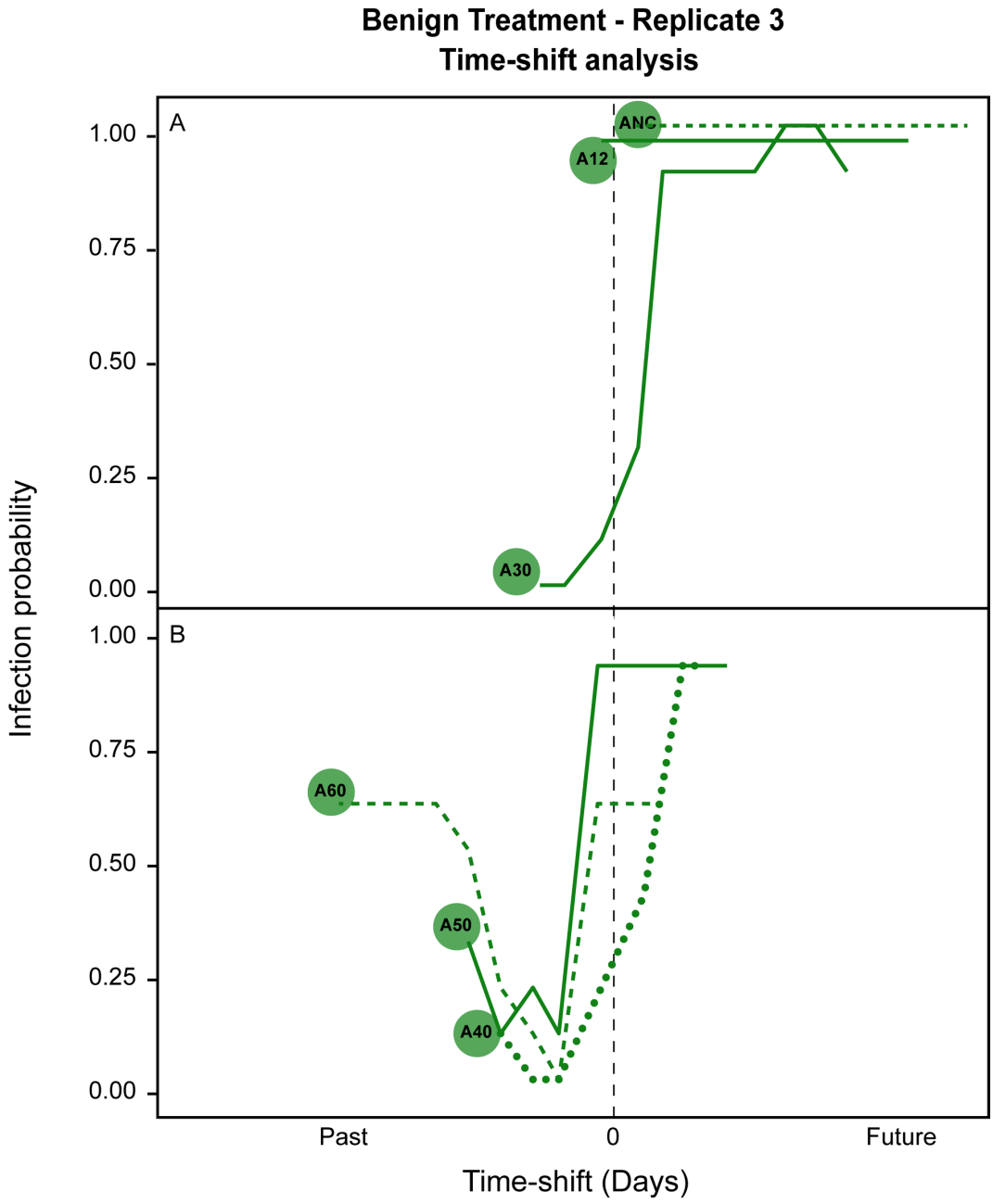

Figure S3: Time-shift analysis of host-virus infectivity over time in the benign treatment-replicate 3. In the centre of the diagram, we placed alga clones and virus populations isolated from the same time point. We placed the interactions between alga clones and their past virus populations on the left of the diagram and interactions between algal clones and their future virus populations on the right of the diagram. Each line matches with the infection probability of ten host-alga clones isolated from specific time points which are indicated by the label in the centre of the green dots. Panel A includes alga clones isolated from the time points “0,12,30” and the ancestral alga clones. Panel B includes alga clones isolated from the time points “40,50,60” over the course of the experiment. In the panel A, when alga clones were challenged with virus populations from past time points their infection probability was low (up to 10%) while when they were challenged with virus populations from future time points their infection probability was high (up to 100%). This finding is consistent with arms-race dynamics where there is directional selection for increased host resistance. In the panel B, when alga clones were challenged with virus populations from the past, contemporary and future points, we observe fluctuations in the infectivity which is consistent with fluctuating selection dynamics.

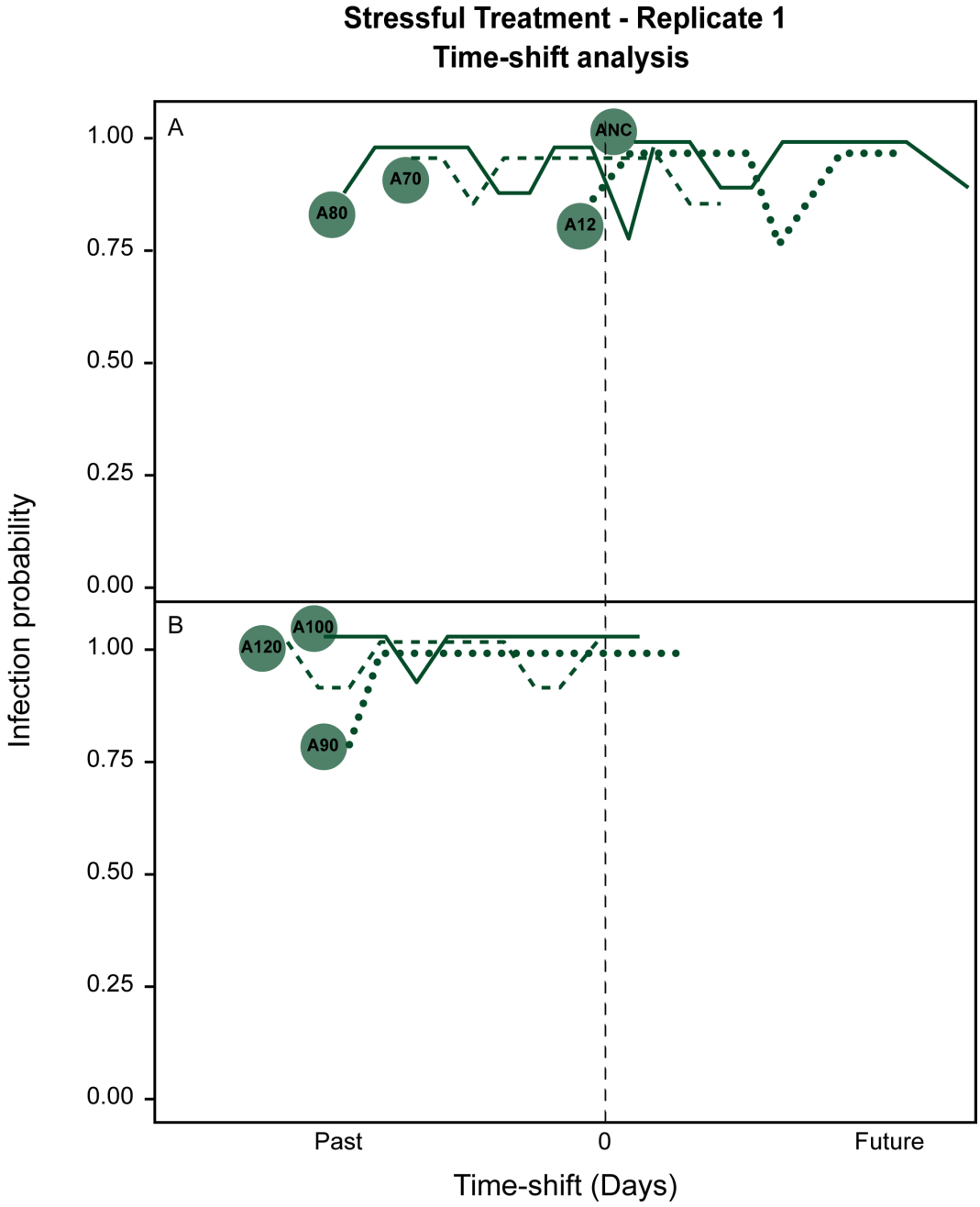

Figure S4: Time-shift analysis of host-virus infectivity over time in the stressful treatment-replicate 1. In the centre of the diagram, we placed alga clones and virus populations isolated from the same time point. We placed the interactions between alga clones and their past virus populations on the left of the diagram and interactions between alga clones and their future virus populations on the right of the diagram. Each line matches with the infection probability of ten host-alga clones isolated from specific time points which are indicated by the label in the centre of the green dots. Panel A includes alga clones isolated from the time points “12,70,80” and the ancestral alga clones. Panel B includes alga clones isolated from the time points “90,100,120” over the course of the experiment. In both panels A and B, when alga clones were challenged with a virus population from the past, contemporary and future points, we observe fluctuations in the infectivity which is consistent with fluctuating selection dynamics. The dynamics are the same in both panels but we still present them in two panels for better visualization.

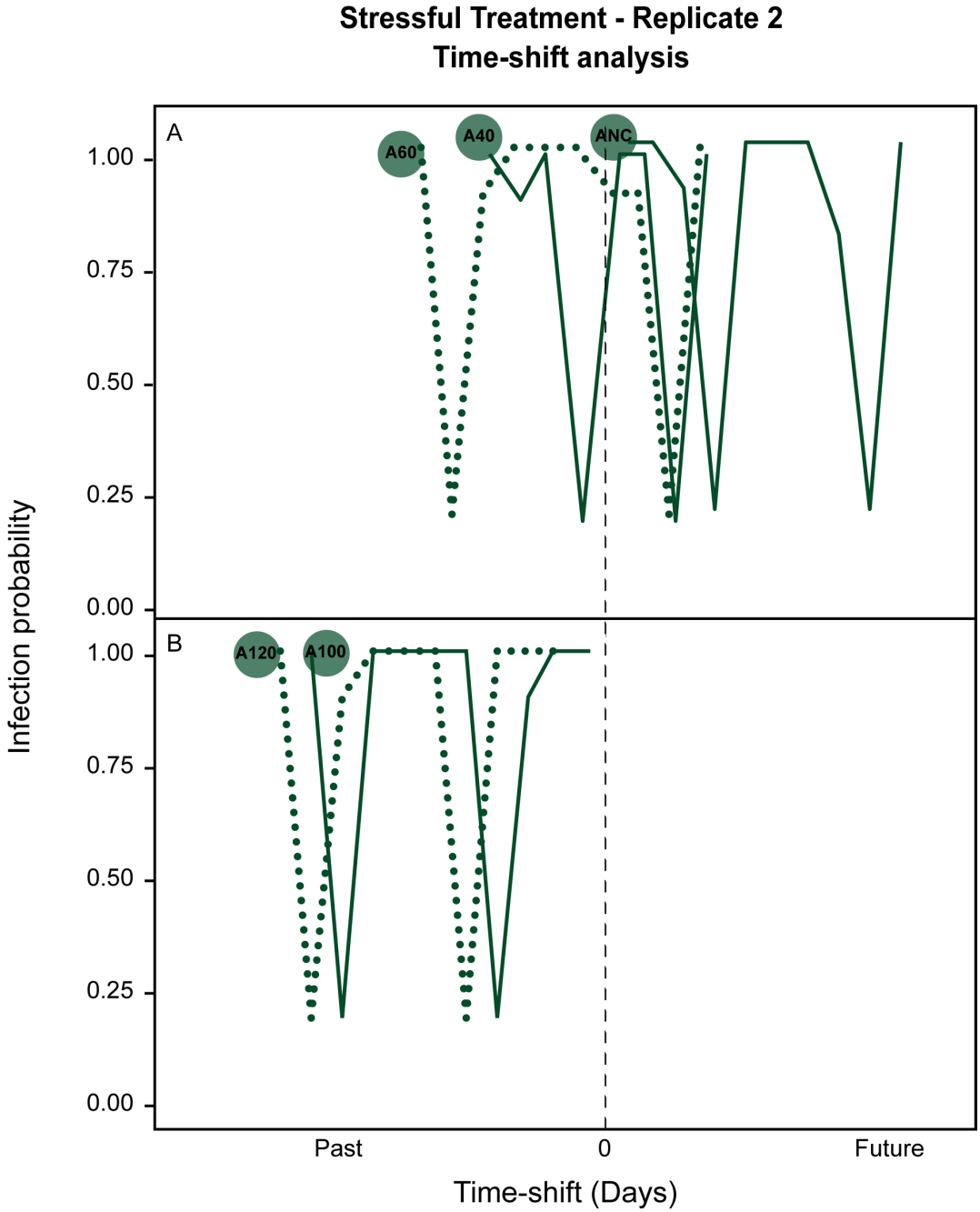

Figure S5: Time-shift analysis of host-virus infectivity over time in the stressful treatment-replicate 2. In the centre of the diagram, we placed alga clones and virus populations isolated from the same time point. We placed the interactions between alga clones and their past virus populations on the left of the diagram and interactions between alga clones and their future virus populations on the right of the diagram. Each line matches with the infection probability of ten host-alga clones isolated from specific time points which are indicated by the label in the centre of the green dots. Panel A includes alga clones isolated from the time points “12,40,60” and the ancestral alga clones. Panel B includes alga clones isolated from the time points “100,120” over the course of the experiment. In both panels A and B, when alga clones were challenged with a virus population from the past, contemporary and future points, we observe fluctuations in the infectivity which is consistent with fluctuating selection dynamics. The dynamics are the same in both panels but we still present them in two panels for better visualization.

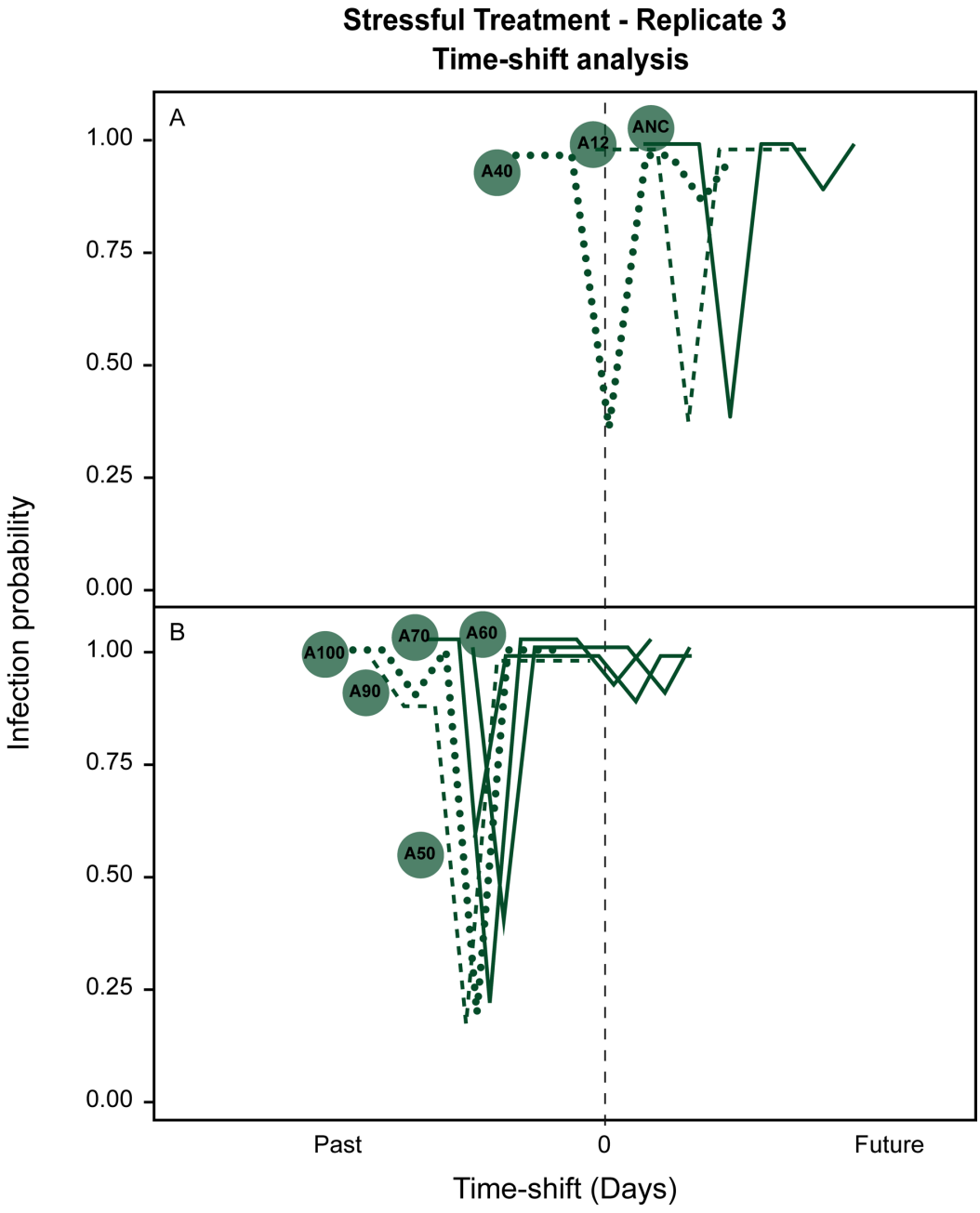

Figure S6: Time-shift analysis of host-virus infectivity over time in the stressful treatment-replicate 3. In the centre of the diagram, we placed alga clones and virus populations isolated from the same time point. We placed the interactions between alga clones and their past virus populations on the left of the diagram and interactions between alga clones and their future virus populations on the right of the diagram. Each line matches with the infection probability of ten host-alga clones isolated from specific time points which are indicated by the label in the centre of the green dots. Panel A includes alga clones isolated from the time points “12,40” and the ancestral alga clones. Panel B includes alga clones isolated from the time points “50,60,70,90,100” over the course of the experiment. In both panels A and B, when alga clones were challenged with a virus population from the past, contemporary and future points, we observe fluctuations in the infectivity which is consistent with fluctuating selection dynamics. The dynamics are the same in both panels but we still present them in two panels for better visualization.

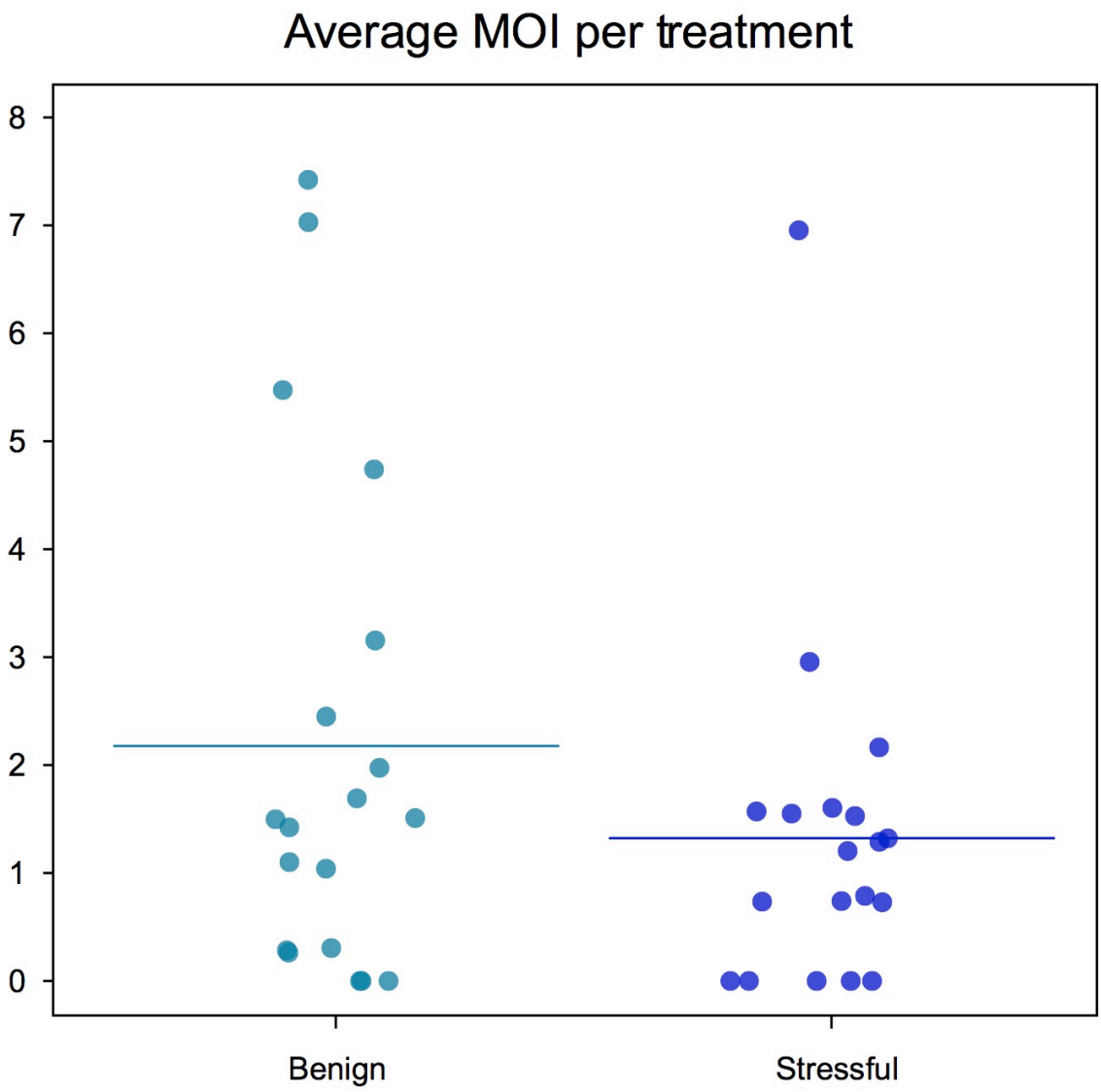

Figure S7: Average MOI (Multiplicity of infection) in the benign and stressful treatment. To calculate MOI in both treatments and for the same time points as in the time-shift experiments we calculated the ratio between the infective virions and susceptible alga clones. We did not find any significant difference in the average MOI between the two treatments. Dots in the graph represent the different MOI ratios over the course of the experiment. The line represents the average MOI ratio in each treatment. The light blue colour indicates MOI ratios in the benign treatment while the dark blue in the stressful treatment.

CHAPTER THREE

Effects of Network Structure on the Eco-Evolutionary Dynamics and Species Coexistence

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Abstract

The idea that ecological change can drive evolutionary change and that evolution feeds back to cause further ecological change, is growing in importance. As knowledge in the eco-evolutionary dynamics field has increased, so has the range of new questions to be answered and problems to be solved. To date, most research centred on antagonistic interactions between two species and simple spatial structures with a maximum of two patches. However, natural communities are rich in species whose populations exist in a network of patches, which are connected through dispersal or migration. We modelled the eco-evolutionary dynamics of an experimental model system consisting of three species in a single patch, and then we extended the single patch environment to dispersal network structures consisting of eight patches. As expected, we found that when patches are spatially homogeneous, the dispersal network does not have a significant effect on the transient dynamics of the species, alga evolution or species coexistence, whether eco-evolutionary dynamic processes are present or not. We suggest further ideas that could be tested by our model as well as experimental directions for studying eco-evolutionary dynamics and feedbacks in communities with more than two species.

1. Introduction

A central question in the fields of ecology and evolution involves understanding how competing species coexist (Holt 1984; Holt & Pickering 1985; Aarssen 1989; Wilson 1990; Huston & Huston 1994; Chesson 2000). Scientists long tried to understand species coexistence by independently exploring the ecological and evolutionary dynamics that develop over time and space. So far, this approach has seemed insufficient to explain species coexistence in many natural communities. Ecologists traditionally focused on niche theory, frequency dependency and species-specific interactions, while mostly ignoring evolutionary change (Hutchinson 1961; Hanski 1998). On the other hand, evolutionary biologists focused on genetic diversity and natural selection to predict species coexistence and neglected the profound effect of community processes on evolution (Hughes *et al.* 2008; Tokeshi 2009; Seehausen 2015; Ehlers *et al.* 2016). However, the evidence that ecology and evolution act on similar timescales (Yoshida *et al.* 2003; Hairston *et al.* 2005) and affect each other (see chapters I and II) leads to new and exciting avenues to explore how eco-evolutionary dynamics can help explain species coexistence.

To date, the evidence for the importance of eco-evolutionary dynamics to species coexistence comes mostly from model systems in single patches with one or two species (Kasada *et al.* 2014; Cortez 2016; Frickel *et al.* 2016; Hiltunen *et al.* 2017). However, natural communities are rich in species with populations that exist in networks of patches and are connected with various patterns and dispersal rates (Toju *et al.* 2017). Currently, we remain unaware of how different spatial structures can affect eco-evolutionary dynamics and how important eco-evolutionary dynamics are for species coexistence in different spatial structures. From the

theory of metacommunity (Hanski 1994, 1998, 1999), we know that spatial differences in the size and habitat quality, as well as the connectivity among habitats can independently influence ecological and evolutionary dynamics and affect species coexistence.

A promising approach to understanding the role of eco-evolutionary dynamics for species coexistence in various spatial structures is to investigate species coexistence in the presence and absence of eco-evolutionary dynamics with and without spatial structure. This study aims to do so by using a mathematical model of the experimental model system described by (Frickel *et al.* 2017). This model includes three species in a single patch environment without spatial structure: the asexually reproducing alga *Chlorella variabilis* as a host, the double-stranded DNA lytic virus PBCV-1 as a viral parasite and the asexual rotifer *Brachionus calyciflorus* as a predator for the algal host. The authors found that in all replicates of their experiment the rotifers went extinct four days after their inoculation likely due to niche overlap with the virus population. At the beginning of the experiment both rotifers and viruses consume the ancestral algae. After the extinction of the rotifers, the algae and viruses showed eco-evolutionary dynamics similar to those previously described for the algae-virus food web (Frickel et al. 2016). One difference was that the evolution of resistance was delayed in the algae-virus system due to the initial presence of the rotifers.

Importantly, when the rotifers were added again to the chemostat system after the evolution of a general resistant alga host, all three species could coexist. The rotifers and viruses coexisted likely due to a reduction in niche overlap, as the rotifers could consume all the algae, while the viruses only consumed those that were susceptible to the specific virus types. The coexistence of algae and rotifers,

as well as algae and the viruses alone, was always possible. Overall, the study of (Frickel *et al.* 2017) shows that evolution of one species interaction (alga-virus) enables coexistence with a previously extinct species.

However, the study lacks a scenario with a spatial structure. In this paper, we designed a mathematical model to expand the model system from one patch to networks of eight patches with different connectivity patterns and dispersal rates. We developed a **regular** network in which each patch is connected to its four nearest neighbours, a **rewired** network in which we randomly rewired the connections of two patches and a **random** network in which all patches were randomly connected to other patches. In each network, patches were connected bidirectionally with different dispersal rates. Specifically we tested the following five different dispersal rates: "0, 0.0005, 0.001, 0.01, 0.1". Here each pattern of connectivity creates a different spatial structure, here after dispersal network structure.

Our aim is to test whether any dispersal network structure allows for the coexistence of all three species, even when the rotifers and viruses have complete niche overlap and if ecological or eco-evolutionary processes play a role in species coexistence by reducing niche overlap. To study the latter, we focused on the length of the transient time i.e., the time before all patches synchronise within a network (ecological dynamics) and the time required for the generally resistant host to evolve (evolutionary dynamics). Coexistence is predicted to be possible under these conditions when population dynamics of patches are asynchronous and populations of rotifers can colonise patches from which they were previously extinct (Levin 1974; Chesson 2000). To estimate the asynchrony of population dynamics among the patches in a network, we measured

the length of the transient dynamics of network. We expected networks, which allow longer transient dynamics to favour the persistence of rotifers in the networks. We then tested whether coexistence is more likely to occur when evolution, and thus eco-evolutionary dynamics are present. Coexistence is predicted to be possible under these conditions, as higher connectivity is predicted to lead to higher infectivity rates (Hanski 1999; Jousimo *et al.* 2014), which we here consider to be synonymous with the faster coevolution of host and virus (i.e., a reduction in niche overlap). We measure the speed of coevolution by measuring when the general resistant host evolves and comprises at least 10% of the algae population. We chose this threshold due to its transferability/detectability into experiments and because we thought that was the point at which a general resistant host could have a significant impact on the population.

The workflow of this study began with the development and demonstration of the two-species (algae-virus) and three-species (algae-virus-rotifers) eco-evolutionary dynamics model in a single patch (Results, section 3.1). Next, we expanded the single-patch model to more complex spatial scales to investigate how the spatial structure affects the potential for coexistence of the three species with (Results, section 3.2) and without eco-evolutionary dynamics (Results, section 3.3) and how dispersal networks and coexistence alters the eco-evolutionary dynamics.

2. Model Description

To describe the interaction between the alga-host and the virus, we applied a modified gene-for-gene interaction with no cost to the virus. In the modified gene-for-gene interactions we assume that a viral mutant P_j can infect a host mutant C_i only if $i \leq j$. In our model, we assume five types of alga-host mutants and four types of viral mutants. Based on the modified gene-for-gene interactions, host mutant C_5 will be generally resistant to all virus types (see Figure 1). An increase in alga resistance is associated with a cost to its growth rate, described by the factor b_c = (0.7, 0.68, 0.66, 0.64, 0.62) in the function $F_c(N)$. Based on the parameter b_c the ancestral alga type, C_1, which is susceptible to all virus types, has the highest growth rate at 0.7, while the general resistant alga type C_5 has the lowest growth rate at 0.62. The functional response curve $F_c(N)$ describes the nutrient uptake of the algae. As the resistance of the alga increases, its palatability for the rotifers decreases. This is indicated by the parameter p = (0.22, 0.21. 0.20, 0.19, 0.18) in the function $F_b(C)$, which describes the feeding rate of the rotifers in each alga-host type. Based on the parameter p, the ancestral alga type, C_1, has the highest palatability at 0.22, while the general resistant alga type C_5 has the lowest palatability at 0.18. In the current model, $n = NV$ represents the quantity of nitrate (the limiting nutrient) in µmol per chemostat, and $c = CV$ is the number of the *Chlorella* alga cells (10^9 cells per chemostat).

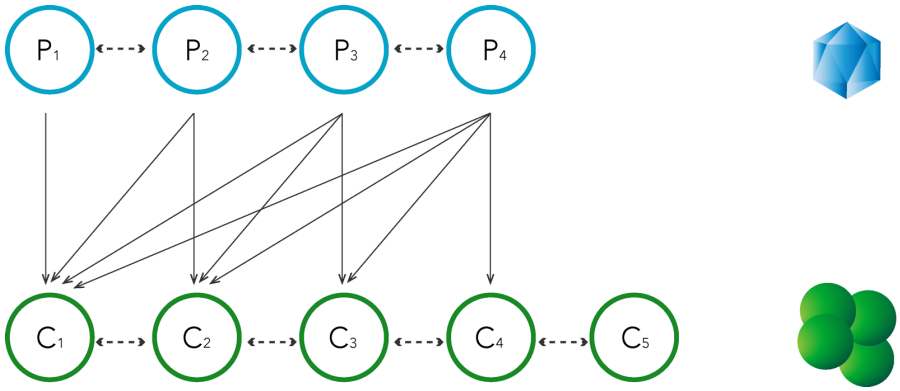


Figure 1: Schematic representation of the modified gene in the gene model. The modified gene-for-gene interactions assume that a viral mutant P_j can infect a host mutant C_i only if i ≤ j. In our model, which is modelled after the experimental system of Frickel *et al.* 2017, we assume five types of alga-host mutants and four types of viral mutants. Based on the modified gene-for-gene interactions, host mutant C_5 will be resistant to all virus types.

The alga-virus-rotifer eco-evolutionary dynamics were modelled using the following five differential equations

$$\frac{dN_j}{dt} = D(VNi - Nj) - \sum_{i=1}^{n=5} F_c\,(N)_i C_j + d\sum_{j=1}^{k=8} dmat_{jk} N_k \quad (1)$$

$$\frac{dC_j}{dt} = M_c * x_c F_c(N) C_j - F_b(C)B - \ \varphi A C_j * P_j - DC_j \ + d\sum_{j=1}^{k=8} dmat_{jk} C_k \quad (2)$$

$$\frac{dP_j}{dt} = M_p b * (\varphi t(A) P * C\ ) - (\varphi t(A) P * C) - DP + \ d\sum_{j=1}^{k=8} dmat_{jk} C_k \quad (3)$$

$$\frac{dB_j}{dt} = x_b F_b(C) R - (D+m) B_j + \ d\sum_{j=1}^{k=8} dmat_{jk} B_k \quad (4)$$

$$\frac{dR_j}{dt} = x_b F_b(C) R - (D+m) B_j + \ d\sum_{j=1}^{k=8} dmat_{jk} R_k \quad (5)$$

Where $F_c(N) = \frac{\omega_c b_c N}{\varepsilon_c\,(K_c+N)}$ and $F_b(C) = \frac{pCG}{K_b + \max\,(pC, C*)}$

Ordinary differential equation (ODE) (1) describes changes in nutrients over time. ODE (2) describes changes in the population of the alga-host *Chlorella variabilis* over time. ODE (3) refers to the changes in the population of the virus

PBCV-I over time. ODEs (4) and (5) represent the total population and the fertile population, respectively, of the rotifer *Brachionus calyciflorus* (individuals per chemostat; see Fussmann 2000). Model parameters which are defined in Table 1 are coming from the studies of Fussmann and co-authors (Fussmann 2000), Suzuki and co-authors (Suzuki & Yoshida 2012). The values of virus adsorption rate and virus burst size have been adapted to represent our experimental data. The symbol "*" in the ODE's refers to component wise multiplication.

Matrix A describes the modified gene-for-gene interaction between the algae and viruses, assuming five types of host and four types of virus.

$$A = \begin{pmatrix} 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

The alga-host evolves by point mutations with a mutation rate of, ε, represented by the matrix, M_c, below.

$$M_C = \begin{pmatrix} 1-\varepsilon & \varepsilon/2 & 0 & 0 & 0 \\ \varepsilon & 1-\varepsilon & \varepsilon/2 & 0 & 0 \\ 0 & \varepsilon/2 & 1-\varepsilon & \varepsilon/2 & 0 \\ 0 & 0 & \varepsilon/2 & 1-\varepsilon & \varepsilon \\ 0 & 0 & 0 & \varepsilon/2 & 1-\varepsilon \end{pmatrix}$$

The virus evolves by point mutations with a mutation rate, ε, represented by the matrix, $M_{p,}$ below.

$$M_p = \begin{pmatrix} 1-\varepsilon & \varepsilon/2 & 0 & 0 \\ \varepsilon & 1-\varepsilon & \varepsilon/2 & 0 \\ 0 & \varepsilon/2 & 1-\varepsilon & \varepsilon \\ 0 & 0 & \varepsilon/2 & 1-\varepsilon \end{pmatrix}$$

In all networks, dispersal is bidirectional and has an average degree of connectivity of four. The different dispersal network matrix structures are designated by the matrices, *dmat,* in the differential equations. Figure 2 displays the graphics for each dispersal network structure and the corresponding dispersal matrix. Presence or absence of dispersal between the patches in each network is indicated by a 1 or a 0, respectively. We replaced the 1 in each simulation with the dispersal rates investigated-i.e., 0, 0.0005, 0.001, 0.01 and 0.1.

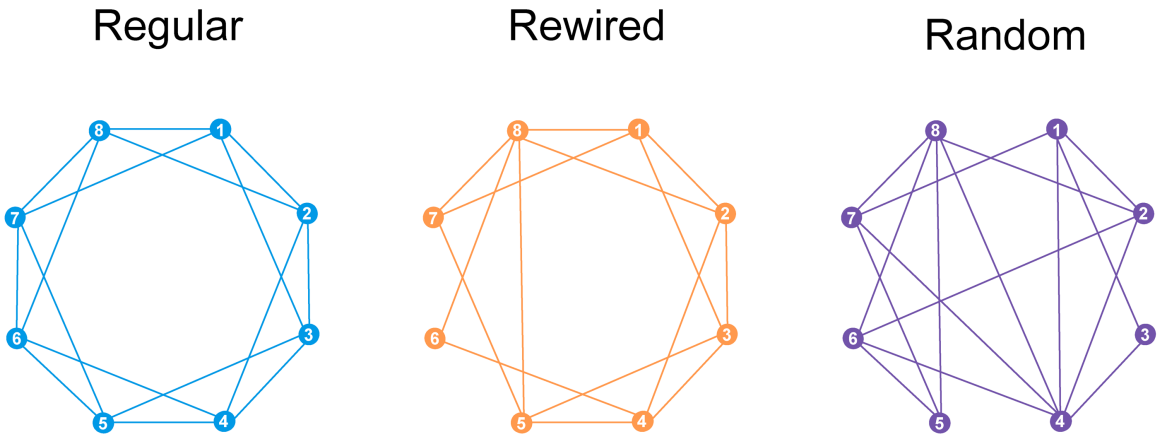
To measure the length of the transient dynamics of all three species in each network and each simulation, we first calculated the transient dynamics of the species in each of the patches using the R-package “changepoint” and applying the function “cpt.meanvar” (Killick & Eckley 2014). This function calculates the shift from transient to asymptotic dynamics by investigating the difference in the mean and variance of the population dynamics over time. After that, we estimated the transient duration for each network in each simulation as the time took to at least six of the eight patches to reach a state of asymptotic behaviour. Later, we report the mean and standard deviation of the network transient dynamics from 100 simulations.

We used the R-package “vegan” (Oksanen *et al.* 2007) and the function Shannon-index to calculate the alga and viral biodiversity in each simulation and for each time point in the time-frame 200-500. Shannon-index calculates biodiversity based on differences in the abundances of the different alga types and viral types per time point. After that, we calculate the mean biodiversity and standard deviation for the 100 simulations.

To calculate the average time necessary for the evolution of the general resistant alga host, we calculated the frequency of all five algal types per time point

and defined the evolution of the general resistant host as occurring at time points at which it comprises 10% of the algal population.

In our differential equations, we considered species extinction when they reached population densities below 10^{-10}. For this, we programmed our differential equations solver to convert every value below to 10^{-10} to 0.



patch:	1	2	3	4	5	6	7	8
1	0	1	1	0	0	0	1	1
2	1	0	1	1	0	0	0	1
3	1	1	0	1	1	0	0	0
4	0	1	1	0	1	1	0	0
5	0	0	1	1	0	1	1	0
6	0	0	0	1	1	0	1	1
7	1	0	0	0	1	1	0	1
8	1	1	0	0	0	1	1	0

1	2	3	4	5	6	7	8
0	1	1	0	0	0	1	1
1	0	1	1	0	0	0	1
1	1	0	1	0	1	0	0
0	1	1	0	1	1	0	0
0	0	0	1	0	1	1	1
0	0	1	1	1	0	0	1
1	0	0	0	1	0	0	1
1	1	0	0	1	1	1	0

1	2	3	4	5	6	7	8
0	1	0	0	0	0	1	0
1	0	0	1	0	1	0	1
0	0	0	1	0	0	1	1
1	1	1	0	0	1	1	1
0	0	0	0	0	1	1	1
0	1	0	1	1	0	0	1
0	0	1	1	1	0	0	1
0	1	1	1	1	1	1	0

Figure 2: Dispersal network structure for eight-patch networks (dmat-parameter). In all networks dispersal is bidirectional and the average degree of connectivity is four. In the regular network, each patch is connected to its four nearest neighbours. In the rewired network we have randomly rewired the connection of two patches and in the random network all patches are randomly connected to other patches. The table below the graphics indicates the dmat matrix that was used in each network dispersal structure. The label 1 indicates dispersal between the patches while 0 indicates no dispersal. Every time we wanted to test the effect of different dispersal rates we were substituting the label 1 with one of the dispersal rates “0, 0.0005, 0.001, 0.01, 0.1”

Table 2: Parameter values of the model.

Parameter	Biological Meaning	Value
D	Chemostat volume dilution rate (per day)	0.69
Ni	Inflow resource concentration (μmole N/L)	80
V	Chemostat volume (L)	0.33
K_c	Minimum half-saturation constant for nutrient uptake by Chlorella (μmole N/L)	4.3
b_c	Maximum recruitment rate, Chlorella (sum of all five alga types)	3.3
x_c	Conversion efficiency by algae	0.05
ω_c	N content in 10^9 Chlorella cells (μ mole)	20
ε_c	Assimilation efficiency	1
C^*	Critical *Chlorella* Concentration ($*10^9$)	0.437
K_b	Half saturation constant for alga consumption by rotifer (10^9 *Chlorella* cells)	4.3
p	Minimum alga food value (sum of all five alga types)	0.9
λ	Rotifer senescence rate (per day)	0.055
x_b	Conversion efficiency by rotifers	5400
G	Rotifer maximum clearance rate (per day)	$3.3*10^{-4}$
m	Rotifer mortality (per day)	0.055
φ	Virus adsorption rate	$9*10^{-2}$
b	Virus burst size	50
θ	Point mutation rates	10^{-3}

3. Results

3.1 Species Coexistence in a Single Patch in the Presence and Absence of Eco-Evolutionary dynamics

The outcome of our mathematical model shows similar dynamics as the experimental data obtained by Frickel et al. (2016; 2017). To study the algae-virus eco-evolutionary dynamics we performed 100 simulations where we pseudorandomized the initial population sizes of the first alga type C_1 and the first viral type P_1 (Figure 3A). To study eco-evolutionary dynamics in the algae-virus-rotifers system, we performed 100 simulations where we pseudorandomized the initial population sizes of the first alga type C_1, the first viral type P_1 and the rotifers (Figure 3B).

In each run we simulated 1000 days. Initially, in the absence of algae-virus coevolution and thus eco-evolutionary dynamics, the rotifers became extinct (Figure 3B) since both rotifers and virus consume ancestral algae and have complete niche overlap and the consumption by both consumer leads to too low algal densities to maintain rotifers. After rotifer extinction, the algae and virus showed eco-evolutionary dynamics similar to those for the alga-virus system (Figure 3A). We observe similar population dynamics and patterns of algal-virus coevolution. However, the presence of rotifers prolonged the average duration of the transient dynamics in the three species food web compared to the two species food web (Figure 4; t-test: t=15.296, $p < 2.2 \times 10^{-16}$). Similarly to the experimental results, the presence of rotifers delayed the average time for the evolution of the general resistant host C_5, in the three species food web compared to the two species food web (Figure 5; t-test comparing the day of simulation when C_5 reached 10%: t-test: t=11.495, $p < 2.2 \times 10^{-16}$). Also, the three species could coexist

only after the evolution of the general resistant host in the system which took place around day 61 (Figure 5 & Figure 3B). As a result of the coexistence of the three species, alga intraspecific diversity was significantly decreased compared to the alga-virus food web (Figure 6; t-test: $t=14.915$, $p<2.2 \times 10^{-16}$).

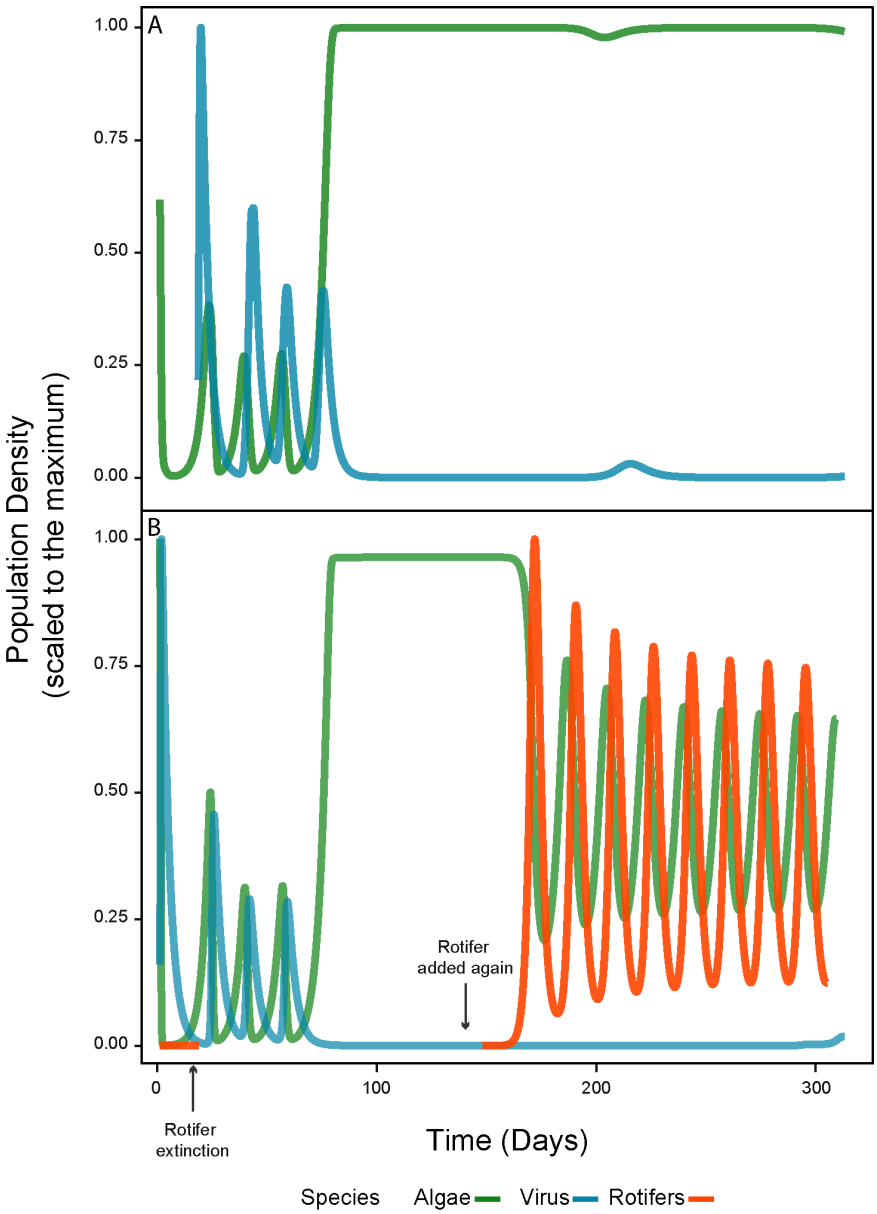


Figure 3: Population dynamics of algae and virus populations (A) and algae, virus and rotifer populations (B). A. Population dynamics of the algae (green) and virus (blue). Algae and virus densities oscillate, and after the evolution of the general resistant host at time point ~58, they stabilize. **B.** Population dynamics of algae (green), virus (blue) and rotifers (red). When we start our system with the ancestral types of alga and virus and the rotifers, the rotifers become extinct. If we add rotifers after the evolution of the general resistant host in the algae (day 61), then all three species can coexist. All population densities are scaled to their maximum. The lines represent the mean of the 100 simulations. The first arrow indicates the rotifer extinction while the second one indicate the second artificial addition of the rotifers.

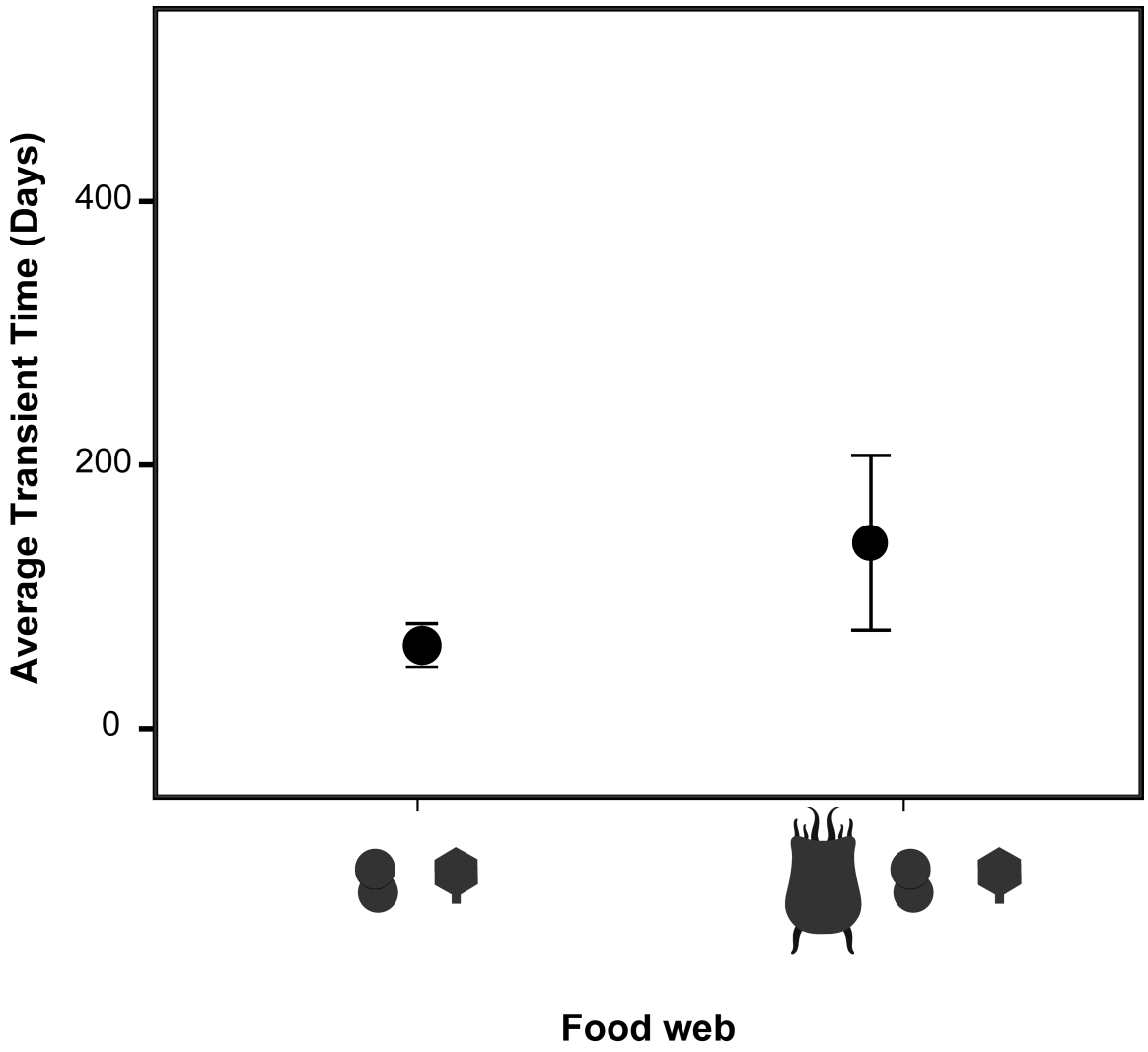


Figure 4: Average length of the transient time after 100 simulations for the three species in a single patch. The presence of rotifers increases significantly the length of the transient dynamics in the three species food web compared to the two species food web. The dots represent the average length of transient dynamics (days) after 100 simulations and the error bars the standard deviation from the mean.

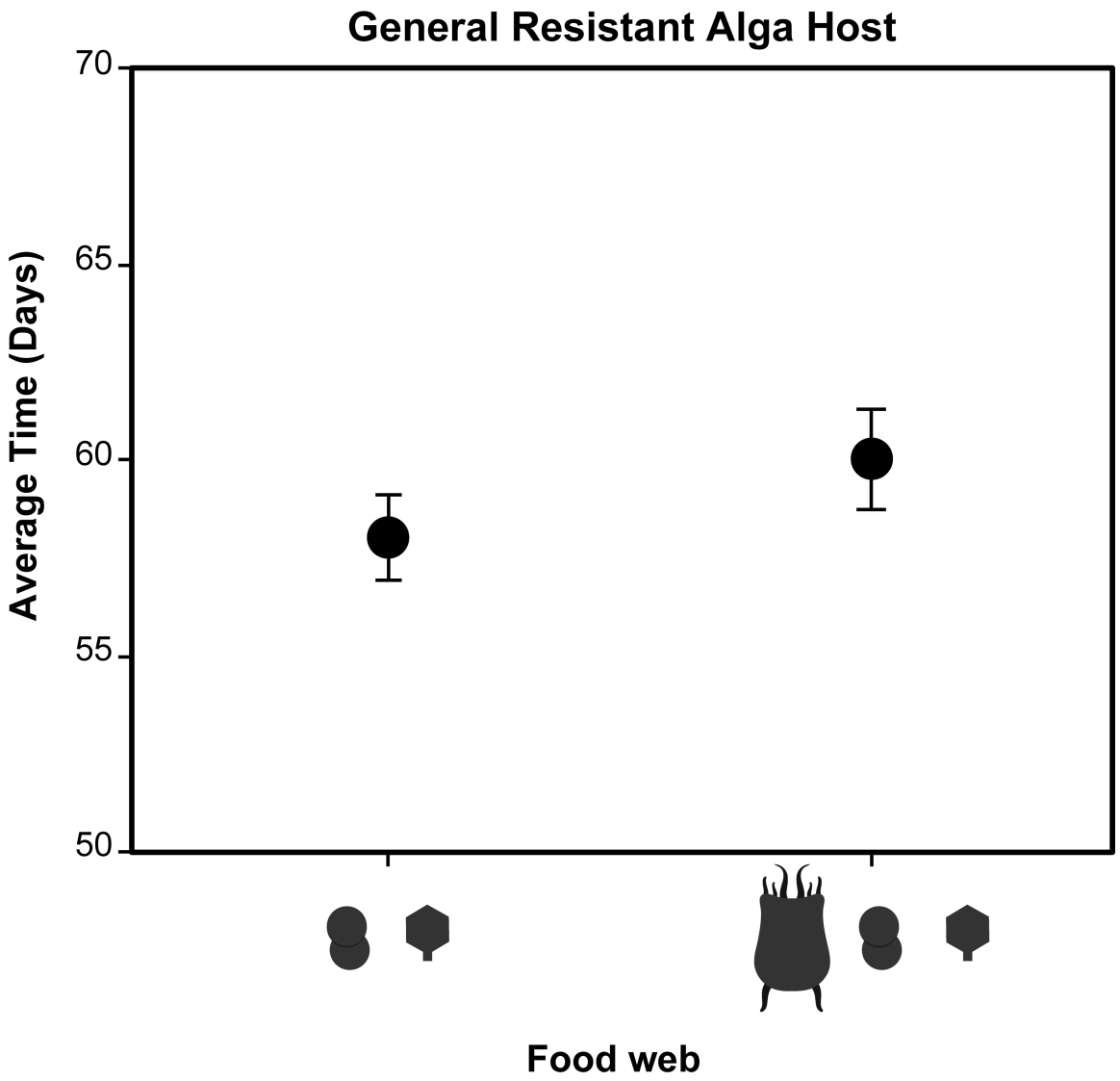


Figure 5: Average time for the evolution of the general resistant host alga. The presence of rotifers increases the average time for the evolution of the general resistant host significantly. The dots represent the average time (days) after 100 simulations for the evolution of a general resistant host and the error bars the standard deviation from the mean.

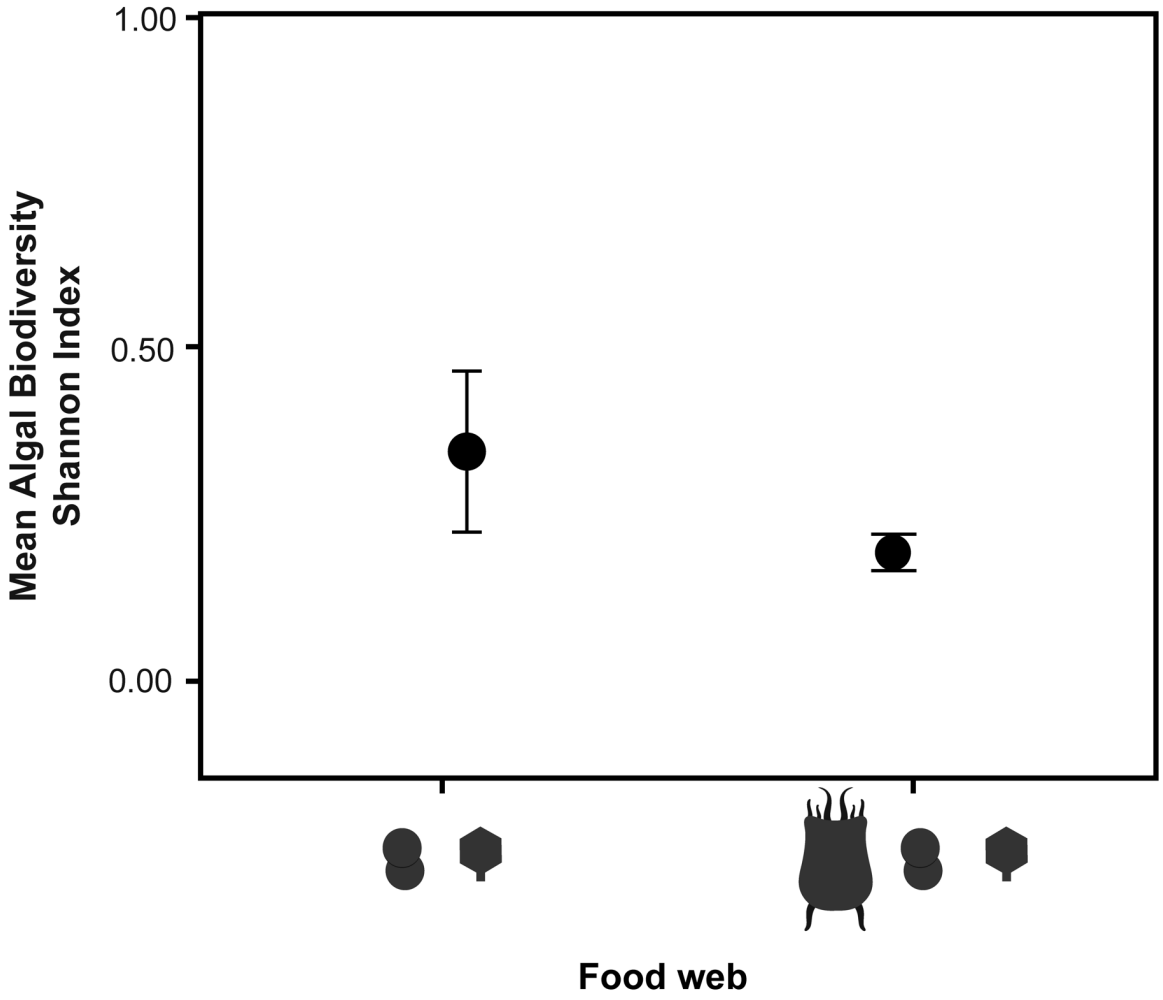


Figure 6: Comparison of the mean alga biodiversity measured as Shannon index in the two food webs (algae-virus and algae-virus-rotifers). The presence of rotifers decreases the mean algal biodiversity significantly. The dots represent the mean alga biodiversity (days) after 100 simulation and the error bars the standard deviation from the mean.

3.2 Dispersal Network Structure and Species Coexistence in in the Presence of Eco-Evolutionary dynamics

We found that in the presence of alga-virus eco-evolutionary dynamics none of the networks allows coexistence of all three species. We initialized all patches with pseudorandom values for the alga C_1, virus P_1 and rotifers, and algae and the virus could evolve over time. We found that algae and virus could coexist in all dispersal networks structures while the rotifers became extinct (Figure 7). In the presence of algal evolution and thus eco-evolutionary dynamics, we found that the network structure does not affect the average duration of the transient time in any of the three species (two-way ANOVA: F-value=1.108, p=0.330). As expected, the duration of the transient dynamics is longer when there is no dispersal among the patches, but the difference is not significant (Figure 8; ANOVA: F-value=0.428, p=0.930).

Finally, we observe that the network structure does not affect the evolution of the general resistant alga host C_5, (Figure 10; two-way ANOVA: F=0.155, p=0.856), even though the evolution of the general resistant host seems to occur earlier in all networks for high dispersal rates (Figure 9).

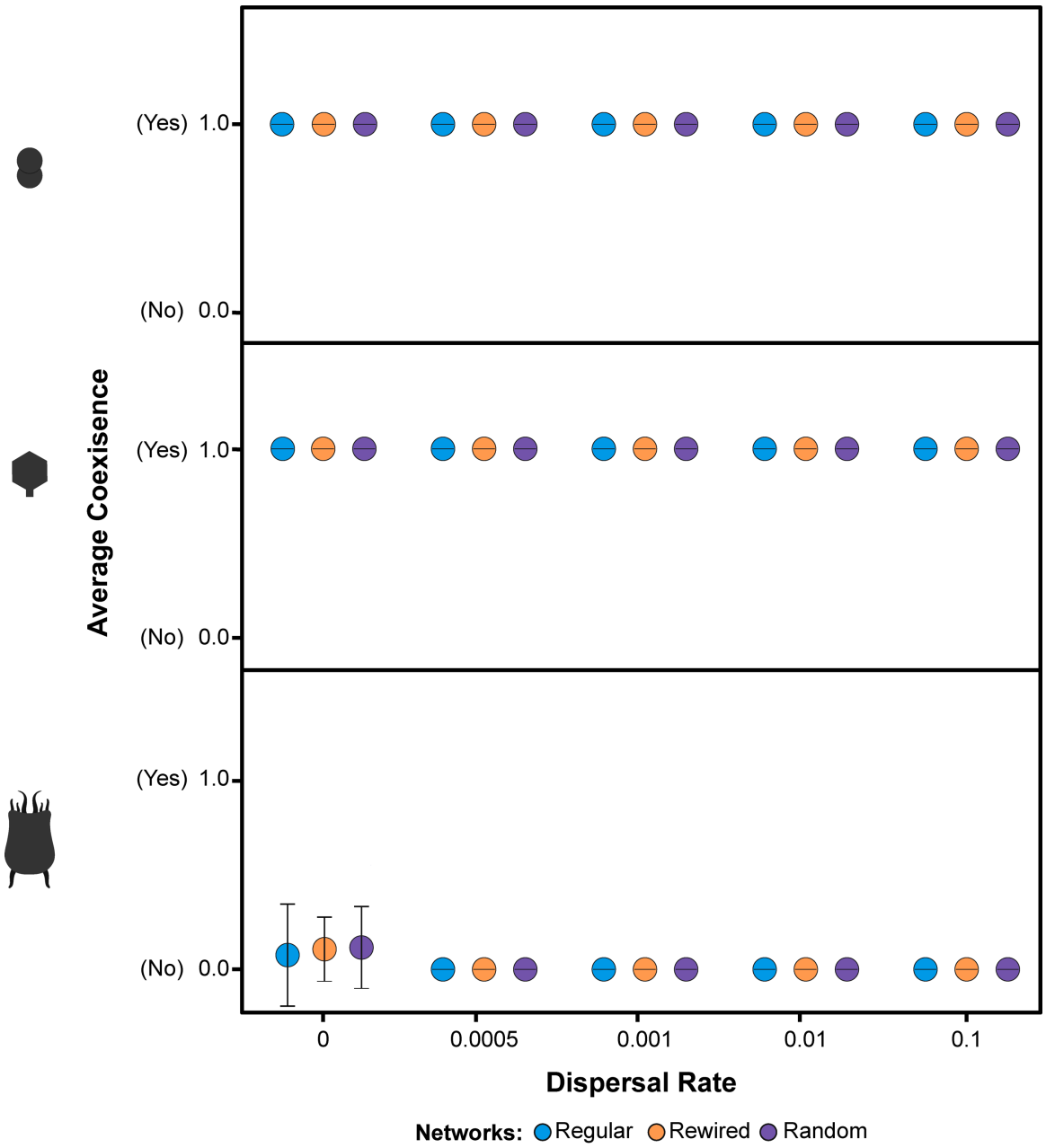


Figure 7: Average coexistence after 100 simulations for the three species model in the presence of eco-evolutionary dynamics. In the presence of eco-evolutionary dynamics, the dispersal network structure does not allow the coexistence of all three species. In all dispersal networks the algae and virus coexist while rotifers become extinct. The dots represent the average coexistence after 100 simulations and the errors bars represent the standard deviation from the mean. The blue coloured dots represent the regular network, the orange dots represent the rewired network and the purple the random network.

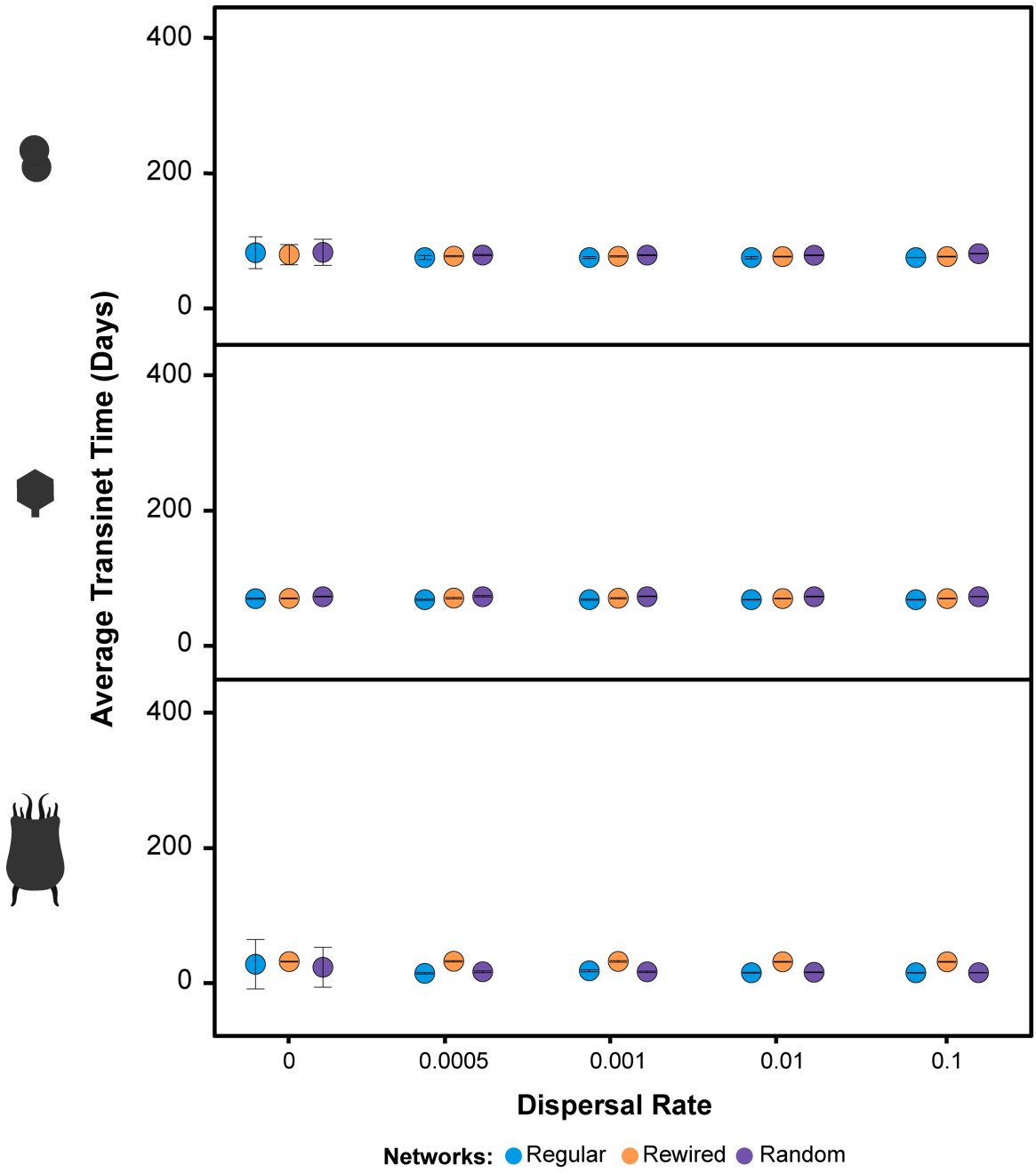


Figure 8: Average length of the transient time after 100 simulations for the three species model in the presence of eco-evolutionary dynamics. In the presence of eco-evolutionary dynamics and spatial homogeneity, the dispersal network structure has no effect on the transient duration of the species. The dots represent the average coexistence after 100 simulations and the errors bars represent the standard deviation from the mean. The blue coloured dots represent the regular network, the orange dots represent the rewired network and the purple the random network.

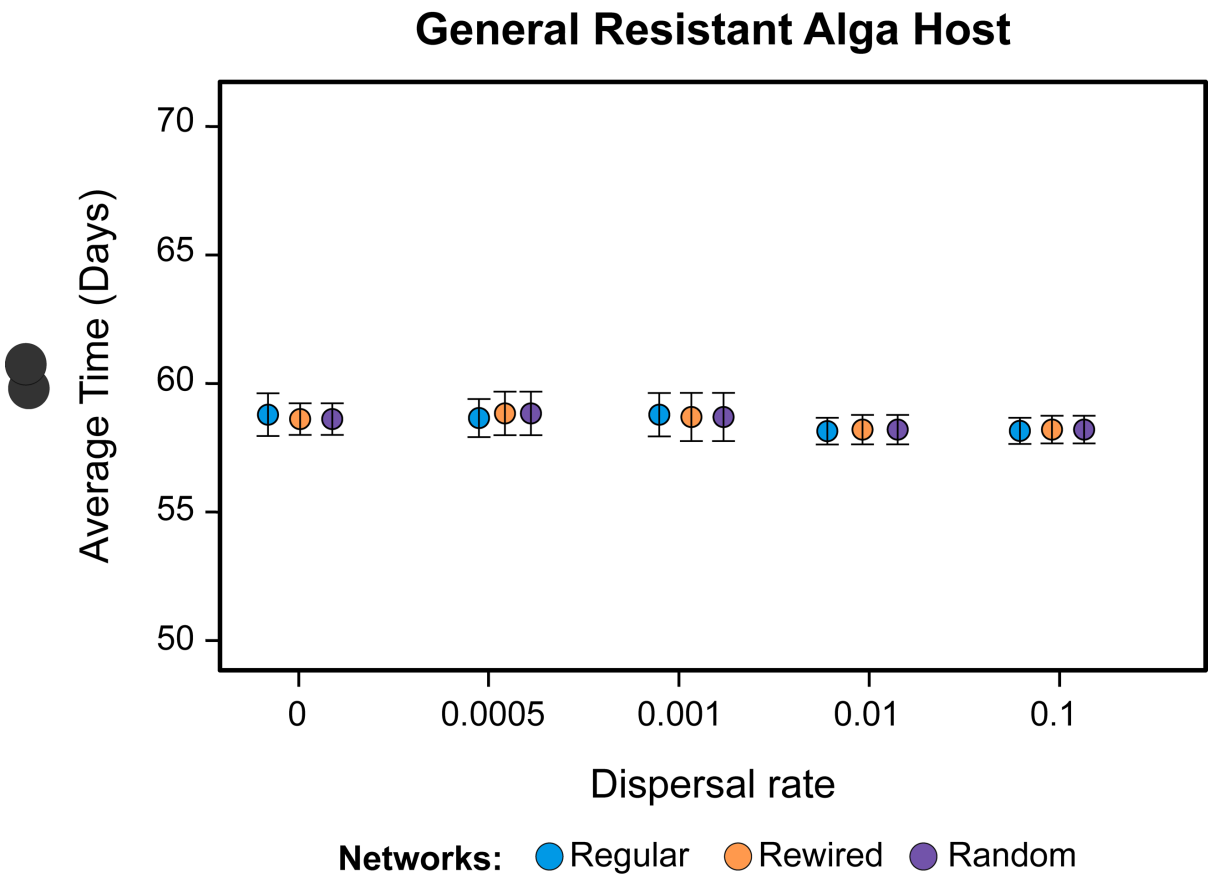


Figure 9: Average time for the evolution of the general resistant alga host in the three different dispersal network structures under different dispersal rates. The network structure does not significantly affect the evolution of the general resistant host. The dots represent the average time for the evolution of the general resistant host after 100 simulations and the errors bars represent the standard deviation from the mean. The blue coloured dots represent the regular network, the orange dots represent the rewired network and the purple the random network.

3.3 Dispersal Network Structure and Species Coexistence in in the Absence of Eco-Evolutionary dynamics

To look at the scenario without evolution and thus without eco-evolutionary dynamics, we initialized all patches in the different networks with only one of the five alga types C_1, C_2, C_3, C_4 or C_5 and we did not allow them to evolve, but we allowed the virus to evolve. Each one of the alga types is infected differently by the ancestral virus P_1, as indicated in Figure 2. We found that, **the infection pattern of each algal host type plays an important role in the coexistence of all three species**. In the presence of C_1, all three species go extinct. In the presence of C_2, C_3, C_4 and C_5 the virus becomes extinct and only the algae and rotifers coexist (Figure 10).

In addition we found that in the absence of eco-evolutionary dynamics, the dispersal network structure has no significant effect on the transient dynamics in any of the three species (Figure 11; two-way ANOVA: F-value = 16.72, p = 0.663). There are differences in the average duration of the algae and virus transient dynamics when the simulations are initiated with alga type C_1 compared to the dynamics for the other alga types. In the presence of C_1, algae and virus densities fluctuate till they become extinct, while in the presence of the other types algae and rotifers coexist and the system reaches an equilibrium after ~20 days (Figure 11).

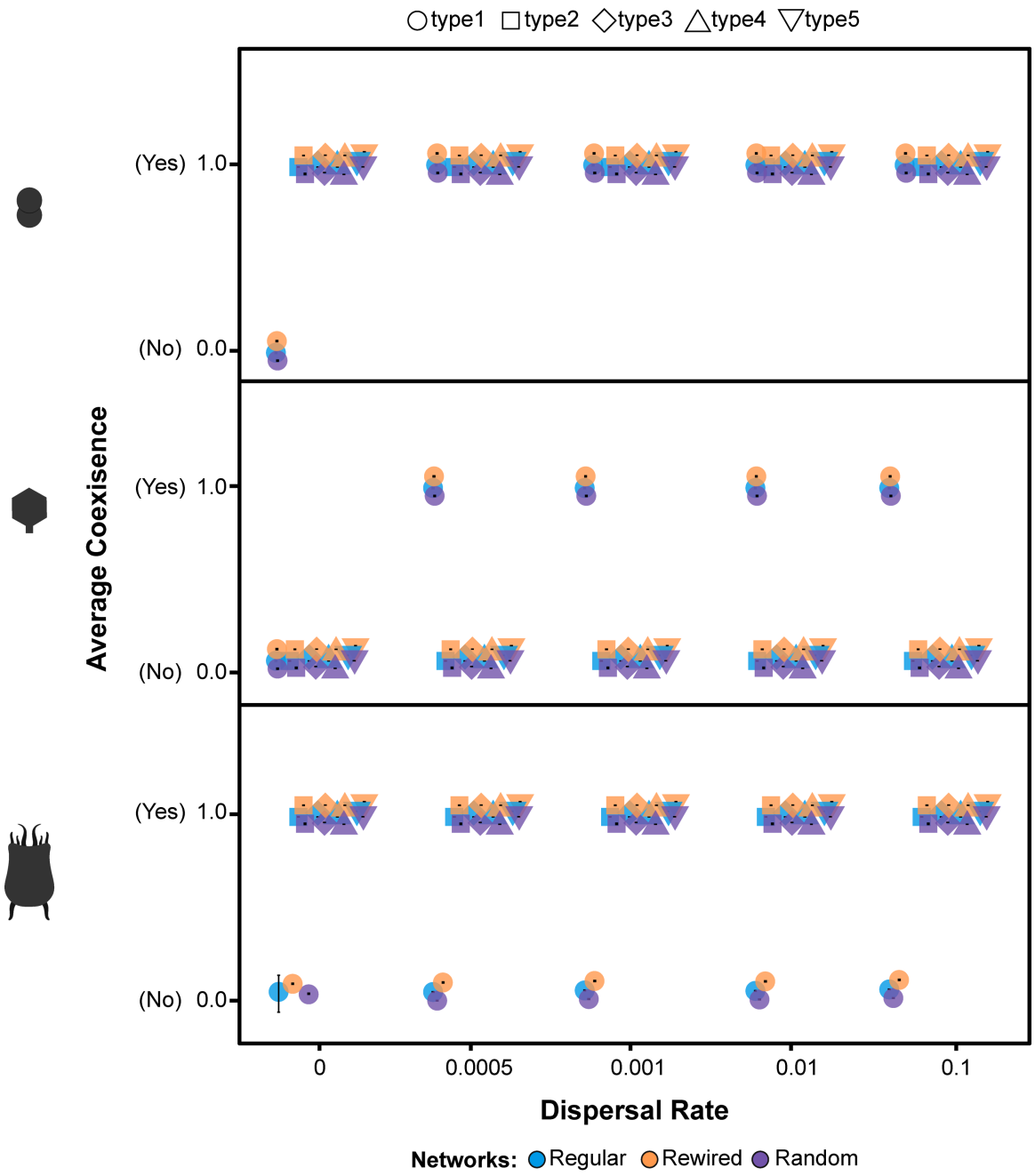


Figure 10: Average coexistence after 100 simulations for the three species in the absence of eco-evolutionary dynamics. In the absence of eco-evolutionary dynamics and spatial homogeneity, the dispersal network structure has no effect on the coexistence between species. The specific interactions of the different alga types with the virus determine if the virus or the rotifers will coexist with the algae. In the presence of alga type 1, algae and rotifers coexist. The blue colour represents the regular network, the orange represents the rewired network and the purple the random network. The circle indicates that all patches were initialized with the first alga type, C_1, which was not allowed to evolve, the square indicates the same conditions for the C_2, the rhombus for the C_3, the triangle for the C_4, the reverse the general resistant alga host C_5. The line represents the standard deviation from the mean.

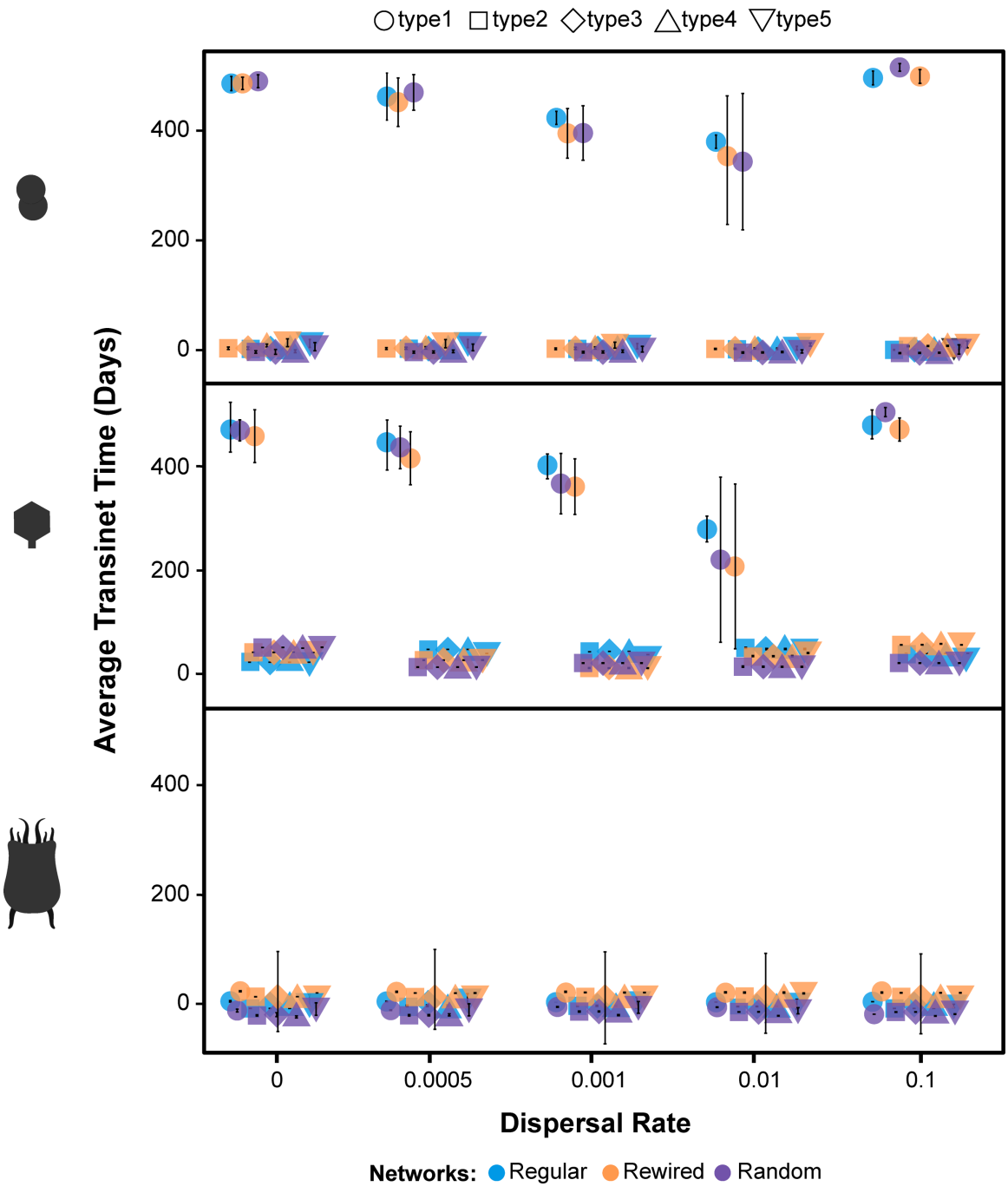


Figure 11: Average length of the transient time after 100 simulations for the three species in the absence of eco-evolutionary dynamics. In the absence of eco-evolutionary dynamics and spatial homogeneity, the dispersal network structure has no effect on the average duration of transient dynamics of the species. The presence of C_1 leads to significantly longer transient dynamics compared to other types. The blue colour represents the regular network, the orange represents the rewired network and the purple the random network. The circle indicates that all patches were initialized with the first alga type, *C_1,* which was not allowed to evolve, the square indicates the same conditions for the *C_2,* the rhombus for the *C_3,* the triangle for the *C_4,* the reverse the general resistant alga host C_5. The line represents the standard deviation from the mean.

4. Discussion

Our mathematical model describes the experimental data obtained by Frickel et al. (2017) as well as allows us to test for the following: whether any dispersal network structure allows for the coexistence of all three species, when the rotifers and viruses have complete niche overlap and if either ecological or eco-evolutionary processes play a role in species coexistence by reducing niche overlap. Our results show that in the presence or absence of eco-evolutionary dynamics none of the dispersal network structure can allow the coexistence of all three species.

The initial presence of rotifers in the system significantly increased the length of the transient dynamics between the alga and the virus. In addition, it delayed the evolution of the general resistant host compared to the food web, which consisted of only of algae and the virus. Therefore, we suggest that rotifers lead to these changes by reducing the mutation supply in both the alga and virus populations via consuming and thus reducing the alga population size. Rotifers can coexist with the algae and the virus after the evolution of the general resistant algal host. The presence of algal biodiversity for the maintenance of all three species is required because it reduces the niche overlap between the algae and the virus.

When we extended our model from a single patch to the regular, rewired and random networks of eight homogenous patches, we found that, in the presence and absence of eco-evolutionary dynamics, the dispersal network structure did not affect the coexistence of the species. Overall, the dispersal network structure did not change the eco-evolutionary dynamics of the system (i.e. the transient dynamics and the evolution of the general resistant host) in contrast

to our hypothesis that random networks will favour asynchrony in the population dynamics and the maintenance of rotifers.

When eco-evolutionary dynamics are not present, as suggested by our results, none of the alga types alone can sustain the coexistence of all three species, which highlights the importance of algal biodiversity for the coexistence of species. Alga biodiversity is essential for the coexistence of the species because it reduces the niche overlap between the rotifers and the virus.

Overall, this study is a first step towards answering new and unexplored questions about the role of the dispersal network structure for the eco-evolutionary dynamics and species coexistence. The mathematical model that we developed will be an important tool for future research in the study of eco-evolutionary dynamics of the multi-species system as it gives us the opportunity to investigate ecological and evolutionary processes for long time and in larger networks scales, which is extremely laborious to perform experimentally.

In this study, the assumption of homogeneity among the patches limited our understanding of the dispersal network structure's role in the coexistence and eco-evolutionary dynamics of the species. Ecological systems are heterogeneous in many aspects, such as in the environmental conditions, the carrying capacity of the patches and dispersal flow (Hesse *et al.* 2015; Toju *et al.* 2017). Potentially, the high mutation rate for the alga as well as the spatial homogeneity among the patches may cover the effect of the dispersal network structure in the evolution of the general resistant host. We could test for example the effect of the dispersal network structure regarding the coexistence of the species when the dispersal is asymmetric among the patches. Previous studies on a two-patch system have shown that asymmetric dispersal between species has significant consequences

for the maintenance of biodiversity in spatially structured populations, and it can lead to inferior competitor dominance in a heterogeneous environment (Salomon *et al.* 2010). Additionally, we could investigate how spatial heterogeneity can affect the coexistence of species with vacant patches as well as patches that maintain only alga and rotifer populations. We expect groups of spatially separated populations to interact with each other and affect algae-virus-rotifer interactions, which in turn affect the network's transient time and the evolution of the general resistant host.

Finally, we could also introduce stochasticity into our model because metapopulation processes, connectivity among patches and viability among patches can be entirely stochastic in natural populations (i.e. regarding how extinction occurs).

REFERENCES

Aarssen, L. W. (1989). Competitive ability and species coexistence: A 'Plant's-Eye' View. *Oikos*, 56, 386-401.

Chesson, P. (2000). Mechanisms of Maintenance of Species Diversity. *Annual Reviews of Ecological Systems*, 31, 343-366.

Cortez, M. H. (2016). How the Magnitude of Prey Genetic Variation Alters Predator-Prey Eco-Evolutionary Dynamics. *American Naturalist*, 188, 329-341.

Ehlers, B. K., Damgaard, C. F. & Laroche, F. (2016). Intraspecific genetic variation and species coexistence in plant communities. *Biology Letters*, 12, 462-482

Frickel, J., Sieber, M. & Becks, L. (2016). Eco-evolutionary dynamics in a coevolving host-virus system. *Ecology Letters*, 19, 450-459.

Frickel, J., Theodosiou, L. & Becks, L. (2017). Rapid evolution of hosts begets species diversity at the cost of intraspecific diversity. *Proceedings of the National Academy of Sciences*, 114, 11193-11198.

Fussmann, G. F. (2000). Crossing the Hopf Bifurcation in a Live Predator-Prey System. *Science*, 290, 1358-1360.

Hairston, N. G., Ellner, S. P., Geber, M. A., Yoshida, T. & Fox, J. A. (2005). Rapid evolution and the convergence of ecological and evolutionary time. *Ecology Letters*, 8, 1114-1127.

Hanski, I. (1994). A practical model of metapopulation dynamics. *Journal of Animal Ecology*, 87, 151–162.

Hanski, I. (1998). Metapopulation dynamics. *Nature*, 396, 41–49.

Hanski, I. (1999). Habitat connectivity, habitat continuity, and metapopulations in dynamic landscapes. *Oikos*, 87, 209-219.

Hesse, E., Best, A., Boots, M., Hall, A. R. & Buckling, A. (2015). Spatial heterogeneity lowers rather than increases host-parasite specialization. *Journal of Evolutionary Biology*, 28, 1682-1690.

Hiltunen, T., Kaitala, V., Laakso, J. & Becks, L. (2017). Evolutionary contribution to coexistence of competitors in microbial food webs. *Proceedings of the Royal Society B: Biological Sciences,* 284, 1673-1684.

Holt, R. D. (1984). Spatial heterogeneity, indirect interactions, and the coexistence of prey species. *American Naturalist*, 124, 377-406.

Holt, R. D. & Pickering, J. (1985). Infectious disease and species coexistence: a model of Lotka-Volterra form. *American Naturalist*, 126, 196–211.

Hughes, A. R., Inouye, B. D., Johnson, M. T., Underwood, N., Vellend, M. (2008). Ecological consequences of genetic diversity. *Ecology Letters*, 11, 609-623.

Huston, M.A. & Huston, M.A. (1994). Biological diversity: the coexistence of species. *Cambridge University Press.*

Hutchinson, G. E. (1961). The Paradox of the Plankton. *American Naturalist*, 95, 137-145.

Jousimo, J., Tack, A. J. M., Ovaskainen, O., Mononen, T., Susi, H., Tollenaere, C. (2014). Ecological and evolutionary effects of fragmentation on infectious disease dynamics. *Science*, 344, 1289-1293.

Kasada, M., Yamamichi, M. & Yoshida, T. (2014). Form of an evolutionary tradeoff affects eco-evolutionary dynamics in a predator–prey system. *Proceeding of the National Academy of Sciences,* 111, 16035-16040.

Killick, R. & Eckley, I. (2014). changepoint: An R package for changepoint analysis. *Journal of Statistical Software*, 58, 1-19.

Levin, S. A. (1974). Dispersion and Population Interactions. *American Naturalist*, 108, 207-228.

Oksanen, J., Kindt, R., Legendre, P., O'Hara, B., (2007). The vegan package. *Community Ecology Package*, 10, 631-637.

Salomon, Y., Connolly, S. R. & Bode, L. (2010). Effects of asymmetric dispersal on the coexistence of competing species. *Ecology Letters*, 13, 432–441.

Seehausen, O. (2015). Process and pattern in cichlid radiations–inferences for understanding unusually high rates of evolutionary diversification. *New Phytologist*, 207, 304-312.

Suzuki, K. & Yoshida, T. (2012). Non-random spatial coupling induces desynchronization, chaos and multistability in a predator-prey-resource system. *Journal of Theoretical Biology*, 300, 81-90.

Toju, H., Yamamichi, M., Guimarães, P.R., Olesen, J.M., Mougi, A., Yoshida, T., Thompson, J. N. (2017). Species-rich networks and eco-evolutionary synthesis at the metacommunity level. *Nature Ecology Evolution*, 1, 1-11.

Wilson, J. B. (1990). Mechanisms of species coexistence: twelve explanations for Hutchinson's "paradox of the plankton": evidence from New Zealand plant communities. *New Zealand Journal of Ecology*, 13, 17-42.

Yoshida, T., Jones, L.E., Ellner, S.P., Fussmann, G.F. & Hairston, N.G. (2003). Rapid evolution drives ecological dynamics in a predator-prey system. *Nature*, 424, 303-306.

Contributions to the thesis

Chapter One

This chapter was submitted as an invited contribution to a special issue in Functional Ecology (May 2018).

Loukas Theodosiou (LT), Teppo Hiltunen (TH), Lutz Becks (LB) conceived the ideas, LT and LB led the writing of the manuscript,

Chapter Two

LT and LB conceived and designed the study, LT performed the experiments and analysed the results, LT wrote the chapter.

Chapter Three

LT, LB Michael Sieber and Laura Hindersin conceived the designed the study, LT performed the simulations and analysed the results, LT wrote the chapter.

General Conclusion

The primary goal of my thesis was to investigate the mechanisms through which common environmental changes such as the introduction of an abiotic stressor and dispersal network structure can either break or enhance the link between evolution and ecology and thus affect the outcome of eco-evolutionary feedback dynamics. Overall, the results of my thesis suggest that the heritable phenotypic traits driving eco-evolutionary dynamics can be expected to be highly dependent on the environment. My thesis strongly suggests that we should not always expect an important role of the interplay between ecology and evolution. This is in particular important when we aim to understand the mechanisms that regulate the fate of natural populations.

But can we predict when and how often the interplay between evolution and ecology happens? The empirical and theoretical results from my thesis contribute to this yet unanswered question, but further empirical and theoretical research is needed to generalise and extend the research findings. To have a more profound image on how frequently ecology and evolution interplay, we need more long-term and detailed studies on the ecological dynamics (e.g., population dynamics, transient dynamics, amplitude dynamics of species abundances) and the evolutionary dynamics of species interactions in the laboratory, in mesocosms and in natural populations.

Although it is challenging at present, we need to conduct empirical and theoretical studies with multiple species in metacommunities. One of the biggest challenges is to evaluate the strength of natural selection imposed by species interactions and their evolutionary responses. Another challenge is to address the possibly prominent role of the indirect effect among species in natural selections.

One way to address these challenges is to study first the interactions between pairs of species and then move stepwise to more complex communities. In all steps it is helpful to define the type and strength of natural selection (e.g., directional, balancing selection) as well as the traits under selection, that are imposed by species interactions and their effect onto ecological dynamics. For this we need a detailed report of the population dynamics (or other ecological change) and evolutionary dynamics. To acquire a better mechanistic understanding of the effect of population dynamics on trait evolution it would be useful to manipulate the strength of species interaction by altering the abundances of the different species. Good examples that follow these patterns are the studies by Gomez *et al.* (2016), Frickel *et al.* (2017), and Cara *et al.* (2017). An alternative approach to investigate multispecies interactions could be the one suggested by Toju *et al.* (2017). Here the authors suggest the incorporation of network theory to understand the ways that species interact and organize the structure of the metacommunity; however, they don't tell us how to identify traits under selection.

Increasing the number of interacting species in a community requires a massive laboratory effort. For this effort, new mechanical engineering techniques need to be developed that allow counting, preserving and testing fitness assays of the different populations of species in a fast, accurate and high-throughput manner. Previous studies, show that the use of mathematical modelling has great potential to help us acquire a considerably deeper understanding of the $eco-evo$lutionary dynamics in multispecies metacommunities. In a study on the guppy fish, *Poecilia reticulata*, which have evolved under environments with different predation pressure, mathematical models were used to assess the sensitivity of the ecological and evolutionary dynamics of the guppies to variations in specific

parameters such as the food availability and have assisted what should be measured in the experimental work (Bassar *et al.* 2012). Also, models can be useful to illustrate assumptions about how an experiment might unfold and even make predictions, as I did in chapter II and chapter III of my thesis. Last but not least, mathematical models can be used to estimate the parameters that are not always possible to measure, such as the indirect effect among species. In a predator-prey system, the presence of the predator has a direct effect on the population of the prey. However, avoidance behaviour from the prey to the predator can have an indirect effect on the demographics, but it is challenging to be quantified.

Integrating genomics into eco-evolutionary dynamics

To acquire a better understanding of the eco-evolutionary feedback dynamics, it is essential to integrate the fields of genetics and genomics with experimental studies. Eco-evolutionary feedback dynamics are the result of rapid genetic changes underlying phenotypic changes that are driven by ecological forces and these genetic changes ultimately shape ecological dynamics. Genomics and genetics can be useful to reveal the genetic make-up of ecological important traits that are under selection, identify their genetic architecture and discover how repeatable the evolutionary change is. All these tools have, however, rarely been placed into an eco-evolutionary context. For this we require more long-term empirical data of eco-evolutionary dynamics where detailed ecological and evolutionary dynamics are combined and correlated with changes on the genomics level. The use of genomics could potentially reveal the genetic architecture that is required for rapid evolution to take place and contribute to the riddle when and how

often eco-evolutionary dynamics interplay in natural settings. For example it would be good to know whether single gene mutations, mutations of large effect, or certain genes and metabolic pathways are involved in rapid evolution with strong effects on ecological changes.

However, it is important to bear in mind that genomics have limitations. Often it is not enough to simply correlate genotypes with phenotypes since changes in the phenotypes can be caused by differences in gene expressions in response to the environment. In these cases, genomic studies need to be combined with gene expression studies or proteomics. Another limitation of genomics is that, although we have the opportunity to acquire much genomic data from many different taxa, it is sometimes difficult to interpret the huge abundance of this data since the annotation of the genes of non-model organisms is often incompatible with that of traditional model organisms.

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REFERENCES

Bassar, R.D., Ferriere, R., López-Sepulcre, A., Marshall, M.C., Travis, J., Pringle, C.M., *et al.* (2012). Direct and Indirect Ecosystem Effects of Evolutionary Adaptation in the Trinidadian Guppy (*Poecilia reticulata*). *Am. Nat.*, 180, 167-185.

Bassar, R.D., Marshall, M.C., Lopez-Sepulcre, A., Zandona, E., Auer, S.K., Travis, J., *et al.* (2010). Local adaptation in Trinidadian guppies alters ecosystem processes. *Proc. Natl. Acad. Sci.*, 107, 3616-3621.

Becks, L., Ellner, S.P., Jones, L.E. & Hairston Nelson G., J.G. (2010). Reduction of adaptive genetic diversity radically alters eco-evolutionary community dynamics. *Ecol. Lett.*, 13, 989-997.

Brunner, F.S., Anaya-Rojas, J.M., Matthews, B. & Eizaguirre, C. (2017). Experimental evidence that parasites drive eco-evolutionary feedbacks. *Proc. Natl. Acad. Sci.*, 114, 3678-3683.

Cortez, M.H. (2016). How the Magnitude of Prey Genetic Variation Alters Predator-Prey Eco-Evolutionary Dynamics. *Am. Nat.*, 188, 329-341.

Fussmann, G.F., Loreau, M. & Abrams, P.A. (2007). Eco-evolutionary dynamics of communities and ecosystems. *Funct. Ecol.,* 21, 465-477.

Haafke, J., Abou Chakra, M. & Becks, L. (2016). Eco-evolutionary feedback promotes Red Queen dynamics and selects for sex in predator populations. *Evolution*, 70, 641-652.

Hairston, N.G., Ellner, S.P., Geber, M.A., Yoshida, T. & Fox, J.A. (2005). Rapid evolution and the convergence of ecological and evolutionary time. *Ecol. Lett.*, 8, 1114-1127.

Hendry, A. (2013). Eco-evolutionary dynamics: Community consequences of (Mal)adaptation. *Curr. Biol.,* 23, 869-871.

Matthews, B., Aebischer, T., Sullam, K.E., Lundsgaard-Hansen, B. & Seehausen, O. (2016). Experimental evidence of an eco-evolutionary feedback during adaptive Divergence. *Curr. Biol.*, 26, 483-489.

Post, D.M. & Palkovacs, E.P. (2009). Eco-evolutionary feedbacks in community and ecosystem ecology: interactions between the ecological theatre and the evolutionary play. *Philos. Trans. R. Soc. B Biol. Sci.*, 364, 1629-1640.

Quigley, B.J.Z., García López, D., Buckling, A., McKane, A.J. & Brown, S.P. (2012). The mode of host-parasite interaction shapes coevolutionary dynamics and the fate of host cooperation. *Proc. Biol. Sci.*, 279, 3742-3748.

Rudman, S.M., Barbour, M.A., Csilléry, K., Gienapp, P., Guillaume, F., Hairston Jr, N.G., *et al.* (2017). What genomic data can reveal about eco-evolutionary dynamics. *Nat. Ecol. Evol.*, 2, 9-15.

Toju, H., Yamamichi, M., Guimarães, P.R., Olesen, J.M., Mougi, A., Yoshida, T., *et al.* (2017). Species-rich networks and eco-evolutionary synthesis at the metacommunity level. *Nat. Ecol. Evol.*, 1, 0024.

Yoshida, T., Jones, L.E., Ellner, S.P., Fussmann, G.F. & Hairston, N.G. (2003). Rapid evolution drives ecological dynamics in a predator-prey system. *Nature*, 424, 303-306.

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3. **"Rapid evolution of hosts begets species diversity at the cost of intraspecific diversity"**
   PNAS | J. Frickel , L. Theodosiou, L. Becks

Affidavit

I hereby declare that this thesis work

- Concerning content and design are my own work under guidance of my supervisor. Contributions of other authors are listed in the “contribution to the thesis: section of the thesis;
- Has not been submitted elsewhere partially or wholly as a part of a doctoral degree and no other materials are published or submitted for publication than indicates in the thesis;
- The work and thesis has been performed and prepared following the Rules of Good Scientific Practice of the German Research Foundation.

Plön, 10.12.2018

Loukas Theodosiou