

Parallel Session

Evolutionary Dynamics II

EVOLUTIONARY BRANCHING VIA REPLICATOR-MUTATOR EQUATIONS

MARIO E. VERUETE

mario.veruete@umontpellier.fr

Institut Montpellierain Alexander Grothendieck, CNRS, Université de Montpellier

Keywords: Evolutionary genetics, Branching phenomena, Long time behaviour, Non-local partial differential equation.

We consider a class of non-local reaction-diffusion problems, referred to as *replicator-mutator* equations in evolutionary genetics. For a confining fitness function, we prove well-posedness and write the solution explicitly, via some underlying Schrödinger spectral elements (for which we provide new and non-standard estimates). As a consequence, the long time behaviour is determined by the principal eigenfunction or *ground state*. Based on this, we discuss (rigorously and via numerical explorations) the conditions on the fitness function and the mutation rate for *evolutionary branching* to occur.

Parallel Session

Evolutionary Dynamics II

**VARIABILITY IN LIFE-HISTORY SWITCH POINTS
ACROSS AND WITHIN POPULATIONS EXPLAINED BY
ADAPTIVE DYNAMICS**

PIETRO LANDI

landi@sun.ac.za

Theoretical Ecology Group, Department of Mathematical Sciences, Stellenbosch University,
Matieland, South Africa

Joint work with James R Vonesh (Virginia Commonwealth University), Cang Hui (Stellenbosch
University).

Keywords: Time of maturation, Phenotypic variability, Evolution, Disruptive selection, Evolutionary branching.

Understanding the factors that shape the timing of life-history switch points (SPs, e.g., hatching, metamorphosis, maturation) is a fundamental question in evolutionary ecology. Previous studies examining this question from a fitness optimization perspective have advanced our understanding of why the timing of life-history transitions may vary across populations and environments. However, in nature we also often observe variability among individuals within populations. Optimization theory, which typically predicts a single optimal SP under physiological and environmental constraints for a given environment, cannot explain this variability. Here we re-examine the evolution of a single life-history SP between juvenile and adult stages from an Adaptive Dynamics perspective, which explicitly considers the feedback between the dynamics of population and the evolution of life-history strategy. The Adaptive Dynamics model, although simple in structure, exhibits a diverse range of evolutionary scenarios depending upon demographic and environmental conditions, including the loss of the juvenile stage, a single optimal SP, alternative optimal SPs depending on the initial phenotype, and sympatric diversification under disruptive selection. Such predictions are consistent with previous optimization approaches in predicting life-history SP variability across environments, and in addition it also explains within-population variability. Thus, our model can provide a simple theoretical tool for exploring how changing environmental conditions may shape the evolution of life-history strategies.

Acknowledgements: PL and CH acknowledge support from the National Research Foundation (NRF) of South Africa (grants 89967 and 109244). JRV acknowledges support from US Fulbright and Centre of Excellence for Invasion Biology, Stellenbosch University, South Africa.

Parallel Session

Evolutionary Dynamics II

GENE-FOR-GENE EPIDEMIC MODELS, SYSTEMIC ACQUIRED RESISTANCE, AND THE EVOLUTION OF PLANT PARASITES

FRÉDÉRIC M. HAMELIN

fhamelin@agrocampus-ouest.fr

IGEPP, Agrocampus Ouest, INRA, Université de Rennes 1, 35000 Rennes, France

Joint work with Pauline Clin (IGEPP), Florence Val (IGEPP), and Frédéric Grognaud (Université Côte d'Azur, Inria, Biocore, 06902 Sophia-Antipolis, France).

Keywords: Plant disease epidemiology, Adaptive dynamics.

Many plant parasites interact with their host through gene-for-gene interactions. Considerable polymorphism for virulence (defined as the ability to overcome a resistance gene) and resistance occurs in agricultural and wild ecosystems. Fitness costs of resistance and virulence are required for polymorphism to be maintained in the long run [1]. A previous study [2] showed that there exist virulence costs in the Great Famine pathogen (*Phytophthora infestans*). These costs are mainly due to a lower spore production. However, virulent genotypes have a shorter latent period (time-to-sporulation). The latter observation is intriguing as virulent genotypes are expected to benefit from shorter latent periods. A key component of plant immunity is termed systemic acquired resistance (SAR): this is a partial resistance response that occurs following an earlier exposure to a pathogen. Through an adaptive dynamics approach, we show that SAR, by increasing the latent period of subsequent infections, may indeed select for shorter latent period in virulent genotypes. This way, we provide an original and possibly testable hypothesis to explain previously puzzling observations.

Acknowledgements: This work was supported by a grant over-seen by the French National Research Agency (ANR) as part of the “Blanc2013” program (ANR-13-BSV7- 0011, FunFit project)

References

- [1] J. K. Brown, A. Tellier, Plant-parasite coevolution: bridging the gap between genetics and ecology, *Annual review of phytopathology*, **49**, (2011) 345-367.
- [2] J. Montarry, F.M. Hamelin, I. Glais, R. Corbière, D. Andrivon. (2010). *Fitness costs associated with unnecessary virulence factors and life history traits: evolutionary insights from the potato late blight pathogen* *Phytophthora infestans*. *BMC Evolutionary Biology*, 10(1), 283.

Parallel Session

Evolutionary Dynamics II

FOOD WEB MODELS WITH EVOLUTION OF TWO TRAITS

CORALIE FRITSCH

coralie.fritsch@inria.fr

Inria & IECL

Joint work with Nicolas Champagnat (Inria & IECL) and Sylvain Billiard (University of Lille).

Keywords: Food web, Adaptive dynamics.

In the literature, several models of food web evolution have been introduced and numerically analysed. However, some biological conditions seem to be artificial in these models.

We will propose a food web model in which the size of individuals and their predation preference are subjected to evolution. We will discuss the mechanisms which have to be introduced in the model in order to obtain satisfactory evolutions of the food webs without artificially constrain the evolution of both traits (for example, constrain the predators to be always bigger than their preys). We will present results depending on the evolution speed of both traits.

Parallel Session

Evolutionary Dynamics II

**THE EFFECT OF SPATIAL HETEROGENEITY ON
EVOLUTION IN SPATIAL MODELS**

KALLE PARVINEN

kalle.parvinen@utu.fi

Department of Mathematics and Statistics, FI-20014 University of Turku, Finland

Joint work with Hisashi Ohtsuki (SOKENDAI, Japan) and Joe Yuichiro Wakano (Meiji, Japan)

Keywords: Metapopulation, Dispersal, Adaptive dynamics, Evolutionary branching, Spatial heterogeneity.

The Wright's island model consists of a large number of ecologically identical patches, in which a fixed number of adults produce offspring and die. Part of the offspring disperse. Those individuals surviving dispersal arrive randomly in any other patch. After dispersal, the n individuals to become adults are randomly chosen among the offspring present in each patch. In this model, classical results about the evolution of dispersal have been obtained [2].

We investigate an extension including spatial heterogeneity, so that patches can be of different quality. By investigating metapopulation fitness, we present analytical expressions for the selection gradient and conditions for convergence stability and evolutionary stability.

In the homogeneous model, evolutionary branching of dispersal is not possible [1]. We show that spatial heterogeneity selects against dispersal, but can promote evolutionary branching.

For a fecundity-affecting trait, Taylor's cancellation result holds in the homogeneous model: Not only singular strategies but also their convergence stability is identical to that in the corresponding well-mixed model. Homogeneous spatial structure also often inhibits evolutionary branching: Evolutionary branching never occurs when the dispersal rate is close to zero, and for a wide class of fecundity functions (including those determined by any pairwise game), evolutionary branching is impossible for any dispersal rate if branching does not occur in the corresponding well-mixed model [3].

In contrast, in a spatially heterogeneous model, evolutionary branching can happen for low dispersal rates, even when it does not happen when everybody disperses.

References

- [1] É. Ajar. (2003) *Analysis of disruptive selection in subdivided populations*. BMC Evolutionary Biology 3:22, 1–12.
- [2] W. D. Hamilton and R. M. May. (1977) *Dispersal in stable habitats*. Nature 269, 578–581.

- [3] Kalle Parvinen, Hisashi Ohtsuki, and Joe Wakano. (2017) *The effect of fecundity derivatives on the condition of evolutionary branching in spatial models*. J. Theor. Biol 416, 129–143.