Epigenetic modifications are associated with propensity to migrate in rainbow trout

Melinda Baerwald[1], Mariah Meek[1], Alisha Goodbla[1], Raman Nagarajan[3], Kat Tomalty[1], Bernie May[1], Krista Nichols[2], Molly Stephens[1]
[1]University of California, Davis, Davis, CA, USA, [2]Northwest Fisheries Science Center, Seattle, WA, USA, [3]University of California, San Francisco, San Francisco, CA, USA

Although migration is a central life-history trait spanning all major branches of the animal kingdom, knowledge of the underlying molecular mechanisms regulating this trait remains limited. We are using the salmonid *Oncorhynchus mykiss* as a model to gain mechanistic insight into one migratory phenotype, the propensity to migrate. Given that gene x environment interactions and phenotypic plasticity are likely critical components to migratory divergence, epigenetic modifications (e.g., DNA methylation) may regulate gene expression and partially underlie migratory phenotypic diversity. An F_2 family created by crossing steelhead (migratory) and rainbow trout (non-migratory) double haploid clonal lines was used to quantitatively measure genome-wide DNA methylation variation of skin tissue, which increases in reflectance prior to migration. Significant differential DNA methylation (hyper and hypo) was discovered when comparing juvenile steelhead and rainbow trout life-history types. Several of the differentially methylated regions are part of *in silico*-predicted CpG islands, suggesting epigenetic regulation of associated gene promoters leading to differential gene expression. This study provides the first empirical example of a relationship between epigenetic variation and alternative migratory behavior.

Incorporating the interaction between evolution and plasticity into management decision-making: a question of time

Marissa Baskett
University of California, Davis, Davis, CA 95616, USA

As research establishing how evolution and plasticity interact in response to global change advances, a key question is how that interactive response affects management decisions. I will provide three examples of modeling exercise that quantify that effect. When exploring the potential for marine reserves to mitigate fisheries-based selection for earlier maturity, model results indicate that the interaction between evolution and adaptive plasticity is crucial to predicting the time scale of trait change, which is central to the monitoring and adaptive management of reserves. When exploring the potential for the evolution of thermal tolerance to affect coral reef persistence under future climate change, model results indicate that tolerance breadth around a genetically-determined optimum temperature is one of the most influential parameters on coral persistence, which can inform conservation priorities based on the vulnerability of different species. When exploring alternative management strategies to minimize the impact of artificially-propagated populations (e.g., hatcheries and aquaculture) under domestication selection on wild populations when spillover occurs, the importance of the order of events in the life cycle to the relative efficacy of different strategies indicates the potential importance of timing of response to the environment when accounting for plasticity. Furthermore, the importance of variability in spillover in time found in evolution-only models will likely increase with plasticity given its effect on the time scale of phenotypic response. Overall, the potential for the interaction between plasticity and evolution to determine the timing and time scale of phenotypic response to environmental change alters management decisions under global change.

Interactions of plastic, genetic, and demographic responses to environmental change

Luis-Miguel Chevin
CEFE, CNRS, Montpellier, France

Rapid evolution of traits affecting population growth breaks down the classical distinction between ecological and evolutionary time scales, requiring the use of evolutionary demography for understanding population dynamics. Most evidence from contemporary evolution indicates that rapid phenotypic change in the wild generally includes a substantial component of phenotypic plasticity, the response of individual genotypes to their environment of development or expression. In a new or changing environment, phenotypic plasticity may also affect responses to selection, or evolve itself (if genetically variable), which can influence population growth and extinction risk. I will briefly review some of the explorations I have made of these questions in recent years, focusing on quantitative traits with linear reaction norms. I will then present two more recent projects that do not directly concern population growth. In the first, I will show how phenotype-environment associations caused by phenotypic plasticity and genetic change in a temporally correlated environment could be used to infer patterns of change of an optimum phenotype with this environment. In the second, I will address multivariate reaction norms, plasticity integration and the evolution of cues. I will conclude by highlighting important open theoretical questions, notably regarding the temporal aspect of phenotypic plasticity within lifetime, under more realistic life cycles.

Speed kills: adaptive evolution of slow growth in microbes

Sinéad Collins
Institute of Evolutionary Biology, University of Edinburgh

Marine microbes have large population sizes and mutational supplies, and are likely to evolve in response to global change. However, they also respond plastically to many environmental changes, and evolutionary and marine biologists have historically put forward contradictory predictions about the relationship between ancestral plasticity and adaptive evolution. First, I will briefly discuss an microbial evolution experiment that shows how plastic responses can be used to predict evolutionary ones, even in the absence of demographic effects. However, the most unexpected result of this experiment was that slow growth repeatedly evolved under conditions typically thought to select for rapid growth, and that these slow growing genotypes could outcompete faster-growing genotypes by overgrowing them. Finally, genotypes that evolved slow growth maintained or evolved more trait plasticity than genotypes that evolved fast growth. This both confused and intrigued me, so most of my talk will focus on the metabolic and ecological reasons that we think slow growth (with or without high plasticity) can be the result of adaptive evolution in microbes, and on what this might mean for how we think about growth rate evolution in systems that, on first glance, appear built for speed.

Selection and plasticity in fish due to decadal oscillations nested within long-term climate change

Lisa Crozier
NOAA Fisheries, Seattle

Decadal variation in climate profoundly affects ecological communities, often altering individual growth and reproduction sufficiently to drive “regime shifts”. Despite the long history of environmental oscillations with periods on the order of 50-70 years, such as the 1500 year history of the Pacific Decadal Oscillation, adaptive plasticity has not evolved to compensate for these relatively predictable fluctuations in climate. Ongoing climate change imposes a long-term trend on these oscillations that will alter the selective regime in the future. Theoretical work in evolutionary biology has explored how phenotypes should respond to selection in a fluctuating environment, but the implications of this theory for the detection of evolutionary responses to climate change have not been widely appreciated. I here use a very simple evolutionary model to demonstrate some expected responses for organisms exhibiting a range of generation times commonly observed. I emphasize some potentially misleading patterns in phenotypic traits that might obscure our detection of responses to anthropogenic climate change. I suggest how consideration of these processes could improve interpretations of short-term studies and comparisons of phenotypes at different time periods, which are the most common means of detecting responses to climate change.

Physiological local adaptation in populations of sockeye salmon: implications for coping with climate change

Erika Eliason[1,2], Tony Farrell[2]
[1]Carleton University, Ottawa, Ontario, Canada, [2]University of British Columbia, Vancouver, BC, Canada

Every year, millions of sockeye salmon return to the Fraser River (BC, Canada) to perform their once-in-a-lifetime upriver spawning migration. Climate change-induced increases in summer river temperature have been associated with exceptionally high mortality in migrating salmon, raising conservation concerns. There are over 100 geographically and genetically distinct populations within the Fraser River watershed, each of which experiences unique upriver migration conditions varying in migration distance (100-1,100 km), elevation gain (10-1,200 m), river temperature (9-22°C) and river flow (2,000-10,000 $m^3 s^{-1}$). This research examined thermal tolerance and local adaptation across sockeye salmon populations over several levels of biological organization, from whole animal swimming and cardiorespiratory performance, organ performance, gross organ morphology, ultrastructure and receptors. Fraser River sockeye salmon populations appear to have physiologically adapted to their local upriver migration environment. Specifically, populations with more challenging migrations had significantly greater aerobic scope, greater cardiac scope, larger relative ventricular mass and more compact myocardium compared to coastal populations traveling shorter distances. In addition, each sockeye salmon population maintained maximum aerobic scope across the range of temperatures typically encountered during the upriver migration. Notably, some populations may be more susceptible to continued river warming, which has clear conservation concerns for biodiversity.

Adaptive and non-adaptive plasticity in response to novel environments: Implications for rapid adaptation

Cameron Ghalambor
Department of Biology, Colorado State University

Evolutionary biologists have long debated if phenotypic plasticity facilitates or constrains adaptive evolution, but debate has persisted as few studies have quantified the role plasticity plays during the initial stages of adaptive divergence. Novel environments, such as those encountered during colonization events or those generated by human activities, are likely to induce a range of both adaptive and non-adaptive plastic responses, thus providing an opportunity to test the relationship between initially plastic responses and subsequent evolutionary change. We experimentally transplanted Trinidadian guppies (<i>Poecilia reticulata</i>) adapted to a stream with cichlid predators to cichlid free streams, and tested if plasticity in the source population predicted evolutionary change in the transplanted populations. We measured a suite of traits, including gene expression, body shape, growth rate, and metabolism. We found evidence for both adaptive and non-adaptive plastic responses in the source population and rapid adaptive evolution in the experimental population. However, traits exhibiting non-adaptive plasticity (i.e. a plastic response in the opposite direction favored by selection) diverged from the source population more rapidly. These results suggest traits exhibiting non-adaptive plasticity are under stronger directional selection compared to traits exhibiting adaptive plasticity. Thus, how suites of traits initially respond through plasticity is therefore likely to influence of the strength of selection and predict the rate of rapid evolution to novel environments.

Reef-specific patterns of osmotic response in larval and adult oysters, *Crassostrea virginica*, from a single estuary

Laura E. Eierman, Matthew P. Hare
Department of Natural Resources, Cornell University, Ithaca, NY, USA

Rapid environmental change is motivating research to predict the capacity for population responses based on plasticity versus natural selection. We collected eastern oyster adults from low and high salinity reefs in a single estuary (~10 and ~25 salinity) and conditioned them for nine weeks in 10 and 30 salinity common garden tanks. Our null hypothesis was that genotypes across the estuary show similar patterns of gene expression plasticity in response to salinity treatments. Our alternative model was that after homogenizing larval dispersal, differential viability selection on postsettlement juveniles recurrently selects for functionally divergent genotypes across the salinity gradient each generation. We used RNA-seq to measure gene expression after acclimation in the common gardens. A total of 9,921 reference transcriptome contigs (reftigs; 23.6%) showed significant differential expression (DE). Among DE reftigs, 0.6% showed a reef effect, 18.9% showed a treatment effect, and 13.9% showed a reef x treatment interaction (G x E). Thus, both hypotheses were strongly supported, suggesting that plastic responses are genomically pervasive, yet selection also leads to reef-specific reaction norms for many genes. Next, we made within-reef pair crosses from low, intermediate and high salinity source oysters to test the salinity tolerance of their larvae. Survival analysis of larval families at high and low salinity indicated a parental source by treatment interaction, supporting heritable differences in the plasticity of oysters from different reefs within an estuary. These results underscore the importance of oyster life history traits that support recurrent selection – high genetic diversity, fecundity and dispersal.

Climate change and temperature-dependent sex determination in turtles

Fredric Janzen
Iowa State University, Ames, IA, USA

Numerous anthropogenic processes increasingly imperil turtles globally. Now, rapid climate change stands to exacerbate these problems, since so many of these species also have temperature-dependent sex determination (TSD). Can these iconic, long-lived animals adapt fast enough to match ongoing thermal change or will they fail by evolving at a turtle's pace instead? I will present findings from >25 years of collaborative study of populations of turtles with TSD, a classic threshold form of phenotypic plasticity. I will first illustrate the considerable sensitivity of offspring cohort sex ratios to annual variation in climatic temperatures and then report on quantitative genetic analyses of three key traits identified by evolutionary theory that could permit TSD in these populations to adapt to biased offspring sex ratios expected under a moderate projection of climate change by the year 2100. Our results indicate moderate among-year repeatabilities, but small overall field heritabilities, for (1) thermal sensitivity of embryonic sex determination, (2) nest-site choice with respect to vegetation cover, and (3) nesting phenology (=onset of the nesting season). Thus, while the repeatability results reveal that these traits embody reasonable phenotypic targets for natural selection in the wild, these traits nonetheless evidently lack much additive genetic variance to fuel evolutionary response. Consequently, the potential for microevolution of TSD to keep pace with expected climate change appears to be limited. I will discuss the implications of these findings in the context of the deep evolutionary history of this clade as well as in terms of possible conservation and management actions.

Mechanistic overlap between plastic and evolved responses to heat stress: implications for adaptive responses to climate change

Morgan Kelly[1], David Plachetzki[2], Sabrina Pankey[2]
[1]Louisiana State University, Baton Rouge, LA, USA, [2]University of New Hampshire, Durham, NH, USA

Organisms and populations may respond to environmental change through plasticity or evolutionary adaptation. While these have historically been viewed as separate processes, the genetic assimilation hypothesis holds that environmentally induced (plastic) phenotypes are often the first step in adaptation, and later become genetically "assimilated," such that the original environmental stimulus is no longer required to produce the phenotype. We tested this hypothesis by combining artificial selection and heat shock experiments with RNA sequencing of the crustacean *Tigriopus californicus*. Transcriptomic responses to heat shock and artificial selection suggest substantial mechanistic overlap between plastic and evolved response to heat stress, and provide some of the first experimental support for the genetic assimilation hypothesis. To the extent that adaptation to changing environments tends to occur through genetic assimilation, our results suggest that plasticity and evolution may provide overlapping, rather than additive benefits to species responding to global change.

Evolution along a variably mutagenic landscape: Lessons from Fukushima and Chernobyl

Timothy Mousseau
University of South Carolina, Columbia, SC, USA

Evolutionary biologists have focused considerable attention on responses to selection, natural and otherwise, and much has been learned concerning the relationship between selection and genetic architecture to predict population responses. Less well explored has been the contribution of variability in mutation rates to the evolutionary process although mutation-selection balance is believed to greatly influence fitness and population persistence. The disasters at Chernobyl, and more recently Fukushima, as well as naturally radioactive regions of the world, provide the opportunity to investigate the genetic, evolutionary and ecological outcomes for individuals, populations and communities facing variably elevated mutation rates. Recent field studies of animals, plants and microbes have found evidence for significant deleterious consequences of elevated mutation rates with many species having gone locally extinct in Chernobyl. Field studies in Fukushima suggest a similar response for many groups..Comparisons between bird communities at Chernobyl and Fukushima suggest that negative fitness effects of radiation exposure in Japan are significantly higher than those currently observed in Chernobyl, leading to the suggestion that there may have been the evolution of adaptive responses within some Chernobyl populations. Recent analyses suggest that individuals of some species living in the Chernobyl region have enhanced antioxidant defenses (at the cost of coloration) resulting in significantly lower oxidative stress, reduced genetic damage, and higher overall fitness. These observations suggest that selection related to radiation exposure can generate adaptive responses in some groups although in most cases such responses are insufficient to overcome the deleterious consequences of radiation-induced mutational loads.

Adapting to a changing environment: modeling the interaction of directional evolution and plasticity

Leonard Nunney
University of California Riverside, Riverside, CA, USA

Human-induced habitat loss and fragmentation constrain the range of many species, so that they are unable to respond to a warming environment by shifting their range. For such species, their fate is likely to be either rapid adaptation or extinction. In a classic theoretical study, Haldane concluded that the “cost of natural selection” limited the rate of adaptation to about one genetic substitution per 300 generations. Using a simulation model integrating population dynamics and mutation, I have shown that in very large populations (of about 10^5 or more) long-term adaptation is possible at rates more than 10x faster than Haldane’s classic limit. Unfortunately, with increasing human impacts on biodiversity, a population size of 10^5 is often an impossibility, with the result that as the pace of environmental change increases, such populations cannot adapt fast enough. Here I focus on the role of plasticity in promoting the long-term survival of small populations. The potential importance of plasticity is in its role of "buying time" for a population, since a given genotype can encompass a greater environmental range, which in the context of directional change, means that it can persist for a longer period of time. However, plasticity is not cost free and, given different cost models, I have been examining two issues: first, the dynamics of genetic variation for plasticity under rapid environmental change; and second, how these dynamics alter the extinction risk of small populations.

Fisheries-induced evolution in largemouth bass - linking vulnerability to angling, parental care, and fitness

David Philipp[1,2], Julie Claussen[1,2]
[1]University of Illinois, Champaign, IL, USA, [2]Fisheries Conservation Foundation, Champaign, IL, USA

Long-term studies in Ontario, Canada on largemouth bass *Micropterus salmoides* and smallmouth bass *M. dolomieu* have demonstrated that angling nesting males (both catch-and-harvest and catch-and-release) can have negative impacts on the reproductive success for the captured individual. They have also demonstrated that within a population the male bass that provide the best and longest parental care for their offspring are the most capable of having the greatest relative contribution to the year class. Furthermore, those males are also the most aggressive toward potential brood predators and hence, the most vulnerable to angling, and angling for nesting bass, results in selection against aggressive individuals in a population, and as a result the angled population evolves to become less aggressive, containing males with diminished parental care attributes - an example of fisheries-induced evolution (FIE). Controlled, long-term selective breeding experiments over 30+ years have documented the heritability of vulnerability of bass to angling. Controlled reproductive competition experiments further demonstrated that the highly vulnerable (HV) strain of bass produced in those selective breeding experiments had greater reproductive success than the less vulnerable strain (LV). Because angling for largemouth bass has been occurring on many bass populations for decades, we also postulated that there should be some evidence in the wild of this FIE. In fact, we did find that the level of vulnerability to angling of nesting male largemouth bass in lakes that have had little to no exploitation is significantly greater than that observed for nesting males in moderately and heavily angled populations.

Does molecular pleiotropy constrain evolution, plasticity or both? A proteomic perspective in a salmonid fish metapopulation

Spiros Papakostas[1], Asbjørn Vøllestad[2], Matthieu Bruneaux[1], Tutku Aykanat[1], Joost Vanoverbeke[3], Mei Ning[1], Erica Leder[1], Craig Primmer[1]
[1]University of Turku, Turku, Finland, [2]University of Oslo, Oslo, Norway, [3]KU Leuven, Leuven, Belgium

Evolutionary change in a population can sometimes proceed rapidly, but there is little understanding regarding the molecular mechanisms that enhance or constrain such rapid adaptation. The significance of gene expression pattern modification in these processes has received considerable attention recently but the relative roles of plastic vs evolutionary expression change remain unclear, as does whether the evolutionary component tends to be neutral or affected by natural selection. We studied the proteomic expression profiles of European grayling sub-populations adapted to different thermal environments in a common garden setting (two temperature treatments, two warm-origin and two cold-origin sub-populations). The proteome expression changes included both evolutionary and plastic components, with each component having an independent, but complementary, effect on the expression profile. A Q_{ST}-F_{ST} analysis indicated that the observed differences in proteomic expression profile between cold and warm origin sub-populations likely include an adaptive component. We also found that temperature-driven gene expression changes were constrained by the level of gene pleiotropy estimated by either the number of protein interactions or gene

biological processes. Genes with low pleiotropy levels were the main drivers of the observed changes in both plastic and adaptive global expression profiles, while highly pleiotropic genes had a limited expression response to temperature treatment. These findings provide important insights into the molecular mechanisms facilitating rapid adaptation ino changing environments. In addition to having implications for climate change adaptation, these results suggest that gene pleiotropy should be considered more carefully when interpreting gene expression profiling data.

Hard and soft selection revisited: how evolution by natural selection works in the real world (Key Lecture)

David Reznick
Department of Biology, University of California, Riverside, CA, USA

The modern synthesis of evolutionary biology unified Darwin's natural selection with Mendelian genetics, but at the same time it created the dilemma of genetic load. Lewontin and Hubby's characterization of genetic variation in natural populations increased the apparent burden of this load. Neutrality or near neutrality of genetic variation was one mechanism proposed for the revealed excessive genetic variation. Bruce Wallace coined the term "soft selection" to describe an alternative way for natural selection to operate that was consistent with observed variation. He envisioned nature as presenting ecological vacancies that could be filled by diverse genotypes. Survival and successful reproduction was a combined function of population density, genotype and genotype frequencies, rather than a fixed value of the relative fitness of each genotype. My goal is to explore the importance of soft selection in the real world. My and my colleagues' motive is not to explain what maintains genetic variation in natural populations, but rather to understand the factors that shape how organisms adapt to natural environments. We characterize how feedbacks between ecology and evolution shape both evolution and ecology. These feedbacks are mediated by density and frequency dependent selection, the mechanisms that underlie soft selection. I will report on our progress in characterizing these types of selection with a combination of a consideration of the published literature and with me and my collaborators' research on natural populations of guppies.

Are plastic changes in tree phenology adaptive in the context of climate change? Insights from a mechanistic model

Anne Duputié[3 ,2], Alexis Rutschmann[4 ,2], Ophélie Ronce[1], Isabelle Chuine[2]
[1]ISEM CNRS-Université Montpellier 2, Montpellier, France, [2]CEFE CNRS, Montpellier, France, [3]GEPV CNRS Université Lille 1, Villeneuve d'Asc, France, [4]Station d'Ecologie expérimentale CNRS, Moulis, France

Phenotypic plasticity is often put forward as a mechanism helping species to cope with changing environments. Phenology is intimately linked to fitness in temperate trees, and is plastic with respect to temperature and photoperiod. Plasticity in phenology may represent an adaptive response to adjust the life cycle to climatic variation in seasonal environments. However, it could also reflect physiological constraints on growth, which make organ development dependant on climatic conditions. Furthermore, there is concern that adaptive plasticity having evolved under a given regime of environmental variation may become maladaptive when the environment changes, in particular when cues mediating change in phenotype become unreliable. Distinguishing between adaptive and non-adaptive plastic responses to climate change is thus an important challenge in the context of climate change. Using a process-based model describing tree fitness as a function of phenology and resistance to abiotic stresses, we assess the contribution of plasticity in phenological traits to fitness, species range and niche breadth in three common European tree species. We investigate this contribution by artificially altering phenotypic plasticity in the model and its expression through space and time. We examine the predicted contribution of plasticity in current and projected future climate at the scale of Europe. Surprisingly, for the 3 species, plastic variation in phenology has a weak effect on fitness in a large part of the range, but strong effects in marginal conditions. In warm and cold margins, plasticity can have either a positive or a negative effect, with patterns varying among species.

Epigenetic transgenerational inheritance of phenotypic variation in evolution: Lessons from Darwin’s finches

Michael K. Skinner
Washington State University, Center for Reproductive Biology, School of Biological Sciences, Pullman, WA, USA

Transgenerational effects of environmental exposures significantly impact the importance of the environment on biology. One of the most sensitive periods to exposure is during embryonic gonadal sex determination when the germline is undergoing epigenetic programming and DNA re-methylation. Previous studies have shown that a variety of toxicants can cause a dramatic increase in adult onset disease such as infertility, prostate, ovary and kidney disease, cancers and obesity. Interestingly, this effect is transgenerational (F1, F2, F3 and F4 generations) and hypothesized to be due to a permanent (imprinted) altered DNA methylation of the germline. The transgenerational epigenetic mechanism involves the actions of an environmental exposure at the time of sex determination to permanently alter the epigenetic (i.e. DNA methylation) programming of the germ line that then alters the transcriptomes of developing organs to induce disease and phenotypic variation. In addition to environmental toxicants, others have shown nutrition and stress can do the same. The observation that environmental factors can reprogram the germline to induce the inheritance of phenotypic variation provides a new form of non-genetic inheritance which is environmentally responsive, and relevant to areas of biology such as

evolution. To experimentally address this we have used Darwin’s Finches as a model of rapid adaptive radiation of species to investigate the phylogenetic relationship of genetic and epigenetic changes between species. A significant correlation with the presence of epimutations between species was identified, with strong associations with genes involved in avian evolution. Observations suggest environmental epigenetics may be an important factor in evolution.

Rapid evolution of plasticity in populations of an invasive plant: Implications for future adaptation

Sonia E. Sultan

Wesleyan University

A central question confronting evolutionary biologists is whether organisms in natural populations will be able to express adaptive phenotypes in the novel environments they will confront in future. The answer depends on potential constraints to both the evolution and the expression of genotypic norms of reaction that confer adaptation to new conditions. Our recent work has demonstrated rapid evolutionary changes of individual plasticity patterns in populations of the Asian shade plant *Polygonum cespitosum* in its introduced range in northeastern North America. In a series of glasshouse resurrection experiments, we tested genotypes sampled from the same 3 field populations in 1994 and again in 2005 to track recent adaptive evolution of this invasive annual species. In only 11 generations, genotypes from these *P. cespitosum* populations have evolved changes in physiological and morphological plasticity that are associated with increased plant fitness in high light conditions. These changes in plasticity are consistent with the very recent spread of the species into more open sites in its introduced range. As a result of global climate change, future environments within the North American range of this species are expected to include high light, greater heat, drought stress, and elevated CO_2 concentration, conditions that the species has not encountered in its previous selective history. We studied the plastic responses of *P. cespitosum* genotypes to these combined stresses in a manipulative field experiment at a Free Air CO_2 Enrichment (FACE) site. As in the previous studies, we used a resurrection approach to determine the effect of recent evolution in 3 field populations on plasticity patterns for physiological, leaf anatomical and life-history traits. Our findings revealed three potential limits to successful adaptation to future environments, even in an evolutionarily labile species such as this invasive annual plant. (1) Although North American populations of *P. cespitosum* have rapidly evolved to increase photosynthetic rate and delay senescence under full-sun, dry conditions, this adaptive plasticity was not expressed under elevated CO_2. (2) The populations differed markedly in reproductive output in these novel, stressful conditions, possibly reflecting the accumulation of ‘cryptic’ genetic variation; and (3) populations differed in the amount of quantitative genetic variation that could fuel further adaptation (a result confirmed in another, larger glasshouse study). The evolutionary potential to cope with rapid, anthropogenic environmental change may thus vary at the population level, creating diverse trajectories for persistence and adaptation.

Coevolution of bet-hedging and reaction norm slope and elevation in temporally autocorrelated environments

Jarle Tufto
Norwegian University of Science and Technology, Trondheim, Norway

Using a quantitative genetic model I consider the coevolution of bet-hedging, plasticity and adaptive tracking through genetic evolution in mean reaction norm elevation. The macroenvironment influencing all individuals of a given generation fluctuates according to an autoregressive process. The expressed and optimum phenotype of a given individual depends on the macroenvironments at the time of development and selection, respectively, and individually correlated, microenvironmental deviations. Independent evolution of the phenotypic variance is accomodated by a plastic response to a second independent white-noise microenvironmental variable. I first show how the covariance between the mean elevation and the macroenvironment decrease with increasing plasticity and with the total phenotypic variance. Secondly, if the variance of the mismatch between the population mean phenotype and the mean phenotypic optimum is sufficiently large, diversifying bet-hedging is adaptive and the total phenotypic variance evolves towards the difference between this mismatch variance and the square of the width of the stabilizing selection fitness function. Finally, simple formulas for the mean reaction norm slope given the outcome of the other processes are derived in two special cases. Through the effect of plasticity on the individual level phenotype-optimum variance, microenvironmental variability may create selection for either less or more plasticity depending on the correlation between microenvironmental deviations at the time of development and selection. The overall coevolutionary outcome is characterized by considerable overlap between the three forms of evolutionary responses throughout large parts of the parameter space.

Ecological and evolutionary dynamics of the amphibian-killing fungus

Kelly Zamudio
Ecology & Evolutionary Biology, Cornell University

One of the consequences of anthropogenic change to natural habitats is the spread of emergent infectious disease agents. Chytridiomycosis, an infectious disease caused by the amphibian-killing fungus *Batrachochytrium dendrobatidis*, has caused widespread declines and extinctions of amphibian populations globally, with high impacts in Central and South American communities. I will present data on the roles of immunogenetic and demographic factors in immunity to this infectious disease that is a serious threat to New World amphibian biodiversity. In my talk I will highlight two research target areas in our laboratory: (1) identification of the genetic basis of host defence strategies (resistance and tolerance) and pathogenicity traits, and (2) ecological characterization of shifts in fitness driving seasonality patterns in host-pathogen interactions. Given the heterogeneity of disease outcomes and broad host diversity for *Batrachochytrium dendrobatidis*, genomic information helps characterize the diverse collection of disease survival strategies for amphibians, which in turn helps build a detailed map of the components of the innate and adaptive immune system acting in infected hosts in varying environments.