

Commentary

Weeds of agricultural importance: bridging the gap between evolutionary ecology and crop and weed science

An undeniable and expensive consequence of agricultural practices is the adaptation of weeds to agricultural systems. Weeds are responsible for significant crop yield losses and for financial losses in agricultural production – in the order of 10% per year worldwide (Oerke, 2006). To address this critical problem, the discipline of weed science has expanded over the past 50 yr into an amalgam of scientists and practitioners who ask a variety of questions and employ a myriad of tools focused on understanding and managing weeds (Holt, 2002). Two predominant foci of this discipline are the fundamental aspects of weed biology and ecology, and the practical aspects of managing these pests (Radosevich *et al.*, 2007). While weeds can infest many types of ecosystems, weed scientists focus on how weed populations affect crop yield and how to best apply this knowledge to prevent, eradicate or control weeds, primarily through the use of herbicides, with the ultimate goal of maximizing crop production (Davis *et al.*, 2009).

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Evolutionary biologists study various aspects of plant biology in order to gain a better understanding of evolutionary processes. Unfortunately, evolution has not been a significant component of weed science, and the question 'What makes these species inherently weedy?' often gets lost between the two fields of study. However, just as crops have

been domesticated to serve the needs of human agriculturalists, weeds have been domesticated indirectly by humans for adaptation to agricultural fields (De Wet & Harlan, 1975). All weed-control methods – including nonchemical methods – exert selection pressure on weed populations, which effectively favors weeds that are better adapted to the method in use.

An extreme example of weed selection is herbicide resistance in response to the repeated use, over several years, of the same herbicide or mode of action, which imposes heavy selection pressure favoring individuals in the population which can survive that herbicide (Holt, 1992; Heap, 2009). Resistance management requires the reduction of herbicide selection pressure through the use of alternative methods of weed control. It naturally follows that considering evolutionary principles when managing resistant weeds should reduce, or even prevent, the evolution of greater resistance problems (Neve, 2007). Furthermore, to gain a clearer picture of how plants become weeds, we need to understand how the genetic architecture underlying weed-related traits interacts with all management practices, not just herbicides, which are ostensibly the environment of the weed (Holt, 1997; Jordan & Jannink, 1997; Sakai *et al.*, 2001).

The continuing evolution of weeds

Weeds, defined anthropocentrically as undesirable plants that are growing 'out of place', have evolved numerous mechanisms to survive field conditions that are optimized for crops. Certain traits are generally associated with weedy plant species, including early germination, rapid growth from seedling to sexual maturity, and the ability to reproduce sexually and asexually (Baker & Stebbins, 1965; Baker, 1974). Baker hypothesized that the 'ideal weed' might exhibit a generalist genotype with a high level of phenotypic plasticity (Baker & Stebbins, 1965; Baker, 1974). However, weeds are known to evolve rapidly in several ways: from colonizers selected by agricultural practices; from hybridization between wild and domesticated cultivars; and from selection on abandoned domesticated cultivars (De Wet & Harlan, 1975). Thus, the question of whether weeds are phenotypically plastic, 'Jacks of all trades' (Richards *et al.*, 2006), or possess single genes/traits that are responsible for weediness, remains unresolved.

There are many well-known examples of the appearance of new weeds or weed complexes following selection by a weed-control practice or cropping system. Annual tillage systems are known to select annual weeds and to disfavour

perennial weeds, while perennial and no-till cropping systems generally select perennial weeds. Mowing often selects weeds with horizontal growth form and low-growing meristems, such as grasses and clovers, or prostrate phenotypes within the same species. In some systems weeds have evolved that mimic crops morphologically and phenologically, such as barnyardgrass (*Echinochloa crus-galli*) growing in rice (*Oryza sativa*) (Barrett, 1983). There are also many examples of biological agents that have had profound effects on weed floras, such as the increase in noxious thistles and other unpalatable species in response to grazing animals on rangelands. In some cases the result is simply a shift or a change in the species composition of a site, similar to succession in natural systems, while in other cases rapid weed evolution has occurred (Holt, 1997; Radosevich *et al.*, 2007). As noted by Baker 1974 (1991), weeds are 'potentially useful for studies of microevolution under human influence'.

Evolutionary ecology in agricultural ecosystems

The very traits that are a bane to those attempting to manage weed infestations are also traits that make weeds excellent scientific model organisms. In fact, many agronomic weeds that have a significant, negative economic impact are also models in ecology and evolutionary biology. For example, morning glories (*Ipomoea* spp.), the wild radish (*Raphanus*), and weedy sunflower and thistles (various genera) are all well represented by some of the major research threads in evolutionary ecology, such as studies of plant mating systems, plant–herbivore interactions, ecological adaptation and speciation (Chang & Rausher, 1999; Tiffin & Rausher, 1999; Stinchcombe & Rausher, 2002; Snow *et al.*, 2001; Rieseberg & Colleagues). Likewise, representative species from these groups are regularly listed among the top 10 'worst' weeds in current-day agriculture and as such are often the subject of applied studies (Holm *et al.*, 1977). Understanding the mechanisms that promote weed persistence, including herbicide resistance, is of practical significance; it also provides us with a model for understanding the genetics of adaptation.

From an evolutionary perspective, the principles and practices of agriculture create a large experiment across the landscape. The integration of the practical side of weed science with hypothesis-driven evolutionary ecology, along with the tools of genetics and genomics, will provide answers to the questions of not only the types of mutations that arise to promote weed persistence and vigor, but also how many genes might be involved in these traits, how they might impact one another, and the specific ecological context that can promote or constrain their persistence in weed populations. Adding to the complexity of the evolutionary ecology of weeds, however, is their phylogenetic diversity, which probably precludes the use of a single model weed species.

Bridging the gap

There is currently little communication between evolutionary biologists/ecologists and applied weed scientists. Given that weeds thrive within an agricultural system, the effect of management regimes on the evolutionary ecology of weeds should not be ignored. Likewise, understanding the evolution of traits that allow weeds to take advantage of an agricultural system will inform applied weed scientists of the best strategy to mitigate their effects and reduce weed population growth. In view of the above, increased communication between the basic and applied sciences is critical. This issue of *New Phytologist* features both reviews and empirical research on the problem of weed evolution from both subdisciplines of plant biology – weed science and evolutionary ecology. First, two reviews by Neve *et al.* (pp. 783–793) and Vila-Aiub *et al.* (pp. 751–767) argue for a continued integration of evolutionary ecology into the study of weeds, and second, four research papers present empirical work that considers the problem of introgression leading to weediness (Campbell *et al.*, pp. 806–818; Dechaine *et al.*, pp. 828–841; Gross *et al.*, pp. 842–850; Trucco *et al.*, pp. 819–827).

The purpose of these special papers is to provoke discussion between evolutionary ecologists and weed scientists in order to stimulate integration between the fields and to integrate thinking about the process of weed domestication to agriculture and the evolution of weediness. It is our hope that these papers will be effective both in stimulating 'cross-talk' and in defining the questions that need to be addressed in order to understand the process of weed adaptation to agroecosystems.

Conclusions

Weed adaptation to agricultural systems provides both a unique view into the process of evolution as well as a challenge to the global food supply. Understanding the mechanisms behind weed proliferation in cropping systems will require detailed knowledge of the processes and causes of weed adaptation, such as the evolution of herbicide resistance, gene flow between transgenic crops and weeds, and evolutionary ecology underlying traits that might be responsible for 'weediness'. Ultimately, a better understanding of weed evolution in the context of human-caused selection could be the key to significant future advances in weed management in agroecosystems.

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Key words: adaptation, agriculture, evolutionary ecology, weed evolution, weed science.

Meetings

Phenology as a tool to link ecology and sustainable decision making in a dynamic environment

Symposium 14, 94th Ecological Society of America Meeting, Albuquerque, New Mexico, USA, August 2009

Adaptation to climate change (i.e. actions that reduce negative and enhance positive climate impacts) is one of the most

pressing issues of our time, from both human and ecological perspectives. Recent rapid changes have already affected the availability of water, the frequency and extent of wildfire, the persistence and distribution of species, the availability of nutrients, and many other ecological and physical processes (IPCC, 2007). At the 2009 annual meeting of the Ecological Society of America, a symposium entitled ‘Phenology, the Interdisciplinary Canary: Linkages between Ecology and Sustainable Decision Making in a Dynamic Environment’ <http://eco.confex.com/eco/2009/techprogram/S4149.HTM> highlighted the ubiquitous role that phenology plays in many of these responses to climate change and described how phenology data can improve our ability to make management decisions in the face of climate change.

'...the strength of a species' phenological response to variations in climate might in fact indicate its vulnerability to climate change...'

The utility and ubiquity of phenology

Phenology is the study of seasonal recurring plant and animal life cycle stages, or phenophases, such as leafing and flowering of plants, maturation of agricultural crops, emergence of insects and migration of birds. The role of phenology in the structure and function of ecological systems is often underappreciated, but its importance is magnified by climate change. Shifts in phenology are among the most sensitive biological responses to climate change (Parmesan, 2007). They occur across trophic levels and are observable at local to global scales. Moreover, changes in the timing of phenological events have widespread impacts on ecological and biophysical processes. Nearly every ecological relationship and process depends on timing to some degree, often to a very large degree – viz., pollination, predation, competition, niche differentiation and primary productivity (Stenseth & Mysterud, 2002). In addition, the phenology of many organisms is plastic and integrates many climate variables, including temperature, precipitation, wind, day-length and even atmospheric concentrations of carbon dioxide. Thus, phenological data contain not just information about organismal timing, but also information about environmental variables.

Taken together, the ability of phenology to integrate climate variables, its ubiquitous role in ecological and physical responses to climate change, and the ease with which it can be observed, make phenological data a critical tool for improving our understanding of ecological processes and for managing resources in the face of climate change. The many applications for phenology data and models include agriculture, drought monitoring, wildfire risk assessment and the management of wildlife, invasive species, agricultural pests and other risks to human health and welfare, including allergies, asthma and vector-borne diseases. More broadly, phenology data can be used to inform the public about climate change science, and its impacts on the environment, through education and outreach programs. In this symposium, an interdisciplinary set of speakers highlighted new insights into how phenology mediates ecological responses to global change, new applications of phenology data and models in management contexts, and key unanswered questions. Speakers in this symposium also described the role of phenology in many ecological relationships and processes, including flower production, plant–pollinator relationships,

invasive species, species distributions, agricultural pest management, ecosystem-level fluxes of carbon and water, and wildfires.

The role of phenology in some of these relationships and processes has been discussed extensively in the literature: the concept of climate-driven, temporal mismatches between an organism and key resources, such as food or pollinators (Visser & Both, 2005), has probably received the most attention. However, it is not clear that those mismatches will often occur or will necessarily lead to rapid declines in population sizes when they do occur, particularly for species with generalist interactions. Examples of climate-driven, temporal mismatches causing populations to decline are rare, possibly because the mismatches themselves are rare, or because the evidence required to describe them is difficult to collect.

The speakers described many other effects of phenological changes that are discussed less often and deserve further attention. For example, as phenology and climatic conditions shift simultaneously, albeit differentially, abiotic conditions at key life-history stages will also change. If leaf-out and flowering dates of early flowering plants shift too quickly relative to temperatures, they could be exposed to an increased incidence of frost, with consequences of reduced survival or reduced reproductive output (Inouye, 2008). If they change too slowly, they risk being out-competed by non-native species that open their leaves or flowers earlier, thereby exploiting the extended growing season (Xu *et al.*, 2007).

At the ecosystem scale, changes in the length of the growing season could alter carbon and water cycling. Warmer temperatures and longer growing seasons that affect leaf and canopy structure or activity (e.g. the carbon-uptake period) are expected to increase both gross primary productivity and respiration, a potential feedback mechanism to the global carbon cycle and climate mitigation. However, the effect on net primary productivity is unclear, and may differ depending on the scale of observation and the type of ecosystem (Piao *et al.*, 2008; Richardson *et al.*, 2009). Much new research on this topic is needed.

Shifting phenologies: impact or plasticity?

Key to understanding and managing plant and animal species within and across changing environments is interspecific variability in the rates and directions of phenological change (Parmesan, 2007). For example, as described above, differential shifts in phenology can disrupt time-sensitive interactions (e.g. plant–herbivore relationships or exposure to environmental stresses such as frost and drought) in ways not necessarily predictable by simple enumeration of species-specific responses. From this variability arises an intriguing question: Is it generally beneficial for a species to track changes in climate by shifting its phenology?

In much research to date, shifts in phenology are used to indicate the effect of an external perturbation on the activity or behavior of plants and animals across space and time. However, investigators are beginning to explore the ecological significance of these changes beyond temporal mismatches. New research suggests that the strength of a species' phenological response to variations in climate might in fact indicate its vulnerability to climate change: populations with phenologies that track climate tend to perform well, whereas those that do not track climate tend to decline (Møller *et al.*, 2008; Willis *et al.*, 2008). The mechanism underlying this pattern is not clear, and analyses to date are restricted to terrestrial systems. However, phenotypic plasticity has been invoked as a conceptual model – shifts in phenology may be a generally beneficial plastic response to rapid climate change, or phenological plasticity may be correlated to plasticity in other key traits. Assessments of species-specific changes in phenology, particularly when considered in light of changes in resources and abiotic conditions, may emerge as a valuable tool to facilitate the rapid assessment of species vulnerability to climate change. For example, managers and conservation biologists could target efforts to preserve species with phenologies that are not shifting in concert with climatic conditions. Species with generally nonplastic phenologies include most long-distance migratory birds and many plants species. Such a conceptual model could help conservation practitioners to take concrete actions to protect the species most vulnerable to climate change.

Coordinating collection of phenology data

The major limitation to our understanding of phenological responses to climate change, their consequences and their use in management decisions, is the lack of abundant, easily accessible data. Several recent studies, however, have shown the utility of nontraditional sources of phenology data, such as herbarium specimens, photographs and personal journals (Lavoie & Lachance, 2006; Miller-Rushing *et al.*, 2006). In addition, new citizen-science programs are being developed to collect phenology data in the USA and other countries. One such program described in the symposium is the USA National Phenology Network (USA-NPN; <http://www.usanpn.org>), a new partnership among federal agencies, the academic community and the general public to establish a national science and monitoring initiative focused on using phenology as a tool to facilitate human adaptation to climate change. The USA-NPN is developing a National Phenology Information Management System that will collect new and historical phenology data and will make it freely available to scientists, managers, educators and the general public. Similar efforts are also underway in Europe and elsewhere (Sparks *et al.*, 2009). Global collaboration on standards, data sharing and joint research could be greatly

facilitated through the development of an international effort towards a Global Phenology Network.

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Key words: adaptation, climate change, global warming, phenology, phenotypic plasticity

From genes to ecosystems: an emerging synthesis of eco-evolutionary dynamics

Symposium 7, 94th Ecological Society of America Meeting, Albuquerque, New Mexico, USA, August 2009

A synthesis is underway between ecology and evolution, partly brought about by the realization that evolutionary change can take place on ecological timescales (Hairston *et al.*, 2005; Whitham *et al.*, 2006; Carroll *et al.*, 2007). This synthesis attempts to understand the dynamic interplay of ecological and evolutionary processes that results from natural or anthropogenic selective forces (Lankau & Strauss, 2007). Moreover, this synthesis represents an integration of several 'genes to ecosystems' approaches, including 'ecological stoichiometry', 'community genetics' (Whitham *et al.*, 2006) and 'niche construction'. United under the framework of 'eco-evolutionary dynamics', these ideas seek to link genetic and phenotypic variation to population dynamics, biodiversity and ecosystem function, and place these disciplines in a dynamic evolutionary framework (i.e. understanding the ecological consequences of evolutionary processes and the evolutionary consequences of ecological interactions). This is not an easy endeavor because any such synthesis needs to be broadly multidisciplinary and integrative (Whitham *et al.*, 2006). And yet the potential pay offs are large given that genetic variation across plant and animal systems can have extended consequences at the population, community and ecosystem levels. These consequences can come in the form of the vital rates of survival, reproduction and migration, as well as arthropod and aquatic macroinvertebrate diversity, soil microbial communities, trophic interactions, carbon storage, soil nitrogen availability, dissolved organic nitrogen and production of primary producers (Whitham *et al.*, 2006; Bailey *et al.*, 2009; Ezard *et al.*, 2009; Harmon *et al.*, 2009; Johnson *et al.*, 2009; Palkovacs *et al.*, 2009; Post & Palkovacs, 2009). The effects of genetic or phenotypic variation are not limited to single systems or to ecologically important species (i.e. keystone species, dominant species, foundation species, ecosystem engineers), although these are excellent places to start looking. Instead, genetic variation seems to have effects that are broadly distributed across plant and animal systems - and these effects can be similar in magnitude to those of nonevolutionary ecological variables, such as climate, species invasion and habitat quality (Hairston *et al.*, 2005; Bailey *et al.*, 2009; Ezard *et al.*, 2009; Palkovacs *et al.*, 2009; Post & Palkovacs, 2009).

While it is clear from the talks presented in this symposium that genetic variation can have significant impacts on population dynamics, biodiversity and ecosystem services in specific instances, research efforts are increasingly focused more generally on factors that influence the strength and form of eco-evolutionary dynamics (Bailey *et al.*, 2009). Active research topics include (1) how evolution and co-evolution influence biodiversity and ecosystem function, (2) the reciprocal influences of ecological and evolutionary causation (i.e. eco-evolutionary feedbacks) and (3) the relative effect sizes of evolutionary processes. In Fig. 1, for example, genetic variation might influence phenotypic variation, which might influence population dynamics or community structure, leading to variation in ecosystem function that might then impose selection on phenotypic variation and thereby cause genetic change. At the 2009 Annual Meeting of the Ecological Society of America, a symposium entitled 'Eco-Evolutionary dynamics: Should ecologists care?' <http://eco.confex.com/eco/2009/techprogram/S4123.HTM> focused on the state of eco-evolutionary research, and here we outline some of the insights that emerged from that symposium.

'...to show that eco-evolutionary dynamics are taking place in a specific system, it is first important to show that genetic variation influences ecological variables. But how important is this variation or these dynamics at different hierarchies of complexity or in relation to nonevolutionary ecological effects?'

Evolutionary and co-evolutionary effects on biodiversity and ecosystem function

Recent research has shown that extended ecological consequences of standing genetic variation/diversity occur across plant and animal systems and across terrestrial and aquatic biomes. Moreover, empirical, mathematical and theoretical studies suggest an emerging mechanistic framework for the multispecies co-evolutionary process that is associated with interspecific indirect genetic effects (i.e. where the genotype of one species influences the fitness and phenotype of associated interacting species) (Thompson, 2005; Shuster *et al.*, 2006; Wade, 2007). Such work suggests that the co-evolutionary process should be common across the landscape and be important for positive and negative plant-soil feedbacks,

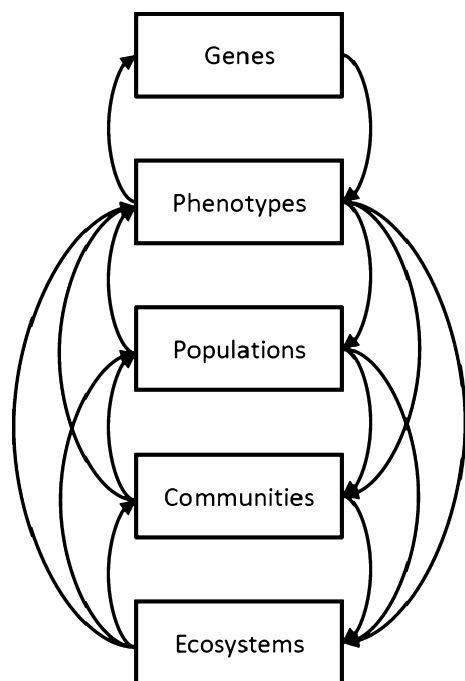


Fig. 1 Conceptual model of dynamic eco-evolutionary feedbacks, demonstrating the potential feedbacks from genes to phenotypes across population, community and ecosystem levels of organization.

plant–plant interactions that range from competitive to complementary, and trophic interactions in plant–herbivore–predator systems. In addition, understanding the indirect consequences of evolution and co-evolution represents an emerging frontier. For example, Palkovacs *et al.* (2009) experimentally compared the effects of two fish species (guppies (*Poecilia reticulata*) and killifish (*Rivulus hartii*)) that had evolved in either the presence or absence of predators (i.e. evolutionary diversity), and under different contexts of sympatry (i.e. co-evolutionary diversity), on aquatic macroinvertebrates and algal biomass. They found that populations which evolved under these different conditions differentially influenced both invertebrate and algal biomass in mesocosms. Overall, three major themes emerged from these and other work on this topic: (1) intraspecific variation can be as important as interspecific variation to ecological processes; (2) the co-evolutionary process is likely to be common across plant and animal systems as more studies specifically begin to address interspecific genotype \times genotype interactions; and (3) the co-evolutionary dynamic may be a particularly important contributor to eco-evolutionary dynamics.

Dynamic ecological and evolutionary frameworks

The demonstration of multiple ecological effects of standing genetic variation within populations, or recently evolved

differences between populations, suggests the potential for true eco-evolutionary dynamics (i.e. ongoing changes in traits influencing ecological interactions, and vice versa), but these dynamics have only rarely been studied explicitly (Pelletier *et al.*, 2009). Very recent examples include empirical analyses of population responses to contemporary trait change (Ezard *et al.*, 2009), mathematical models of population or community dynamics (Johnson *et al.*, 2009; Zheng *et al.*, 2009) and experimental designs that either capture (Jones *et al.*, 2009) or mimic longitudinal time series (Barbour *et al.*, 2009; Harmon *et al.*, 2009). This framework is critical for revealing (1) how ecology and evolution mutually interact to shape population persistence in the face of environmental change, (2) the origins (speciation) and maintenance of biodiversity (Cavender-Bares *et al.*, 2009) and (3) the ecological trajectories of populations, communities and ecosystems (Jones *et al.*, 2009). Although there are a number of nice examples of how genetic and phenotypic variation within species influences ecological processes, as presented in this symposium, the relative rarity of dynamical studies of reciprocal eco-evolutionary feedbacks highlights the difficulty of such work (Post & Palkovacs, 2009). This difficulty probably arises, at least in part, because two-way interactions are difficult to document and disentangle in nature. However, this means that detailed manipulative experiments are called for that also extend to more natural contexts, rather than only the laboratory or field mesocosms that have been used so far (Harmon *et al.*, 2009; Post & Palkovacs, 2009).

Measuring and predicting effect sizes

In order to show that eco-evolutionary dynamics are taking place in a specific system, it is first important to show that genetic variation influences ecological variables. But how important is this variation or these dynamics at different hierarchies of complexity (populations, communities, ecosystems) or in relation to nonevolutionary ecological effects? Only by addressing these questions can we determine the potential importance of eco-evolutionary patterns at different hierarchical levels or in relation to traditional ecological effects. These studies present compelling evidence that eco-evolutionary effects can be surprisingly large, even relative to the effects of traditional ecological factors (Fig. 2; Bailey *et al.*, 2009; Palkovacs *et al.*, 2009). Such effects may be greatest (on average) at the population level and somewhat less intense at levels more removed from variation within a target species, such as community structure or ecosystem function (Bailey *et al.*, 2009). This is not always the case, however, given that genetic variation can sometimes have very large direct effects on community or ecosystem variables that are not simply mediated by population abundance. Quantitative assessments of effect sizes represent a significant advance in the field as it may ultimately enable

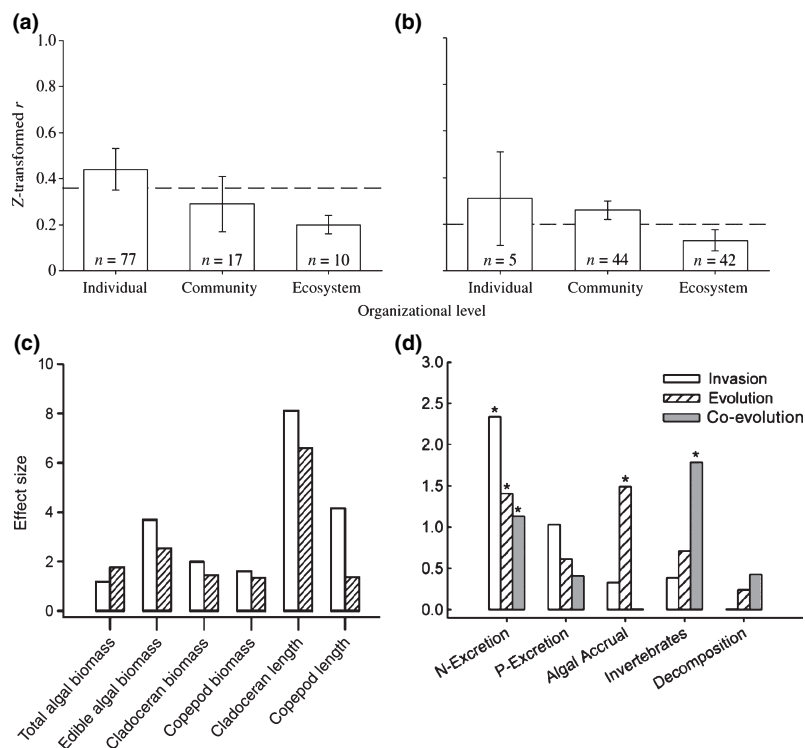


Fig. 2 Ecological effect sizes across population, community and ecosystem response variables in aquatic and terrestrial ecosystems. In terrestrial plant systems the effects of genetic introgression (a) and genotypic diversity (b) demonstrate strong effects across levels of organization (i.e. population, community, ecosystem). Bars represent the mean effect size (\pm 95% CI) while the dashed lines indicate the average effect size across all levels of organization (modified from Bailey *et al.*, 2009). In aquatic systems, large effect sizes (Cohen's *d*) exist on community and ecosystem response variables in association with alewife (c) populations and stream fishes in Trinidad (d). Panel c represents the effect size of the presence/absence or incidence of alewife (open bars) and intraspecific phenotypic variation (i.e. the difference between anadromous and land-locked populations of alewives; hashed bars). The data are modified from Post *et al.* 2008. Panel d represents effect sizes with guppy invasion, guppy evolution and *Rivulus*-guppy co-evolution. Significant contrasts at the $\alpha = 0.05$ level are indicated with an asterisk; data are modified from Palkovacs *et al.*, 2009).

scientists to predict where ecological and evolutionary effects are likely to be weak or strong. Moreover, attention to such effect sizes may be important from a very practical standpoint, given the possibility that studies quantifying ecological effect sizes may at times be confounded by the contemporaneous ecological effects of evolution and co-evolution (Strauss *et al.*, 2008).

Conclusions and future directions

Population-level genetic differentiation in quantitative traits can lead to variation in genetically based species interactions that may feed back to affect the phenotype and fitness of the interacting species (i.e. the co-evolutionary process) (Thompson, 2005). While there are an abundance of plant systems and experimental approaches to examine such hypotheses, including provenance trials with plants (see Barbour *et al.*, 2009) and genotype-by-genotype interactions, the majority of studies to date have focused on predator-prey systems (Pelletier *et al.*, 2009), leaving the door open to many important questions in many diverse systems, including the following. (1) Are eco-evolutionary effects stabilizing or disruptive processes in ecology (Palkovacs *et al.*, 2009)? (2) How common is rapid evolution and can it influence biodiversity and ecosystem services on similar timescales? (3) How do phenotypic/genetic effects depend on density regulation? (4) Do evolutionary effects decrease from populations to ecosystems (Bailey *et al.*, 2009)?

(5) Under what conditions do ecological and evolutionary feedbacks take place, and when are they positive or negative (Post & Palkovacs, 2009)? These questions all represent important areas of research and synthesis in the growing field of ecological and evolutionary dynamics. As the discussion at the symposium demonstrated, eco-evolutionary dynamics are common on an ecological timescale in nature, which means that addressing these and other questions is important if we are to understand and predict the dynamic interplay of ecological and evolutionary processes that result from natural or human-driven environmental changes.

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