New frontiers in community and ecosystem genetics for theory, conservation, and management

Community and ecosystem genetics: the extended genetic effects of plant species, XVII International Botanical Congress 2011, Melbourne, Australia, August 2011

The effects of genetic variation in species can have large impacts on direct and indirect species interactions, associated biodiversity and ecosystem function. Biodiversity and ecosystem function can change as a consequence of evolutionary dynamics (Barbour et al., 2009), thus, linking evolution strongly with community and ecosystem ecology. At the 2011 International Botanical Congress in Melbourne, Australia, a symposium entitled, ‘Community and ecosystem genetics: the extended genetic effects of plant species’, examined new research in the field of community and ecosystem genetics. Talks focused on: links between contemporary ecological interactions and historic evolutionary dynamics; the role of feedbacks as mechanisms in driving patterns of biodiversity and ecosystem function; and application of these approaches to management and conservation issues as they relate to global change. The symposium concluded that an understanding of evolutionary divergence and adaptation, and the role of ecological feedbacks in natural systems, will be fundamental to successful outcomes in future conservation, restoration and management decisions.

‘Extended genetic effects of a forest dominant: The case of Eucalyptus globulus’, while the second by Joe Bailey (University of Tennessee, USA) on ‘Historical evolutionary dynamics result in convergent ecological consequences for biodiversity and ecosystem function’ focused on how phylogenetic divergence may lead to change in biodiversity and ecosystem function. Emerging from both talks was the recognition that Eucalyptus, as a broad group, represents a model for understanding the genetic basis to biodiversity and ecosystem function irrespective of the genetic scale of interest. Eucalyptus globulus, a dominant tree of lowland forests of south-eastern Australia, is widely grown in plantations in temperate regions of the world and its molecular and quantitative genetic diversity are amongst the most extensively studied of any forest tree. The natural colonization of pedigreed field trials by local fungi, insect and marsupial species has provided a robust system in which to study individual species, as well as community responses to genetic variation (Barbour et al., 2009). Community and ecosystem responses have been explored at multiple genetic levels from genetically divergent geographic races, additive genetic effects within-populations and within-races, to within-family quantitative trait loci (QTL) effects. Because of this system’s established quantitative and molecular genetics, there is a strong foundation for understanding the genetic drivers of insect, marsupial and fungal responses to genetic variation at the species (including genetic co-variance amongst these organisms) and community level, the relative importance of direct and indirect genetic effects as a mechanism, and the potential for co-evolution through feedbacks on tree fitness.

The role of feedbacks as mechanisms in driving patterns of biodiversity and ecosystem function

There were three talks in the symposium on this topic. First, Jennifer Rowntree (University of York, UK) discussed plant–plant parasite feedbacks, second Mark Genung (University of Tennessee, USA) spoke about plant–plant intra- and inter-specific indirect genetic effects in Solidago, and third, Jennifer Schweitzer (University of Tennessee, USA) examined plant–soil genetic feedbacks. Feedbacks among interacting species are fundamental to the co-evolutionary process (Thompson, 2005), local adaption (Johnson et al., 2010), and the maintenance of biodiversity (Laine, 2009). Little is understood, however, about how feedbacks influence patterns of biodiversity and ecosystem function, or if they stabilize (i.e. by negative feedback) or destabilize (i.e. by positive feedback) eco-evolutionary patterns in community or ecosystem ecology. Genetic variation in a single species can influence many facets of ecological communities and ecosystem function, thus one may expect to observe genetically based feedbacks on ecological communities stemming from a variety of species interactions.
As a consequence of genotype by genotype interactions (i.e. where the fitness and phenotype of an interacting individual or species is affected by the genotype of an associated individual or species), feedbacks between interacting species may lead to divergence at the population scale and perhaps even in deep evolutionary time. For example, the net effects of diverse components of the soil community that either interact with the living plant (including root herbivores, pathogens, mutualists) or plant detritus (heterotrophic decomposers) can result in both positive and negative feedback to plant performance or persistence that can vary through time (Kulmatiski et al., 2008; Diez et al., 2010, Felker-Quinn et al., 2011; Van der Putten et al., 2001). Negative plant–soil feedbacks from accumulation of pathogens or herbivores may largely affect the direction of natural selection and prevent species from persisting at fixed locations or at high abundances and also promote species co-occurrence (Diez et al., 2010). Positive plant–soil feedbacks may affect the direction of natural selection and are mechanisms for persistence and even increased genetic variation (sensu Pregitzer et al., 2010).

The importance of ‘plant–neighbor’ interactions in feedbacks has yet to be fully realized, although recent data suggests they may be critical. For example, biodiversity studies that have manipulated genotypic diversity almost always invoke genotype interactions as mechanisms for any observed non-additive (i.e. unpredictable) effects (Bailey et al., 2009). Studies which manipulate G × G interactions may illuminate mechanisms that are important in mixtures containing greater numbers of genotypes. Additionally, if these G × G interactions have fitness consequences, such studies can inform how ‘plant–neighbor’ (including parasitic plants, herbivores as well as species at higher trophic levels) interactions affect both the ecology and evolution of the interacting species at small spatial scales (Genung et al., 2011; Rowntree et al., 2011). Recent research, including the talks in this symposium, suggest the novel idea that natural selection in the context of feedbacks is at least partially responsible for the non-additive effects observed in biodiversity studies.

**Application of community genetic approaches to management and conservation**

Finally, a talk by Tom Whitham (Northern Arizona University, USA) on ‘Conservation issues associated with the community genetics of foundation forest trees as drivers of community diversity, structure, stability and evolution’ raised new issues for our understanding management and conservation in an uncertain climatic future. As genetic variation in species (especially foundation species that are community and ecosystem drivers) can define community structure, ecosystem processes, species interactions, evolution and biodiversity, it is important to consider their management and conservation implications (Whitham et al., 2010). For example, because different plant genotypes can support different communities and ecosystem processes (reviewed by Bailey et al., 2009), genetic diversity in a common foundation species such as a forest tree is likely to be associated with the biodiversity of the dependent community (see review by Hughes et al., 2008). Similarly, with the demonstration that there is a genetic component to community stability (i.e. the consistent response of arthropod communities across years; Keith et al., 2010), we now realize that so called ‘emergent properties’ of communities such as stability can be due, in part, to underlying plant genetic variation.

A community genetics approach to management and conservation is likely to be productive in three major and interactive areas (climate change, exotic invasions, and habitat restoration). For example, climate change is likely to make locally adapted species locally maladapted (e.g. O’Neill et al., 2008); climate change is thought to interact with exotic invasive species to either promote or hinder their expansion (Bradley et al., 2009); and restoration of endangered habitat types has a strong genetic component with some genotypes of a foundation species far exceeding the performance of other genotypes. Recent studies have even identified specific genes and mutations associated with invasive species that allow them to dramatically alter community structure and/or make them difficult to remove or control (Wymore et al., 2011). Because there are genetic components to understanding the response of plants to climate change, exotic invasions, and habitat restoration, and they can strongly interact, we believe that community genetics has a strong role to play in the successful merger of these fields, which constitute some of the most pressing biological issues of our time.

We predict that two major tools will become increasingly important in merging climate change, exotic invasions, and habitat restoration. First, common gardens that use multiple foundation species and replicated genotypes of species along elevation and latitude gradients are crucial. By incorporating exotic species into these experiments, we can identify the genotypes of native species best able to survive climate change and interactions with exotic species, as well as those genotypes or genotype combinations that support the greatest biodiversity. This approach elevates the time honored provenance trial approach to a new level of complexity to development strategies and calibrate climate change models for the more realistic conditions of gene by biotic environment by abiotic environment interactions (G × E). Second, the application of network theory (e.g. Bascompte, 2009) to quantify the interactions among species in a community is crucial to understanding the functioning of an ecosystem. Because climate change, exotic invasions and other anthropogenic factors change species interactions and evolutionary trajectories, the conservation of species interactions may be critically important. Thus, just as population genetics has played a major role in agriculture and the green revolution, we argue that community genetics can play a vital role in the management and conservation of whole ecosystems.

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