Chapter 14

CURRENT STATUS, FUTURE OPPORTUNITIES, AND REMAINING CHALLENGES IN LANDSCAPE GENETICS

Niko Balkenhol,[1] Samuel A. Cushman,[2] Lisette P. Waits,[3] and Andrew Storfer[4]

[1]*Department of Wildlife Sciences, University of Göttingen, Germany*
[2]*Forest and Woodlands Ecosystems Program, Rocky Mountain Research Station, United States Forest Service, USA*
[3]*Fish and Wildlife Sciences, University of Idaho, USA*
[4]*School of Biological Sciences, Washington State University, USA*

14.1 INTRODUCTION

Just over a decade ago, advances in geographic information systems and genetic methodology helped usher in the field of landscape genetics, an amalgamation of landscape ecology, population genetics, and spatial statistics aimed at testing how landscape heterogeneity shapes patterns of spatial genetic variation. It is clear that the tools developed in landscape genetics have shaped a new paradigm for conducting empirical population genetics studies; although population genetics theory itself remains largely unchanged, the majority of empirical studies of spatial genetic structure now include spatially explicit tests of landscape influences on gene flow. As a result, landscape genetics has essentially replaced the isolation-by-distance paradigm with spatially explicit tests of effects of landscape variables on genetic population structure. More generally, landscape genetics has advanced the field of evolutionary ecology by providing a direct focus on relationships between landscape patterns and population processes, such as gene flow, selection, and genetic drift.

Since the inception of landscape genetics, there have been many calls for: (1) better communication among spatial statisticians, landscape ecologists, and population geneticists (Storfer et al. 2007; Balkenhol et al. 2009a); (2) more rigorous hypothesis testing (Storfer et al. 2007, 2010; Cushman & Landguth 2010; Segelbacher et al. 2010; Manel & Holderegger 2013); (3) increased consideration of proper sampling design (Storfer et al. 2007;

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Holderegger & Wagner 2008; Anderson et al. 2010; Spear et al. 2010; Landguth et al. 2012; see Chapter 4); (4) developing predictive models for conservation and management, particularly in the face of climate change (Landguth & Cushman 2010; Segelbacher et al. 2010; Manel et al. 2010; Bollinger et al. 2014); (5) selecting appropriate analytical methods and understanding their underlying assumptions (e.g., Balkenhol et al. 2009b; Wagner & Fortin 2013; Chapters 3 to 5): and (6) understanding the interactions of scale and landscape definition with the heterogeneity of the environment in affecting the strength and detectability of landscape effects on genetic variation (e.g., Cushman & Landguth 2010; Cushman et al. 2013a; Chapter 2).

In this book, it was our goal to summarize the current state of knowledge with respect to these topics and foreshadow a number of emerging opportunities and challenges the field will face in the coming decades. Landscape genetics is a field in its infancy and is characterized by rapid growth, multiple lines of parallel and sometimes contradictory work, and an apparent cultural and conceptual divide between practitioners coming from genetic versus landscape ecological backgrounds. Given this, the field appears to be producing a confusing thicket of ideas. We are confident that over time the competition among ideas and approaches will lead to increasing clarity and, we hope, a true synthesis of population and evolutionary genetic theory with spatial ecology. For now, we will offer our own view of some of the current and emerging challenges and opportunities, which we hope may focus and facilitate future progress in the field. Based on the previous book chapters and other published literature, we believe that at least ten conclusions can be drawn about the current state-of-the-art in landscape genetics.

14.2 CONCLUSION 1: ISSUES OF SCALE NEED TO BE CONSIDERED

Most landscape genetic studies have not carefully considered the effects of spatial scale and the definition of the landscape, even though these aspects can substantially affect our ability to detect relationships between population genetic structure and landscape features. As explained in Chapter 2, landscape definitions that differ in thematic content, thematic resolution, and spatial scale may dramatically alter the statistical relationships between genetic variation and landscape structure (e.g., Blair & Melnick 2012; Keller et al. 2013). While there have been a few empirical and simulation studies on the effects of scale and landscape definition in the field (e.g. Cushman & Landguth 2010; Galpern et al. 2012), the vast majority of studies published in landscape genetics have not addressed these issues at all. Indeed, many past studies have naively sought correlations between the genetic structure of a population and a putative barrier feature, such as a road or river, without considering that other landscape features might also be important. Similarly, too few studies quantitatively assess the influences of alternative scales or landscape definitions. While some researchers have begun to address these challenges by different optimization procedures (e.g. Shirk et al. 2012; Galpern & Manseau 2013; Castillo et al. 2014), this topic has not been thoroughly explored. Given the fundamental importance of scale optimization and correct landscape definition in quantifying any pattern–process relationship, we strongly feel that much more attention should be given to investigating the relationships between landscape definition, spatial scale, and the accurate quantification of landscape–genetic relationships.

14.3 CONCLUSION 2: SAMPLING NEEDS TO SPECIFICALLY TARGET LANDSCAPE GENETIC QUESTIONS

One of the largest limitations of most landscape genetics research conducted to date is that sampling is often done without *a priori* consideration of expected landscape effects on genetic variation and underlying processes. However, sampling for landscape genetics can only be effective if it is based on these expectations, which should be stated as testable hypotheses (see below and Chapter 4). To derive such hypotheses, we need to develop a theory that includes the multifaceted influences of landscape heterogeneity on genetic variation (see conclusion 10). Nevertheless, even if hypotheses are clearly formulated at the beginning of a study, the complexity of landscape genetic research will always be a challenge for optimal study design and sampling. Thus, we strongly advocate simulations as a means to test different sampling options before beginning a study, and to conduct a power analysis to determine whether certain landscape–genetic relationships can actually be detected within a given study (Cushman 2014).

14.4 CONCLUSION 3: CHOICE OF APPROPRIATE STATISTICAL METHODS REMAINS CHALLENGING

We have not yet reached a true consensus on which analytical methods to use for the three analytical steps of landscape genetics described in Chapter 1. Reflective of the rapid growth of a new field, there are a number of alternative methods currently in use to analyze landscape genetic data in node-, neighborhood-, and link-based frameworks (see Wagner & Fortin 2013; Chapter 5). Few of these methods have been rigorously compared, and there is no general agreement as to which methods are best for a specific question. This is an area of utmost importance to advance the field and should receive very high priority for future research. Given the complexity of the task, we will probably never have a single method that fits all research questions and data, but the conceptual framework suggested by Wagner and Fortin (2013; see Chapter 5) helps to guide future efforts for developing appropriate methods. To address some of the challenges associated with existing methods used in landscape genetics, increasingly complex statistical approaches are suggested. Unfortunately, some of the more complex analytical approaches seem to be viewed as all-embracing and impeccable, and are simply used "as is" in many landscape genetic studies. A good example is the use of genetic assignment and clustering methods, which are often simply used to infer a single "best" number of populations contained in the data. As shown in Chapter 7, this task is far from trivial, making the appropriate use of assignment-based methods much more challenging than is often realized. At the same time, assignment and clustering methods can do much more than infer the most likely number of populations (e.g., Murphy et al. 2008; Balkenhol et al. 2014), and their potential for landscape genetic analyses remains high. Overall, the overwhelming variety of different analytical options will continue to be one of the most challenging aspects in landscape genetics in the next years, especially for beginners. However, we are actually encouraged by the great diversity of alternative methods that are being developed and evaluated, as they are proof of the tremendous interest of the scientific community in the field. This "free-market" of ideas will eventually select the best approaches, provided that competing methods are thoroughly evaluated using empirical and simulated data.

14.5 CONCLUSION 4: SIMULATIONS PLAY A KEY ROLE IN LANDSCAPE GENETICS

Simulation modeling will play a vital role for the future development of landscape genetics. Analysis of data is the foundation of empirical science, and is critical to advance landscape genetics. However, when analyzing empirical data a researcher never knows the true process that governs the observed response. One can only *infer* the process from the pattern of response and its association with one or multiple hypotheses. The great power of simulation is that it allows this inferential pathway to be inverted. That is, in simulation modeling the researcher stipulates and controls the process being modeled and then can generate the patterns of genetic structure that would result from that process. This provides critical control over the pattern–process relationship that is essential to reliably evaluate such things as effect of different landscape definitions, spatial scale, effectiveness of alternative sampling schemes, and power of different statistical methods (Cushman 2014). While there is clearly much more work to be done in developing realistic and efficient simulation models for landscape genetics, much progress has already been made (Chapter 6). Importantly, simulations will also be an essential component for developing and testing general theories of landscape genetics (see conclusion 10). However, to realize the full potential of landscape genetic simulations, there is a need to incorporate the various influences of landscape heterogeneity on neutral and adaptive genetic variation (see conclusion 6), so that we can directly evaluate the interaction between landscapes, processes, and resulting patterns in genetic variation (e.g. Balkenhol & Landguth 2011; Cushman 2014, 2015).

14.6 CONCLUSION 5: MEASURES OF GENETIC VARIATION ARE RARELY DEVELOPED SPECIFICALLY FOR LANDSCAPE GENETICS

To accurately and reliably quantify landscape–genetic relationships, we also need to develop measures of genetic variation that explicitly account for the spatial complexity of reality. For the quantification of landscape heterogeneity (analytical step 2), multiple novel approaches have been suggested in recent years, and several of them are specifically intended for landscape genetics (e.g.,

McRae 2006, Van Strien et al. 2012). In contrast, very few measures of genetic diversity and structure (analytical step 1) have been designed specifically for landscape genetics (Chapter 3). Some of the existing measures are not ideal for the field, because populations that inhabit heterogeneous landscapes rarely conform to classical population genetic assumptions such as random mating and Hardy–Weinberg equilibrium, and more often are characterized by metapopulation or gradient structure (Chapter 2). Nevertheless, a few notable exceptions exist. For example, Shirk and Cushman (2011) developed a spatially explicit estimate of genetic diversity (*sGD*) based on grouping individuals into potentially overlapping genetic neighborhoods that match the population structure, whether discrete or clinal. Recently, Shirk and Cushman (2014) further explored spatial effects on genetic diversity by applying Wright's neighborhood concept (Wright 1943) to isolation-by-resistance to produce spatially explicit estimates of local population size from genetic data in continuous populations. Similarly, to estimate genetic structure within a network of potentially connected metapopulations, the ***conditional genetic distance*** (*cGD*) was developed by Dyer and Nason (2004) (see also Dyer et al. 2010; Chapter 10). This distance reflects gene flow among subpopulations in a much more realistic way than traditional measures of genetic differentiation, because it does not assume a simple stepping stone model of migration; nor does it assume gene flow to be homogeneous across the landscape. Thus, both *sGD* and *cDG* were designed specifically to avoid some of the problematic assumptions of classical measures of genetic variation, and improve our ability to accurately quantify genetic patterns in heterogeneous environments. These recent efforts illustrate that it is both possible and important to develop measures of genetic variation that more explicitly match the data and research questions typical of landscape genetics. We particularly encourage geneticists to help us advance towards measures that better reflect the spatial complexity of natural populations and the various processes that influence them.

14.7 CONCLUSION 6: LANDSCAPE RESISTANCE IS JUST ONE OF THE POSSIBLE LANDSCAPE–GENETIC RELATIONSHIPS

The majority of published landscape genetics studies has focused on quantifying the effects of landscape features *in between* sampling locations on gene flow and resulting genetic structure, for example, by incorporating barriers or estimates of landscape resistance (Chapters 2 and 8). However, landscape characteristics *at* or *around* sampling locations also affect the processes that shape genetic variation. These should find more consideration in future studies, as suggested by Wagner and Fortin (2013; Chapter 5), Murphy et al. (2010; Chapter 9), and Pflüger and Balkenhol (2014). For example, under isolation-by-environment (IBE; Wang & Bradburd 2014), genetic differentiation can be predicted based on the dissimilarity of local environmental variables. Such isolation-by-environment was shown to explain more variation in gene flow than isolation-by-resistance (IBR) in 17 species of Caribbean *Anolis* lizards (Wang et al. 2013). In order to evaluate the relative importance of IBE versus IBR more generally, we need to incorporate both local environmental variables and matrix resistance in our studies. For example, Cushman et al. (2013b), in a study comparing IBE and IBR models of genetic differentiation of a riparian tree found that both riverine network connectivity and climatic gradients contribute to genetic differentiation. Overall, landscape genetics should not limit itself to evaluating the effects of landscape resistance on genetic structure, but embrace the full complexity of interactions between spatial environmental heterogeneity, ecological and evolutionary processes, and the resulting genetic patterns.

14.8 CONCLUSION 7: GENOMICS PROVIDES NOVEL OPPORTUNITIES, BUT ALSO CREATES NEW CHALLENGES

Landscape genomics is one way to fully grasp the various influences that landscape can have on neutral and adaptive genetic variation. Genomic approaches are increasingly used in landscape genetics and offer revolutionary abilities to understand selection and adaptation in complex landscapes (Chapter 9). Next-generation sequencing has allowed collection of vast amounts of sequence data, even in non-model organisms. Development of numerous analytical methods has followed, but several issues still plague landscape genomics studies with complicating factors that make detecting true signatures of selection difficult. A major challenge in landscape genomics has been differentiating signals of selection as detected by changes in allele frequencies from demographic history. For example,

nearby populations tend to have correlated allele frequencies, as well as shared environmental variables, which can result in high false-positive rates of correlations between allele frequencies and environmental variables (Coop et al. 2010; Joost et al. 2013). Moreover, recent range expansions can confound drift caused by serial founder effects (also known as "allele surfing"; Excoffier & Ray 2008) with selection, resulting in false positives. In general, the absence of demographic data can result in overestimation of rates and strengths of selection because not accounting for population structure can bias diversity and allele frequency estimates among populations (Joost et al. 2013; Lotterhos & Whitlock 2014). Some researchers have developed methods for joint estimation of demographic parameters and selection (Eyre-Walker & Keightley 2009). However, due to their stepwise nature, the resulting models tend to over-fit the data (Joost et al. 2013).

Overall, these new ways for deriving genetic data also provide new challenges, as summarized in Chapter 9. A major challenge, then, is to analyze data sets that integrate both the genomic landscape and the ecological landscape in order to understand the spatial distribution of adaptive genetic variation. Landscape genomics has an exceptionally high potential for increasing our understanding of the feedbacks between ecological and evolutionary dynamics, but only if we realize that correlation tests to detect selection are only a first step, and that local adaptation is not only influenced by local environmental pressures but also by the complex interactions between local selection, gene flow, and drift – and all of these aspects can be affected by landscape heterogeneity and change (e.g., Lowe & McPeek 2014; Fordham et al. 2014; Richardson et al. 2014). Thus, linking complex genotypes to phenotypes and local adaptation is one of evolutionary ecology's grand challenges in the coming decade(s) (Cushman 2014).

14.9 CONCLUSION 8: THE SCOPE OF LANDSCAPE GENETICS NEEDS TO EXPAND

In addition to considering neutral and adaptive processes, landscape genetics generally must broaden its scope, for example, with respect to study organisms. A large number of studies have used landscape genetics for various organisms in aquatic and terrestrial systems (Chapters 11 to 13; Storfer et al. 2010). However, the taxonomic range of landscape genetic research should be substantially expanded. Studying taxonomic groups, such as insects, which are small in size, highly mobile, and have short generation times, will facilitate controlled and replicated experiments, which are necessary to confirm putative relationships seen in empirical field studies or suggested in simulation modeling (e.g. Cushman 2014, 2015). Such experimental landscape genetics will help to clarify pattern–process relationships governing genetic patterns, especially if they are conducted in multiple study areas (e.g. Short Bull et al. 2011). In addition, it is essential for more studies to combine landscape genetic approaches with other research methods, so that the actual processes underlying observed genetic patterns can be identified and their relative importance evaluated (e.g. Cushman and Lewis 2010; Reding et al. 2013; Shafer et al. 2012; Weckworth et al. 2013). Another way that landscape genetics needs to broaden is in the geographic focus of studies and training of scientists. Currently landscape genetic studies are strongly biased toward temperate climates and developed countries (Storfer et al. 2010).

14.10 CONCLUSION 9: SPECIFIC HYPOTHESES ARE RARELY STATED IN CURRENT LANDSCAPE GENETIC STUDIES

In our opinion, one of the most important steps for increasing scientific rigor and broadening the scope of landscape genetics is the formulation of clear, testable hypotheses that describe how genetic variation and underlying processes are expected to be influenced by the landscape. Currently, a disturbingly large portion of the published landscape genetics literature does not define clear hypotheses and considers only a few of the possible landscape-genetic relationships (see conclusion 6). If we were to derive such hypotheses before beginning a study, we would probably often realize that factors other than landscape resistance can affect our genetic data, and it would help us to identify how other types of data and research approaches could help to answer specific research questions and disentangle the influence of multiple underlying processes. Indeed, we argue that we need to move away from single-species, single-landscape studies that focus on finding statistical significant correlations between spatial patterns in genetic and landscape data (statistical, pattern-focused;

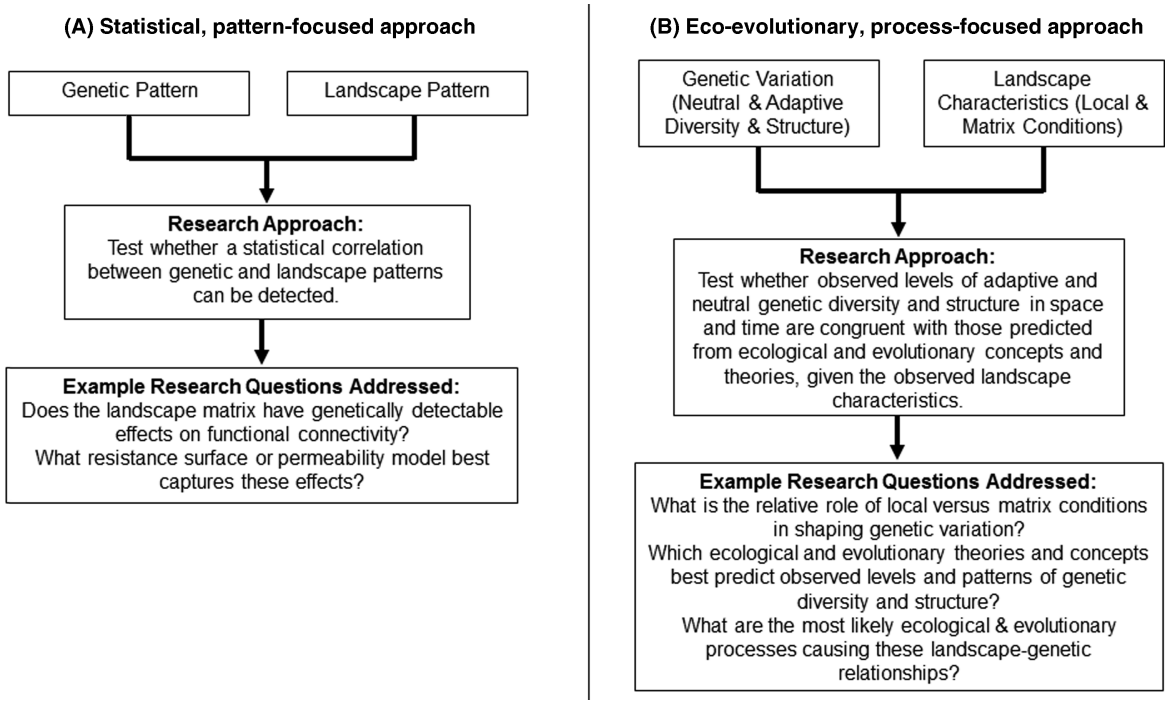

Fig. 14.1 Schematic comparison of (A) current landscape genetic approaches that are often pattern-focused and correlation-based with (B) a suggested approach that focuses on the eco-evolutionary processes shaping landscape–genetic relationships.

Fig. 14.1A) and towards studies that focus on finding meaningful relationships between landscape characteristics and the processes that shape genetic variation across space and time (eco-evolutionary, process-focused; Fig. 14.1B).

14.11 CONCLUSION 10: A COMPREHENSIVE THEORY FOR LANDSCAPE GENETICS IS CURRENTLY MISSING

One aspect related to all of the above conclusions is the current lack of a comprehensive theory that links landscape heterogeneity in space and time to patterns in neutral and adaptive genetic variation, by considering the many different processes that affect gene flow, drift, and selection. One major goal of landscape genetics should be to develop a more mechanistic understanding of how genetic variation interacts with species distribution, population size and density, dispersal ability, differential resistance, selection gradients, and individual fitness in heterogeneous environments. Trying to move towards a theoretical framework that accomplishes this would substantially improve our ability to derive testable hypotheses, to sample and analyze landscape and genetic data in a targeted way, and to combine it with other data and research approaches for more meaningful inferences. We urge researchers in landscape genetics to focus more strongly on developing conceptual and theoretical foundations for landscape genetics, and suggest that synthesizing results provided by existing studies is one way to achieve a more general understanding of landscape influences on genetics.

14.12 THE FUTURE OF LANDSCAPE GENETICS

As can be seen above, much remains to be done in landscape genetics. We are convinced that, despite the current challenges, the field has a bright and dynamic future and that landscape genetic approaches will

continue to provide exciting new insights in various scientific disciplines.

This is a time of explosive growth in landscape genetics, with a panoply of different ideas, methods, and scopes of analysis. It is likely that this complexity is going to increase even more, for example, because whole genome sequencing and bioinformatics are driving a transformative paradigm shift that presents tremendous opportunities and challenges to our field. Similarly, increasingly sophisticated approaches for analyzing data related to landscape genetics, such as animal movement and population demography, are constantly being developed (e.g., Kranstauber et al. 2014; Merow et al. 2014). We believe that for our field to take full advantage of these opportunities, we must effectively combine the ongoing work in landscape genetics, which has focused on describing population structure and associating it with landscape features, with genomics, bioinformatics, and other research approaches in experimental and field settings (Cushman 2014). To accomplish this, landscape geneticists need to think even more carefully in advance about hypotheses, suitable data, study design, and data analysis so that results can be generalized and their implications can be explored across scales of biological organization, from nucleotides to ecosystems.

We are very interested to see what directions landscape genetics will take in the future. On the one hand, we foresee that the different ways landscape genetics can be used (see Chapter 1) will lead to more differentiated and more disparate developments in "landscape genetics for ecology" versus "landscape genetics for genetics". Ecologists will focus even more on evaluating the processes that can be inferred from analyzing landscape genetic data and will hopefully develop new ways for combining landscape genetic data with other types of research methods, including telemetry, stable isotopes, mark-recapture, or demographic population modeling. In contrast, geneticists will put more emphasis on developing novel ways for analyzing genomic data in a landscape context, on testing existing evolutionary theory, and on deriving new theory for adaptive processes in complex landscapes. Importantly, we also see much potential for merging ecological and evolutionary principles within a landscape genetic framework. Neutral and adaptive processes do not occur isolated from one another and need to be considered in combination to analyze eco-evolutionary dynamics (Cushman 2014; Landguth et al. 2011), which is a prerequisite for truly understanding the emergence and maintenance of biological diversity in spatially and temporally varying environments (Hand et al. 2015).

Currently, it seems that our technical abilities to gather genetic data in the field, to analyze it in the lab, and to obtain landscape data over very large spatial extents (e.g., via remote sensing) have surpassed our abilities to draw meaningful conclusions from these data. Landscape genetics is probably not the only scientific field where this is currently evident.

Given the complexities and current challenges in landscape genetics, it is not surprising that many researchers diving into the field are somewhat overwhelmed by the variety of research approaches, and feel that they urgently need help with analytical aspects of landscape genetics. This book tries to provide some help to get started, but we also hope that the book shows that landscape genetics is not just a set of tools, and thus requires much more than the combined use of landscape and genetic data. While we absolutely realize the importance of using appropriate methods for this task (see conclusion 3), we feel that too little emphasis is currently given to the development of landscape genetic theories, the derivation of explicit hypotheses, and the synthesis of results obtained from existing landscape genetic studies. We should keep in mind that the ultimate goal of landscape genetics is not just to provide new tools for the joint analysis of genetic and landscape data but also to enhance our understanding of how landscapes shape patterns in neutral and adaptive genetic diversity and structure. Thus, we hope that in the not too distant future, we can move away from the currently dominating question in the field of "*How do we do it?*" towards the more fundamental question of "*What do we learn from it?*" This book hopefully serves as another small step towards reaching this ambitious goal.

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