

Landscape Genetics

How Landscapes Affect Ecological Processes

Landscape genetics evaluates the effect of landscape structure and composition on the movement, dispersal and gene flow of animals and plants.

It is applied, for instance, to test whether de-fragmentation measures such as green bridges or landscape corridors effectively enhance the movement of individuals in fragmented landscapes.

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Combining Population Genetics and Landscape Ecology

Landscape genetics seeks to assess how landscape structure and composition affect movement, dispersal and gene flow of animals and plants. Landscape genetics has recently been promoted in review articles (e.g., Holderegger and Wagner 2008) and at international conferences (e.g., Balkenhol et al. 2009). The research field amalgamates population genetics and landscape ecology by combining the theory and methods of the former with the GIS-applications, spatial analyses and modelling of the latter (Manel et al. 2003). While landscape ecology stresses the dynamics of patterns and processes in changing landscapes by characterizing landscape structure (e.g., suitable versus unsuitable habitats, barriers versus corridors, etc.), population genetics uses various genetic techniques to indirectly measure how animals and plants

(and therefore their genes) move and disperse across landscapes. By merging the two fields, landscape genetics provides a powerful tool to identify the effects of landscape properties on movement, dispersal and gene flow. Given the appeal of landscape genetics, both in science and application, ETH Zurich will offer a one-week winter school on landscape genetics next February (box 1) and SAGUF will introduce this new field to its members at its annual meeting in 2011 (box 2).

An Innovative Research Field

The combination of genetic and landscape or environment data with modelling approaches in landscape genetics offers a setting to test emerging questions of species behavior under land-use and climate change. A prominent example of landscape genetic research and its application in conservation management relates to the effectiveness of de-fragmentation measures. The basic question is whether implemented structural connectivity measures lead to functional connectivity; the latter being the effective exchange of individuals or genes among populations. For instance, cantonal authorities in Switzerland already use landscape genetic approaches to assess the degree of population fragmentation due to highways, major roads, fenced railways or

settlements in wildlife corridors of national importance. This knowledge of the present situation will also enable the future assessment of the effectiveness of mitigation measures such as green bridges or underpasses once they have been implemented. Similarly, landscape genetic methods are used to study the effectiveness of connectivity measures taken on agricultural land under national or international agri-environmental schemes. In doing so, landscape genetics develops into a valuable planning and monitoring tool in practical management. What we have learned from landscape genetics so far shows that especially animals but also plants more often spread over larger distances than had been suggested hitherto (Holderegger and Wagner 2008).

Approaches and Challenges

Currently, landscape genetics is using three approaches to detect the effects of landscape structure and composition on movement, dispersal and gene flow, namely 1. approaches based on genetic discontinuities (*Where can distinct gene pools be found in a landscape?*), 2. approaches based on genetic distance (*How different are two populations or individuals in genetic terms?*) and 3. approaches assessing current movement and gene flow.

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1. Approaches based on **genetic discontinuities** investigate whether the boundaries between genetically distinct populations (i. e., populations that are not in contact with each other) spatially coincide with particular landscape structures (e. g., roads, rivers or settlements) on topographic or land use/land cover maps, which potentially act as barriers to movement and dispersal. Various clustering methods are used to assign individuals to genetic pools. An empirical example is provided by Riley et al. (2006). They showed that coyotes and bobcats form genetically isolated groups on different sides of a Californian highway and that the highway therefore acts as a barrier to gene flow.
2. **Genetic distance** provides a measurement of how often populations or individuals come into mating contact. In other words, genetic distance is a measure of the abundance of movement, dispersal and gene flow between two localities. Approaches based on genetic distance use GIS data on landscape elements such as forests, roads, open fields or meadows. Most often, a resistance value is given to each landscape element, reflecting the permeability of the element to the movement of a given species. This procedure allows calculating a minimum cumulative landscape resistance between two localities. This least cost distance describes a potential movement path minimizing the costs of movement through a particular landscape. The correlation between genetic distance and different least cost distance models can then be evaluated and allows identifying those landscape elements that mainly influence movement, dispersal and gene flow. Using such an approach, and regarding roe deer dispersal in a fragmented landscape, Coulon et al. (2004) showed that roe deer strongly follows woodland patches and avoids crossing open land without shelter.
3. The last approach estimates the **contemporary movement of individuals or current gene flow**. Assignment tests determine contemporary migrants among populations based on their genetic com-

BOX 1:**Winter School in Landscape Genetics at ETH Zurich**

February 14 – February 19, 2011

WSL Swiss Federal Research Institute, Birmensdorf, Switzerland

This course will be held by *Rolf Holderegger*, *Janine Bolliger* and *Gwenaëlle Le Lay*. It will introduce students to major concepts and methods of landscape genetics. Special emphasis is given to current state-of-the-art methods and to hands-on exercises. The course will deal with types of genetic and landscape ecological data for landscape genetic analysis, landscape resistance and gene flow (least cost paths, Mantel tests, regression with permutation), overlays and genetic boundaries (clustering, barrier detection, kriging), contemporary gene flow (paternity analysis, assignment tests), identification of genetic markers of adaptive relevance (i. e., landscape genomics) and methods for model evaluation. The benefits and limitations of landscape genetics will also be highlighted. Basic knowledge in population genetics and GIS is required.

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position. In other words, given the genetic composition of a given individual, to which population of origin does it most probably belong? The genetic composition of most individuals matches that of the population where they were sampled – these are residents. However, some individuals will be assigned to a population different from where they were sampled – these are migrants from other populations. Using such an assignment test, Angelone and Holderegger (2009) showed that functional connectivity at the landscape scale in the valley of the Swiss river Reuss could be achieved through the construction of new ponds; the ponds increased the movement of tree frogs, thus acting as stepping stones between existing populations. Another method to identify contemporary gene flow,

called parentage analysis, has mainly been used in plants. Kamm et al. (2009) found that even widely scattered individuals of a rare forest tree species in northern Switzerland form part of an extensive network connected by regular pollen exchange over distances of more than ten kilometres. These trees, although spatially isolated, were functionally well connected.

Outlook

Many of the above mentioned methods and approaches still suffer from conceptual and methodological shortcomings (Balkenhol et al. 2009). Future progress in landscape genetics depends on the development of appropriate analytical tools allowing a better assessment of the relationships between genetic and landscape data. Hence, close collaboration between land-

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BOX 2:**SAGUF-Jahrestagung 2010****Erfahrungsaustausch zu inter- und transdisziplinärer Praxis**

25. November 2010, 9 bis 16 Uhr, Altes Spital, Solothurn, Schweiz

Die diesjährige SAGUF-Jahrestagung findet statt als Workshop zum Thema **Erfahrungsaustausch zu inter- und transdisziplinärer Praxis** und wird von der SAGUF und dem Nationalen Forschungsprogramm *Nachhaltige Wassernutzung* (NFP 61) gemeinsam organisiert. Die Teilnahme am Workshop ist beschränkt auf SAGUF-Mitglieder und Forschende des NFP 61.

Anmeldung bis 31. Oktober 2010 an: SAGUF Geschäftsstelle, *Dr. Claudia Zingerli*, ETH Zentrum CHN, 8092 Zürich, Schweiz, E-Mail: saguf@env.ethz.ch

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Vorschau: Thema der SAGUF-Jahrestagung 2011: **Landschaftsgenetik**

scape ecologists and population geneticists is required, since only statistically robust and easy-to-use approaches will allow landscape genetics to expand its full power with respect to application in management practice (Segelbacher et al. 2010). One particular advantage of landscape genetics is that large spatial areas (i. e., whole landscapes) can be monitored over extended time periods. Therefore, landscape genetics can provide the whole landscape view of functional fragmentation or connectivity that is urgently needed in conservation and landscape management.

Landscape genetics offers a setting to test emerging questions of species behavior under land-use and climate change.

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Landscape genetics is well suited to complement small-scale ecological studies on the dispersal of marked animals – here a marked damselfly – on larger spatial scales.

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