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Research Article

Adaptive vs. neutral genetic diversity: implications for landscape genetics

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Abstract

Genetic diversity is important for the maintenance of the viability and the evolutionary or adaptive potential of populations and species. However, there are two principal types of genetic diversity: adaptive and neutral – a fact widely neglected by non-specialists. We introduce these two types of genetic diversity and critically point to their potential uses and misuses in population or landscape genetic studies. First, most molecular-genetic laboratory techniques analyse neutral genetic variation. This means that the gene variants detected do not have any direct effect on fitness. This type of genetic variation is thus selectively neutral and tells us nothing about the adaptive or evolutionary potential of a population or a species. Nevertheless, neutral genetic markers have great potential for investigating processes such as gene flow, migration or dispersal. Hence, they allow us to empirically test the functional relevance of spatial indices such as connectivity used in landscape ecology. Second, adaptive genetic variation, i.e. genetic variation under natural selection, is analysed in quantitative genetic experiments under controlled and uniform environmental conditions. Unfortunately, the genetic variation (i.e. heritability) and population differentiation at quantitative, adaptive traits is not directly linked with neutral genetic diversity or differentiation. Thus, neutral genetic data cannot serve as a surrogate of adaptive genetic data. In summary, neutral genetic diversity is well suited for the study of processes within landscapes such as gene flow, while the evolutionary or adaptive potential of populations or species has to be assessed in quantitative genetic experiments. Landscape ecologists have to mind these differences between neutral and adaptive genetic variation when interpreting the results of landscape genetic studies.

Introduction: the meaning of genetic diversity

> "According to the neutral theory, the frequency of alleles is determined by purely stochastic rules, and the picture that we obtain at any given time is merely a transient state representing a temporary frame from an ongoing dynamic process" (Li and Graur 1991, p. 39).

In their seminal paper, Manel et al. (2003) stated that landscape genetics, the amalgamation of molecular population genetics and landscape ecology, aims at providing information about the interaction between landscape features and evolutionary processes within species such as gene flow or local adaptation. The authors further stressed that the understanding of such processes requires detailed knowledge of how landscape

characteristics influence the local gene pools of populations. We thus need data on the genetic diversity and differentiation of populations. Genetic differentiation can for instance be defined as how much of the genetic diversity present in a sample of several populations is found among vs. within these populations (Pearse and Crandall 2004). Additionally, we also need data on local adaptation, i.e. information on how natural selection might have changed local gene pools. However, what seems to be an easy task, namely to infer differential adaptation and evolutionary potential from patterns of genetic diversity and differentiation, is far from being trivial and, indeed, one of population genetics' most controversially debated topics.

One could argue that there are two different types of genetic diversity instead of just one genetic diversity. One type, the neutral genetic variation, is straightforward to measure in the laboratory with the help of the ever increasing arsenal of molecular-genetic markers. The other, the adaptive or selective genetic variation, is more difficult to estimate, namely in quantitative genetic experiments (see below). For landscape ecologists entering the field of landscape genetics, it is important to know the distinction between neutral and adaptive genetic diversity. Therefore, a short introduction to neutral and adaptive genetic variation seems relevant and should also point to the usefulness and pitfalls of the application of these two principal types of genetic diversity (a glossary of some basic genetic terms is given in Table 1). This distinction between neutral and adaptive genetic variation is largely unrecognised outside of population or conservation genetics (Pearman 2001).

We give a brief introduction to the two basic types of genetic diversity and try to outline consequences for landscape genetic studies. This should help landscape ecologists to better understand the results that population genetics can provide and to better embrace the limits of genetic data, whose potential is sometimes overrated. However, it is not the aim of this article to thoroughly introduce the reader to population genetics. Hence, we do not give much detail on theoretical models and their assumptions. Corresponding information can be found in several, excellent textbooks (e.g. Falconer and MacKay 1996; Hartl and Clark 1997). Instead, we want to show how population genetics is generally used (or sometimes misapplied) in practise and what landscape ecologists can expect from population genetic data.

We start by presenting some theory and examples of applications for both neutral and adaptive genetic diversity, subsequently discuss their relationship and end with some general comments on the different spatial and temporal scales investigated and the different concepts of landscape used by landscape ecologists and population geneticists.

Neutral genetic variation

The term 'neutral' refers to a gene (or a locus) that has no (or almost no) effect on fitness, e.g. in terms of offspring produced. Assume that at a given gene only two gene variants (alleles) occur, namely *a* and *b*. In a diploid species (with two chromosome sets), three different genotypes can occur, namely the homozygotes *aa* and *bb* and the heterozygote *ab*. However, it does not matter for a given individual which of these three genotypes it carries, since this has no effect on its performance. As natural selection does not act upon these alleles, they are of no direct adaptive value and are selectively neutral or, in short, neutral (Kimura 1983; Conner and Hartl 2004). Neutral genetic variation is the genetic variation estimated at such neutral genes.

Neutral genetic variation and laboratory techniques

Molecular-genetic methods have seen unprecedented progress during the last two decades in terms of analytical power and throughput. It is now possible to generate genetic data for large sample sets including many individuals and populations. A wide array of different molecular markers is available that differ with respect to the kind of data generated (co-dominant or dominant; see below), degree of detectable variation as well as in their mode of inheritance (Lowe et al. 2004).

The nuclear genome (nDNA) of organisms is biparentally inherited, from mother and father. In plants, it is transmitted both through seed and

Table 1. Glossary of some population genetic terms (modified from Conner and Hartl 2004; Frankham et al. 2004; Lowe et al. 2004; Futuyma 2005).

Term	Explanation
Adaptive	A phenotypic trait that has evolved to help an organism cope with the environment or to increase its fitness is adaptive; adaptation always has a genetic basis
Additivity	When the alleles at a locus do not affect each other's expression, neither at the same nor at a another locus, they are purely additive; this genetic variation is responsible for the evolutionary potential of populations
Allele	An allele is a particular variant of a given gene; diploid (with two chromosome sets) organisms have two alleles per locus, one from the mother and one from the father
Co-dominant	A locus where all its alleles are expressed is co-dominant; heterozygotes can therefore be distinguished from homozygotes
Dispersal	Dispersal is the movement of individuals to different localities; through individuals in animals and seed in plants
Dominant	A locus is dominant if one allele is dominant over another one (the recessive) and is therefore solely expressed; dominant homozygous individuals can not be distinguished from heterozygotes
Fitness	Fitness is the ability of an organisms to survive and reproduce; a common measure of fitness is the lifetime number of offspring produced
Gene	In molecular genetics, a gene is a region of DNA; in population genetics, it is the functional unit of heredity; the term 'gene' has many different meanings
Gene diversity	Gene diversity is one particular measure of genetic variation, namely H_e
Gene flow	Gene flow is the movement of genes between populations caused by migration and subsequent mating; gene flow is through individuals in animals and through pollen *and* seed in plants
Genetic differentiation	Genetic differentiation refers to differences of populations at neutral, molecular markers or adaptive, quantitative traits; in other words, how different are the populations?
Genetic diversity	Genetic diversity is any measure of the genetic variation at neutral or adaptive loci of a population or a species; in other words, how diverse are the populations
Genotype	Genotype refers to the allelic composition of an individual at any specified number of loci
Heterozygous	An individual that possesses different alleles at a locus is heterozygous
Homozygous	An individual that posses only one allele (but two times the same in a diploid organism) at a locus is homozygous
Locus	A locus (plural: loci) is the site on a chromosome occupied by a specific gene; often used interchangeably with gene
Migration	In ecology, migration refers to directional large-scale movement of organisms; in population genetics, it is the movement of individuals among populations; often used interchangeably with gene flow
Molecular marker	A molecular marker is a sequence of DNA or a protein (in case of allozymes) that can be screened for genetic variation in the laboratory using molecular-genetic methods
Neutral	A locus that does not help an organism to cope with the environment or to increase its fitness is neutral; large parts of an organism's DNA are effectively neutral
Phenotype	Phenotype refers to the outward appearance of a genotype; it is the outcome of the interaction between genotype and environment
Quantitative trait	A phenotypic character that varies continuously and can easily be measured is a quantitative trait

pollen. There are two principal types of (mainly) nDNA molecular markers, namely co-dominant and dominant markers (for the use of these different markers and the information they can provide also see Latta 2006). Co-dominant markers provide the possibility to score the identity of the two gene variants (alleles) that a diploid individual possesses at a given gene. Scorings might therefore be: *aa*, *ab*, *cc*, *cd* etc. Co-dominant markers include allozymes (proteins) and the highly variable microsatellites. In contrast, dominant markers (Lowe et al. 2004) create banding patterns that resemble a barcode. For each individual, tens to hundreds of bands can be generated, resulting in a DNA fingerprint. Each band of this fingerprint refers to a locus with only two alleles. Let us assume that one of these alleles, *a*, is dominant over the other allele, *b*. The genotypes carrying the dominant allele, i.e. *aa* and *ab*, thus show the same band: One cannot discriminate the heterozygote from the homozygote genotype. In contrast, the genotype *bb* does not show a band. As a consequence, dominant genetic markers are usually scored in a band presence/band absence manner. Corresponding marker types are RAPDs (random amplified polymorphic DNAs), ISSRs

(inter simple sequence repeats) or AFLPs (amplified fragment length polymorphisms). These marker types are highly variable, comparatively cheap, easy to use and fast, but limited in their information content.

In contrast to nDNA, the genome of organelles (mitochondria (mtDNA) in both animals and plants and chloroplasts (cpDNA) in plants) is usually uniparentally transmitted, either through the father or the mother. Organelles have a single-copy genome (haploid) with only one gene variant per gene. In fact, the whole organelle genome behaves like a single gene, since there is no recombination (Lowe et al. 2004). Both mtDNA and cpDNA are most often analysed either as RFLPs (restriction fragment length polymorphisms) or as DNA sequences. Short descriptions of all the above mentioned molecular markers and techniques can be found in many textbooks (e.g. Frankham et al. 2004; Lowe et al. 2004).

Most of the molecular markers presently used in population genetics have one thing in common: They are essentially neutral and do not undergo selection. As a consequence, these markers do not allow referring to the adaptive or evolutionary potential of populations or species. (Note that there are some specific molecular markers that are adaptive; Conner and Hartl 2004).

How are neutral genetic variation and differentiation estimated?

The most commonly used statistical measure of neutral genetic variation of a population is gene diversity, H_e. It is calculated as

$$H_e = 1 - \sum_{i=1}^{n} p_i^2$$

where p_i is the frequency of the ith allele at a given locus in a population, and n refers to the number of alleles at this locus. The formula can be interpreted as the probability of sampling two different genes from a population (Hartl and Clark 1997). Gene diversity, H_e, is usually calculated per locus and subsequently averaged over several loci. This average gene diversity represents a measurement of the genetic variation of a population. It should be noted that there is a multitude of different statistical measurements available to estimate genetic variation of populations. Some of them are universal, others are marker type specific and depend, e.g., on the particular mode of inheritance or mutational change (Lowe et al. 2004).

Similarly, population geneticists use many different measurements to refer to population differentiation (with some of them correcting for sampling variance; Lowe et al. 2004). The most commonly used measure of genetic differentiation is Wright's F-statistics (Wright 1951; Conner and Hartl 2004).

$$F_{ST} = 1 - H_S/H_T$$

where H_T is the average gene diversity calculated for the whole data set (according to the formula of H_e given above) of usually several populations ($N \geq 2$), and H_S is the mean of the average gene diversity calculated for each of these populations. F_{ST} gives an estimate of the amount of genetic variation found among populations and refers to the genetic differentiation or the genetic structure of these populations. If F_{ST} approximates unity, all genetic variation is found among the populations (i.e. different alleles are found in the different populations) and if F_{ST} is zero, the populations are not differentiated at all (i.e. the same alleles are found in the same frequencies in all the populations). F_{ST} can either be calculated over the whole sample set of populations (mean differentiation) or in a pairwise fashion for each pair of populations. F_{ST} can also be hierarchically structured by introducing additional levels, e.g., to estimate regional differentiation in a set of populations.

An application of neutral genetic variation: gene flow in space and time

Landscape ecologists are much interested in the connectivity of landscapes. Connectivity has both structural and functional aspects. The structure of a landscape can readily be quantified by any kind of landscape index. However, as Li and Wu (2004) and Holderegger et al. (in press) have stressed, a validation of such indices asks for a test of the functional connectivity of a landscape. This may include estimations of gene flow patterns. In other words, does structural connectivity lead to an increased exchange of individuals or genes?

Gene flow homogenises the genetic diversity found within populations and thus leads to a decrease of their genetic differentiation. An often used estimate to refer to past gene flow, *Nm* (i.e. number of migrants exchanged among populations per generation), relies on the differentiation of populations, F_{ST}, under the assumptions of Wright's island model (Conner and Hartl 2004; Vandewoestijne and Baquette 2004) with

$$Nm = (1 - F_{ST})/4F_{ST}$$

Gugerli et al. (WSL Birmensdorf, unpublished data) have investigated several oak populations (*Quercus* spp.) in Switzerland. Their sampling was far from being complete. There were many more individuals present in the populations and many unsampled oak populations in between the sampled ones. From the genotypic data based on microsatellites (nDNA), the authors calculated (1) the gene diversity, H_e, per population, (2) F_{ST} values between pairs of populations and (3) transposed these F_{ST} values into past gene flow estimates, N_m.

The oak populations had high values of genetic variation (average $H_e = 0.85$; range 0.72–0.89). However, it would be wrong to conclude that all of them are thus of similar importance in conservation or forestry (e.g. as seed sources), although this is often done (O'Meally and Colgan 2005). As shown above, microsatellites refer to neutral genetic variation, and the populations could well exhibit different amounts of adaptive genetic variation and, therefore, different evolvability at adaptive genes (see below; Holderegger et al. in press).

Figure 1a shows that a focal oak population in Central Switzerland was weakly differentiated from any other studied population. Hence, high past gene flow over large distances of dozens of km was inferred (mean $Nm = 8.80$).

As Gugerli et al. (WSL Birmensdorf, unpublished data) sampled and genotyped adult trees, the *Nm* values do (at best) reflect gene flow at the time when the seeds from which the adult trees grew up had been fertilised and dispersed, but they do not reflect, as often assumed, current gene flow. In reality, *Nm* values refer to long time periods, as they integrate evolutionary effects over several generations. What is currently going on in terms of gene flow can be quite different, especially if we face the dramatic landscape changes (e.g. fragmentation) that occurred during the last 150 years (Turner et al. 2001).

However, there is a way to infer current gene flow patterns from neutral genetic markers. Paternity analysis can detect mating events as a result of pollen transfer in plants. In brief, the fathers of the progeny of single mothers are genetically identified from the sample of all potential fathers (i.e. all the fathers in a given area). With the knowledge of the spatial position of all potential fathers, exact gene flow trajectories can be drawn. A detailed description of corresponding methods is given by Smouse and Sork (2004) and Sork and Smouse (2006). Figure 1b provides an example of a paternity analysis of the seeds of a single oak tree (Gugerli et al., WSL Birmensdorf, unpublished data). It shows that pollen is transferred by wind over more than 200 m and that, for this particular tree, about 30% of the seeds were sired by trees that were situated outside of the sampled population (Figure 1b). This latter value refers to current interpopulation gene flow by pollen. In a similar way (parentage analysis), one can study the current gene flow in animals or gene flow by seed in plants (Godoy and Jordano 2001; Sork and Smouse 2005).

So, why use neutral genetic markers to estimate processes such as gene flow in a landscape? In order to test processes in a landscape, we need a marker, genetic or not, that reflects gene flow independently of selective forces. That is exactly what neutral genetic markers do. In contrast, adaptive genetic markers are selected by environmental conditions (see below). In an extreme case, there could be gene flow between two populations, but the genes being adaptive at one site would strongly be selected against and vanish at the other site. Based on adaptive genes, one would therefore infer missing gene flow, when in fact the two populations were functionally connected.

Adaptive genetic variation

The terms 'adaptive' or 'selective' refer to a gene (or a quantitative trait; see below) that has an effect on fitness. Let us assume, as before, that only two gene variants (alleles) occur at a given gene, namely *a* and *b*. Again, three different genotypes

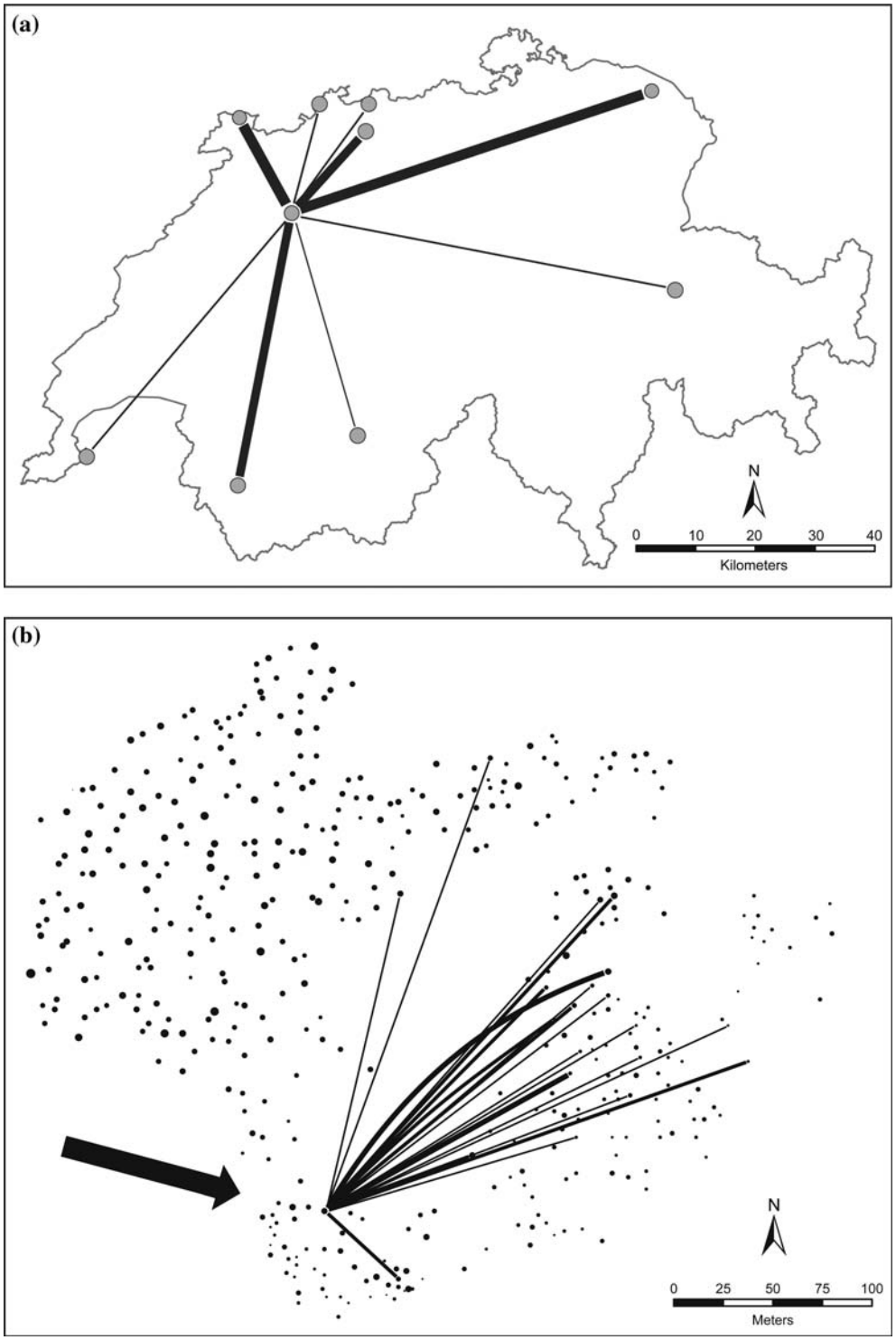

Figure 1. Historical and current gene flow in oaks (*Quercus* spp.) from Switzerland (Gugerli et al., WSL Birmensdorf, unpublished data). (a) Historical gene flow patterns (based on *Nm* estimates inferred from genetic population differentiation, F_{ST}) between a focal population and several other populations. The thickness of the lines refers to the amount of historical gene flow, *Nm*. (b) Current gene flow by pollen (based on paternity analysis) in a single oak population. The thickness of the lines refers to how many times a given father sired seed of the focal mother tree, and the black arrow indicates gene flow by pollen (about 30%) from outside the population (i.e. current gene flow by pollen among populations).

exist, namely the homozygotes *aa* and *bb* and the heterozygote *ab*. This time, however, it matters for a given individual which of the three genotypes it carries on its chromosomes, since they are selectively non-equivalent. For instance, the genotype *bb* might have a higher general fitness than the genotypes *aa* or *ab*. Hence, natural selection will directly act on these genotypes favouring genotype *bb*. The genotypes are thus of adaptive or selective significance (Conner and Hartl 2004). Selected genes have a tendency to be monomorphic within populations, because selection removed all the unfit variants. Adaptive genetic variation is the genetic variation that is estimated at such adaptive genes. It is this type of genetic variation we are used to, because it is what Charles Darwin referred to in his theory of evolution due to natural selection (Darwin 1859).

Adaptive genetic variation and quantitative genetic studies

So far, it is rarely possible to directly study the alleles at genes that are responsible for adaptive genetic variation in most organisms. (Note that this is what functional genomics seeks to achieve in model organisms; Jackson et al. 2002.) Instead, the variation at traits which are of potential adaptive value, such as body size in animals or frost resistance in plants, has to be investigated in quantitative genetic experiments. Most of the quantitative traits are not determined by a single gene but by several to many genes (Conner and Hartl 2004). Alleles may therefore be additive in their effects across many genes. (Again, not all quantitative traits are necessarily under selection; there are quantitative traits which are effectively neutral; Conner and Hartl 2004). Selected loci are, as neutral markers are, affected by drift and gene flow, but selection is superimposed on the latter two processes.

To assess genetic variation at traits that are under natural selection in quantitative genetic experiments, individuals with a known genetic relationship are grown under constant environmental conditions. For instance, one samples seeds from several naturally pollinated mother plants (i.e. half-siblings) and germinates them in a glasshouse, subsequently plants the seedlings in a randomised way in a common garden (e.g. an experimental or botanical garden) and monitors the performance or expression of several traits of interest throughout the life cycle. The reasoning behind this setup is (1) that the differences of individuals grown in the same environment must be due to genetic differences and (2) that family members share alleles and are therefore more similar to one another than to members of other families. Hence, the higher the degree of similarity of family members, the greater is the genetic component of the total measurable phenotypic variation. It is evident that quantitative genetic experiments are labour-, time- and cost-intensive.

How are adaptive genetic variation and differentiation estimated?

As gene diversity, H_e, is a measurement of the genetic variation at neutral genes, heritability, h^2, is used as a measurement of genetic variation of a population at an adaptive gene (or a quantitative trait). In its usual form (narrow-sense heritability), it is defined as

$$h^2 = V_A/V_P$$

where V_A is the additive genetic variance, and V_P is the phenotypic variance of a trait that varies with genotype *and* environment. Under additivity, the effects of the alleles in a genotype can be summed up to determine the total effect on the phenotype. Hence the alleles at a locus do not affect each other's expression or the expression of alleles at other loci (Conner and Hartl 2004). The additive genetic variance is responsible for the evolutionary potential of populations. To calculate h^2, we have to separate genetic from environmental (i.e. non-genetic) variances. This is done by estimating variances of phenotypic measurements from individuals with a known genetic relationship (e.g. half-siblings) grown in the same environment. The exact calculation of h^2 depends on the design of the experimental approach and is beyond the scope of this article (for methods see Conner and Hartl 2004). A typical approach is to estimate variance components from an analysis of variance (ANOVA) with individuals (offspring) nested within families (e.g. offspring of a known mother, but with unknown fathers). Heritability, h^2, is of-

ten misinterpreted as the degree to which a phenotype is determined by its genotype. This is not correct, because there can be many fixed (i.e. with only one allele) loci per population that have a large influence on the genotype but do not add to the variance. In fact, heritability is a variance ratio (as seen from the above formula). Note that heritability, h^2, is specific to a particular trait and a particular environment (Conner and Hartl 2004).

As shown before, F_{ST} represents population differentiation at neutral genes. The equivalent measurement referring to population differentiation at adaptive genes is Q_{ST}, which can be written as (Savolainen et al. 2004):

$$Q_{ST} = V_G/(V_G + 2V_A)$$

where V_G is the between-population variance component, and V_A is now the average additive genetic variance within populations (Latta 2003). As for F_{ST}, unity indicates complete differentiation at quantitative adaptive traits and zero indicates genetic homogeneity of populations. The most convenient experimental approach is a nested ANOVA design with individuals nested within families nested within populations (Latta 2003). A reader-friendly introduction to quantitative genetics is given by Conner and Hartl (2004).

An application of adaptive genetic variation: oaks in Europe

Adaptive genetic variation is of great importance in conservation biology, e.g., with respect to adaptation under environmental change, or for economic reasons in agriculture or forestry. In forestry, common garden experiments with trees originating from different locations (i.e. provenance tests) have long been used to find populations with economically favourable traits such as high growth rates.

Petit et al. (2002) surveyed the spatial arrangement of cpDNA in European oak species and inferred three glacial refugia on the Iberian and Italian Peninsulas and on the Balkans. From these refugia, the species re-colonised central and northern Europe. The molecular markers used by Petit et al. (2002) were RFLPs of cpDNA (see above), which are essentially neutral. The historical oak populations surviving in the three major refugia with potentially different selective forces were separated from each other for long time periods of at least several ten thousand years during the last glaciation. Hence, the question arises of whether this led to differential adaptive evolution (Widmer and Lexer 2001).

For this aim, Kremer et al. (2002) used data on 62 quantitative traits from 16 common garden tests on European oaks and correlated them with neutral genetic data from laboratory studies. They showed that there is no or, at best, a weak association between differentiation in cpDNA and nDNA markers and differentiation in the quantitative data set from the common garden experiments. In other words, Kremer et al. (2002) found no consistent correlation between neutral and adaptive genetic differentiation among populations. This leads to the general question of whether there is a common relationship between genetic variation and differentiation at neutral and adaptive genes.

Is neutral genetic variation correlated with adaptive genetic variation?

If there was a strong correlation between neutral and adaptive genetic variation, we could use the former as a relatively cheap and fast surrogate for the latter, which is much more troublesome to measure (Holderegger et al. in press). Several recent reviews have dealt with the question of whether there is a common correlation between neutral and adaptive genetic variation or differentiation. These reviews often came up with different conclusions even when they analysed similar data sets. It is therefore no surprise that the topic is still strongly debated in population genetics (Pearman 2001).

Reed and Frankham (2001) performed a meta-analysis of 71 published data sets. Each study provided estimates of gene diversity (H_e) measured by neutral genetic markers and of adaptive genetic variation as measured by heritability (h^2) for each of many populations. Then, these pairwise values per population were correlated across all populations per species. Reed and Frankham (2001) found a significant overall correlation coefficient of $r = 0.217$ in the 71 studies surveyed. However, the variation of the correlation coefficients among studies was extremely large, ranging from -0.88 to

0.90. For instance in *Phlox drummondii*, Schwaegerle et al. (1986) found a tendency for a higher h^2 in populations with a higher H_e at allozyme loci for one quantitative trait ($r = 0.42$), but showed a lower h^2 with a higher H_e for two other quantitative traits ($r = -0.61$ and -0.48, respectively). Frankham and Reed (2001) therefore concluded that molecular measurements of genetic diversity (i.e. neutral markers) only have a very limited ability to predict quantitative genetic variation.

If there is no clear correlation between adaptive and neutral genetic variation, could there be one between adaptive and neutral genetic differentiation? What is about population genetic differentiation then? Merilä and Crnokrak (2001) used data from 14 studies providing estimates of F_{ST} and Q_{ST} for the same study species. They found a significant and strong correlation between F_{ST} and Q_{ST} ($r = 0.75$). In contrast, McKay and Latta (2002), in a survey of 29 species, detected an only marginally significant correlation of these variables ($r = 0.363$). Figure 2 shows an analysis of the combined data sets of Merilä and Crnokrak (2001) and McKay and Latta (2002) using 30 data sets. A linear regression of non-transformed values (Kolmogorv-Smirnoff tests indicated normality of the data at $\alpha = 0.05$) showed a significant relationship ($R^2 = 0.225, p = 0.008$).

What is evident from Figure 2 is the large scatter in the relationship. Many studies found low F_{ST} values with larger Q_{ST} values, while the results of other studies were close to a one-to-one relationship. In general, Q_{ST} values were larger than F_{ST} values (Figure 2; Latta 2005), which suggests that natural selection plays a significant role in shaping contemporary populations (Conner and Hartl 2004).

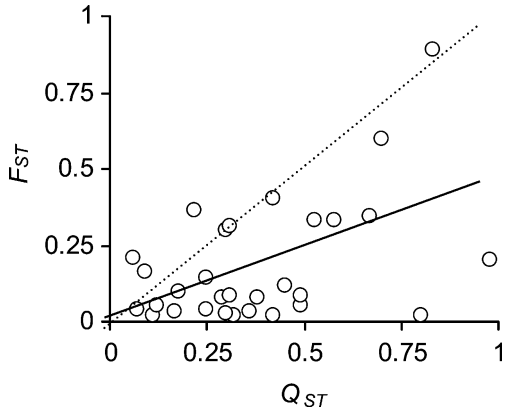

Figure 2. Relationship between measurements of population differentiation at quantitative, adaptive traits (Q_{ST}) and neutral, molecular loci (F_{ST}). The solid line refers to the linear regression of the data ($R^2 = 0.225, p = 0.008$) and the broken line to the expected one-to-one relationship. Combined data sets ($N = 30$) from Merilä and Crnokrak (2001) and McKay and Latta (2002).

We can deduce from these results (1) that the relationship between F_{ST} and Q_{ST} is far from being simple and (2) that quantitative genetic data are needed for the evaluation of a population's evolutionary or adaptive potential and its conservation value (Reed and Frankham 2001; McKay and Latta 2002). Hence, neutral genetic data should not be used as a surrogate of adaptive genetic variation (Holderegger et al. in press). However, neutral genetic variation at the level of the individual (i.e. heterozygosity) is correlated with individual fitness (Reed and Frankham 2002).

Conclusions: genetic diversity and differentiation in landscape genetics

What are the take-home messages with respect to genetic diversity and differentiation?

(1) There are two principal forms of genetic diversity, namely neutral and adaptive variation. Neutral genetic diversity is usually measured by various molecular laboratory methods, while adaptive genetic diversity is estimated in quantitative genetic experiments under uniform environmental conditions. Neutral genetic information should not be used as a surrogate for adaptive genetic information, neither with respect to the genetic diversity of populations nor to their population differentiation.
(2) Whenever information on the adaptive potential, the evolvability or the conservation value of populations is needed, it is necessary to directly study quantitative traits.
(3) In contrast, neutral genetic markers are highly valuable for investigating processes in the landscape (Antolin 2006; Pannell and Dorken 2006; Wagner et al. 2006). Particularly prominent examples are gene flow, migration or dispersal. Here, molecular-genetic markers also allow for the discrimination between historical and current processes. Selected genes

do not adequately reflect such demographic processes.

Landscape genetics aims at providing information about the interaction between the landscape and microevolutionary processes (Manel et al. 2003). Hence, the scientists involved approach questions in landscape genetics from the traditional fields of landscape ecology or population genetics. The different schools have to understand each other and integrate their findings. We therefore urge landscape ecologists (in fact all of us) to mind the difference between neutral and adaptive genetic diversity when interpreting the results of genetic studies. Population geneticists, on the other hand, should be aware of the fact that their use of the term 'landscape' is not necessarily identical with that of landscape ecologists (Turner et al. 2001). Population genetic studies are often carried out at two different spatial levels that imply different scales. The first is local, i.e. detailed studies within populations with often complete sampling of individuals, but ignores the landscape context of the population studied. The second level refers to spatial scales that are often beyond the extent of a single landscape. Here, a set of populations is studied with the 'landscape' often reduced to geographic distance, thus ignoring the landscape's qualitative and quantitative characteristics (Turner et al. 2001). Hence, the spatial scales considered by population geneticists are either considerably smaller or larger than the landscape of landscape ecologists. One might therefore argue that there is a spatial gap in population genetic studies, namely at the spatial scale of real landscapes. In addition, many population genetic studies do not, for reasons of the work load, incorporate samples from all populations of a species within a given landscape. However, if we want to establish gene flow patterns, we should evaluate the potential effect of the un-sampled populations. As Slatkin (2005) showed, it will generally be impossible to predict the influence of these un-sampled populations. This refers to the problem of scaling: genetic results obtained at one spatial scale cannot easily be transferred to another spatial scale, a scaling problem well known by landscape ecologists (Wiens 1989; Wu and Hobbs 2002). We argue that it is at the level of adjacent populations, i.e. the 'landscape' of a given species, where landscape genetics has great potential to give insight into processes that are otherwise difficult to investigate such as exact measurements of gene flow (Wu and Hobbs 2002). In doing so, landscape genetics can also help defining the appropriate scale for the evaluation of landscapes in an organism perspective (Wiens 1989). Similarly, there is a gap in the time scale of population genetic investigations, with studies either referring to short periods (e.g. one particular year) or to extended, but usually unknown, time periods, i.e. many generations or even evolutionary time frames (see discussion of historical and current gene flow above).

Finally, we want to stress that landscape genetics is more than just spatial genetics. It is the interactions between genetics (or the processes that population genetics can trace) and the landscape in which we are interested. Real landscape genetic studies have to include the quantitative *and* qualitative characteristics of the landscape studied, such as the types, size and spatial arrangement of potential barriers to migration. Then, and only then, will landscape genetics hold the great expectations that it presently evokes.

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