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Adaptive population divergence: markers, QTL and traits

John K. McKay and Robert G. Latta

Molecular markers appear to be poor indicators of heritable variation in adaptive traits. Direct comparison of population structure in markers with that in traits is made possible by the measure Q_{st} , which partitions quantitative genetic variation in a manner analogous to F_{st} for single gene markers. A survey of the literature reveals that mean Q_{st} is typically larger than and poorly correlated with mean F_{st} across 29 species. Within species, Q_{st} varies widely among traits; traits experiencing the strongest local selection pressures are expected to be the most divergent from molecular F_{st} . Thus, Q_{st} will be particularly relevant to conservation efforts where preserving extant adaptation to local environments is an important goal. Recent theoretical and simulation studies suggest however that F_{st} is a better predictor of the pattern of allelic differentiation at quantitative trait loci (QTLs) than is Q_{st} in random mating populations, in which case allelic variation at QTLs might be better assessed by molecular markers than will extant variation in the traits themselves.

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John K. McKay
Center for Population
Biology, One Shields
Avenue, University of
California, Davis,
CA 95616-8515, USA.
e-mail:
jkmckay@ucdavis.edu

Robert G. Latta*
Dept of Biology,
Dalhousie University,
Halifax, Nova Scotia,
Canada B3H 4J1.
*e-mail: rglatta@is.dal.ca

'A major unresolved issue is the relationship between molecular measures of genetic diversity and quantitative genetic variation' (Frankham [1])

Molecular genetic markers have played a major role in evolutionary biology. As molecular methods have become cheaper, faster and involve less invasive sampling, they have become increasingly popular in conservation [2,3], where there is often a clear need for rapid decision making. For example, because genetic differences among populations are often considered

worthy of conserving [2–5], many studies apply a criterion, assigning conservation priority to populations (or clades of populations) that are reciprocally monophyletic, because these probably represent independently evolving clades or evolutionarily significant units (ESUs) [5]. There are several definitions of ESU in the literature, which vary in the degree of emphasis placed on molecular versus ecological criteria [2–6]. Such definitions have crucial importance in the light of conservation legislation, where boundaries of ESUs must be drawn before legal protection status can be assigned [2–4]. However, locally adaptive genetic diversity within units is likely to be of greater importance when choosing populations that are most suitable as translocation or restoration sources. In this case, adaptive genetic differences among populations can lead to outbreeding depression if divergent populations are mixed [7].

Several reviews have identified testing the assumption of an association between marker diversity and adaptive diversity as a pressing research concern [1,8–10], and warn against the gradual replacement of ecological data with molecular criteria when diagnosing units of conservation [2,3,10]. Two recent studies use a formal meta-analysis to test the relationship between molecular and quantitative variation, both within [10] and among populations [11]. Here, we focus on measures of divergence or population structure [11], because these are most relevant to the

Box 1. Population divergence in molecular markers and ecological traits

Wright's [a] F_{st} and related statistics [b] provide a useful measure of the level of population genetic structure at single genes by quantifying the proportion of the total allelic variation that occurs between populations. Imagine that several populations derive from a common ancestor with genetic variance $\sigma_{g(0)}^2$ and diverge through drift. Wright [c] showed that the partitioning of genetic variance at a quantitative polygenic trait into within $\sigma_{g(w)}^2$ and between $\sigma_{g(b)}^2$ population components is related to the partitioning of allelic variation as (Eqn I–III)

$$\sigma_{g(b)}^2 = 2F_{st}\sigma_{g(0)}^2 \quad [\text{Eqn I}]$$

$$\sigma_{g(w)}^2 = (1 - F_{st})\sigma_{g(0)}^2 \quad [\text{Eqn II}]$$

$$\sigma_{g(t)}^2 = (1 + F_{st})\sigma_{g(0)}^2 \quad [\text{Eqn III}]$$

Such that (Eqn IV)

$$\frac{\sigma_{g(b)}^2}{\sigma_{g(t)}^2} = \frac{2F_{st}}{(1 + F_{st})} \quad [\text{Eqn IV}]$$

We can therefore define a quantitative trait analog of F_{st} labeled Q_{st} by Spitze [d] as (Eqn V)

$$Q_{st} = \frac{\sigma_{g(b)}^2}{\sigma_{g(b)}^2 + 2\sigma_{g(w)}^2} \quad [\text{Eqn V}]$$

and therefore $Q_{st} = F_{st}$ for neutral traits.

We have retained the subscript g throughout the above to emphasize that Q_{st} must be calculated from components of genetic, not phenotypic variance. In practice, Q_{st} is measured by quantifying the genetic components of variance within and among populations in randomized common garden experiments, where all individuals are assayed in the same environment. In such experiments, the phenotypic differences between populations can be ascribed to genetic differentiation among populations. Phenotypic variation within populations includes both a genetic and an environmental component that can be partitioned by assaying multiple individuals within (say) half-sib families [e]. Thus, the most common experimental design is a nested ANOVA with individuals nested within families within populations.

The evolutionary forces influencing Q_{st} for neutral traits have been well worked out by Lande [f]. Briefly, variation among n demes is determined by the migration (m) and mutation rates (σ_m^2) (Eqn VI)

$$\sigma_{g(b)}^2 = \frac{(n-1)\sigma_m^2}{m} \quad [\text{Eqn VI}]$$

whereas the variance within populations is determined by N (the effective population size, which determines how much variation is fixed through drift) and the mutation rate (Eqn VII)

$$\sigma_{g(w)}^2 = 2nN\sigma_m^2 \quad [\text{Eqn VII}]$$

Thus, by substituting Eqn VI–VII into Eqn V, we get (Eqn VIII)

$$Q_{st} = \frac{\frac{(n-1)\sigma_m^2}{m}}{\frac{(n-1)\sigma_m^2}{m} + 2 * 2nN\sigma_m^2} \quad [\text{Eqn VIII}]$$

which simplifies to (Eqn IX)

$$Q_{st} = \frac{1}{1 + 4Nm\left(\frac{n}{n-1}\right)} \quad [\text{Eqn IX}]$$

(Eqn 10a of Ref. [f]), which is equivalent to F_{st} for large numbers of demes. The relationship between F_{st} and Nm applies strictly to large numbers of demes at equilibrium in an island model, a situation that is observed rarely in nature. However, it can be shown using a coalescent approach [g] that departures of F_{st} from its equilibrium (e.g. because of historical contingency) influence Q_{st} in a parallel manner, because (Eqn X)

$$Q_{st} = F_{st} = \frac{t_{total} - t_{within}}{t_{total}} \quad [\text{Eqn X}]$$

for coalescence times t (Eqn 10, 11 of Ref. [g]).

Thus, for a species with any population structure, it is possible to test the null hypothesis that a given trait evolved by genetic drift, in which case F_{st} (from neutral markers) will be equal to Q_{st} [f–h]. If we instead find a trait with an estimate of Q_{st} that is significantly different from F_{st} , we reject the hypothesis that this trait is neutral, because the difference between Q_{st} and F_{st} reflects the relative influence of natural selection. When two populations have adapted to different habitats, we expect Q_{st} values for traits involved in adaptation to be $>F_{st}$. If both populations are experiencing stabilizing selection for the same phenotype, we expect Q_{st} to be $<F_{st}$.

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definition of 'units' in conservation. Much recent theoretical work is relevant to the identification of ecologically adaptive divergence among populations. We review the comparison of population genetic structure in markers, traits and quantitative trait loci (QTLs), drawing upon both the empirical studies available to date as well as theoretical arguments. For brevity, we focus on local adaptation of quantitative traits, recognizing that other sources of fitness (e.g. inbreeding depression) are relevant to conservation efforts [1]. We suggest that genes, markers and traits will each behave differently in the adaptive divergence of populations, and therefore extrapolating from one type of variation to another must be done with caution. However, these considerations also suggest promising approaches for future research, or highlight outstanding questions, and will help determine the appropriate

role for molecular markers in defining units for the conservation of local adaptation within taxa.

Comparing divergence at marker loci and quantitative traits

Tests for adaptive variation proceed most easily by comparison against the null hypothesis that variation is selectively neutral [12–14]. Neutral theory is well developed for molecular markers [14], and a similar body of theory has been developed recently for neutral quantitative genetic traits [12] (Box 1). For several marker types and mutation models, population genetic structure is often quantified using F_{st} or related statistics [15]. A precisely analogous measure for quantitative genetic traits is Q_{st} [16]. Provided that quantitative genetic techniques are applied to measure and partition genetic variation (rather

Table 1. Q_{st} and F_{st} from published data for 29 species

Species	Refs ^a	Q_{st}	Q_{st} range ^b	Markers ^a	Refs ^a	F_{st}
<i>Arabidopsis thaliana</i>	[17]	0.83	0.29,1	A,M	[17]	0.890
<i>Arabis fecunda</i>	[43]	0.98	0.3,1	A	[43]	0.200
<i>Brassica insularis</i>	[47]	0.06	0.023,0.09	A	[47]	0.210
<i>Centaurea corymbosa</i>	[47]	0.22	0.11,0.34	A	[47]	0.364
<i>Clarkia dudleyana</i>	[17]	0.38	0.16,0.61	A	[17]	0.075
<i>Daphnia obtusa</i>	[16]	0.30	0.08,0.4	A	[16]	0.300
<i>D. pulex</i>	[17]	0.31	0.0,0.69	A,M	[17]	0.310
<i>D. pulicaria</i>	[48]	0.53	0.21,0.7	A,M	[48]	0.33
<i>Drosophila buzzatii</i>	[17]	0.17	N/A	A	[17]	0.032
<i>D. melanogaster</i>	[17]	0.70	0.38,1	A	[17]	0.600
<i>Larix laricina</i>	[49]	0.49	0.39,0.55	A	[50]	0.050
<i>L. occidentalis</i>	[51]	0.49	0.04,0.83	A	[52]	0.086
<i>Medicago truncatula</i>	[17]	0.58	0.03,0.93	RAPDs	[17]	0.330
<i>Phlox drummondii</i>	[53]	0.25	0.03,0.5	A	[53]	0.038
<i>Picea glauca</i>	[46]	0.36	0.04,0.25	A	[46]	0.035
<i>P. sitchensis</i>	[54]	0.29	0.13,0.44	A	[55]	0.079
<i>Pinus brutia</i>	[56]	0.25	0.004,0.66	A	[57]	0.140
<i>P. contorta</i> ssp. <i>latifolia</i>	[17]	0.11	0.01,0.2	A	[17]	0.019
<i>P. sylvestris</i>	[18]	0.80	N/A	A,M,R	[18]	0.018
<i>Pseudotsuga menziesii</i>	[58]	0.42	0.06,0.71	A	[59]	0.022
<i>Quercus petraea</i>	[17]	0.32	N/A	A	[17]	0.022
<i>Rana arvalis</i>	[11]	0.42	N/A ^b	M	[11]	0.404
<i>R. temporaria</i>	[11]	0.31	N/A ^b	M	[11]	0.083
<i>Salix viminalis</i>	[11]	0.07	N/A ^b	A	[11]	0.041
<i>Scabiosa canescens</i>	[17]	0.09	0.02,0.22	A	[17]	0.160
<i>S. columbaria</i>	[17]	0.45	0.15,0.75	A	[17]	0.120
<i>Sequoiadendron giganteum</i>	[60]	0.18	0.14,0.22	A	[60]	0.097
<i>Silene diclinis</i>	[11]	0.12	N/A ^b	A	[11]	0.052
<i>Wyomea smithii</i>	[17]	0.67	N/A	A	[17]	0.346

^a[11,17] are reviews that contain references to the original studies.
^bData were collected on more than one trait: see references within [11].
^cAbbreviations: A, allozymes; M, microsatellites; R, restriction fragment length polymorphisms; RAPD, random amplified polymorphic DNA.

than phenotypic variation) within and between populations, Q_{st} is straightforward to calculate and can be compared directly to F_{st} .

For neutral additive traits, F_{st} and Q_{st} should be equal (Box 1). Therefore, the magnitude of the difference between Q_{st} and F_{st} can be used to infer the degree of local adaptation [11–13,16,17]. For traits under divergent selection pressure, Q_{st} is expected to be greater than F_{st} of marker loci [11–13,16–18]. For example, across a latitudinal cline in Scots pine *Pinus sylvestris*, a common garden screening revealed that among-population divergence in the timing of bud burst was much greater ($Q_{st} = 0.80$) than was population divergence in allozyme, microsatellite, RAPD and RFLP markers ($F_{st} < 0.02$) [18]. Although this is a particularly striking example, the general result appears to be the rule rather than the exception. Table 1 and Fig. 1 summarize data for 29 species in which it was possible to compare statistically F_{st} and Q_{st} directly (see [11] for a formal meta-analysis of the relationship between F_{st} and Q_{st} across species). Three patterns emerge (Fig. 1). First, for 24 of 29 species, Q_{st} averaged across traits is higher than F_{st} averaged across marker loci [11]. This represents a significant departure (2-tailed sign test, $P < 0.001$) from the 50:50 odds that one would expect if Q_{st} and F_{st} were equal on average.

There is no *a priori* reason for this departure, and although $Q_{st} > F_{st}$ for most traits, a minority exhibit a Q_{st} that is significantly $< F_{st}$ [16], suggesting that selection acts on those traits towards the same optimal phenotype in each population. Second, these empirical studies reveal little evidence that the differentiation of neutral molecular markers predicts population differentiation at quantitative traits well (Fig. 1). What little relationship exists between Q_{st} and F_{st} (Fig. 1) seems to derive primarily from the tendency for Q_{st} to be $> F_{st}$. In Fig. 1b, we re-plot the data against the number of migrants inferred from F_{st} (Nm) (Box 1) to illustrate that high levels of neutral gene exchange do not seem to prevent adaptive differentiation. Finally, there is considerable scatter (i.e. range of Q_{st}) among the different quantitative traits assayed within each species, indicating that the balance between selection and drift is specific to individual traits. The overall picture from empirical studies is of adaptive divergence of specific traits taking place in the face of gene flow, with little relationship to patterns exhibited by molecular markers.

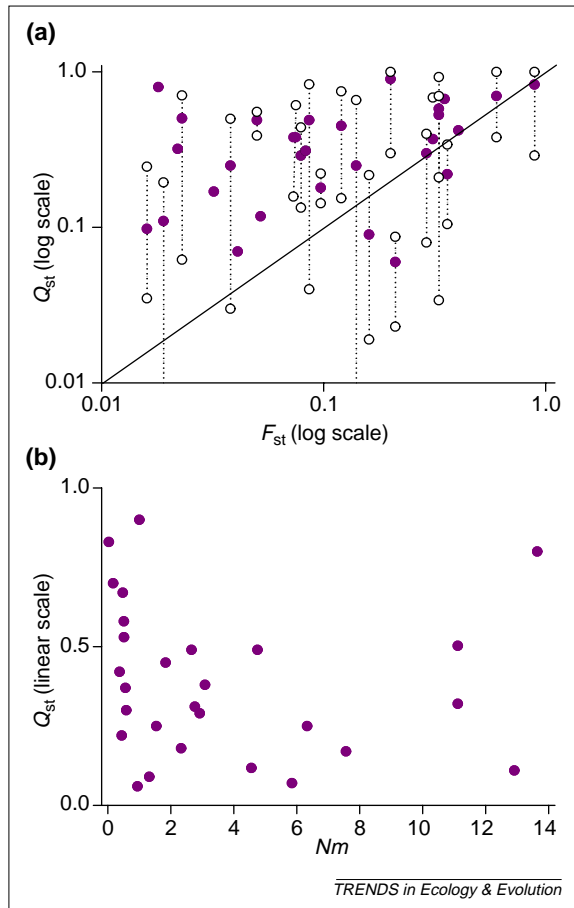
Theoretical considerations of adaptive and neutral divergence

Selection and migration constrain but do not eliminate one another

Rather than gene flow 'overcoming' selection (or vice versa), there exists a balance between them that determines both the equilibrium level of differentiation and the rate of approach to that equilibrium [19]. Adaptive differences between populations develop in spite of considerable gene flow [20–22], and strong selection can rapidly remove the genetic load imposed by immigrants, maintaining differences among populations [23,24]. At the same time, studies comparing populations that are experiencing different levels of isolation show that gene flow constrains adaptive differentiation, such that populations connected by high levels of gene flow are less differentiated than might be expected based upon the locally optimal phenotypes [21,25–27].

For example, in the Lake Erie water snake *Nerodia sipedon*, King and Lawson [21] document (1) adaptive differentiation in the banding patterns between mainland and island populations as well as (2) high levels of gene flow. Selection 'overcomes' gene flow in that the populations are more differentiated for banding pattern than they might be under migration drift balance. At the same time, the high levels of gene flow constrain local adaptation in that the populations are less differentiated than expected by selection alone (i.e. the populations do not exhibit fixed differences). Moreover, the selection against the immigrant type is not strong enough to eliminate gene flow at allozyme markers, which exhibit F_{st} values in the range 0.019–0.093 between island and mainland populations. The conservation implications of such studies are clear. If the island populations were in some way endangered and in need of restoration, a

Fig. 1. Values of F_{st} and Q_{st} in 29 species. In Fig. 1a, each filled circle represents the mean value of F_{st} and Q_{st} for a given species and the vertical lines and open circles show the large range of Q_{st} across different traits (Table 1). The diagonal line represents the neutral expectation $F_{st} = Q_{st}$. A paired t -test shows that, across species, mean Q_{st} is greater than mean F_{st} (t-test on the log-transformed variables, $t = -4.93$, $df = 28$, $P < 0.00005$). Figure 1a shows that there is a marginal but nonsignificant positive correlation between log-transformed variables Q_{st} and F_{st} ($r = 0.363$, $P = 0.053$) and Q_{st} does not approach zero as F_{st} approaches zero. This is also apparent in Fig. 1b where F_{st} has been 'transformed' into an estimate of Nm (Box 1) and again there is no significant correlation. See Table 1 for a list of species included.



large-scale translocation of snakes from the mainland would greatly reduce the mean fitness of the island population. But neutral markers do not reveal this differentiation at the adaptive trait. Indeed, had the island and mainland snakes been differentiated for a more cryptic (say, physiological) trait, the adaptive differences might well have gone undetected.

There are two important reasons for the disconnection between geographical patterns at neutral and selected traits. First, the number of migrants might be high enough ($Nm > 1$) to prevent neutral differentiation, whereas the proportion is low enough ($m < s$, where s is the selection coefficient) to permit adaptive differentiation. Moreover, selection against immigrant alleles at a locally adaptive locus will present little barrier to the effective migration of neutral loci, unless such loci are linked tightly to the locus under selection [28]. Second, unless population size is extremely small, the rate of approach to equilibrium is likely to be higher for loci experiencing selection than for those that are drifting. Adaptive differentiation occurs at a rate (R) that is proportional to the product of trait heritability (h^2) and the selection intensity (S) (the familiar $R = h^2 S$ breeders equation of quantitative genetics). Typical rates of short-term evolutionary change are ~ 0.1 – 0.5 phenotypic standard deviations per generation [29] and cases of very rapid evolution are famous [30–33]. For local adaptation occurring over fairly short periods (~ 50 – 100 generations),

substantial differentiation of quantitative traits can be achieved under sustained directional selection of moderate to strong intensity. By contrast, differentiation because of drift will be much slower for many organisms, in the order of N_e generations [34].

Selective differentiation of polygenic traits might cause little differentiation of the underlying loci

For adaptive traits controlled by single Mendelian loci, we expect among-population divergence of the allele frequencies at these loci. However, many adaptive differences among populations involve polygenic traits, controlled by two or more unlinked QTL. (We use the term polygenic rather than quantitative traits to distinguish from continuously varying traits controlled by a single QTL.) With multiple loci affecting a polygenic trait, selection on the trait is diluted over many loci, such that each locus can itself behave as if it was nearly neutral [35]. Recent simulation studies [36] show that, under random mating within populations, QTLs differentiate little in the face of pronounced diversifying selection on trait values. In the simulations, neutral marker loci conformed to the expectations of migration/drift equilibrium regardless of the selective regime imposed on the polygenic trait. More importantly, F_{st} calculated from the QTLs themselves was almost identical to that seen at the neutral markers. Thus, if divergence in a polygenic trait is caused by local adaptation, not only will Q_{st} be greater than the F_{st} value seen at neutral markers, but it will also be $> F_{st}$ of the QTLs (Box 2).

Because the trait value is the sum of each allelic effect, the variance of the trait includes a contribution of the covariance of allelic effects. With neutral differentiation of the trait, unlinked loci differentiate independently among populations, giving covariances that are zero on average (Box 2). Adaptive differentiation of a polygenic trait among populations creates a parallel differentiation (i.e. a covariance) of allele frequencies at the underlying QTLs because each QTL is responding to the same selection pressure. These covariances increase trait differentiation beyond what would be expected from the sum of each allele frequency difference. Thus, counter-intuitively, substantial trait differentiation is possible with only minor differentiation of allele frequencies at the underlying loci (or vice versa). Moreover, as the number of loci affecting the trait increases, the relative contribution of covariances increases exponentially. In the extreme, very large Q_{st} is possible with only trivial allele frequency differences acting in parallel over very many loci. If the QTLs (which are the targets of selection at the genetic level) themselves differentiate only slightly, there can be no reason to expect neutral molecular markers to reflect the adaptive differentiation of populations.

Conserving present and future evolutionary potential
This theoretical result suggests a crucial distinction between the differentiation of traits and of their

Box 2. Adaptive divergence at polygenic traits and quantitative trait loci

Under the simplest model of polygenic trait variation, the trait value is simply the sum of the allelic effects at each of two underlying loci [quantitative trait locus (QTL)]. The variance of a sum is determined both by the variance of each of the parts (here the genetic variation at each locus) and the pattern of covariance among the parts (which can be interpreted as linkage disequilibrium among loci) (Eqn 1) [a,b].

$$\sigma_g^2 = \sigma_{loc1}^2 + \sigma_{loc2}^2 + 2Cov(loc1, loc2) \quad [\text{Eqn 1}]$$

Because σ_g^2 is partitioned within and among populations (Box 1), so are each of the terms on the right side of the equation. Thus, the variance among populations (i.e. the numerator in the calculation of Q_{st}) will be determined both by the differentiation of QTL allele frequencies (i.e. F_{st} of the QTLs), but also by the correlation of allelic frequencies across populations.

This among-population linkage disequilibrium of QTLs can be seen intuitively in Fig. 1. If the correlation is negative (Fig. 1a), opposite changes in allele frequencies at locus 1 and locus 2 cancel each other out, such that there is strong allele frequency differentiation, but no trait differentiation (the mean trait value in this example is exactly the same for each population). The more likely situation is depicted in Fig. 1b, where parallel clines in allele frequencies produce a stronger differentiation of trait values than would be predicted from either locus considered individually [c]. To put it another way, pronounced adaptive differentiation of traits can be achieved with little differentiation of allele frequencies at the underlying QTLs. Moreover, the contribution of the covariances increases as the square of the number of loci [because there are $n(n-1)/2$ locus pairs among n loci]. Thus, the more loci influence a trait, the greater the impact of parallel differentiation of allele frequencies on trait differences, and the less differentiation is expected of the allele frequencies themselves.

Although this model assumes additive effects of genes on the trait, epistatic effects on fitness are implicit in the assumption of stabilizing selection [d], because it is likely that several combinations of alleles will create intermediate trait values [e]. Epistatic interactions in the determination of the trait itself have not been modeled directly. However, the suggestion that differentiation for combinations of alleles effectively decouples F_{st} and Q_{st} suggests that the presence of epistatic interactions will blur the association between population structure of QTLs versus traits further.

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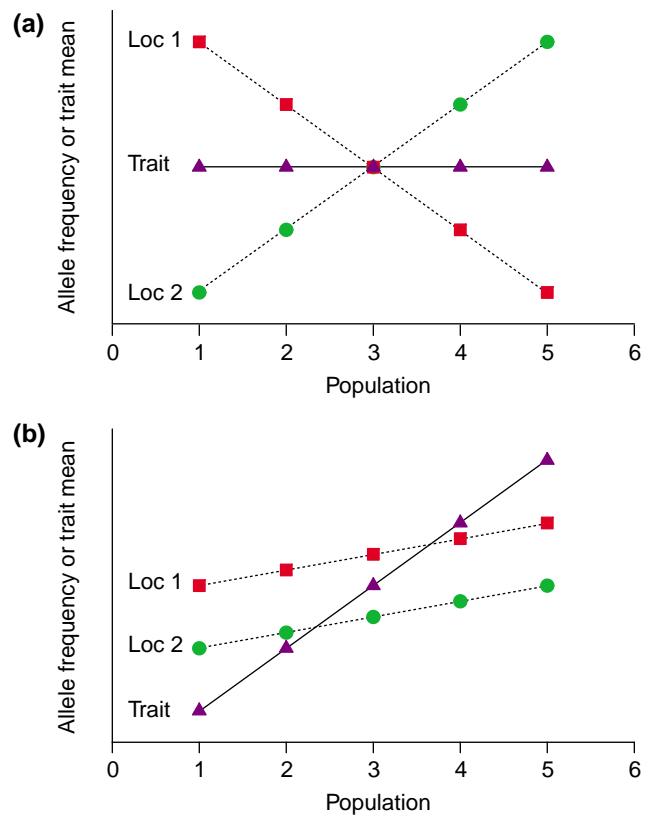


Fig. 1

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underlying loci. To illustrate this, consider a hypothetical riparian species occurring along parallel streams that traverse steep elevational gradients. If populations at the same elevation experience the same environment, then trait means will be most similar among populations at the same elevation in different drainages (Q_{st} highest among different elevations). But, if gene flow occurs mostly along the riparian zone within drainages, allele frequencies (at both QTLs and molecular markers) will be most similar within drainages (F_{st} highest among different drainages). In the short term, evolutionary potential to respond to environmental changes will be determined by the standing pool of phenotypic variation (Q_{st}). However, the allelic variation (whose spatial distribution is reflected by F_{st}) represents the underlying potential for longer term evolutionary change.

Perhaps the major motivation for studies of genetic differentiation in conservation is the identification of ESUs, populations that are sufficiently distinct to merit conservation status under existing legislation [2–5].

Such ESUs are thought to preserve evolutionary potential that can recreate lost biodiversity, provided that evolutionary processes are able to operate [5]. We tend to favor ESU criteria that include as much ecological information as possible [2,3]. Nevertheless, molecular genetic markers appear to provide considerable opportunity to make inferences about allelic variation underlying adaptive traits [36–39], and thus potentially the longer term evolutionary potential of the species concerned.

However, genetic criteria are also invoked frequently to guide short-term actions, such as transfer of individuals between existing populations as well as restoration efforts where populations have been extirpated [7,40,41]. With rapid translocations, it seems unlikely that evolutionary processes can operate rapidly enough to prevent significant loss of fitness in endangered populations [7]. From the perspective of the recipient population, translocations can represent a very high proportion of immigrants, enough to erode substantially any existing local adaptation.

Alternatively, from the perspective of the translocated individuals, the change in the environment will potentially occur faster than adaptive change can take place without threat of extinction [42]. Thus, long-term evolutionary potential might not be enough to preserve populations through short-term stresses imposed by movement between sufficiently different environments. Although such translocations are extremely beneficial in many cases (e.g. in reducing inbreeding depression, which might well outweigh the loss of local adaptation, at least in the short term), both theoretical (Box 2) and empirical (Fig. 1) results suggest that molecular genetic markers might provide a poor guide to locally adapted units. Such short-term efforts should in all cases emphasize the ecological criteria over and above molecular genetic markers when assessing local adaptation. In some cases, the geographical distribution of adaptive variation might be predicted most reliably (and conveniently) by available data on ecological and climatic gradients [43].

Research needs

Ecological genetic experiments can directly estimate genetic variation in traits that affect fitness and therefore the demography of rare and endangered species. This is crucial information that cannot be inferred from molecular data. However, although molecular genetic markers are applicable to almost any taxon, common garden studies are not feasible for many endangered or intractable species. Recent methods have been developed that combine molecular markers to infer relatedness with field measures of ecologically important variation [44]. These methods allow the estimation of both heritability and Q_{st} from field studies of natural populations [44], and so hold promise for the analysis of adaptive variation in any species. To help interpret such studies, however, it will be useful to apply detailed common garden methods to well-studied organisms, so that the evolutionary processes that shape quantitative trait and QTL variation are understood thoroughly.

Does F_{st} reflect QTL distribution?

Whereas techniques for the identification of QTL are becoming ever more sophisticated [45], assaying the allele frequencies at QTLs in most natural populations remains out of reach. Significant promise for estimating allele frequencies at QTL comes from genetic model species and their close relatives for which QTLs have been mapped and, in some cases, cloned. We have conjectured that, although Q_{st} and related approaches might be most relevant to the distribution of trait variance and local adaptation (short-term conservation), F_{st} might better reflect the distribution of allelic variation at QTL (an evolutionary potential, which is more relevant to longer term conservation). However, we cannot overstate that this conjecture is based entirely upon theoretical arguments assuming random mating,

and thus might not be relevant to many species. It remains to be demonstrated empirically that molecular markers do indeed reflect allelic variation at QTLs or other genes underlying fitness. Uncritical inference from molecular markers to QTLs might be just as damaging as the uncritical inference from markers to adaptive variation.

Theoretically, preserving allelic variation at QTLs should allow a greater potential response to selection, but the fitness consequences of recombining the genetic backgrounds in which these QTL alleles exist remains an unknown risk.

What evolutionary forces influence quantitative traits?

It will be useful to compare Q_{st} and F_{st} across species representing a variety of life histories, breeding systems and metapopulation demographics. Several authors (Table 1) have used Q_{st} to infer selection acting on individual quantitative traits by their departure from patterns seen at neutral molecular genetic markers, but other comparisons are possible. For example, comparisons across breeding systems will help us to identify the nature of quantitative trait evolution in mixed mating and selfing systems in which both neutral and QTL alleles are more likely to be fixed through drift [11,17]. As $Q_{st}-F_{st}$ studies accumulate, comparing across taxa will allow inferences to be made about the relative influences of selection on particular traits. For example, bud-set date appears to be particularly important in climatic adaptation in conifers [18,46]. Similarly, in well-studied organisms for which QTLs have been mapped, it would be instructive to compare Q_{st} across traits with different numbers of QTLs or with nonadditive inheritance (dominance and/or epistasis). If molecular surveys of candidate loci can be included in such studies, a complete understanding of the relationship between marker and trait variance should be possible.

Summary

We emphasize that none of the foregoing is intended to argue against the use of molecular markers or translocations, both of which can be extremely beneficial in ecological, evolutionary or conservation studies [1–5,37–40]. However, we caution against an oversimplified interpretation of the results, in which it is assumed that low marker differentiation inevitably precludes adaptive differentiation. We have shown on both theoretical and empirical grounds that the interpretation of genetic variation must distinguish among: (1) (putatively neutral) molecular genetic markers; (2) quantitative genetic (polygenic) traits; and (3) the genes (QTLs) underlying quantitative traits. Each type of variation is likely to have its own pattern of geographical distribution, which is likely to be poorly correlated across the types. Moreover, the relevance of these three classes of variation to the definition of ecologically and evolutionarily relevant groupings will vary depending upon the short- and long-term purpose of defining those groups.

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