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Online links

FURTHER INFORMATION

American Museum of Natural History: http://www.amnh.org
Calouste Gulbenkian Foundation: http://www.gulbenkian.org.uk
Geneculture: http://www.geneculture.org
Lehmann Maupin Gallery: http://www.ohwy.com/ny/l/lehmauga.htm
Marion Goodman Gallery: http://www.mariangoodman.com
Mendel Museum of Genetics: http://www.mendel-museum.org
National Portrait Gallery, London: http://www.npg.org.uk
Sperone Westwater: http://www.contemporaryart.com/speronewestwater
The Wellcome Trust: http://www.wellcome.ac.uk
The Wellcome Trust Sanger Centre: http://www.sanger.ac.uk
Universal Concepts Unlimited, New York City: http://www.u-c-u.com

Access to this interactive links box is free online.

OPINION

Quantitative genetic analysis of natural populations

Allen J. Moore and Penelope F. Kukuk

Quantitative genetic studies in natural populations have been rare because they require large breeding programmes or known pedigrees. The relatedness that has been estimated from molecular markers can now be used to substitute for breeding, allowing studies of previously inaccessible species. Many behavioural ecologists have a sufficient number of markers and study species with characteristics that are amenable to this approach. It is now time to combine studies of selection with studies of genetic variation for a more complete understanding of behavioural evolution.

R. A. Fisher, one of the architects of the modern syntheses in evolutionary biology, showed how a knowledge of Mendelian inheritance was required to complete our understanding of evolution. Indeed, the first words of Fisher's seminal work were "Natural selection is not evolution"[1] (page vii), referring to the risk of ignoring the effects of inheritance on evolution. Whereas phenotypes that do worse than others are eliminated by selection, the changes of a trait only persist over time in a population if there are genetic influences that underlie the variation of that trait, that is, if selection is filtered through the system of inheritance[1]. So, changes that result from selection can be constrained or altered by the pattern of inheritance for a particular trait of interest[2]. The most fundamental constraint is a lack of genetic variation, because if there is no underlying genetic variation, the changes that occur in response to selection do not persist to the next generation. In addition, if two traits share common genetic influences, then selection acting on one will necessarily change the other even if this second trait is not subject to direct selection. If selection pressures conflict, or the genetic association among traits is negative, then this too can act as a constraint and can delay or stop evolutionary changes.

Given the role of genetics in evolution, evolutionary interpretations of selection studies without information about the mode of inheritance can be misleading[3,4]. It is therefore crucial to examine the extent of genetic variation in a population (genetic VARIANCE) and the genetic associations among traits (covariance), which are often conveniently expressed as HERITABILITIES and GENETIC CORRELATIONS, respectively (BOX 1). These parameters can then be assessed in combination with selection if we wish to extrapolate the potential EVOLUTIONARY TRAJECTORY of a set of traits[2]. However, because of the difficulties of identifying genetic influences in most populations, researchers are often limited to studying patterns of selection alone and inferring evolution from this partial information. In addition, many characters of interest to evolutionary biologists (morphology, behaviour and LIFE-HISTORY CHARACTERS) are usually COMPLEX and therefore require a quantitative genetic approach, which can be even more daunting[5–11]. However, recent advances in statistical methodology[12–17] should facilitate the combined studies of natural selection and genetics in natural populations. In this article, we suggest how such studies might be conducted, with a particular focus on how these methods can be used to explore the evolution of behaviour. As we discuss, several conditions and assumptions must be met for the statistical methods to be applicable, so not all areas of research can capitalize on these developments. In addition, the methods are relatively untried, and the extent to which these methods are robust is unknown until more data are collected[18]. Nonetheless, we argue that behavioural ecologists in particular will benefit, as they are likely to study species with the required characteristics, including molecular markers and information on population structure, which facilitate the use of these statistical methods. Such studies will verify or refute their usefulness.

Natural quantitative genetics

Perhaps more than most fields, behavioural ecology is characterized by studies that relate fitness to variation in behaviour, and that interpret behavioural patterns in an evolutionary context[2–4], but ignore genetics. This is not due to a lack of interest in the genetic contribution to behaviour[9,10]. There are several barriers to examining patterns of genetics for ecologically relevant behaviour, mostly owing to the lack of tractable species to which previous methods could be applied[8] (although avian studies have been a notable exception[19,20]). First, behaviour is perhaps the ultimate complex character and is almost always

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Box 1 | **Questions and approaches in quantitative genetics**

Evolutionary quantitative geneticists often ask: Are some of the differences between individuals due to heritable differences? Do several traits share common genetic influences (is there genetic covariation)? These two questions are classically expressed in terms of heritabilities and genetic correlations, respectively.

The starting point for quantitative genetics is to measure the variance (dispersion about the mean) or covariation (strength of association between two variables, such as phenotypic traits) in a population. The causes of differences between individuals can then be assigned by investigating the genetic or environmental factors that contribute to the variance or covariance observed. The most frequently used statistical models are described below. The particular statistical model that is used depends on the research question, the experimental design used to investigate genetic and environmental influences, and the species studied[5–7]. Commercial statistical packages (for example, S-Plus, SYSTAT, SAS and SPSS; see Online links box) are available that readily partition the total variance into its component genetic and environmental parts, regardless of the model.

Analysis of variance

This remains the most common method of partitioning variances in quantitative genetics[7]. Genetic influences are inferred on the basis of phenotypic resemblances among relatives in the breeding design compared with lower or lack of resemblance among unrelated individuals. In analysis of variance (ANOVA), the factor under experimental control is the type of relative (sib, half-sib and so on) that is measured. For more than one trait measured, multivariate ANOVA (MANOVA) is used to generate the covariances that are associated with different factors[7].

Regression

Regression allows inferences to be made about how independent variables determine or predict a dependent variable. Generally, both the dependent (for example, offspring phenotypes) and independent (for example, parental phenotypes) variables are continuous. Both simple linear regression (when a single independent variable is present) and multiple regression (multiple factors under experimental control) can be used.

Standard ANOVA and regression assume that the data are normally distributed and often require balanced designs (equal sample sizes in each sub-category). Incorporating more than two generations can also be difficult. Maximum-likelihood methods overcome these restrictions but are computationally intensive[7].

Maximun likelihood

Rather than requiring a known distribution function, a computer is used to search for the most likely variance estimate on the basis of the observed data. This approach is useful with either ANOVA or regression approaches and increases the flexibility of the data that can be analysed. This technique might be familiar to many geneticists in terms of tests of LOD SCORES.

Using molecular markers, such as microsatellites, rather than information derived from breeding to estimate relatedness does not change the basic statistical approach. Because relatedness can take on a continuum of values rather than falling into neat categories, a form of regression is preferred over ANOVA. Other issues that influence the statistical approach are detailed in the main text.

under polygenic influences. So, a statistical approach to understanding its genetic basis must be adopted[5–7,10]. Second, behavioural researchers often follow long-lived species in their natural habitat[9]. Therefore, genealogical studies are rarely possible with such species[2,10,16–22]. Third, even in short-lived species, many model organisms that are used for behavioural ecology research are not easily reared in sufficient numbers or bred under the controlled conditions that are necessary for quantitative genetic analyses. Finally, even studies of organisms that can be reared in the laboratory might not allow ecological interpretations to be drawn[8–10] as the laboratory environment can alter the behaviour or trait of interest in unpredictable ways[6,11]. So, extending the ability to study genetics in natural populations has the potential to expand, if not alter, our view of the inheritance of behaviour under natural conditions for most species.

Studies that aim to estimate quantitative genetic parameters depend on two factors: reliable measurements of the traits of interest and identification of individuals with known relatedness[5–7]. Although the former is not necessarily limiting for natural populations, the latter can be difficult to obtain. The traditional approaches to quantitative genetics use analysis of variance (ANOVA) (BOX 1) to compare the phenotypic similarity of relatives to unrelated individuals[5–7]. When there are genetic influences on traits, related individuals will be more similar to each other than they are to unrelated individuals, and the degree of similarity will be associated with the degree of relatedness. So, full-sibs are expected to be more similar than half-sibs, and half-sibs are more similar than unrelated individuals. Categorizing individuals into relationships (full-sib, half-sib) allows a partitioning of variances, or separation of the causes of variation into genetic and environmental[5–7], as first described by Fisher[7].

Estimates of relatedness have traditionally been generated by controlled mating in the laboratory or by exploiting a known pedigree. Manipulated breeding is not impossible in field studies[10]; for example, manipulating breeding by CROSS-FOSTERING has been used successfully for studies of bird behaviour in natural populations (for example, REFS 19,20). When genealogical records are available, it is possible to estimate genetic relatedness and therefore estimate genetic variation from measurements made on all individuals[7]. Measurements for such studies are often limited, and are most likely to be applied to morphological (for example, REFS 16,21) or perhaps life-history (for example, REFS 19,22) characters rather than behavioural ones. Moreover, for most vertebrates and nearly all invertebrates, parentage cannot be traced in the field, and it is often impossible to study more than one generation. Documenting patterns of genetic variance in natural populations therefore requires a technique that is relatively powerful, reliant on indirect measurement of relatedness and applicable to a single reproductive season.

Recently, methods have been described that exploit our ability to estimate relatedness on the basis of molecular markers and can be applied to natural populations in a single generation[7,12–17,23–26]. Like all statistical approaches, these marker-based methods have limitations and assumptions that might restrict their use in analysing quantitative genetic traits, although many organisms of interest to behavioural ecologists probably meet the requirements. The advent of PCR-based, highly variable and presumably neutral genetic markers, such as microsatellites, allow the genetic identity of individuals in a single population to be determined, so that relatedness values between two individuals can be estimated more precisely than ever before. Under certain conditions, which are detailed below (in the section entitled 'Limitations and assumptions'), we can combine pairwise estimates of genetic relatedness with pairwise measures of phenotypic resemblance to determine heritabilities and genetic correlations.

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Using molecular markers

Estimating parameters in the field. Ritland was the first to develop an approach that used molecular markers to estimate relatedness values and to apply it to a quantitative genetic study[12,13]. In BOX 2, we provide a brief overview of the basic statistical methods that can be used, but the underlying concept is straightforward. As in all quantitative genetics, more closely related individuals are expected to be more phenotypically similar than unrelated individuals. Any two individuals in a population might share alleles that are identical-by-descent, and therefore might be related on a continuous scale by r_{ij}, which is known as the coefficient of kinship or the relationship coefficient. Given an estimate of this measure (R), and measures of phenotypic similarity, genetic variances can be estimated using regression analysis (BOX 2). However, unlike traditional approaches in which relatedness is known because breeding is controlled, both relatedness and genetic variances must be estimated, so large sample sizes are needed (BOX 3).

This simple model can be easily expanded to incorporate additional factors. For example, it is likely that many behavioural ecologists will be concerned with common environmental influences, such as shared parenting or shared experiences, which can accentuate the phenotypic similarities among unrelated individuals. Indeed, including this information where available will help to avoid artificially inflating the estimates of genetic effects. Another potentially important cause of phenotypic similarity is the variation that is introduced by temporally subdivided populations, such as that seen in species that have more than one generation in a season, with each generation experiencing unique influences. The approach detailed by Ritland accommodates environmental and other genetic factors (dominance or inbreeding, for example) by using multiple regression analysis[13,24,25] (BOX 1). The previous knowledge of how a population is structured or potentially influenced is the limitation on other factors that can be estimated. In addition, sample sizes that are already large will need to be considerably larger whenever the simple model is extended. Like all biological applications of multiple regressions, choosing which factors to include or exclude should reflect the understanding of the biology of the species in question. Simply indiscriminately adding variables causes problems with interpretation and power.

The method of Ritland can be extended to estimate genetic correlations in natural populations, as well as to estimate heritabilities[26] (BOX 2). Genetic correlations reveal shared genetic influences on traits and are important because the genetic structure of a population dictates the speed and direction of evolution. Patterns of genetic covariances (correlations)

Box 2 | Quantitative genetics from phenotypes and molecular markers

Several recent reviews[7,18,24–26] provide greater detail on these methods. Here, we provide a brief overview to illustrate the basic concepts.

Heritabilities

To estimate heritabilities, we need an estimate of relatedness between individuals and a measure of a variable phenotype. The regression technique for estimating genetic variances and covariances depends on phenotypic similarity between two individuals i and j for a given trait z (Z_{ij}), and on the pairwise estimate of relatedness (R_{ij}). Phenotypic similarity is calculated by cross-products (the average of which is the phenotypic correlation), as

$$Z_{ij} = \frac{(z_i - \bar{z})(z_i - \bar{z})}{\mathrm{Var}(z)} . \qquad (1)$$

Pairwise relatedness (R_{ij}) can be estimated using several methods that we discuss further below. After a measure of phenotypic similarity between individuals has been obtained, genetic (and other) components of similarity can be estimated by a linear model:

$$Z_{ij} = 2r_i h^2 + e_{ij} , \qquad (2)$$

where r and Z_{ij} are as before, h^2 is the heritability and e_{ij} is the residual deviation. So, replacing actual relatedness (r) with an estimate (R), heritability can be estimated as

$$\hat{h}^2 = \frac{\mathrm{Cov}(Z,R)}{\mathrm{Var}(r)} \qquad (3)$$

where Cov(Z,R) is the sample covariance between the measure of phenotypic similarity and the estimate of relatedness, and Var(r) is the actual variance of relatedness among all pairs estimated from the sample.

Genetic correlations

Quantifying the extent of genetic influences on a trait is usually only half of the information that is needed to begin to understand evolutionary trajectories. The extent to which other traits share genetic influences, and therefore share changes that result from selection across generations, is quantified with genetic covariances. Genetic covariances can take on any value, which can make comparisons difficult. Therefore covariances are often converted to correlations, a standardized measure of joint association that can take on values from –1 to +1.

For genetic correlations, we again need an estimate of relatedness and measures of two or more variable characters on the individuals being compared. After Lynch[26], for two characters (z_x and z_y), and two individuals (i and j), the measure of how the phenotypic expressions of these two traits covary is

$$C_{xy,ij} = (z_{x,i} - \bar{z}_x)(z_{y,j} - \bar{z}_y) . \qquad (4)$$

The additive (A) genetic correlation ($r_{Ax,y}$) is then given by

$$r_{Ax,y} = \frac{R_{ij}C_{xy,ij}}{\sqrt{R_{ij}C_{xx,ij}R_{ij}C_{yy,ij}}} . \qquad (5)$$

Evolutionary biologists often infer constraints if there is a negative genetic correlation[2,3,6,7,26–28], as a negative correlation indicates that directional selection acting on one trait will cause an opposite change in the other trait. If only the sign is of interest, rather than the magnitude, the numerator alone suffices. This can be estimated with fewer individuals.

An equivalent method for estimating the additive genetic covariance can be obtained by regressing $C_{xy,ij}$ on R_{ij}. The sign of this regression gives the sign of the genetic correlation. The slope of this regression, b_{xy}, along with the slope of $C_{xx,ij}$ on R_{ij} (b_x), and $C_{yy,ij}$ on R_{ij} (b_y), provide the estimate of the full genetic correlation:

$$r_{Ax,y} = \frac{b_{xy}}{\sqrt{b_x b_y}} . \qquad (6)$$

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Box 3 | **Experimental design issues**

Number of individuals

Sample sizes must be large. The number of pairwise comparisons should be greater than 10^4 (and preferably 10^5) to obtain reasonable heritability estimates[13]. This requires a sample of between 150 and 450 individuals. If a greater spatial scale is required for a larger sample, this will probably reduce the number of related pairs that will be obtained and will increase the sample size needed. If genetic correlations are estimated, higher rather than lower numbers of individuals must be sampled[13,26]. One way to minimize the size of the sample required is to have highly accurate estimates of relatedness. For this, highly variable, co-dominant markers must be available.

Number of loci

The quantity $n(m-1)$ should be between 25 and 100, where n is the number of loci and m is the number of alleles per locus. This minimum can be achieved with as few as five loci, each with five alleles in relatively even frequencies. Increased precision in estimating pairwise relatedness values is obtained through increasing the number of loci or the number of alleles per locus. Better estimates of pairwise relatedness values are obtained using 20 such marker loci and 250 pairs of individuals than with 10 loci and 500 pairs[25], but unfortunately more individuals might need to be sampled to obtain a sufficient number of related pairs[30]. Both the number of markers scored and the number of individuals sampled must be larger than is the current 'norm' for studies in behavioural ecology.

Variation in relatedness

There should be substantial variance in pairwise relatedness values in the sample, indicating that relatives, not just unrelated individuals, are included. There should be an expectation that at least 20% of the individuals sampled will be relatives. Selecting species with specific mating or social structures can help. A male POLYGYNOUS mating system would result in a population consisting of sets of individuals, each set fathered by the same male. A lack of dispersal, PHILOPATRY, by either males or females, will also increase spatial population structure and increase the variance in pairwise relatedness values. Knowledge of non-behavioural factors can sometimes help. For example, the possible range of pairwise relatedness values in haplodipoid species is 0.00–0.75, an increase of 50% over that of diplodiploid species, which makes the method especially useful for groups such as the social Hymenoptera.

In populations in which a family structure is known to exist, the problem becomes one of classification (for example, sib or non-sib) rather than an estimation of relatedness: Markov chain Monte Carlo methods are suggested in these cases[31–33]. Fewer loci are needed depending on family size, allele frequency and heritability — as few as five loci with six alleles each might be sufficient. However, inaccurate estimates of family size and expected relatedness among family members (full- versus half-sibs) can result in substantial errors[30].

are therefore often more informative for evolutionary studies than heritability[2,6,7]. Genetic correlations are also potential indicators of EVOLUTIONARY TRADE-OFFS and the FUNCTIONAL INTEGRATION of characters[2,6]. For example, negative genetic correlations are expected for many life-history traits (for example, between the rate of reproduction and longevity) that are expected to place conflicting demands on an organism[27]. The elements of morphology that contribute to a common function are expected to show strong positive genetic correlations and coordinated development[28]. A knowledge of genetic variances and covariances therefore allows us to understand how populations might respond to selection. Applying these methods where possible should increase our understanding of the nature of quantitative genetic variation in populations, allowing us to evaluate the need for genetic studies that are coupled to studies of selection.

Extensions to the statistical methodology. Ritland's method is based on simple linear regression procedures and asks: How does some pairwise measure of the relationship coefficient (the independent variable) predict the pairwise phenotypic similarity (dependent variable)? Improvements in the measurement of either of these variables, then, will improve the method. In addition, other researchers have proposed alternative statistical methods that improve on the simple linear regression model if additional information about a population is available.

Mousseau *et al.* suggest a technique that is based on maximum likelihood as an alternative method[14]. The likelihood approach (BOX 1) is appropriate for populations in which a specific structure of relationships in the sample is likely. A further advantage is that it might allow the use of fewer markers as fewer relationships are estimated; indeed, only relationships (such as full-sib and maternal half-sib) rather than pairwise relatedness measurements are needed. Thomas *et al.* provide a further refinement of the likelihood method that requires fewer initial assumptions about population parameters[17]. Furthermore, they show that likelihood methods have larger average bias but smaller variances over the estimates than the regression approach[17]. So, if specific relationships are known or expected in a population, likelihood methods might provide a more powerful alternative to estimating heritabilities. An important limitation to the use of a likelihood approach, however, is the requirement of previous knowledge of the size of the relationship classes. For many behavioural ecologists, the relationships in a population are unknown or more variable than sibs and half-sibs, which leaves the regression technique as the only option.

Estimating pairwise relatedness. There are several techniques for estimating pairwise relatedness from molecular markers[15,23,29]. All seek to estimate the probability that genes are identical-by-descent when two individuals share the same band or sequence of a marker gene and all techniques assume that loci are sampled from large populations, allowing reasonable estimates of allele frequencies. For each method, the number of alleles at each locus and the frequency of each allele in the population must be known. From these, we score whether each allele (band or sequence) at each locus is the same or different both within and between each pair of individuals. This information is then entered into an equation, and it is the form of the equations that differs among the approaches. Queller and Goodnight's equation[29] assumes highly polymorphic loci and is widely used in behavioural ecology; however, this approach is not applicable when marker loci are diallelic, for example when ALLOZYMES are used as markers. Ritland proposes an alternative formula that can be used under these circumstances[23]. Lynch and Ritland[15] suggest a regression approach to estimating pairwise relatedness, and this method is especially useful when the marker loci are highly variable (more than five alleles). Lynch and Ritland's approach is also computationally simple, as it relies on standard regression to obtain multilocus estimates of relatedness. Van de Casteele *et al.*[30] compare the three approaches and conclude that the best-performing estimator depends on the proportion of the population that form related pairs.

If a likelihood approach to estimating heritability in a population that is structured by relatedness is adopted, the problem is not one of determining the exact values of relatedness

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itself but in estimating the individuals that fall into expected relationships. Most often, this is a problem of identifying sibships (sibs and half-sibs) from markers. An extra problem is that allele frequencies are assumed to be known. In reality, these frequencies are estimated from the data themselves. This has led to the suggestion of adopting a MARKOV CHAIN MONTE CARLO APPROACH, which can be used even when no information on parents is available[31–33]. These techniques do extremely well when only a few forms of relationship are expected.

Limitations and assumptions

There is no such thing as a free (or even inexpensive) lunch in quantitative genetics, and these new techniques offer hope to field biologists but will not be appropriate or feasible for all species. Like all statistical techniques, some necessary assumptions are made when applying the theory to reality. This is no different to any laboratory study of genetics or any field study of selection. However, populations are required to have certain characteristics for the techniques outlined above to be applied successfully. Nonetheless, we feel that neither the assumptions nor the necessary conditions should be limiting for behavioural ecologists.

Perhaps the single most vexing issue for quantitative genetic analyses is sample size. We therefore detail in BOX 3 some of the issues related to the question of "how many?" The simple answer is, of course, as many as possible. If there is a trade-off between the molecular work and sampling more pairs of individuals, it is usually better to sample more individuals, although increased sample size cannot compensate for inadequate markers. If genetic correlations are of interest, and we suggest they usually are or should be, sample sizes depend on the strength of the heritability of each character and therefore even larger sample sizes are needed. Nonetheless, given the potential pay-off, the effort seems to us to be worthwhile. Unlike the classical quantitative genetic approaches, the effort is not directed towards rearing organisms or taking accurate measurements over many generations or long times in the laboratory, but is substantial nonetheless. Sample sizes might be daunting, but judicious sampling to ensure maximum variance in pairwise relatedness values might increase the power of the test (BOX 3).

Although pairwise relatedness and pairwise measures of phenotypic similarity are all that are required to apply any of these methods, it is the variation in these measures that ultimately is important for calculating heritabilities (BOX 3). The techniques for determining relatedness all use the ready availability of PCR-based markers that typically show considerable variability, thereby making them particularly useful for determining relatedness. Unfortunately, the variation in relatedness measures between pairs of individuals has rarely been investigated. Many researchers have already carried out studies that will allow them to estimate variance in pairwise relatedness values, which provides insights into the feasibility of these methods. In BOX 4, we use our own data from previous studies to illustrate the point that researchers might already have data that allow them to evaluate whether these techniques might reasonably be applied to their systems.

In quantitative genetic studies, it is important to ensure that measurement error contributes as little as possible to the error variance. This is especially true for calculations of heritability, in which increased error variances inflate phenotypic variance and therefore provide an underestimate of heritability. So, phenotypic measures should be as

Box 4 | **Quantitative behavioural genetics: an application**

Lasioglossum hemichalceum **is a communal bee species with an annual colony cycle of two generations. Molecular markers (microsatellites) exist in this species and have been used to study the detailed genetic structure of these bee colonies[48,49]. It is possible to measure several socially relevant behaviours: such as food sharing, the timing of foraging and the division of labour in nest excavation[50,51]. Below, we show how these markers can be evaluated for potential use in quantitative genetic studies of natural populations, even though they were developed for other purposes[48,49].**

Image courtesy of Museum Victoria, Melbourne, Australia.

Sample size

Each *L. hemichalceum* nest contains 3–5 adult females along with the developing brood, so that there are enough individuals in a single site (3–5 aggregations of 150–200 nests) to sample. Obtaining data from 70 colonies, with an average of 3 females per colony, results in about 22,200 pairwise comparisons, which is reasonable and would not obliterate the population.

The most efficient way to achieve this large number, while minimizing environmental variance, is to conduct all the experimentation in a single season on a single population. This also increases the proportion of pairs that are related. If sampling between sites is necessary, this information can be included in the regression. Colony membership or colony size could be included as factors that potentially indicate common environmental effects. The more factors we have in our regression, however, the larger the sample sizes that would be required.

Markers

For *L. hemichalceum* there are 12 microsatellite loci with an average of 12.5 alleles per locus available so $n(m-1) = 138$ (BOX 3). In addition, if the sampling variance for the pairwise relatedness estimates were to be unacceptably large, seven other microsatellite primers are available.

Variance in pairwise relatedness values

Using the nine loci that have been used in previously published work[48,49], we can calculate pairwise relatedness values for 180 adult and immature females from nine natural colonies in a single aggregation using the relatedness program of Queller and Goodnight[29]. The 16,110 pairwise relatedness values range between −0.43 and +1.0 with a mean of −0.004 (variance = 0.03). Simulations using the allele frequencies from these data show that the variance due to sampling error drops sharply from one to six loci, and levels off between eight and ten loci at ~0.01 for full sisters and ~0.02 for unrelated pairs. If these results were representative of the population, we would not need more than nine loci for a full study.

A much larger number of nests would be needed to add a consideration of behavioural similarity, and therefore lead to quantitative genetic estimates. However, it is clear by simply examining data that has already been published that we can apply the regression approach to these bees.

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accurate as possible. This might be especially crucial for behaviour because, as most behavioural ecologists quickly learn, measuring behaviour can be daunting[11]. Hoffmann provides a particularly lucid discussion of this problem relative to behavioural genetics, pointing out that one solution is to estimate repeatability, thereby providing a method for removing measurement error[11]. We echo his recommendation that each individual should be measured more than once if possible when studying behaviour.

Glossary

ADDITIVE GENETIC VARIATION
The genetic variation that can be statistically associated with the effects of genes that are independent of other loci or alleles. This is the component of variance that contributes to the response to selection.

ALLOZYME LOCI
Loci that code for different electrophoretic forms of the same enzyme as a result of allelic differences.

COMPLEX CHARACTERS
Traits that are determined by many genes, almost always interacting with environmental influences.

CROSS-FOSTERING
Transplantation of some progeny from a biological mother to an unrelated foster mother. Under this design, all resemblance among unrelated individuals reared by the same mother are ascribed to a common rearing environment, eliminating genetic effects.

EVOLUTIONARY TRADE-OFF
This occurs when the evolution of one trait is limited by the evolution of an associated trait in the opposite direction or because of negative genetic correlations. Trade-offs limit the number of traits that can be maximized simultaneously through evolutionary responses to selection.

EVOLUTIONARY TRAJECTORY
The expected direction of evolutionary change in a trait over time. In adaptive evolution, the trait is expected to evolve towards an adaptive peak, or point of maximum fitness for the population.

FUNCTIONAL INTEGRATION
Traits that together form a functional unit or character, such as the anatomical regions of the skull. Such traits are expected to have experienced stabilizing selection that favours functionally compatible trait values.

GAME-THEORY PREDICTION
A model that investigates phenotypic evolution, particularly behaviour, when the fitness of the phenotypes depends on their frequency in the population.

GENETIC CORRELATION
The correlation between traits that is caused by genetic as opposed to environmental factors. Genetic correlations are the standardized measures of genetic covariation and can take on values between +1 and –1. A genetic correlation results between two traits if the same gene affects both traits (pleiotropy) or if genes that affect the two traits are in linkage disequilibrium.

HAPLODIPLOID SPECIES
Species in which males develop from haploid (unfertilized) eggs, and therefore have only a single set of chromosomes contributed by the female. Females develop from fertilized eggs that have a full complement of chromosome pairs, one from each parent.

HERITABILITY
The proportion of the total phenotypic variation in a trait that can be attributed to additive genetic effects. Heritabilities are standardized measures, taking on values from zero (no genetic variation contributing to phenotypic variation in the population) to one (all of the variation in the population reflects genetic differences).

KIN SELECTION
The selection that results from a behaviour or trait that contributes not only directly to the fitness of the organism, but also indirectly (that is, enhancing an individuals fitness by increasing the reproduction of a relative beyond that which could be achieved without the assistance of the relative).

LIFE-HISTORY CHARACTERS
Traits that are associated with survival or reproduction of an individual, such as longevity, reproductive output, size and growth.

LOD SCORE
(Base 10 'logarithm of the odds' or 'log-odds'). A method of hypothesis testing that uses the logarithm of the ratio between likelihoods under the null and alternative hypotheses.

MARKOV CHAIN MONTE CARLO APPROACH
A computational technique for the efficient numerical calculation of likelihoods.

OPTIMALITY MODEL
A quantitative evolutionary model that defines the maximum (or minimum) fitness values for a given trait under specified constraints. They are often used to investigate life-history evolution.

PHILOPATRIC SPECIES
Those that remain in the same geographical location as at their birth.

POLYGYNY
Multiple mating by males, such that families consist of both full-sibs (having the same mother and father) and half-sibs (siblings with the same mother but different fathers).

SEXUAL CONFLICT
The evolution of phenotypic characteristics by sexual selection, when the trait confers a fitness benefit to one sex but a fitness cost to the other.

SEXUAL SELECTION
The selection that results from differential mating success. It includes competition for mates (usually among males) and mate choice (usually by females).

VARIANCE
A statistic that quantifies the dispersion of data about the mean. In quantitative genetics, the phenotypic variance (V_p) is the observed variation of a trait in a population. V_p can be partitioned into components, owing to genetic variance (V_g), environmental variance (V_e) and gene-by-environment correlations and interactions.

Applications in behavioural ecology

Behavioural ecologists have been using molecular measures of relatedness for more than a decade in studies of KIN SELECTION, breeding systems and dispersal. So, behavioural ecology is pre-adapted to add genetic studies of natural populations to its quantitative research portfolio. Here, we suggest a few specific topics in which we see tremendous potential for adding information on inheritance to our already rich repertoire of studies of selection.

One area that quickly adopted molecular markers to determine relatedness is the study of social evolution. For animals, terrestrial ecosystems are dominated by social species, and social cooperation is the most recent and experimentally most accessible transition in the evolutionary trajectory of ever increasing complexity. Theoretical and empirical investigation of kin and social selection, and of the fitness benefits derived from social behaviour, is an exceedingly productive focus of evolutionary studies, spanning nearly 40 years (REFS 34–36). With rare exceptions (for example, see REF. 37), there is a lack of complementary studies of genetics. This is because classical quantitative genetic approaches could not be applied to most species.

A marker-based approach to quantitative genetics might be especially valuable in understanding how genetic variation influences the evolution of sociality. Relatedness has been a topic of great interest to students of social behaviour, particularly of those studying social Hymenoptera (ants, bees and wasps), and many studies using genetic markers have been conducted (for example, see REFS 29,36 and BOX 4). In these HAPLODIPLOID SPECIES, full sisters are expected to have $r = 0.75$ (where r is relatedness), which is 50% greater than the $r = 0.50$ that is expected between full-sibs in diplodiploid species[35,38]. In addition, kin remain in social groups, and this leads to highly structured populations. So, many social-insect biologists have available the necessary tools and conditions to explore the genetic variation that underlies socially relevant behaviour (BOX 4).

Another area in which behavioural ecologists have often argued evolution strictly from studies of fitness components without regard to genetics is SEXUAL SELECTION and SEXUAL CONFLICT. Empirical studies of genetic variation show that sexually selected traits might harbour more genetic variation than most traits, even though the theoretical expectation is that such traits should have low ADDITIVE GENETIC VARIATION[39,40]. However,

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empirical work on the genetics of sexually selected traits is primarily laboratory based. It would be especially useful to compare field and laboratory estimates of heritability for sexually selected traits, as has been done for other characters[6,11]. In many species in which mate choice, sperm competition and male–male competition are examined, molecular markers are used to determine extra-pair matings and paternity. These species might be especially amenable to the use of regression-based methods for determining patterns of genetic variance and covariance in sexually selected traits under natural conditions. It could be that field studies will provide insight into the true generality, or otherwise, of patterns for sexually selected traits. A potential further advantage of such studies is that morphology, as well as behaviour, might be studied[41].

OPTIMALITY MODELS and GAME-THEORY PREDICTIONS prevail in nearly all areas of behavioural ecology. Such models, however, assume that populations are at an evolutionary equilibrium and, importantly, that selection has been unconstrained[3,4]. Combining optimality approaches with quantitative genetics studies to examine the genetic 'filter' through which selection must pass to produce evolutionary change will provide an especially powerful tool for understanding behavioural evolution, and the limits thereof[6].

Finally, one of the growing areas in behavioural ecology is the recognition that populations might be subdivided or structured as a result of non-random behavioural interactions[42–45]. For example, social grouping or neighbourhoods might result in greater within-group than between-group interactions. The consequences of behavioural subdivision can be profound and include altering the nature of selection[42–45]. Such populations are especially amenable to the techniques described here; indeed, without adopting a behavioural genetics approach, we might have a misleading view of evolution in these populations[44,45]. Furthermore, the methods can be adapted to consider how quantitative genetic variation might exist between subpopulations[13,24,25]. Quantitative genetic variation at both of these levels could be especially informative for behavioural ecologists, as it is they who have identified species in which social structuring occurs.

This list of examples is by no means exhaustive. Patterns of foraging, learning and anti-predator behaviour occupy the attention of behavioural ecologists but are rarely studied from a genetic perspective apart from a few model (and therefore laboratory) species, such as *Drosophila* or mice[8,10]. It can be difficult to study the genetic influences on parental care and parental investment outside the laboratory, but these topics might be amenable to the marker-based approach. Similarly, traits such as territoriality, dominance and other social interactions have rarely been addressed from a quantitative genetics perspective[45]. However, it is exactly these traits that are expected to have different patterns of genetic influences and to evolve differently to other traits[42,45]. Our intent is to stimulate the creativity of behavioural ecologists and others who study complex characters in natural populations. Genetic information on virtually any ecologically relevant trait would be valuable.

Prospects and conclusions

The advent of highly variable PCR-based genetic markers has allowed a burgeoning of studies in behavioural ecology that are focused on selection, social evolution, sexual selection, parental care, communication and many more topics — the limit has been the imagination of researchers rather than the tools. The use of these same molecular techniques will allow a new burgeoning of studies that examine the rest of the evolutionary equation — that is, the genetic filter through with selection passes to produce evolutionary change. Both the regression method (workable where pairwise relatedness values are expected to be distributed continuously) and the maximum-likelihood methods (useful where categorization of individuals into sibships is a better reflection of the natural situation) will allow quantitative genetic parameters to be estimated in a wide range of natural settings. The approaches we have outlined provide the only avenues that are available at present for investigating the genetics of evolutionarily important behaviour for many species. For example, species in which parents and offspring can experience vastly different seasonal conditions during development are usually neglected from a quantitative genetics perspective. The flexibility of the methods we describe allows such complications to be included in the analyses.

There is now hope that we can begin to assess genetics under natural conditions. This is particularly important, given the (albeit limited) current evidence that heritabilities differ between field and laboratory settings[11]. Such studies require potentially heroic sample sizes to provide enough power for reasonable comparisons, but are feasible. We need studies that allow comparisons of magnitude under different conditions of selection or for different categories of characters[6]. Comparing the field and laboratory patterns of genetic variance will provide an indication of how genetic traits might change under laboratory selection[6,11]. Simply estimating heritabilities has been argued to be of limited value for many characters[7,26] because with adequate sample sizes, quantitative genetic variation seemingly always exists[7]. Although this might be true for laboratory estimates, the paucity of field estimates of heritability mitigates this argument. In addition, as heritabilities differ in field populations, so too will genetic correlations. Knowledge of the extent to which traits share common genetic influences has important consequences for predicting evolutionary trajectories and for investigating life-history theory, and provides insights into constraints and functional units. In addition, documenting patterns of heritability and genetic correlation from natural populations will verify our ability to generalize from laboratory studies of quantitative genetics[6,41].

The approach we have outlined has limitations, particularly in its requirement that researchers know they will encounter relatives in their population. Common environmental effects might also be problematic. Clearly, not all species are amenable to these studies, but we believe the range of organisms in which quantitative genetic information can be obtained has been broadened. Studies that apply these methods to species in which heritabilities or genetic correlations are known from more traditional methods[19] would be especially valuable (for example, see REF. 18). We are confident that many behavioural ecologists have the species, experience (or collaborators) and information needed to make such studies feasible. We also hope that we can help to stimulate the empirical work that is the first step in proving the genetic information that has been revealed in animal systems that are behavioural model organisms rather than genetic model organisms. One pleasing aspect of the marker-based methods for determining quantitative genetic variation is their similarity to regression-based methods for quantifying selection[2,46,47] — methods that were quickly adopted in evolutionary ecology. We think that a revitalization of both behavioural ecology and quantitative genetics is likely to be imminent, as is a more complete view of evolution.

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