Testing the Aerobic Model for the Evolution of Endothermy: Implications of Using Present Correlations to Infer Past Evolution

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Submitted February 4, 2013; Accepted July 9, 2013; Electronically published November 12, 2013

abstract: The evolution of endothermy is one of the most puzzling events in vertebrate evolution, for which several hypotheses have been proposed. The most accepted model is the aerobic model, which assumes the existence of a genetic correlation between resting metabolic rate (RMR) and maximum aerobic capacity (whose standard measure is maximum metabolic rate, MMR). This model posits that directional selection acted on maximum aerobic capacity and resting metabolic rate increased as a correlated response, in turn increasing body temperature. To test this hypothesis we implemented a simple two-trait quantitative genetic model in which RMR and MMR are initially independent of each other and subject to stabilizing selection to two separate optima. We show mutations that arise that affect both traits can lead to the evolution of a genetic correlation between the traits without any significant shifting of the two trait means. Thus, the presence of a genetic correlation between RMR and MMR in living animals provides no support in and of itself for the past elevation of metabolic rate via selection on aerobic capacity. This result calls into question the testability of the hypothesis that RMR increased as a correlated response to directional selection on MMR, in turn increasing body temperature, using quantitative genetics. Given the difficulty in studying ancient physiological processes, we suggest that approaches such as this model are a valuable alternative for analyzing possible mechanisms of endothermy evolution.

Keywords: aerobic model, evolution of endothermy, house-of-cards model, evolutionary modeling, genetic correlations..

Introduction

Because of their high metabolic rate, birds and mammals can maintain a high and constant body temperature (i.e., above 30°C, mostly between 35°and 41°C), independently of the environmental temperature (Bennett and Ruben 1979; Hayes and Garland 1995; Lovegrove 2012). In contrast, ectotherms experience fluctuations in body temperature depending on their immediate environment. It has been argued that birds and mammals attained their ecological success as lineages because of endothermy which promoted a suite of changes such as thermal homeostasis, sustained capacity for activity, efficient gestation, and lactation (see Lovegrove 2012 and references therein). However, it is also true that ectotherms require on average only one-fifth of the daily energy that an endotherm of the same size needs. This has obvious advantages under conditions of resource limitation (Pough 1980; Else and Hulbert 1981).

Evidence suggests that incremental changes extending over a long time period were involved in the evolution of endothermy, a process named by Kemp (2006) the "correlated progression model" (Kemp 2006; Lovegrove 2012). At least five hypotheses or models that focus on changes in body size, thermal niche, aerobic capacity, parental care, and assimilation capacity have been proposed (for reviews, see Clarke and Portner 2010; Lovegrove 2012). These models fall into three categories, those that posit that (1) body temperature was the target of directional selection (thermoregulatory models; see Crompton et al. 1978; Bennett et al. 2000; Farmer 2000), (2) aerobic capacity was the target of directional selection (aerobic capacity or aerobic scope models; Bennett and Ruben 1979; Koteja 2000), and (3) selection promoted the joint maximization of body temperature and aerobic capacity (Clarke and Portner 2010). All of these models are based on the assumption, for which there is good empirical support, that body temperature is correlated with resting metabolic rate (Clarke and Portner 2010; Clarke et al. 2010; Lovegrove 2012). Aerobic capacity models (AC models) presume a genetic correlation between resting metabolic rate and aerobic capacity and that resting metabolic rate increased as a correlated response to selection on aerobic capacity (Hayes and Garland 1995). With varied emphasis, AC models are an important part of the explanation for the evolution of endothermy (Koteja 2000; Clarke and Portner 2010; Hayes 2010).

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Am. Nat. 2014. Vol. 183, pp. 74–83.
DOI: 10.1086/674093

Hayes (2010, reviewed in Nespolo et al. 2011) introduced two forms of the AC model, the "weak" and "strong" form. These two forms make a crucial distinction on how the AC model should be tested. The weak form assumes that genetic correlations are labile and can change because of mutation, selection, and drift, as classic population and quantitative genetics predict (Arnold et al. 2008). The weak version of the AC model cannot, therefore, be tested using quantitative genetics on living species because current patterns of correlation need not reflect past selection. The strong form of the AC model, on the other hand, assumes the existence of an inescapable structural link between resting and maximum metabolic rates. If this link between resting metabolic rate (RMR) and maximal metabolic rate (MMR) is an essential feature of the design of vertebrates, then it should be constant, at least with respect to sign, irrespective of other forces (Wone et al. 2009; Hayes 2010). In contrast to the weak model, the strong model predicts a measurable, positive genetic correlation between RMR and MMR in extant species of endotherms.

Endotherms evolved from ectothermic ancestors at least twice in the phylogeny of amniotes, a process that lasted not less than 100 million years, from an unquestionably ectothermic synapsid (in the Permian) or dinosaur (in the Triassic) to present-day mammals and birds, respectively (Nespolo et al. 2011). This time span involves several millions of generations if we think conservatively (some turtles have a generation time of 25 years; see Congdon et al. 1994), and tens of millions of generations for a typical amniote. Hence, the possibility of testing the strong form of the AC model in extant species is based on the crucial supposition that the genetic correlation is such a fundamental component of the basic vertebrate design that it should be constant during millions of generations (Hayes 2010).

From the preceding arguments it follows that if one could show that a genetic correlation could arise and be maintained for many generations, in the absence of any necessary structural links between traits, then the utility of examining genetic correlations in extant species would be brought into question. In other words, the crucial supposition would be falsified. In this article, we present a model and analysis demonstrating that a positive genetic correlation can arise without assuming a necessary structural link between traits and can be maintained for hundreds of thousands of generations. From this we conclude that the measurement of the genetic correlation between RMR and MMR, in present-day species, is of limited utility in testing the AC model.

Our Model

The aerobic model for the evolution of endothermy, as initially proposed, assumed a mechanistic link between RMR and MMR. This assumed link was based on the recurring observation that the ratio MMR/RMR is remarkably constant in vertebrates, typically ranging from 5 to 10 (Bennett and Ruben 1979; Bozinovic 1992; Hinds et al. 1993). However, as pointed out by Hayes and Garland (1995), phenotypic correlations are not appropriate parameters with which to make evolutionary predictions. Under the AC model, the MMR/RMR association is assumed to be based on additive genetic effects, and thus, evolutionary predictions depend upon the genetic correlation between MMR and RMR (Hayes and Garland 1995).

In vertebrates, aerobic metabolism is generated mainly by oxidative phosphorylation, whose proteins are assembled by a set of approximately 90 mitochondrial and nuclear genes (Grossman et al. 2001; Das 2006; Ballard et al. 2007). Both resting and activity metabolism rates are affected by these genes, but the exact contributions of effect from either source remains unknown. However, some genes act specifically on RMR or MMR, whereas RMR depends on the aerobic metabolism of leaky membranes in visceral organs (Else et al. 2004), and MMR depends on the performance of red fibers in skeletal muscle, particularly associated with actomyosin ATPase and Ca^{++} ATPase (Hochachka and Burelle 2004). In our model, we assumed that there are genes that separately affect RMR and MMR and other genes that could mutate to affect both traits.

To simulate the genetic basis of RMR and MMR we used the house-of-cards model, suggested by Turelli (1984), which assumes that the variance of mutational effects is large compared to the standing genetic variance. The consequence of this is that only a small number of discrete alleles are possible at each locus (Reeve 2000; Reeve and Fairbairn 2001). We simulated the scenario of a large synapsid or theropod population (1,000 individuals) with nonoverlapping generations. Sexes were assumed to be separate, mating was at random, and MMR and RMR were initially uncorrelated traits, determined by autosomal, diploid loci. We assumed that there were $n_{\mathrm{MMR}} = 50$ loci that affected MMR only and $n_{\mathrm{RMR}} = 50$ loci that affected RMR only. Genotypic trait values were assumed to be additive (no dominance or epistasis) with allelic values of $-a$ or $+a$ at each locus. We assumed that mutations at other loci, which we label C loci, can arise that have pleiotropic effects on MMR and RMR. There were n_{C} of these loci and mutations at these loci have effects of $\pm a$ on both MMR and RMR.

We assumed stabilizing selection

$$w_i = \frac{\exp\left[-0.5^{*}(\mathbf{Z}_i + \boldsymbol{\theta})^{\mathrm{T}}\mathbf{W}^{-1}(\mathbf{Z}_i - \boldsymbol{\theta})\right]}{\max(w)}, \tag{1}$$

where w_i is the relative fitness (=probability of reproducing) of the ith individual, $\mathbf{Z}_i$ is a vector of length 2 holding the values of MMR and RMR for the ith individual, $\boldsymbol{\theta}$ is the vector of optimal trait values, T indicates transpose, $\mathbf{W}$ is a 2 × 2 matrix of stabilizing (diagonal), correlational (off-diagonal, assumed to be zero) selection coefficients (Lande 1980), and $\max(w)$ the maximum individual fitness. To mimic the difference in the two traits, we set values in the vector $\boldsymbol{\theta}$ at 150 (MMR) and 30 (RMR), respectively, reflecting values of oxygen consumption (mL h^{-1}) in a small vertebrate (ca. 100 g; Nespolo et al. 2003; Sadowska et al. 2005). The strength of stabilizing selection (diagonal elements of $\mathbf{W}$) was set at 1,000 for both traits. Following Reeve (2000) the number of mutations per generation was drawn from a Poisson distribution with a mean of $2(0.0001)Nn_{I(=\mathrm{MMR, RMR, C})}$, where N is population size.

Analysis of the Model in the Absence of Pleiotropy

We initially assumed that there were no pleiotropic (C) loci. In the absence of such loci, at Hardy-Weinberg equilibrium the mean trait value, μ_I, where I = MMR or RMR, is given by

$$\begin{aligned}\mu_I &= 2n_I pa - 2n_I(1-p)a \\ &= 2n_I a[p - (1-p)a] \\ &= 2an_I(2p-1),\end{aligned} \tag{2}$$

where p_I is the proportion of $+a$ alleles and n_{I} is the number of MMR or RMR loci. Hence the equilibrium frequency, $\hat{p}_I^{*}$, is

$$\hat{p}_I^{*} = \frac{\mu + 2an_I}{4an_I} = \frac{1}{2} + \frac{\mu_I}{4an_I}. \tag{3}$$

Because of selection, the loci will not be in multivariate Hardy-Weinberg (H-W) equilibrium, but an approximate estimate of the equilibrium heritability can be obtained assuming H-W equilibrium. The additive genetic variance, V_{A} (I = MMR or RMR), is given by

$$V_{\mathrm{A},I} = 2n_I p_I q_I a^2, \tag{4}$$

where $q_I = 1 - p_I$. Based on the review of heritability estimates of metabolic parameters given by Bushuev et al. (2010), we set heritability at 0.5 with an initial frequency of $p = 0.5$. Therefore, the environmental variance, V_{E} (for convenience, the subscript I designating MMR or RMR has been dropped) is

$$\begin{aligned}V_{\mathrm{E}} &= \frac{(1-h^2)V_{\mathrm{A}}}{h^2}, \\ &= \frac{0.5 \times 2n \times 0.5 \times 0.5a^2}{0.5} = 0.5na^2.\end{aligned} \tag{5}$$

Thus, the heritability at equilibrium is approximately

$$h^2 = \frac{2npqa^2}{2npqa^2 + 0.5na^2} = \frac{4pq}{4pq+1}. \tag{6}$$

Although the allelic value a cancels out in the above equation, it still has an influence via its determination of allelic frequencies (e.g. eq. [3]). Stabilizing selection will lead to a reduction in the additive genetic variance, and hence the equilibrium heritability will be lower than predicted by equation (6).

To test the above predictions we ran 10 replicate simulations with $|a| = 0.5, 1, 2, 3, 4, 5, 10$. Equilibrium was achieved within 500 generations, but to ensure that the equilibrium was stable, we ran each replicate for 10,000 generations and calculated the parameter values by averaging over the last 1,000 generations. The predicted frequencies at the two optima (30, 150) were calculated by insertion in equation (3). At the lowest two values of $|a|$, the allelic frequencies given by equation (3) were greater than 1.0 (2.0, 1.25) for MMR, and thus, we predict that in these cases there will be fixation of allele $+a$, with mutation supplying some $-a$ alleles which will reduce the value slightly from 1. Substituting $p_{\mathrm{MMR}} = 1$ in equation (2) gives equilibrium mean values of MMR of 50 and 100 when $a = 0.5$ and 1, meaning that at these values of a, it is not possible attain the optimum value of MMR as specified by the stabilizing selection function.

As predicted, setting $p_X = 1$ for a equal to 0.5 or 1 resulted in mean trait values of 49.9 and 99.8, respectively. Simulation results also closely matched the predicted values for the other allelic values (fig. 1). Further, as predicted, the observed heritabilities were somewhat less than given by equation (6).

Analysis of the Model in the Presence of Pleiotropy

We next examined the scenario in which there was pleiotropic mutation at the C loci after equilibrium to the two separate optima had been attained. The reason for doing this was to separate the effects of mutation from the effects of stabilizing selection: allowing mutations at the initiation of the simulation made no difference to the final results. With pleiotropy, the predicted trait means are

$$\mu_{MMR} = 2an(2p_{MMR} - 1) + 2an_C(2p_C - 1),$$
$$\mu_{RMR} = 2an(2p_{RMR} - 1) + 2an_C(2p_C - 1). \quad (7)$$

Now

$$\mu_{MMR} - \mu_{RMR} = 4an(p_{MMR} - P_{RMR}). \quad (8)$$

Substituting for the assigned values ($\mu_{MMR} = 150$, $\mu_{RMR} = 30$, $n = 50$) and rearranging gives

$$p_{MMR} - p_{RMR} = \frac{3}{5a}. \quad (9)$$

Since $p_{MMR} - p_{RMR} \geq 1$, then $a \geq 0.6$. If, however, $a < 0.6$ we might expect p_{MMR} to go to fixation, as in the previous scenario. Equilibrium frequencies of p_{MMR}, p_{RMR}, and p_C can be calculated from equation (7) for particular values of n_C: for example, if $n_C = 50$, then $p_{MMR} - p_C = 3/20a$, which in conjunction with equation (9) fixes the three values. Unfortunately, there is no unique combination and thus the analytic approach does not provide unique predicted values.

The predicted additive genetic variance in the presence of n_C pleiotropic loci is

$$V_{A,I} = 2n_I p_I q_I a^2 + 2n_C p_C q_C a^2. \quad (10)$$

And thus, the heritability is

$$h_I^2 = \frac{2n_I p_I q_I a^2 + 2n_C p_C q_C a^2}{2n_I p_I q_I a^2 + 0.5n_I a^2 + 2n_C p_C q_C a^2 + 0.5n_C a^2}$$
$$= \frac{2n_I p_I q_I + 2n_C p_C q_C}{2n_I p_I q_I + 0.5n_I + 2n_C p_C q_C + 0.5n_C}. \quad (11)$$

The additive genetic covariance, $Cov_{X,Y}$, depends only on the *C* loci

$$Cov_{MMR,RMR} = 2n_C p_C q_C a^2. \quad (12)$$

The additive genetic correlation is thus

$$r_G = \frac{2n_C p_C q_C a^2}{\sqrt{2a^2(n_{MMR}p_{MMR}q_{MMR} + n_C p_C q_C)\,2a^2(n_{RMR}p_{RMR}q_{RMR} + n_C p_C q_C)}}$$
$$= \frac{n_C p_C q_C}{\sqrt{(n_{MMR}p_{MMR}q_{MMR} + n_C p_C q_C)(n_{RMR}p_{RMR}q_{RMR} + n_C p_C q_C)}}. \quad (13)$$

Although the allelic value cancels out in the above equation, it is still expected to have an effect as it influences the allelic frequencies. From the above equation it can be seen that a large genetic correlation could result from a large number of pleiotropic loci relative to the number of nonpleiotropic loci or if the frequencies of the nonpleiotropic loci (p_{MMR}, p_{RMR}) are close to 1 or 0.

To investigate the effect of pleiotropic mutations we ran the simulation for 1,000 generations without pleiotropic mutation at the *C* loci and then allowed such mutations to occur. Each simulation was run for 100,000 generations to ensure that equilibria were stable (some runs were for 150,000 generations and gave the same results) and parameter values were calculated by averaging over the last 10,000 generations. In one set we used 10 n_C loci and in the other 50 n_C loci. In the latter case we ran five replicates for each allelic value.

The qualitative pattern was the same in all simulations and is illustrated with the example shown in figure 2. There was a rapid evolution of the traits to the optima (in fewer than 100 generations) and thereafter little divergence from these values (*top row*, fig. 2). Mutation at the pleiotropic loci generated genetic covariance between the two traits and altered their heritabilities within a span of about 3,000 generations (fig. 2). Both a genetic and a phenotypic correlation evolved, though the phenotypic correlation was consistently substantially less than the genetic correlation (*bottom row*, fig. 2).

With 10 pleiotropic loci, the heritabilities were sensitive to the allelic value, but there was only a small genetic correlation generated, the frequency of the *a* allele at the pleiotropic loci remaining very low (fig. 3). Trait means remained within 1.5 units of the optimum values for all allelic values (a) > 2. As in the scenario with no pleiotropic mutations, mean MMR was less than the optimum of 150 (59 and 120) for allelic values of $a = 0.5$ and 2, respectively.

Although the two fitness equilibria can be satisfied by multiple combinations of frequencies of p_{MMR}, p_{RMR}, and p_C, the five replicate simulations run with $n_C = 50$ showed that only a single combination was ever achieved (*top right panel*, fig. 3: note that the standard deviation bars lie within or only slightly project from the symbol). Trait means were influenced by the invasion of pleiotropic mutations, decreasing MMR and increasing RMR (fig. 4). As with the case of 10 *C* loci, heritabilities were sensitive to the allelic value except that here heritabilities declined with increased allelic values (*middle panels*, fig. 3). The frequencies of the *a* allele increased in the MMR and RMR loci whereas the frequency of the *a* allele in the pleiotropic loci remained low. However, the high frequencies of *a* in the former types of loci enabled variation in the *C* loci to generate a significant genetic correlation, as predicted by equation (13) (*bottom right panel*, fig. 3). The genetic correlation between the two traits did, in a relatively minor manner, affect the subsequent evolution of the optima (fig. 4). However, the phenotypic correlation gave no indication of the underlying genetic correlation. This final point serves as a critical

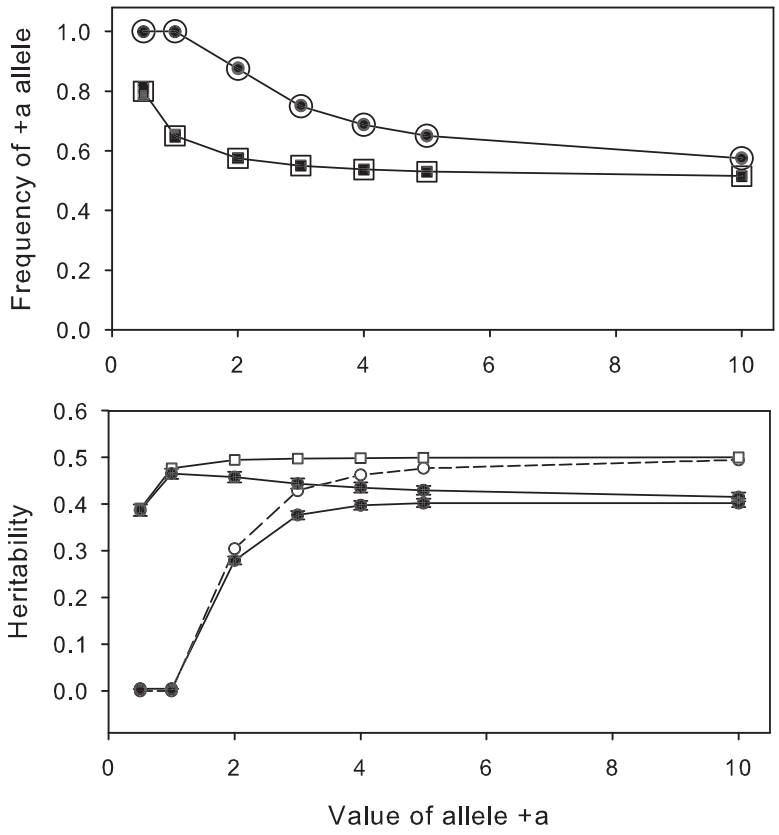

Figure 1: Predicted and observed (mean ± 1 SD) allelic frequencies and heritabilities for the case of no pleiotropic loci. Maximum metabolic rate indicated by circles, resting metabolic rate by squares. Predicted values indicated by open symbols, observed values by filled symbols.

warning that a phenotypic correlation that might have evolved between metabolic rates may not be a reliable indicator of the genetic correlation (Cheverud 1988).

Discussion

In this study, we analyzed a quantitative genetic model of the strong form of the aerobic capacity model (AC model; defined in Wone et al. 2009; see also Hayes 2010), one of the most accepted hypotheses for the evolution of endothermy (Clarke and Portner 2010; Hayes 2010; Lovegrove 2012). In brief, the strong form of the AC model assumes that (1) during the evolution of endothermy, directional selection targeted aerobic capacity (MMR), (2) RMR increased as a correlated response to selection, and (3) the sign of the genetic correlation remained constant. Our results indicate that mutations affecting both traits can arise, leading to the evolution of a pleiotropic correlation, without further significant shifts in the trait means. This result neither supports nor falsifies the aerobic model in explaining the evolution of endothermy. But it calls into question the testability of the hypothesis using quantitative genetic analysis.

The assumption of sustained and constant directional selection on MMR of the AC models implies that the elevation of metabolic rate via a correlated response was achieved gradually during a remarkably long period (Nespolo et al. 2011). However, empirical evidence does not support this assumption. Data suggest that selection is highly variable in most cases (Hoekstra et al. 2001; Kingsolver et al. 2001; Kingsolver 2007; Gonçalves et al. 2011; Olsen and Moland 2011; Scheihing et al. 2011), which is true also for physiological traits (Hayes and O'Connor 1999; Boratynski and Koteja 2010). Recently, Lovegrove (2012) proposed a model describing the transitions from proto-endothermy ("basoendothermy") to full endothermy ("supraendothermy"), passing through intermediate forms ("mesoendothermy"). According to this model, this path was far from continuous, showing cases of backward transitions (from mesoendothermy to basoendothermy; see Lovegrove 2012). On the other hand, Clarke and Portner (2010) proposed that proto-endotherms were eurythermal organisms, living in cool and

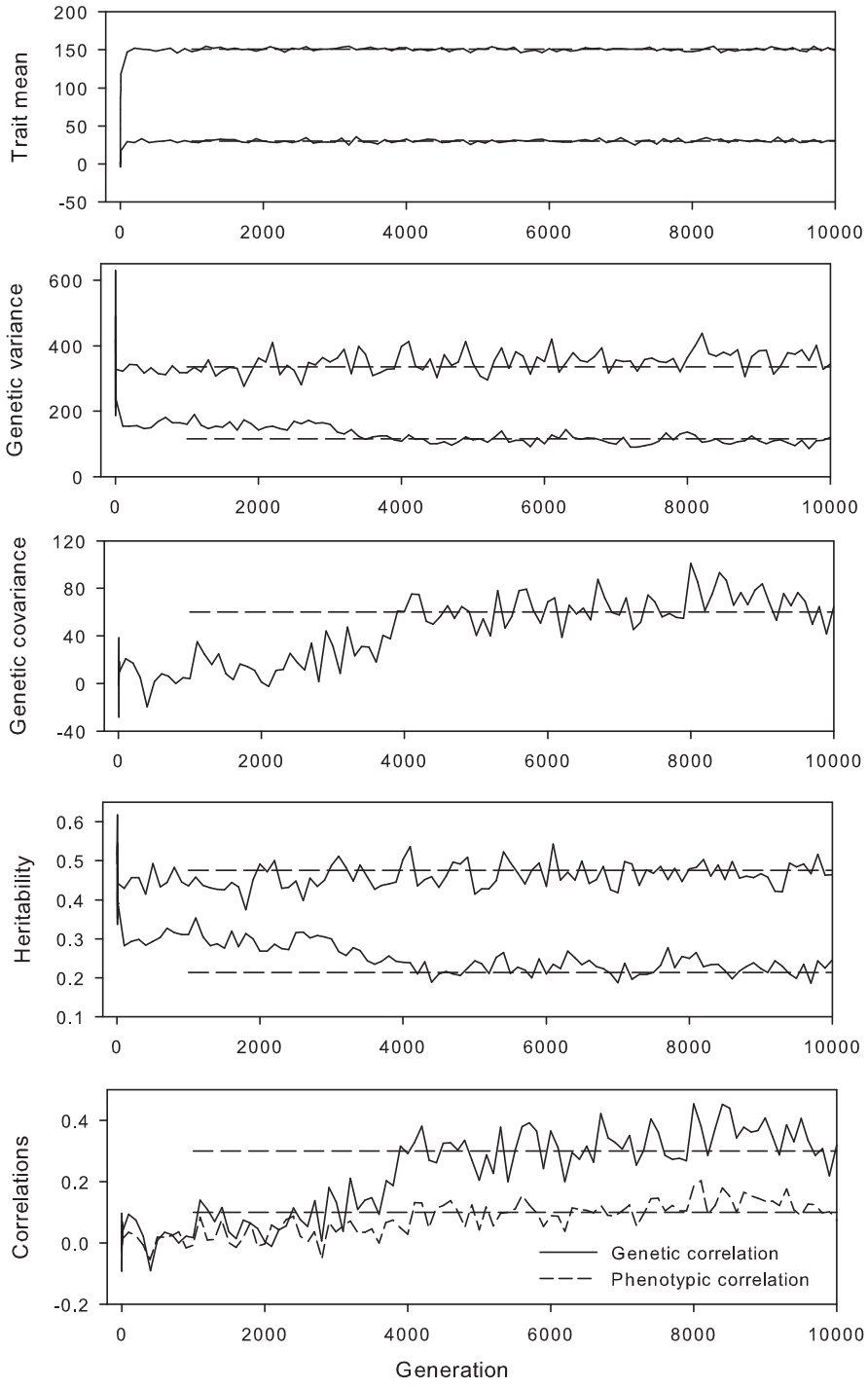

Figure 2: Illustrative time trace (generations) for the simulation in which there are 50 *C* (i.e., $n_C = 50$) loci that have pleiotropic effects on maximum metabolic rate (MMR) and resting metabolic rate (RMR). Data are plotted every generation for the first 100 generations and then every hundredth generation thereafter. For the first 1,000 generations there are no pleiotropic mutations at the *C* loci. After generation 1,000, mutations can occur in these loci that convert them to $+a$ or $-a$, that contribute additively to the values of MMR or RMR. In the simulation shown $a = 2$. The horizontal dashed lines show the means calculated over the last 10,000 generations of 100,000 generations for which the simulation was run. New equilibria after generation 1,000, when pleiotropic mutations arise, are achieved by generation 4,000. The change in the genetic correlation is generated primarily by a change in the genetic covariance.

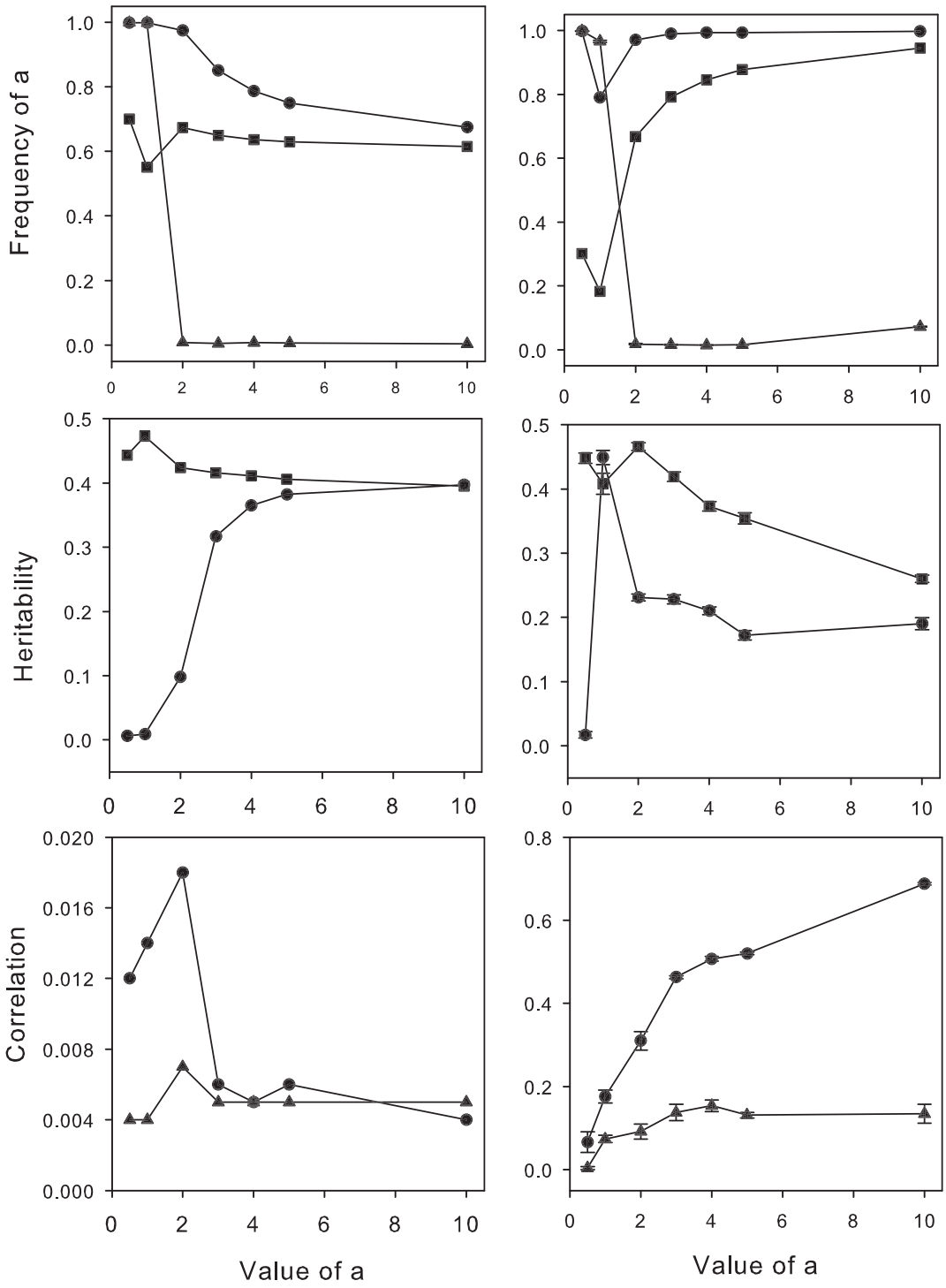

Figure 3: Equilibrium values (mean ± 1 SD) after 10,000 generations, of allelic frequencies, heritability, and genetic correlation when there are 10 (*left*) or 50 (*right*) loci with possible pleiotropic effects. *Top row*: circles indicate maximum metabolic rate (MMR) loci, squares indicate resting metabolic rate (RMR) loci, and triangles indicate C loci. *Middle row*: circles indicate MMR, squares indicate RMR. *Bottom row*: circles indicate genetic correlation, and triangles indicate the phenotypic correlation.

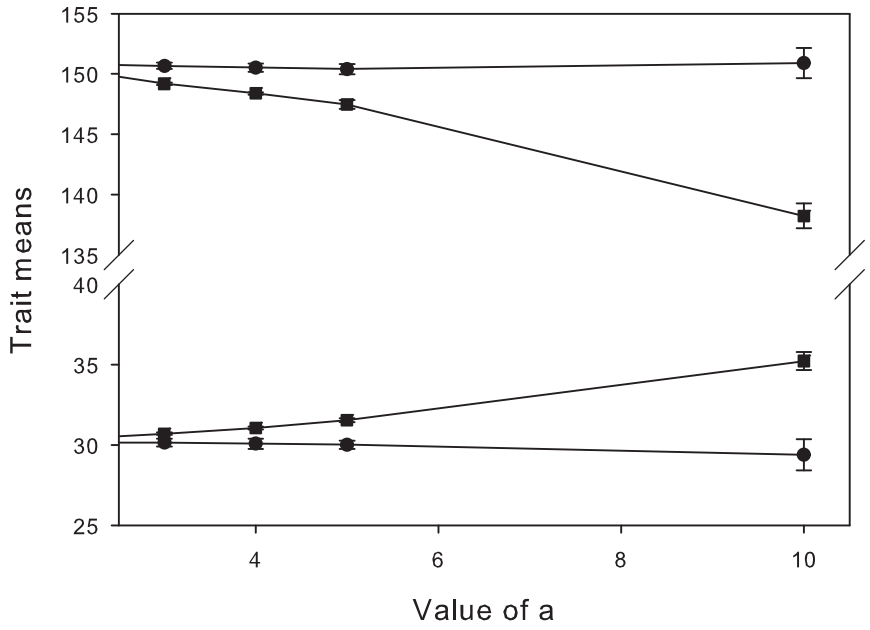

Figure 4: Equilibrium trait means (±1 SD) after 10,000 generations, when there are no pleiotropic loci (circles) and when there are 50 potentially pleiotropic loci (squares).

variable environments, thus suggesting fluctuating selection pressures. It seems unlikely then, or at least simplistic for this single pair of traits, that directional selection on MMR was large and constant enough to produce the observed increase in RMR of endotherms.

The assumption of a positive genetic correlation in the AC models was based on the frequent observation of positive phenotypic correlations between RMR and MMR (mass-specific) in a range of extant species, either inter- or intraspecifically, including amphibians, reptiles, birds, and mammals (reviewed in Wone et al. 2009). Subsequent quantitative genetic experiments performed in mammals yielded zero (i.e., nonsignificant) and positive correlations of varied magnitudes (Dohm et al. 2001; Nespolo et al. 2005; Sadowska et al. 2005; Swanson et al. 2012; reviewed in Swallow et al. 2009). However, the magnitude of the genetic correlation needed to generate an increase in RMR is small if the ratio of the genetic variance for MMR divided by the genetic variance for RMR is large (Hayes 2010). More studies might shed light on the magnitude of the genetic correlation between RMR and MMR in several groups of vertebrates, which, of course, is important in its own right. However, the relevance of the genetic correlation for inferring past processes of selection, we believe, is less clear. In our model both traits evolved rapidly to their separate optima and mutation of loci with pleiotropic effects invaded the population, generating a genetic correlation between the traits that was maintained for the length of the simulation (100,000 to 150,000 generations). Thus, the presence of a genetic correlation at the end of the simulation provided no information as to the evolutionary history of these traits.

While this analysis was directed at the hypothesis for the evolution of endothermy, a more general message applies, namely, the utility of estimating genetic correlations to infer past evolutionary trajectories. Our analysis shows that past evolutionary trajectories cannot be ascertained using current estimates of genetic variances and covariances. It may be argued that such estimates at least can be used to generate hypotheses about such past trajectories. However, the effort required to determine these estimates may be far beyond the confidence with which such trajectories can be viewed. As an example, consider the problem of estimating the genetic correlation between RMR and MMR using a half-sib pedigree design. The sampling effort required to obtain approximate standard error estimates for a half-sib pedigree design can be estimated using the equations from Robertson (1959*a*, 1959*b*). Based on the data from Bushuev (2010), Hayes and Garland (1995), and Wone et al. (2009), we used heritabilities of 0.33 (the mean) and genetic correlations of 0.3 and 0.8. We assumed a half-sib design consisting of 3 dams per sire and 5 offspring per dam, which is close to optimal and realistic using either a mammal or bird species. Given heritabilities of 0.33 and a genetic correlation of 0.3, one must measure 3,000 individuals (200 sires, 600 dams) to

obtain a confidence region that excludes zero (95% confidence region of 0.07 to 0.59). For a genetic correlation of 0.8, the required number is reduced to 90 individuals (6 sires, 18 dams, estimated SE = 0.37). While the number in the last case is not absurdly high, it is not sufficient to provide an accurate estimate of the genetic correlation. Suppose we wish to obtain a confidence region of ±10%: in this case we would need to measure more than 6,000 individuals (400 sires, 1,200 dams, estimated SE = 0.04). So, even in the case of a very high genetic correlation, an enormous effort must be expended to obtain a useful estimate.

Invoking genetic correlations to predict or explain long-term evolutionary changes is at best speculative and at worst misleading (Houle 1991; Roff and Fairbairn 2007; Delph et al. 2011). To understand and predict current and future evolutionary changes, which given global warming is likely to become an important endeavor, we need accurate estimates of genetic parameters. Under this circumstance the effort needs to be expended. Expending less than the required effort to obtain accurate estimates is likely to be a waste of time as the prediction error increases rapidly with increasing projection into the future.

Acknowledgments

This study was funded by international collaboration funds associated with Fondo Nacional de Desarrollo Científico y Tecnológico (FONDECYT) grant 1090423. We thank and recognize the important works of evolutionary physiologists such as J. Hayes and T. Garland Jr., who initiated a fruitful debate when they proposed quantitative ways of testing the aerobic model for the evolution of endothermy. We also thank A. Beckerman and three anonymous reviewers for their thoughtful suggestions for the manuscript.

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Associate Editor: Gregory E. Demas
Editor: Judith L. Bronstein