

The Place of Development in Mathematical Evolutionary Theory

SEAN H. RICE*

Department of Biological Sciences, Texas Tech University, Lubbock, Texas

**ABSTRACT**

Development plays a critical role in structuring the joint offspring–parent phenotype distribution. It thus must be part of any truly general evolutionary theory. Historically, the offspring–parent distribution has often been treated in such a way as to bury the contribution of development, by distilling from it a single term, either heritability or additive genetic variance, and then working only with this term. I discuss two reasons why this approach is no longer satisfactory. First, the regression of expected offspring phenotype on parent phenotype can easily be nonlinear, and this nonlinearity can have a pronounced impact on the response to selection. Second, even when the offspring–parent regression is linear, it is nearly always a function of the environment, and the precise way that heritability covaries with the environment can have a substantial effect on adaptive evolution. Understanding these complexities of the offspring–parent distribution will require understanding of the developmental processes underlying the traits of interest. I briefly discuss how we can incorporate such complexity into formal evolutionary theory, and why it is likely to be important even for traits that are not traditionally the focus of evo–devo research. Finally, I briefly discuss a topic that is widely seen as being squarely in the domain of evo–devo: novelty. I argue that the same conceptual and mathematical framework that allows us to incorporate developmental complexity into simple models of trait evolution also yields insight into the evolution of novel traits. *J. Exp. Zool. (Mol. Dev. Evol.)* 314B, 2011. © 2011 Wiley-Liss, Inc.

J. Exp. Zool.
(*Mol. Dev. Evol.*)
314B, 2011.

How to cite this article: Rice SH. 2011. The place of development in mathematical evolutionary theory. *J. Exp. Zool. (Mol. Dev. Evol.)* 314B:[page range].

Most of the attention given to developmental evolutionary biology has focused either on the evolution of developmental processes themselves or on phenomena, such as novelty and genetic assimilation, which seem to force us to acknowledge development. My initial goal in this article is to consider how developmental biology must ultimately be a part of the rest of evolutionary theory. In other words, I aim to identify where development necessarily enters into any truly general evolutionary theory, even when we are not explicitly studying the evolution of development per se. Having considered this broad question, I will return to a more traditional concern of evolutionary developmental biology—novelty—and discuss how the same principles that link development to directional, incremental, change can shed light on the evolution of novel traits.

Offspring–Parent Distribution

I shall argue that the principle place where development necessarily enters into evolutionary theory is in transmission across generations. Specifically, developmental processes are

critical to evolutionary theory because they determine the distribution of phenotypes among the offspring of an individual (or pair of individuals) with a particular phenotype. Because evolution is a population-level process, we are ultimately concerned with the set of offspring distributions associated with each parental phenotype in the population. We thus arrive at the joint distribution of offspring and parental phenotypes (Fig. 1). This distribution is a central element of any formal evolutionary theory.

Transmission was long considered the domain of genetics, not development. This, however, was an artifact of focusing on alleles, which seem to be transmitted directly—without any

Grant Sponsor: Social Sciences and Humanities Research Council of Canada; Grant number: 410-2008-0400; Grant Sponsor: NSF; Grant number: EF 0928772.

*Correspondence to: Sean H. Rice, Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409. E-mail: sean.h.rice@ttu.edu

Received 4 January 2011; Revised 5 July 2011; Accepted 11 July 2011

Published online in Wiley Online Library (wileyonlinelibrary.com).

DOI: 10.1002/jez.b.21435

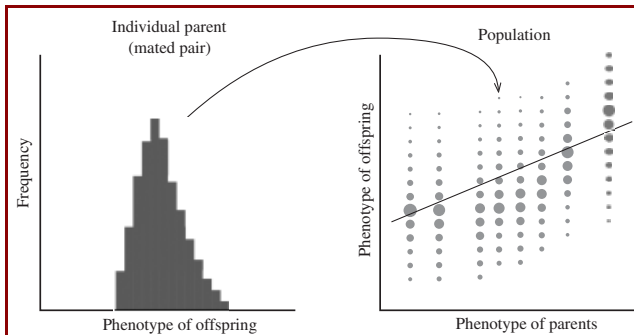


Figure 1. Offspring distribution for an individual or mated pair and offspring-parent distribution for a population.

intervention by development. Classical population genetics is framed in terms of allele (or haplotype) frequencies, and genotype is generally mapped directly to fitness. Of course, this mapping includes (at least) two distinct parts: mapping genotype to phenotype (largely the domain of development) and then mapping phenotype to fitness (the domain of ecology, biomechanics, etc.). Because of the complexity of this mapping, though, population genetics often takes it simply as a given, without reference to the mechanics underlying why a particular genotype has a particular fitness.

Quantitative genetics, by contrast, explicitly considers the joint distribution of offspring and parent phenotypes. However, in most cases, a single quantity is abstracted from the distribution. This quantity is either a measure of heritability (the slope of the linear regression of offspring on parents) or the “additive genetic variance” (the covariance between offspring and parents). Originally, quantitative genetics was seen as an extension of multilocus population genetics, made tractable by assuming many loci, each of small, additive, effect. As a result, quantities such as additive genetic variance (V_A) and heritability (h^2), were defined in terms of the contributions to phenotype of individual loci. Under this definition, the covariance between offspring and parents was seen as an estimator of V_A , which was assumed to be the *real* value of interest.

General Phenotype-Based Theories. Recently, there has been a trend toward treating quantitative genetics as a first order approximation to a general, phenotype-based, evolutionary theory (Rice, 2004b; Heywood, 2005). Under this formulation, what really matters is the offspring-parent distribution, and this leads to a subtle but important shift in definitions: although additive genetic variance and heritability were classically seen as latent properties of an individual that could be *estimated* by the relationship between offspring and parents, under phenotype-based theories, they are *defined* by the offspring-parent distribution. Specifically, heritability is defined as the regression of expected offspring phenotype on midparent phenotype.

To see why the offspring-parent distribution plays such a crucial role, we need to look at the basic equation underlying any

evolving system. We denote an individual’s phenotype by ϕ and the average phenotype of an individual’s offspring by ϕ^o (this is the average phenotype of the offspring that the individual actually produces; it is thus a random variable and is distinct from the expected offspring phenotype, which is the expected value of the distribution of possible offspring phenotypes). An individual’s relative fitness (the number of descendants that it leaves divided by the average number of descendants for all individuals in the population) is denoted by Ω . Both ϕ^o and Ω are random variables, meaning that they have distributions, rather than specific numerical values (i.e. we cannot know ahead of time exactly how many descendants an individual will leave or exactly what they will look like; Rice, 2008).

The fact that mean offspring phenotype and fitness for an individual have distributions, rather than fixed values, means that we will be concerned with means, variances, and covariances of these distributions. We will also, though, be concerned with the means, variances, and covariances of various values across individuals in the population. We thus need to distinguish operations over random variables from operations over individuals in a population. Consequently, we will denote operations over individuals in a population with straight symbols (such as $\bar{\phi}$ for the mean phenotype in a population, $[[\phi^2]]$ for variance in ϕ , and $[[\phi, \hat{\Omega}]]$ for covariance between phenotype and expected relative fitness), and operations over random variables with angled symbols (such as \hat{w} for the expected fitness of an individual), $\langle\langle w^2 \rangle\rangle$ for variance in an individual’s fitness distribution, and $\langle\langle h^2, \Omega \rangle\rangle$ for covariance between an individual’s relative fitness and heritability of some trait.

Using this notation and defining $\hat{\delta}$ as the expected difference between mean offspring phenotype and mean parent phenotype in the absence of selection, the most general description of change in mean phenotype in a closed population (i.e. one with no migration) is then (Rice, 2008)

$$\widehat{\Delta\phi} = [[\hat{\phi}^o, \hat{\Omega}]] + \overline{\langle\langle \phi^o, \Omega \rangle\rangle} + \hat{\delta}. \quad (1)$$

The first term on the right in Equation (1) captures the change due to deterministic associations between expected relative fitness and expected offspring phenotype. The second term captures the stochastic contributions, resulting from correlations between relative fitness and heritability (the biological interpretation of this term will be discussed below). The final term, $\hat{\delta}$, captures change, such as that due to mutation or recombination, that occurs in the process of reproduction.

The key thing to note for now is that parental phenotype, ϕ , does not appear anywhere on the righthand side of Equation (1). What appears instead is offspring phenotype, ϕ^o . In other words, what ultimately matters in evolution is the relationship between the fitness of parents and the phenotype of their offspring (Frank, ’97; Rice, 2004b; Heywood, 2005). If we are to describe evolution in terms of the relationship between fitness and parental

phenotype, we thus need a description of how the phenotypes of offspring are derived from those of their parents.

Reemergence of Development

Much of quantitative genetics tacitly assumes that a single value derived from the offspring–parent distribution is all that we need to know to calculate evolutionary change, and that this value is relatively consistent over time. If this were the case, it would be reasonable to say that, although developmental processes clearly underlie the phenotypic traits that we study, understanding development would not improve our ability to model evolution of those traits. Under this approach, heritability (or additive variance) “screens off” development from evolution (Reichenbach, '56), meaning that knowledge of how a trait develops would provide no extra information not already contained in the heritability value. In fact, though, there are a number of reasons that fixed heritability alone is insufficient as a descriptor of transmission. I will focus on two such reasons: the fact that the relation between offspring and parents is often not linear and the fact that heritability is a function of the environment.

The Relation Between Offspring and Parent Phenotypes is Often Nonlinear. The idea that we can collapse transmission genetics and development into a single term (either heritability or additive genetic variance) is predicated on the assumption that the actual relationship between expected offspring and parent phenotype is linear. If this relationship is nonlinear, then not only are more terms necessary to describe the response to selection, but also the shape of the relationship becomes an object of study itself. Figure 2 shows two examples of offspring–parent distributions that appear to show significant nonlinear elements.

Though the majority of quantitative genetics studies do not even consider the issue of nonlinear offspring–parent regression (the two distributions in Fig. 2 are from articles that did not mention the apparent nonlinearity in the data, reporting only that

the linear regression is significantly greater than 0). There is now a substantial body of experimental and theoretical work suggesting that the regression of expected offspring phenotype on parent or midparent phenotype is often nonlinear; furthermore, this nonlinearity is sufficient to cause the response to selection to differ notably from the predictions of linear models.

In one of the earliest attempts to experimentally evaluate the adequacy of linear models, Clayton et al. ('57) found that, although overall responses to selection on *Drosophila* were in “fair” agreement with expectations, they differed in some important ways, including that the responses to upward and downward selection were different. This phenomenon is often taken as evidence that the offspring–parent regression is nonlinear. Clayton et al. suggested that some of the unexpected results could be owing to genetic idiosyncrasies of *Drosophila* (and, in a classic case of advice that was not taken, suggested that *Drosophila* “should therefore be used with care in experiments intended for extrapolation to other species”; Clayton et al., '57; p 150).

Other studies have confirmed that nonlinear offspring–parent regressions are not unique to one trait in *Drosophila*, but in fact appear in a variety of traits and organisms, including body weight in mice (Nishida, '72) and chickens (Shimizu and Awata, '79), milk yield in cattle (Beardsley et al., '50; Fuerst-Waltl et al., '98), and pupal weight in *Tribolium* (Meyer and Enfield, '75), as well as several traits in *Drosophila* (Gimelfarb, '86; Gimelfarb and Willis, '94). Theoretical studies that have addressed the conditions under which the offspring–parent regression is expected to be nonlinear (Nishida and Abe, '74; Robertson, '77) suggest that the phenomenon can arise readily, resulting from epistasis (Bradford and Vleck, '64; Gimelfarb, '86) or differential contributions of genetic and environmental factors (Robertson, '77). Most importantly, Gimelfarb and Willis ('94) showed that nonlinear transmission in *Drosophila* can significantly alter the response to selection and creates a situation in which the “realized heritability” (the response to selection divided by the selection differential) is a function of the strength of selection. This last observation shows that a single heritability parameter, defined before selection, is inadequate to describe evolution even in characters such as body size and wing length. (It also suggests that simply arguing that a large portion of phenotypic variance can be assigned to additive genetic variance (Hill et al., 2008) does not address the question of how nonlinearities influence the response to selection.)

All this raises the question of how to expand our formal theory to incorporate the nonlinearities that are clearly there. Because heritability is defined as the slope of a linear regression of expected offspring phenotype on parent phenotype, it is tempting to simply substitute a nonlinear regression. Unfortunately, the coefficients derived from a standard polynomial regression are all functions of how many terms we include in the polynomial. This means that the linear term in a quadratic

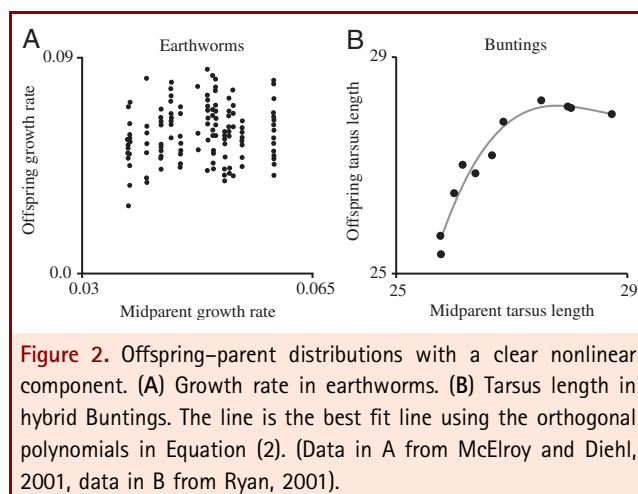


Figure 2. Offspring–parent distributions with a clear nonlinear component. (A) Growth rate in earthworms. (B) Tarsus length in hybrid Buntings. The line is the best fit line using the orthogonal polynomials in Equation (2). (Data in A from McElroy and Diehl, 2001, data in B from Ryan, 2001).

regression (which includes both linear and second order terms) is not the same as heritability (the sole regression term from a purely linear regression), and that the linear term in a cubic regression (which includes linear, second, and third order terms) will be different from both of these. The coefficients of a standard nonlinear regression thus cannot be assigned to distinct biological interpretations. This is one of the things that has hindered development of a formal theory of evolution with nonlinear offspring–parent relationships.

One way around this problem is to regress expected offspring phenotype on a series of orthogonal polynomials. These are polynomials of increasing order (a zero order polynomial, followed by a first, then a second, and so on) that are defined by the distribution of parent phenotypes, such that changing the regression of some variable on one of them has no effect on the regressions on the others. The regression coefficient associated with each polynomial thus does not change as we consider successively higher order polynomials.

Orthogonality, for functions, is defined over a specific region. In our case, the region of interest is the distribution of parental phenotypes, which may take on nearly any form. Because of this, we cannot use standard sets of orthogonal polynomials (such as the Legendre polynomials used by Kirkpatrick et al. ('90) to model growth trajectories), because these are defined over sections of the real line, rather than arbitrary distributions of points. Fortunately, we can construct a set of orthogonal polynomials that are defined in terms of the distribution of parental phenotypes. Denoting the n th central moment of the distribution of parent phenotypes as $[[^n\phi]]$, the first four orthogonal polynomials for an arbitrary distribution of phenotypes are:

$$\begin{aligned} P_0 &= 1 \\ P_1 &= \phi \\ P_2 &= \phi^2 - \frac{[[^3\phi]]}{[[^2\phi]]}\phi - [[^2\phi]] \\ P_3 &= \phi^3 - \gamma\phi^2 - \frac{[[^4\phi]] - \gamma[[^3\phi]]}{[[^2\phi]]}\phi + [[^2\phi]]\gamma - [[^3\phi]] \end{aligned} \quad (2)$$

where

$$\gamma = \frac{[[^2\phi]][[^5\phi]] - [[^3\phi]][[^4\phi]] - [[^2\phi]]^2[[^3\phi]]}{[[^2\phi]][[^4\phi]] - [[^3\phi]]^2 - [[^2\phi]]^3} \quad (3)$$

The set of all such orthogonal polynomials is the basis of a function space that, by virtue of being defined by the distribution of variation within a population, can be thought of as the natural space in which to study population level processes, such as heritability and selection. A variant of P_2 was presented in the Appendix to Lande and Arnold ('83), but has not been subsequently incorporated into quantitative genetics theory.

We can now write expected offspring phenotype ($\widehat{\phi}^o$) as a function of these polynomials. Because $P_1 = \phi$, the regression of $\widehat{\phi}^o$ on P_1 is just the expected heritability, \widehat{h}^2 , denoting the

regression of expected offspring phenotype ($\widehat{\phi}^o$) on polynomial P_i as $[[\widehat{\phi}^o/P_i]]$ (and noting that, by convention, $[[\widehat{\phi}^o/P_1]] = \widehat{\phi}^o$, which is the expected value of the average offspring phenotype), we now have:

$$\widehat{\phi}^o = \widehat{\phi}^o + \widehat{h}^2\phi + [[\widehat{\phi}^o/P_2]]P_2 + [[\widehat{\phi}^o/P_3]]P_3 + \dots \quad (4)$$

Substituting Equation (4) into Equation (1) gives us an equation for evolutionary change written in terms of the full shape of the offspring–parent distribution:

$$\begin{aligned} \widehat{\Delta\phi} &= \boxed{\widehat{h}^2[[\phi, \widehat{\Omega}]]} + [[\widehat{\phi}^o/P_2]] [[P_2, \widehat{\Omega}]] + [[\widehat{\phi}^o/P_3]] [[P_3, \widehat{\Omega}]] + \dots \\ &+ [[\phi, \langle h^2, \Omega \rangle]] + [P_2, \langle [[P_2], \Omega \rangle]] + [P_3, \langle [[P_3], \Omega \rangle]] + \dots \\ &+ \boxed{\frac{\widehat{\phi}^o}{\widehat{\phi}}} \end{aligned} \quad (5)$$

The three lines on the right in Equation (5) are just the three terms on the right in Equation (1), the first two terms expanded to write offspring phenotype in terms of parental phenotype. The boxed terms in Equation (5) are equivalent to the standard model of population and quantitative genetics ($[[\phi, \widehat{\Omega}]]$ is equal to the “selection differential,” often denoted S , so considering just the first term on the right yields the standard “breeder’s equation”).

The unboxed terms in Equation (5) represent the consequences of nonlinear offspring–parent relationships and stochasticity. An important thing to note is that the higher order polynomials also contain first order terms (P_2 and P_3 in Equations (2) each contain terms involving ϕ raised to the first power). This means that nonlinearities in the offspring–parent regression influence the response of the population even to the directional component of selection (captured by the linear relationship between $\widehat{\Omega}$ and ϕ).

To see this, consider just the first two terms in Equation (5) (corresponding to a case in which expected offspring phenotype is a deterministic quadratic function of parent phenotype). Using the equation for P_2 from Equation (2) and rearranging yields:

$$\widehat{\Delta\phi} = \left(h^2 - \frac{[[\widehat{\phi}^o/P_2]]}{[[^2\phi]]} \right) [[\phi, \widehat{\Omega}]] + \frac{[[\widehat{\phi}^o/P_2]]}{[[^2\phi]]} [[\phi^2, \widehat{\Omega}]] \quad (6)$$

Note that the linear selection differential ($[[\phi, \widehat{\Omega}]]$) is no longer multiplied only by the heritability, but also by $\frac{[[\widehat{\phi}^o/P_2]]}{[[^2\phi]]}$, which measures the curvature of the offspring–parent function. Including higher order P functions would add still more first order terms. Thus, accurately predicting even the simplest selection response requires knowing the full shape of the offspring–parent regression. Note that a model that assumes that phenotype is exactly normally distributed (as most quantitative genetics does) would miss this term, even if it allowed a curvilinear offspring–parent relation, because this extra term is also multiplied by $[[^3\phi]]$ (the third central moment of the distribution of parent phenotypes) and the third central moment of the normal distribution is zero.

The response to selection thus depends on the full shape of the offspring–parent distribution. Because understanding why this distribution has the form that it does will almost always require some understanding of the developmental processes underlying the trait of interest, it is much harder to sweep development under the rug than it was when we were considering only a single value to capture the entire offspring–parent distribution. Note that the traits that we are discussing here, body weight, wing length in *Drosophila*, growth rate in Annelids, and bone length in Birds, are not the sorts of traits that evo–devo advocates tend to hold up as examples. These are the sorts of traits used in introductory texts to illustrate the use of the breeder's equation. Upon close examination, though, they all show complexity that simultaneously reduces the value of linear models and prompts the question of why these particular developmental processes produce these distributions.

Heritability is a Function of the Environment. Even if we consider only heritability in the traditional sense (the linear regression of offspring on parents), this value often changes if the environment in which organisms develop changes (Merila and Sheldon, 2001; Charmantier and Garant, 2005; Wilson et al., 2006; Husby et al., 2011). By itself, stochastic variation in heritability does not influence expected change in mean phenotype (Rice and Papadopoulos, 2009). This changes, though, when variation in heritability is correlated with variation in fitness (Rice et al., 2011). Figure 3 shows how adaptive evolution can be altered by covariation between heritability and selection (the figure is modified from Rice et al., 2011). In this example, a population encounters two different environments at random, with very different optimal phenotypes in different environments. When heritability is the same in each environment ($h_1^2 = h_2^2 = 0.5$ in

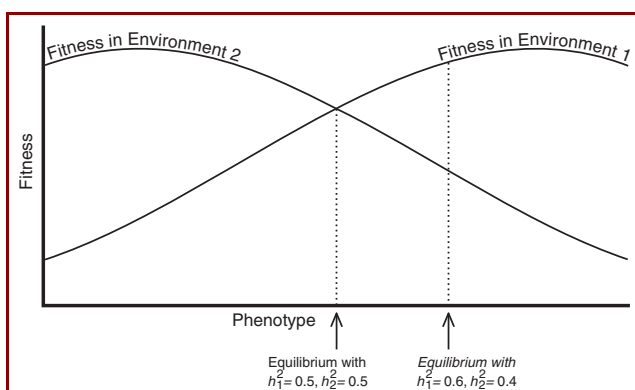


Figure 3. Illustration of the consequences of covariation between heritability and selection. Heritability in environments 1 and 2 are designated h_1^2 and h_2^2 , respectively. The arrows indicate the evolutionary equilibrium phenotypes when heritability is a constant ($h_1^2 = h_2^2 = 0.5$) and when heritability covaries with the environment such that $h_1^2 = 0.6$ and $h_2^2 = 0.4$.

the example), then the population evolves to an intermediate phenotype that does moderately well in both environments. By contrast, when heritability is correlated with environment, such that $h_1^2 = 0.6$ in environment 1 while $h_2^2 = 0.4$ in environment 2, the population evolves to an equilibrium at which it is well adapted to environment 1, but quite poorly adapted to environment 2. This is despite the fact that the organisms encounter environment 2 half the time and have appreciable heritability in it ($h^2 = 0.4$ is well within the range of observed heritability values).

The effects of covariation between selection and inheritance emerge from the second term on the righthand side of Equation (1), $\langle\langle\phi^0, \Omega\rangle\rangle$. This is the average, across the population, of the covariance *within an individual* between the mean phenotype of that individual's offspring and the number of those offspring produced. Rice et al. (2011) show that, under the standard quantitative genetic assumption of a linear offspring–parent regression (but making the slope a random variable), this term becomes $[\langle\phi, \langle\langle h^2, \Omega\rangle\rangle]$ (this is the first term on the second line in Equation (5)). This is the covariance, across the population (square brackets), between individual phenotype and the covariance, within an individual (angle brackets), between that individual's relative fitness and the heritability experienced by the population (note the need to distinguish the two kinds of covariances).

There is good reason to expect covariation between selection and heritability, because both are strongly influenced by the same thing—the environment in which the organisms in question develop and function. It is well established that offspring phenotype is often influenced by environmental factors; this is the basis of phenotypic plasticity. That the environment also causally influences fitness is the basis of the very idea of selection. The key here is to note that if any of the same environmental factors influence both offspring phenotype and the direction of selection, then we expect a correlation between selection and transmission of the type shown in Figure 3. There is also some direct empirical evidence suggesting covariation between selection and heritability. Heritability is often reduced in environments in which the organisms are stressed, and thus are likely to have reduced fitness (Charmantier and Garant, 2005; Wilson et al., 2006). Similarly, a recent study of breeding in Great Tits (Husby et al., 2011) found a significant correlation, across years, between selection differentials and heritability.

As with nonlinearity of the offspring–parent regression, the fact that inheritance correlates with the environment immediately suggests the question of why it does so. Because the basic machinery of genetic transmission is relatively insensitive to environmental variation while development is sometimes strongly influenced by it, this seems to be another case in which development finds its way into even simple (and in this case linear) evolutionary models.

Novelty

Unlike the examples discussed above, understanding the evolution of novel traits has long been seen as requiring an explicit

consideration of development. Biologists have proposed a number of different criteria for identifying evolutionary novelty (Müller and Wagner, '91; Moczek, 2008; Brigandt and Love, 2010). Some of these focus on the history of a trait (Müller and Wagner, '91; Hall and Kerney, this issue), whereas others emphasize its future consequences (Erwin, this issue). I shall argue that these ideas can be clarified and unified by focusing instead on change in the offspring–parent distribution.

A phenotypic trait can be any property of an organism to which we can assign a value (the “value” may be a number or a vector). Such traits include simple functions like body mass or the ratio of lengths of two bones, as well as complicated functions of many elements, such as the uniformity of position and orientation of spicules in the mantle of an Aplacophoran mollusk.

What determines if and how such a trait can evolve under selection or drift is the shape of the offspring–parent distribution for the trait. A century of experimentation shows that the vast majority of simple traits (measuring the size or position of a single structure) are heritable, meaning that they show at least a significant linear relationship between offspring and parents (as mentioned above, nonlinear terms have often been observed as well, but not systematically investigated). This is why nearly all such traits respond to selection. For more complex traits, though, such as the joint orientation of a large number of separate elements, offspring phenotype may be largely random relative to that of their parents. In such cases, even though we can measure the character in question, it would not be a true evolutionary trait.

I thus suggest the following definition for evolutionary novelty: A novel evolutionary trait appears when there is a change in the expected offspring–parent distribution for some character of an organism, such that there is sufficient heritable variation in that character for it to evolve under selection or drift. Such a newly evolvable character is a novel evolutionary trait. This is essentially saying that a new evolutionary trait comes into existence when there is sufficient additive variance for it to respond to selection.

An important property of this idea of evolutionary novelty—and one way in which it differs from many definitions of novelty discussed in the literature (Brigandt and Love, 2010)—is that it makes no reference to whether or not a striking morphological change occurs that a taxonomist or paleontologist would notice. We thus could be in the situation of saying that a novel trait has arisen, even though the morphology of the organisms in question has not changed. Conversely, a striking morphological change might occur in a trait that was previously under stabilizing selection. If that trait was already able to respond in this way but simply had not encountered the right selection regime, we would say that the new changes do not constitute an instance of evolutionary novelty.

In this view, novelty is about evolutionary potential, rather than how distinct the trait is or how poorly we understand how it

arose. It is informative to compare this notion of novelty with biological species concepts. The very idea of species arose because different groups of organisms consistently look different. Despite this, the most widely used species concepts, variants of the biological species concept or the closely related genetic species concept, say nothing about morphology. This is because the key to understanding species is to understand what allows two populations to evolve independently of one another.

The increasing number of recognized “cryptic species”—that are morphologically indistinguishable but show genetic evidence of having been isolated for a long time (Suatoni et al., 2006)—shows that the potential for morphological divergence does not always lead to such divergence. Nonetheless, we call these organisms different species because permanent reproductive isolation has allowed them to evolve independently, even if that independent evolution has not produced striking morphological differences. In the same way, the idea of evolutionary novelty discussed here focuses on the conditions that would *allow* evolution to go in a new direction.

As a hypothetical example, consider the molluscan shell. The mineralized shell is presumably derived from spicules, such as those seen in the mantle of modern Aplacophorans, and putative fossil molluscs, such as *Wiwaxia*. It seems likely though that merely having calcium carbonate secreting cells in the mantle is insufficient to allow for selection of a shell. Getting a shell gland from spicule-producing cells distributed in the mantle requires that those cells be coordinated and concentrated in a particular way. If spicule-producing cells are sparse and randomly distributed within the tissue, then it is unlikely that selection for a rigid covering would produce a shell.

If, however, the spicule-producing cells become concentrated in distinct areas near the surface, as has been recently observed in one modern Aplacophoran (Scheltema and Ivanov, 2002), and if there is significant heritable variation in the density and orientation of these cells, then the potential exists to select for increasing local coverage that would lead to the appearance of a shell. Under this view, the appearance of a novel trait occurred when the distribution of spicule-producing cells was such that selection for a rigid shell could lead to the appearance of such a structure, even though the shell itself was probably not yet present.

I say that this example is hypothetical because we do not know, even for modern Aplacophorans, the pattern of heritable variation in the density and orientation of spicules. This is, however, something that could be determined experimentally. In fact, one of the potential advantages of the approach to novelty that I am advocating is that we could unambiguously catch it in the act. Selection experiments or just estimates of heritability could tell us whether a particular population has heritable variation for a trait that is lacking in related species (or even other populations of the same species). We could thus potentially identify the appearance of an evolutionary novelty as it happens.

The idea of a change in the distribution of variation is not a new concept in ideas about novelty (Müller and Wagner, '91; Brigandt and Love, 2010). A number of authors have argued that novelty results from regulatory changes in development that allow for new kinds of phenotypic change (Britten and Davidson, '71; Carroll, 2000; Wray et al., 2003). Such developmental genetic changes could certainly facilitate the kind of change in heritable variation that I am highlighting here, but they are not necessary. The expected offspring–parent distribution is, in part, not only a function of developmental processes generating an offspring distribution for each parental phenotype, but it is also a function of the distribution of phenotypes among the parents. Thinking about novelty in terms of the offspring–parent distribution is thus compatible with ideas about the evolution of novelty that focus on genetic architecture, as well as those that focus on environmental effects on the phenotype distribution.

Role of Genetic Architecture. All complex phenotypic traits are influenced both by heritable underlying factors, such as gene products, and nonheritable factors, such as unpredictable environmental fluctuations. The way in which heritable and nonheritable underlying factors contribute to a trait is something that can itself evolve. Figure 4 shows an example of how a new evolutionary trait could come into existence through change in the underlying genetic architecture of the trait (the figure is

modified from Rice (2004a), where the specific functions are derived). The solid black lines are contours of equal phenotypic value on a phenotype landscape defined by the function $\phi = u_1^2 + u_2 u_3$, where u_1 and u_2 are heritable underlying factors, and u_3 is a nonheritable “environmental” factor (I am using the term “environmental” in the quantitative genetics sense of “not heritable,” regardless of whether it is internal or external to the organism).

The colors in Figure 4 show the heritability of the trait ϕ for different values of the heritable underlying factors (the nonheritable factor is not shown but has mean value 1). In the blue regions, the trait has very low heritability (close to 0), whereas the heritability is very high (close to 1) in the red regions. A population moving along the $\phi = 10$ contour from upper left to the bottom of the diagram experiences no immediate change in the mean value of ϕ , but its potential for future evolution is changed because ϕ changes from being simply an arbitrary function of the underlying factors to being an evolutionary trait—able to respond to selection and undergo drift.

Various different processes could cause the population to move along a contour in this way. If either u_1 or u_2 also influences some other trait, then selection on that other trait could pull this trait into a region in which it is heritable. It is also possible for drift alone to move the population along a contour. One thing to note, though, is that, in general, selection acting on the trait in question is unlikely to move it out of a region of low heritability. Thus, the appearance of a novel evolutionary trait in this way may be prompted by many different changes in the organism or its environment, but it will generally not result from selection on this trait.

Role of Phenotypic Plasticity. Some authors have emphasized the importance of environmental modifications of phenotype in the evolution of novelty (West-Eberhard, '89; Palmer, 2004). There are two ways that this could alter the offspring–parent distribution. First, changing an environmental factor that interacts nonlinearly with some heritable underlying factors will change the shape of the phenotype landscape over the set of heritable underlying factors, potentially exposing new traits to selection. This is essentially the same thing as shown in Figure 4, except with the population moving along a nonheritable axis.

Second, the offspring–parent distribution, and in particular the evolutionary importance of nonlinearities in this distribution, is a function of the distribution of phenotypes actually present in the parent generation. This is apparent from Equation (2), which includes functions of the central moments of the parent distribution. For instance, if the distribution of parent phenotypes is symmetrical, then $[[^3\phi]] = 0$ so the second order polynomial, P_2 , contains only a ϕ^2 term and a constant, with no term involving ϕ to the first power. Making the parent distribution asymmetrical will cause the $\frac{[[^3\phi]]}{[[^2\phi]]}\phi$ part of P_2 to matter in evolution. As we saw in Equation (6), this will change the

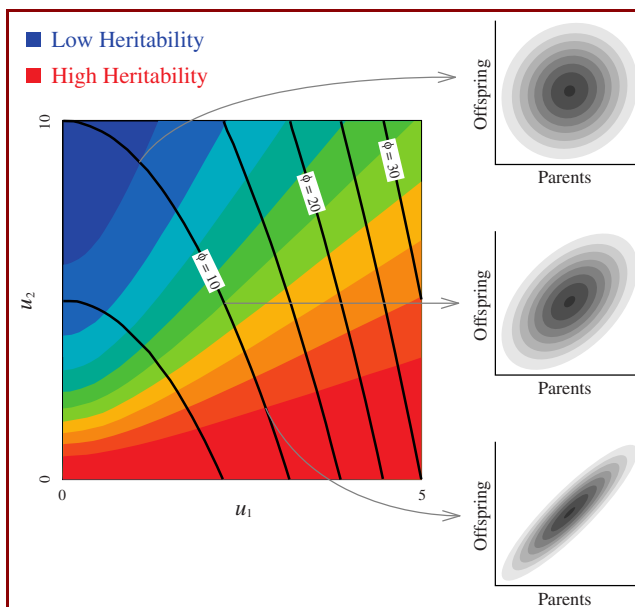


Figure 4. Evolution of heritability. The contour lines are for a trait defined as $\phi = u_1^2 + u_2 u_3$, where u_3 is an environmental factor. As a population moves along the $\phi = 10$ contour, the heritability changes from very low to near 1. In this example, all underlying factors are uncorrelated and normally distributed with variance 1. The mean value of the environmental factor is 1.

response to selection. This formalizes the idea that the appearance of a novel trait may result purely from a change in the distribution of parental phenotypes (see Palmer, this issue).

Thus, seemingly disparate ideas concerning the evolution of novelty can be unified when we think of novelty in terms of the offspring–parent distribution. This is not surprising given that, as illustrated by Equation (1), what matters in evolution are the relative fitnesses of individuals in the current generation and the phenotypes of individuals in the next generation. This is not to say that developmental biology and ecology are not critical to our understanding of novelty, only that to fully understand how they influence evolutionary novelty we need to understand how they impact the offspring–parent distribution.

CONCLUSIONS

It has long been recognized that the relationship between offspring and parents may be nonlinear and may change over time and across environments. Until recently, though, we have lacked the mathematical tools to fully capture the offspring–parent distribution. Consequently, much of formal evolutionary theory has distilled from this distribution a single value, variously the additive genetic variance or heritability, which has had to summarize all the complexities of transmission. This has discouraged focusing on the role of development in evolution, for although development must play a role in determining heritability, there does not seem to be much need to elaborate on the origins of a single value that can be measured by comparing relatives and is assumed to change slowly if at all.

Using orthogonal polynomials and an explicitly stochastic description of evolution, we can now incorporate complex nonlinear offspring–parent relationships into our mathematical evolutionary theories. In so doing, we find that the entire shape of the offspring–parent distribution influences the response to even simple directional selection. Because we are now dealing with a much more complex object (a multivariate distribution, rather than a single numerical value), we naturally seek explanations as to why this distribution has the form that it does. Development thus reemerges as a potential explanatory factor, even in the study of incremental change in quantitative traits.

Another consequence of using a more detailed description of the offspring–parent distribution is that we can ask questions about how this distribution changes. This means that we can use formal evolutionary theory to address some questions, such as the origin of evolutionary novelty, that were essentially invisible when we used a very simplified description of transmission. This also challenges a pervasive idea in recent discussions of evo–devo: that there is a distinction between mathematical and mechanistic descriptions of evolution (Laubichler, 2010). The *mechanics* of evolution involve stochastic processes acting at the level of populations. Such processes can be captured accurately only with a formal mathematical description. Furthermore, unlike

development, all evolutionary processes satisfy certain basic mathematical rules. Thus, any theory connecting the mechanics of development with the mechanics of evolution (which presumably both evo–devo and devo–evo must do) will necessarily involve mathematical descriptions. This is not to diminish the importance of empirical descriptions of developmental processes, but merely to say that mechanistically linking those processes with evolution must ultimately involve mathematical descriptions of processes at the population level.

ACKNOWLEDGMENTS

I thank John Harting, Alan Love, Benedikt Hallgrímsson, and Rich Palmer for valuable discussion of the ideas presented here, and Ingo Brigandt and an anonymous reviewer for valuable comments on the manuscript. This work was supported by Standard Research Grant 410-2008-0400 to Ingo Brigandt from the Social Sciences and Humanities Research Council of Canada, and by NSF grant EF 0928772 to Sean H. Rice.

LITERATURE CITED

- Beardsley JP, Bratton RW, Salisbury GW. 1950. The curvilinearity of heritability of butterfat production. *J Dairy Sci* 33:93–97.
- Bradford GE, Vleck LDV. 1964. Heritability in relation to selection differential in cattle. *Genetics* 49:819–827.
- Brigandt I, Love AC. 2010. Evolutionary novelty and the evodevo synthesis: field notes. *Evol Biol* 37:93–99.
- Britten RJ, Davidson EH. 1971. Repetitive and non-repetitive DNA sequences and a speculation on the origins of evolutionary novelty. *Q Rev Biol* 46:111–138.
- Carroll SB. 2000. Endless forms: the evolution of gene regulation and morphological diversity. *Cell* 101:577–580.
- Charmantier A, Garant D. 2005. Environmental quality and evolutionary potential: lessons from wild populations. *Proc R Soc B Biol Sci* 272:1415–1425.
- Clayton GA, Morris JA, Robertson A. 1957. An experimental check on quantitative genetical theory. *J Genet* 55:131–151.
- Erwin D. This issue. Novelty that change carrying capacity. *J Exp Zool (Mol Dev Evol)*.
- Frank SA. 1997. The price equation, Fishers fundamental theorem, kin selection, and causal analysis. *Evolution* 51:1712–1729.
- Fuerst-Waltl B, Solkner J, Essl A, Hoeschele I, Fuerst C. 1998. Non-linearity in the genetic relationship between milk yield and type traits in Holstein cattle. *Livest Prod Sci* 57:41–47.
- Gimelfarb A. 1986. Offspring–parent genotypic regression: how linear is it? *Biometrics* 42:67–71.
- Gimelfarb A, Willis JH. 1994. Linearity versus nonlinearity of offspring–parent regression: an experimental study of *Drosophila melanogaster*. *Genetics* 138:343–352.
- Hall BK, Kerney R. This issue. Levels of biological organization and the origins of novelty. *J Exp Zool (Mol Dev Evol)*.

- Heywood JS. 2005. An exact form of the breeder's equation for the evolution of a quantitative trait under natural selection. *Evolution* 59:2287–2298.
- Hill WG, Goddard ME, Visscher PM. 2008. Data and theory point to mainly additive genetic variance for complex traits. *PLoS Genet* 4:e1000008.
- Husby A, Visser ME, Kruuk LEB. 2011. Speeding up microevolution: the effects of increasing temperature on selection and genetic variance in a wild bird population. *PLoS Biol* 9:e1000585.
- Kirkpatrick M, Lofsvold D, Bulmer M. 1990. Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979–993.
- Lande R, Arnold SJ. 1983. The measurement of selection on correlated characters. *Evolution* 37:1210–1226.
- Laubichler M. 2010. Evolutionary developmental biology offers a significant challenge to the neo-Darwinian paradigm. In: Ayala F, Arp R, editors. *Contemporary debates in the philosophy of biology*. Malden: Wiley-Blackwell. p 199–212.
- McElroy TC, Diehl WJ. 2001. Heterosis in two closely related species of earthworm (*Eisenia fetida* and *E. andrej*). *Heredity* 87:598–608.
- Merila J, Sheldon BC. 2001. Avian quantitative genetics. In: Nolan V, editor. *Current ornithology*, Vol. 16. New York: Kluwer/Plenum. 179p.
- Meyer HH, Enfield FD. 1975. Experimental evidence on limitations of the heritability parameter. *Theor Appl Genet* 45:268–273.
- Moczek AP. 2008. On the origins of novelty in development and evolution. *BioEssays* 30:432–447.
- Müller GB, Wagner GP. 1991. Novelty in evolution: restructuring the concept. *Annu Rev Ecol Syst* 22:229–256.
- Nishida A. 1972. Some characteristics of parent–offspring regression in body weight of *Mus musculus* at different ages. *Can J Genet Cytol* 14:292–303.
- Nishida A, Abe T. 1974. The distribution of genetic and environmental effects and the linearity of heritability. *Can J Genet Cytol* 16:3–10.
- Palmer AR. 2004. Symmetry breaking and the evolution of development. *Science* 306:828–833.
- Palmer AR. This issue. Developmental plasticity and the origin of novel forms: unveiling of cryptic genetic variation via use and disuse. *J Exp Zool (Mol Dev Evol)*.
- Reichenbach H. 1956. *The direction of time*. Berkeley, CA: University of California Press.
- Rice SH. 2004a. Developmental associations between traits: covariance and beyond. *Genetics* 166:513–526.
- Rice SH. 2004b. *Evolutionary theory: mathematical and conceptual foundations*. Sunderland, MA: Sinauer Associates.
- Rice SH. 2008. A stochastic version of the price equation reveals the interplay of deterministic and stochastic processes in evolution. *BMC Evol Biol* 8:262.
- Rice SH, Papadopoulos A. 2009. Evolution with stochastic fitness and stochastic migration. *PLoS ONE* 4:e7130.
- Rice SH, Papadopoulos A, Harting J. 2011. Stochastic processes driving directional evolution. In: Pontarotti P, editor. *Evolutionary biology: concepts, biodiversity, macroevolution and genome evolution*. Berlin: Springer-Verlag.
- Robertson A. 1977. The non-linearity of the offspring–parent regression. In: Pollak E, Kempthorne O, Baily Jr EB, editors. *Proceedings of the international conference on quantitative genetics*. Ames IA: Iowa State University Press. p 297–304.
- Ryan PG. 2001. Morphological heritability in a hybrid bunting complex: *Neospiza* at inaccessible island. *Condor* 103:429–438.
- Scheltema AH, Ivanov DL. 2002. An Aplacophoran postlarva with iterated dorsal groups of spicules and skeletal similarities to paleozoic fossils. *Invertebr Biol* 121:1–10.
- Shimizu H, Awata T. 1979. On the linearity of heritability and genetic correlation for juvenile body weight and weight gain in meat-type chickens. *J Fac Agr Hokkaido Univ* 59:333–345.
- Suatoni E, Vicario S, Rice S, Snell T, Caccone A. 2006. An analysis of species boundaries and biogeographic patterns in a cryptic species complex: the rotifer–*Brachionus plicatilis*. *Mol Phylogenet Evol* 41:86–98.
- West-Eberhard MJ. 1989. Phenotypic plasticity and the origins of diversity. *Annu Rev Ecol Syst* 20:249–278.
- Wilson AJ, Pemberton JM, Pilkington JG, Coltman DW, Mifsud DV, Clutton-Brock TH, Kruuk LEB. 2006. Environmental coupling of selection and heritability limits evolution. *PLoS Biol* 4:e216.
- Wray GA, Hahn MW, Abouheif E, Balhoff JP, Pizer M, Rockman MV, Romano LA. 2003. The evolution of transcriptional regulation in eukaryotes. *Mol Biol Evol* 20:1377–1419.