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THE CONTRIBUTION OF MATERNAL EFFECTS TO SELECTION RESPONSE: AN EMPIRICAL TEST OF COMPETING MODELS

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Maternal effects can dramatically influence the evolutionary process, in some cases facilitating and in others hindering adaptive evolution. Maternal effects have been incorporated into quantitative genetic models using two theoretical frameworks: the variance-components approach, which partitions variance into direct and maternal components, and the trait-based approach, which assumes that maternal effects are mediated by specific maternal traits. Here, we demonstrate parallels between these models and test their ability to predict evolutionary change. First, we show that the two approaches predict equivalent responses to selection in the absence of maternal effects mediated by traits that are themselves maternally influenced. We also introduce a correction factor that may be applied when such cascading maternal effects are present. Second, we use several maternal effect models, as well as the standard breeder's equation, to predict evolution in response to artificial selection on flowering time in American bellflower, *Campanulastrum americanum*. Models that included maternal effects made much more accurate predictions of selection response than the breeder's equation. Maternal effect models differed somewhat in their fit, with a version of the trait-based model providing the best fit. We recommend fitting such trait-based models when possible and appropriate to make the most accurate evolutionary predictions.

KEY WORDS: **Artificial selection, breeder's equation, life-history evolution, natural selection, parental effects, quantitative genetics.**

Mothers often influence the phenotype of their offspring above and beyond the contribution of genes (Dickerson 1947; Mousseau and Fox 1998; Wolf and Wade 2009). For example, substances such as nutrients, antibodies, and hormones may be transmitted to offspring via the placenta, egg, or seed, with consequences for offspring growth and development (Roach and Wulff 1987; Schwabl 1996; Grindstaff et al. 2003; Maestripieri and Mateo 2009). In addition, mRNA transcribed from the maternal genome is used to make proteins during early development before many of the offspring's own genes become active (Telford et al. 1990). Maternal effects have the potential to profoundly affect the evolutionary process when they influence traits linked to offspring fitness (Kirkpatrick and Lande 1989; Bernardo 1996; Mousseau and Fox 1998).

Maternal effects have been suggested to both facilitate and hinder adaptation. Examples of adaptive maternal effects are often responses to environmental cues; if the offspring's environment is predictable, maternal induction of phenotypes that will thrive in that environment should be favored by selection (Riska et al. 1985; Rossiter 1996; Donohue and Schmitt 1998; Fox and Mousseau 1998; Lacey 1998; Galloway 2005; Galloway and Etterson 2007). The ability to alter offspring phenotypes in response to environmental conditions may facilitate colonization of and adaptation to new habitats (Fox and Savalli 2000; Badyaev et al. 2002;

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Duckworth 2009). Conversely, genetic maternal effects are often expected to slow adaptive evolution (Donohue 1999; Räsänen and Kruuk 2007; Hoyle and Ezard 2012). Maternal genetic effects often act in opposition to direct genetic effects, effectively reducing the additive genetic variance available to selection. This phenomenon can be quantified by the direct–maternal genetic correlation. This correlation displays a wide range of values across studies of captive and wild organisms, but tends to be negative more often than positive (Riska et al. 1985; Robinson 1996; Byers et al. 1997; Thiede 1998; Wilson and Reale 2006; Räsänen and Kruuk 2007). Negative direct–maternal correlations are expected to be favored in relatively stable environments, where they act to stabilize a population in the face of short-term fluctuations in directional selection (Hoyle and Ezard 2012).

When attempting to understand how a population will respond to selection, identifying and quantifying maternal effects is crucial, as was realized by animal breeders as early as the 1940s (Dickerson 1947). Quantitative genetic models incorporating maternal effects, which were first developed by animal breeders and subsequently adopted and extended by evolutionary biologists, can be classified into two categories: variance-components and trait-based models (McGlothlin and Brodie 2009; Hadfield 2012). The first category of models, associated primarily with Dickerson (1947) and Willham (1963, 1972), partitions genetic variance into direct and maternal components. In these models, the response to selection is a function of the direct and maternal variance components and the direct–maternal covariance. By contrast, in trait-based models, which were originally developed by Falconer (1965) and later elaborated by Kirkpatrick and Lande (1989), maternal effects are attributed to specific traits in the mother. Trait-based models generally allow for more complexity, such as time lags in evolutionary response to selection (Kirkpatrick and Lande 1989). Such time lags occur because selection in the maternal generation can cause phenotypic change through two distinct pathways: by altering the genes passed on to offspring and by altering the distribution of traits that cause maternal effects.

Recent work has shown that variance-components and trait-based models make equivalent predictions for models of indirect genetic effects that occur within generations (i.e., social genetic effects). Parameters estimated using a variance-components approach may be used to calculate crucial parameters of trait-based models (McGlothlin and Brodie 2009), and the predictive equations for evolutionary response are translatable between frameworks (McGlothlin et al. 2010). Although maternal effects are simply indirect genetic effects that occur across generations (Wolf et al. 1998), it is unclear whether a similar equivalence between modeling approaches exists for maternal effects. (Parallels have been demonstrated for special cases, e.g., Kirkpatrick and Lande 1989; Hadfield 2012.) Although Kirkpatrick and Lande's **M**, a matrix that quantifies the effects of maternal traits on offspring traits, can indeed be calculated from empirical estimates of variance-components from the variance-components framework (Galloway et al. 2009; McGlothlin and Brodie 2009), the general relationship between the predictive equations for response to selection remains obscure. In particular, because variance-components models do not explicitly account for time lags in evolutionary response, it is unclear under what conditions the two types of models make the same predictions.

This article has two primary aims. First, we examine the similarities and differences between variance-components and trait-based models of maternal effects and demonstrate that under certain conditions, the two frameworks predict equivalent responses to selection. We introduce a correction factor that can be applied when the assumptions of the variance-components model are not met. Second, we test the utility of various maternal effect models for predicting selection response using data collected from two experiments in American bellflower, *Campanulastrum americanum*. The first of these studies applied artificial selection to a single life-history trait, days to flower (Burgess et al. 2007), and the second estimated genetic parameters for days to flower and three additional traits (Galloway et al. 2009). Because genetic parameters and response to selection were estimated from independent data sets, we can use these data to ask how well different models of maternal effects predict observed evolutionary change. We compare the accuracy of several quantitative genetic models of maternal effects, including both variance-components and trait-based models. To examine the consequences of ignoring maternal effects when they are present, we also compare the predictions of maternal effect models to those of the standard multivariate breeder's equation (Lande 1979; Lande and Arnold 1983).

Theory

In this section, we draw a general parallel between the two primary models of maternal effects. We rely heavily upon the approach of McGlothlin and Brodie (2009; McGlothlin et al. 2010; see also Bijma 2013), which we extend to show that the variance-components and trait-based models of maternal effects produce similar equations for the response to natural selection. Most of the mathematical detail is presented in the Supplementary Appendix.

VARIANCE-COMPONENTS MODELS

In variance-components models (e.g., Willham 1963, 1972), total genetic variance is partitioned into direct and maternal components and the covariance between them. The maternal components reflect the total contribution of maternal performance to expression of the offspring phenotype, without attributing these effects to a specific maternal trait. In its generalized multivariate form,

the predictive equation for response to selection in this framework can be written as

$$\Delta\bar{\mathbf{z}} = (\mathbf{G}_{dd} + \frac{1}{2}\mathbf{G}_{dm} + \mathbf{G}_{md} + \frac{1}{2}\mathbf{G}_{mm})\boldsymbol{\beta}. \quad (1)$$

(See the Supplementary Appendix for derivation.) In equation (1), $\Delta\bar{\mathbf{z}}$ is a column vector representing evolutionary change in the population mean between the parental and offspring generations, $\mathbf{G}_{dd}$ is a variance-covariance matrix of direct genetic effects, $\mathbf{G}_{dm}$ and $\mathbf{G}_{md}$ are covariance matrices between direct and maternal genetic effects, $\mathbf{G}_{mm}$ is a variance-covariance matrix of maternal genetic effects, and $\boldsymbol{\beta}$ is a vector of selection gradients (Lande and Arnold 1983).

Two important assumptions of Willham's model are that maternal performance is neither under selection nor itself influenced by maternal effects. As we will see later, these assumptions are relaxed in trait-based models, creating important differences between the two frameworks (see also Cheverud 1984; Hadfield 2012).

TRAIT-BASED MODELS

Kirkpatrick and Lande's (1989) trait-based model differs from Willham's in that maternal effects are assumed to be mediated by specific traits of the mother. In a multivariate framework, this mediation is represented by $\mathbf{M}$, a square matrix of maternal effect coefficients m_{ij}. These maternal effects coefficients quantify the effect of maternal trait j on offspring trait i. Kirkpatrick and Lande (1989) derive two equations for response to selection (see also Hadfield 2012). The first explicitly accounts for time lags in evolutionary response that arise due to effects of selection in the maternal generation:

$$\Delta\bar{\mathbf{z}}(t) = (\mathbf{C}_{az} + \mathbf{MP})\,\boldsymbol{\beta}(t) + \mathbf{M}\Delta\bar{\mathbf{z}}(t-1) - \mathbf{MP}\boldsymbol{\beta}(t-1). \quad (2)$$

Here, time t represents the current generation, time $t-1$ is the maternal generation, $\mathbf{P}$ is the phenotypic variance-covariance matrix, and $\mathbf{C}_{az}$ is a matrix of covariances between additive genetic values and phenotype, which Kirkpatrick and Lande show can be estimated at equilibrium by

$$\mathbf{C}_{az} = \mathbf{G}\left(\mathbf{I} - \frac{1}{2}\mathbf{M}^{\mathrm{T}}\right)^{-1}, \quad (3)$$

where $\mathbf{G}$ is the additive genetic variance-covariance matrix, $\mathbf{I}$ is the identity matrix, and T denotes matrix transposition. (Note that the Kirkpatrick–Lande model ignores dominance and epistatic contributions to genetic variance, as do the other models discussed here.)

The complexity of equation (2) arises primarily because selection alters the distribution of traits that mediate maternal effects before reproduction, leading to a partial generational lag between selection and evolutionary response (Kirkpatrick and Lande 1989). The first two components of equation (2) are due to selection in the current generation, including a change in the genetic component ($\mathbf{C}_{az}\boldsymbol{\beta}(t)$) and a purely phenotypic change in the maternal component ($\mathbf{MP}\boldsymbol{\beta}(t)$). The next term ($\mathbf{M}\Delta\bar{\mathbf{z}}(t-1)$) represents a change in the maternal contribution in the current generation due to evolution in the previous generation, and the final term represents the loss of the purely phenotypic change in the maternal contribution caused by selection in the previous generation ($\mathbf{MP}\boldsymbol{\beta}(t-1)$). The evolutionary lags caused by selection in the previous generation are of most concern when selection differs from generation to generation, that is, when $\boldsymbol{\beta}(t) \neq \boldsymbol{\beta}(t-1)$ and $\Delta\bar{\mathbf{z}}(t) \neq \Delta\bar{\mathbf{z}}(t-1)$. Rearranging equation (2) as

$$\Delta\bar{\mathbf{z}}(t) = (\mathbf{I} - \mathbf{M})^{-1}(\mathbf{C}_{az}\boldsymbol{\beta}(t) + \mathbf{MP}\delta(\boldsymbol{\beta}) - \mathbf{M}\delta(\Delta\bar{\mathbf{z}})), \quad (4)$$

where δ represents a difference between generation t and generation $t-1$, makes this dependence clear.

Kirkpatrick and Lande's (1989) second equation to estimate selection response makes the simplifying assumption that selection and thus the rate of evolution remains constant across generations, that is, $\delta(\boldsymbol{\beta}) = \mathbf{0}$ and $\delta(\Delta\bar{\mathbf{z}}) = \mathbf{0}$. (This is also an assumption of the variance-components model, which includes a selection gradient for only a single generation.) Under this assumption, response to selection is predicted by

$$\Delta\bar{\mathbf{z}} = (\mathbf{I} - \mathbf{M})^{-1}\mathbf{C}_{az}\boldsymbol{\beta} = (\mathbf{I} - \mathbf{M})^{-1}\mathbf{G}\left(\mathbf{I} - \frac{1}{2}\mathbf{M}^{\mathrm{T}}\right)^{-1}\boldsymbol{\beta} \quad (5)$$

Kirkpatrick and Lande (1989) note that when selection is constant, the rate of evolution predicted by equation (5) will be approached asymptotically after a number of generations. Equation (5) may thus be a reasonable approximation in periods of relatively constant selection.

The extent to which the time-lag models (eqs. (2), (4)), and the asymptotic model (eq. (5)) make similar predictions depends upon the extent to which the assumptions of constancy of selection and the rate of evolution are valid. Because the effects of these both depend upon $\mathbf{M}$, the importance of explicitly considering time lags will depend upon the strength of maternal effects as well. As an illustration, consider a single trait model with maternal effect coefficient m. Making the additional assumptions that the change in selection is constant each generation and that the change in evolutionary rate each generation depends only on the change in selection, equation (4) may be written as

$$\Delta\bar{z}_{\mathrm{time-lag}} = \frac{G\beta}{(1-m)(1-m/2)} + \frac{mP\delta(\beta)}{(1-m)} - \frac{mG\delta(\beta)}{(1-m)^2(1-m/2)}. \quad (6)$$

The ratio of the prediction made by the time-lag model and that by the asymptotic model (a one-trait version of eq. (5)) is

then

$$\frac{\Delta\bar{z}_{\text{time-lag}}}{\Delta\bar{z}_{\text{asymptotic}}} = 1 + m\frac{\delta(\beta)}{\beta}\left(\frac{(1-m/2)}{h^2} - \frac{1}{(1-m)}\right), \qquad (7)$$

where h^2 is narrow-sense heritability, the ratio of G to P. It is evident from equation (7) that the extent to which the two models differ in their predictions depends upon three parameters: heritability, the strength and direction of the maternal effect (m), and the relative difference in the strength and direction of selection between generations ($\delta\beta/\beta$). For a representative heritability of 0.5, there is a large parameter space where the two models make similar predictions (Fig. 1). However, for very strong maternal effects and/or very large differences in selection across generations, the predictions of the two models diverge. The divergence between the two models is also more pronounced when heritability is lower (not shown).

CORRESPONDENCE BETWEEN FRAMEWORKS

At first glance, the expressions for predicted response to selection presented in the two frameworks appear quite distinct. However, it is possible to show correspondence between variance-components and trait-based models of within-generation indirect genetic effects by expressing them in a common mathematical language (McGlothlin and Brodie 2009), suggesting maternal effect models are likely to display underlying similarities as well. Because the trait-based model includes only a single selection gradient, we will focus on the correspondence of equation (1) with equation (5), Kirkpatrick and Lande's asymptotic model. We thus ask how similar the trait-based and variance-component approaches are when selection is treated as constant across generations.

By applying the translations given in the Supplementary Appendix (eqs. A9a–A9d), it is possible to express equation (1) as

$$\Delta\bar{\mathbf{z}} = (\mathbf{I}-\mathbf{MM})^{-1}\left(\mathbf{G} + \frac{1}{2}\mathbf{G}\mathbf{M}^{\mathrm{T}} + \mathbf{M}\mathbf{G} + \frac{1}{2}\mathbf{M}\mathbf{G}\mathbf{M}^{\mathrm{T}}\right)(\mathbf{I}-\mathbf{M}^{\mathrm{T}}\mathbf{M}^{\mathrm{T}})^{-1}\boldsymbol{\beta}. \qquad (8)$$

Kirkpatrick and Lande's asymptotic equation (5) can be expressed in a similar form by a simple algebraic manipulation given in the Supplementary Appendix, yielding

$$\Delta\bar{\mathbf{z}} = (\mathbf{I}-\mathbf{MM})^{-1}\left(\mathbf{G} + \frac{1}{2}\mathbf{G}\mathbf{M}^{\mathrm{T}} + \mathbf{M}\mathbf{G} + \frac{1}{2}\mathbf{M}\mathbf{G}\mathbf{M}^{\mathrm{T}}\right)\left(\mathbf{I} - \frac{1}{4}\mathbf{M}^{\mathrm{T}}\mathbf{M}^{\mathrm{T}}\right)^{-1}\boldsymbol{\beta}. \qquad (9)$$

The resemblance between equations (8) and (9) is striking: they differ only by the multiplier $\frac{1}{4}$ in the penultimate factor. Thus, the response to selection predicted by the two equations will be similar when **MM** is small relative to **I** and will be identical when $\mathbf{MM} = \mathbf{0}$. In the latter case, equations (8) and (9) reduce to

$$\Delta\bar{\mathbf{z}} = \left(\mathbf{G} + \frac{1}{2}\mathbf{G}\mathbf{M}^{\mathrm{T}} + \mathbf{M}\mathbf{G} + \frac{1}{2}\mathbf{M}\mathbf{G}\mathbf{M}^{\mathrm{T}}\right)\boldsymbol{\beta}. \qquad (10)$$

The discrepancy between the two models appears to arise from the neglect of what may be called "cascading maternal effects" in the standard variance-components model. Cascading maternal effects occur when a trait mediating a maternal effect is itself influenced by a maternal effect in the previous generation. As a result, an offspring's phenotype becomes dependent upon not only the phenotypes of its own mother, but also those of its grandmother, its great-grandmother, and so on. Falconer's (1960) result for litter size in mice, which led to the development of the trait-based model (Falconer 1965), is a classic case of cascading maternal effects: females born in large litters tend to produce relatively small litters. Mathematically, whenever cascading maternal effects are present, **MM** will be nonzero, and thus the simplest version of the variance-components model will make predictions that are not equal to those of the trait-based model. In the absence of such cascades, $\mathbf{MM} = \mathbf{0}$, and the trait-based and variance-components models should be equivalent. A nonzero **MM** may occur either when maternally affected traits cause maternal effects themselves (i.e., when any diagonal element of **M** is nonzero) or when maternally affected traits influence a different trait in the next generation (i.e., when particular combinations of off-diagonal elements of **M** such as m_{12} and m_{21} are nonzero).

As noted earlier, Willham's original (1963) formulation of the variance-components model assumes the absence of cascading maternal effects (Hadfield 2012). By contrast, this condition is built into the trait-based model (Kirkpatrick and Lande 1989; Hadfield 2012). Willham's later (1972) model addressed the problem by incorporating cascading maternal effects into grandmaternal variance components. In empirical applications, however, this formulation introduces the problem of estimating a large number of additional parameters that may not be estimable in most data sets. An alternative approach is to introduce a correction factor to the variance-components model that will allow it to make correct predictions when cascading maternal effects are present. Examination of equations (5) and (6) suggests that this correction factor should be

$$\mathbf{K} = (\mathbf{I}-\mathbf{M}^{\mathrm{T}}\mathbf{M}^{\mathrm{T}})\left(\mathbf{I} - \frac{1}{4}\mathbf{M}^{\mathrm{T}}\mathbf{M}^{\mathrm{T}}\right)^{-1} \qquad (11a)$$

or equivalently,

$$\mathbf{K} = \left(\mathbf{I} - \mathbf{G}_{dd}^{-1}\mathbf{G}_{dm}\mathbf{G}_{dd}^{-1}\mathbf{G}_{dm}\right)\left(\mathbf{I} - \frac{1}{4}\mathbf{G}_{dd}^{-1}\mathbf{G}_{dm}\mathbf{G}_{dd}^{-1}\mathbf{G}_{dm}\right)^{-1} \qquad (11b)$$

(see the Supplementary Appendix for details). The modified version of Willham's predictive equation that includes a correction

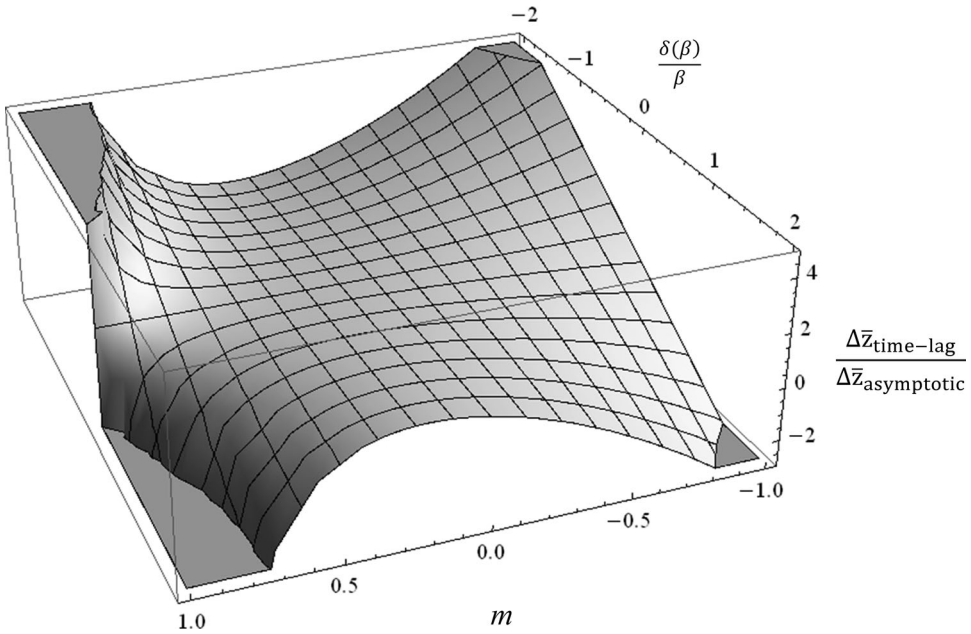

Figure 1. Ratio of evolutionary predictions made by two versions (time-lag and asymptotic, see text) of Kirkpatrick and Lande's trait-based maternal effect model as a function of the maternal effects coefficient (*m*) and the relative difference in the selection gradient across generations ($\frac{\delta(\beta)}{\beta}$, see eq. (7)). Heritability is set at $h^2 = 0.5$. In the relatively flat central region of the graph, the models are roughly equivalent (ratio ≈ 1), but the models diverge as maternal effects and/or differences in selection become stronger.

for cascading maternal effects is

$$\Delta\bar{\mathbf{z}} = \left(\mathbf{G}_{dd} + \frac{1}{2}\mathbf{G}_{dm} + \mathbf{G}_{md} + \frac{1}{2}\mathbf{G}_{mm}\right)\mathbf{K}\boldsymbol{\beta}. \quad (12)$$

The effect of including **K** tends to be to reduce the predicted rate of evolution when compared to the uncorrected variance-components model. Unless the elements of **M** are very large, this reduction will be relatively modest. As an illustrative case, consider a single trait model where the maternal trait influences the expression of the same trait in the offspring. Here, the correction factor K will equal $\frac{1-m^2}{1-(m^2/4)}$. By definition, m ranges between -1 and 1 (Kirkpatrick and Lande 1989), so K will range from 0 to 1. Interestingly, at modest values of m, the difference between the uncorrected and corrected models is not large; for example, when $m = \pm 0.2$, the correction factor equals 0.97. Employing the correction becomes increasingly crucial as cascading maternal effects become stronger; for example, at $m = \pm 0.7$, the correction factor equals 0.58, indicating that the uncorrected variance-components model severely overestimates the response to selection.

Empirical Methods

As demonstrated earlier, the performance of maternal effect models for making predictions from empirical data sets should depend upon both the nature of maternal effects and selection in a given system. Comparing these models is thus essentially an empirical question. In this section, we use experimental data to evaluate the utility of quantitative genetic models of maternal effects for predicting response to selection. We ask how well the predictions of each model correspond to empirical measurements of selection response from an artificial selection study. Specifically, we evaluate the importance of including maternal effects in general, cascading maternal effects, and variation in selection across generations in predictive models. We also compare the fit of variance-components vs. trait-based models.

To address these questions, we used parameters estimated from two independent studies of genetics and selection in *C. americanum* to fit six models, including the maternal effect models discussed earlier. Quantitative genetic parameters for four traits derive from a breeding design that allowed estimation of maternal genetic effects (Galloway et al. 2009). The genetic parameters from this study, which were estimated for transformed traits (natural log for all traits except rosette size, which was square-root transformed), may be found in Galloway et al. (2009; $\mathbf{G}_{dd}$, Table 3a; $\mathbf{G}_{mm}$, Table 3b; $\mathbf{G}_{dm} = \mathbf{G}_{md}{}^{\mathrm{T}}$, Table 3c). In Galloway et al. (2009), **M** was calculated using mean- and variance-standardized traits to facilitate comparisons among traits. To use **M** in the predictive equations here, we recalculated it for unstandardized traits using equation (A10a; Table S1).

In a separate study of the same population, three generations of artificial selection were applied to one of these traits, days to flower, in four replicate selection lines (Burgess et al. 2007). Two lines were selected for early flowering (E1 and E2),

and two were selected for late flowering (L1 and L2). In each generation, the top or bottom 20% were selected to be the parents of the next generation. We estimated the resulting selection gradient using linear regression of total number of offspring selected to contribute to the next generation on ln-transformed days to flower. Despite using a consistent criterion each generation, selection gradients were not equal (Table S2). The other three traits were only measured after the third generation of selection, and therefore we ignore any inadvertent selection that may have occurred on these traits and set their selection gradients equal to zero.

We predicted the evolution of days to flower after three generations of selection for a number of different genetic models. For each model, we used the starting mean (ln-transformed) for each line and iteratively applied it across generations. Although we used multivariate models to calculate predicted values, we used only the predictions for days to flower to assess fit, as this was the phenotype under selection. All parameters used for model fitting are given either in Galloway et al. (2009) or in the Supporting Information.

We compared six different models, two in each of three families of models. The first two models did not incorporate maternal effects in their prediction of evolutionary change. In *Model 1* (*breeder's equation*), we used a naïve estimation of $\mathbf{G}$ that assumed the absence of maternal effects. This $\mathbf{G}$ was estimated in ASReml 3.0 (Gilmour et al. 2009) using the data set presented in Galloway et al. (2009) and was inserted into the multivariate breeder's equation, $\Delta\bar{\mathbf{z}} = \mathbf{G}\boldsymbol{\beta}$ (Lande 1979; Lande and Arnold 1983; Table S3). In *Model 2* (*breeder's equation*, *maternal effects removed*), we accounted for maternal effects when measuring genetic parameters, but did not use them in the prediction of response to selection. In other words, $\mathbf{G}_{dd}$ was inserted into the multivariate breeder's equation in place of $\mathbf{G}$. The next two models both belong to the variance-components framework, accounting for maternal effects via matrices of maternal variance and direct-maternal covariance. In *Model 3* (*variance-components model*), direct and maternal (co)variance matrices were substituted into equation (1) without correcting for potential cascading maternal effects. In *Model 4* (*variance-components model, corrected*), these matrices were instead substituted into equation (12), which includes a correction for cascades. The remaining two models were trait based, using the matrix $\mathbf{M}$ to assign maternal effects to specific maternal traits. *Model 5* (*trait-based model with time lag*) explicitly accounted for carryover effects across generations. In the first generation, effects of previous generations were considered negligible, and response was predicted using

$$\Delta\bar{\mathbf{z}}(t) = (\mathbf{C}_{az} + \mathbf{MP})\,\boldsymbol{\beta}(t). \tag{13}$$

Table 1. Mean absolute difference (in days) between predictions of quantitative genetic models to observed response to artificial selection on days to flower in *Campanulastrum americanum*, calculated using data plotted in Figure 2. Models are listed from best to worst fit. See "Empirical Methods" section for definitions of models.

Model	Mean absolute difference (days)
5: Trait-based, with time lag	2.27
6: Trait-based, asymptotic	5.25
2: Breeder's equation, maternal effects removed	6.64
4: Variance-components, corrected	6.67
3: Variance-components	7.40
1: Breeder's equation	19.35

In subsequent generations, we used equation (2), which has terms that include selection and evolutionary change from the previous generation. Equation (3) was used to calculate $\mathbf{C}_{az}$, with $\mathbf{G}$ calculated from equation (A10b; Table S4). The phenotypic (co)variance matrix was calculated following Willham (1972) as

$$\mathbf{P} = \mathbf{G}_{dd} + \frac{1}{2}\mathbf{G}_{dm} + \frac{1}{2}\mathbf{G}_{md} + \mathbf{G}_{mm} + \mathbf{E}_{dd} + \mathbf{E}_{mm}, \tag{14}$$

(Table S2 of Galloway et al. 2009). *Model 6* (*trait-based model, asymptotic*) assumes that selection is constant across generations and hence the rate of evolution has reached an asymptote. As a consequence of this assumption, it is not necessary to explicitly model the lag across generations due to maternal effects. $\mathbf{G}$ was calculated as above and substituted into equation (5).

We did not statistically test the fit of models using information criteria (Burnham and Anderson 2002) or other methods, as our data sets did not readily conform to standard model comparison techniques. Rather, we simply present summary statistics of the average absolute difference between predicted and observed values of days to flower at the end of the selection experiment and rank the models from least to greatest difference between observed and predicted.

Empirical Results

The trait-based model incorporating time lag (Model 5) fit the observations substantially better than all other models (Fig. 2 and Table 1). Model 1, which completely ignored maternal effects, provided the worst fit (Fig. 2 and Table 1). The other four models clustered in the middle, providing a similar fit to the data (Fig. 2 and Table 1).

Comparing the two variance-components models, our proposed correction factor increased the goodness of fit (Model 3 vs.

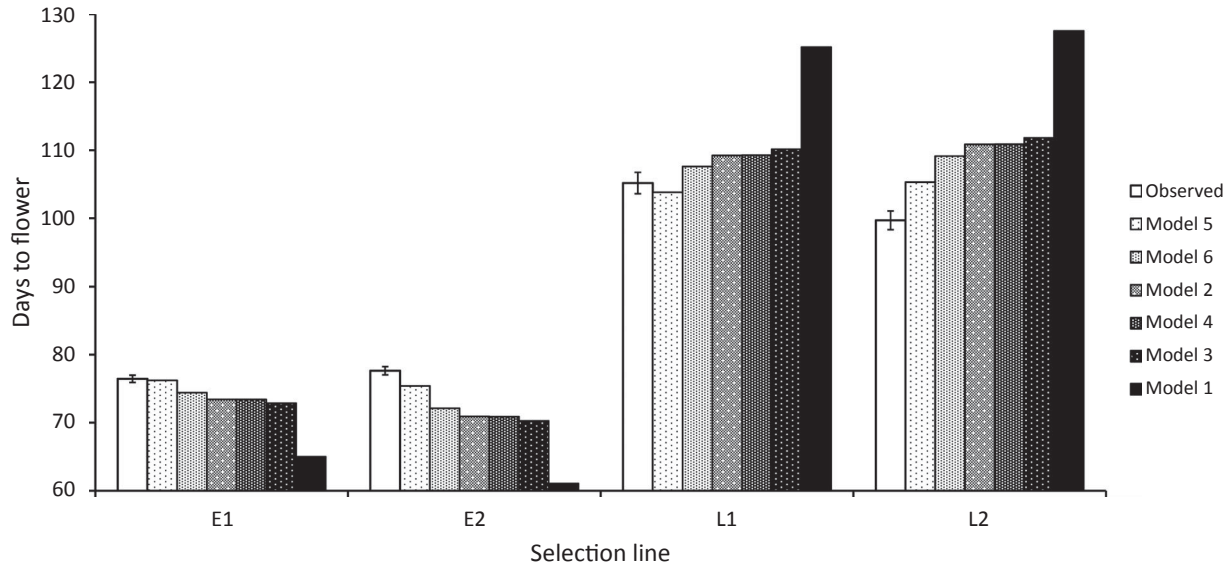

Figure 2. Observed (± SE) and predicted (back-transformed) means for days to flower after three generations of artificial selection. Selection was for earlier flowering in E lines (negative selection gradients) and later flowering in L lines (positive selection gradients; Table S2). The six models, which are ordered from best fit to worst (Table 1), represent three families: breeder's equation (models 1 and 2), variance-components (models 3 and 4), and trait-based (models 5 and 6).

Model 4); however, the magnitude of this difference was not large. Despite the presence of cascading maternal effects in our results (e.g., days to flower has a negative effect on itself, Table S1), these cascades were not strong enough for the correction factor to have a large impact. When considering the two trait-based models, the asymptotic model provided a notably worse fit to the data than the time-lag model. This likely occurred because selection gradients differed enough across generations that the assumptions of the asymptotic model did not hold (Table S2).

Across the two model types, the variance-components model provided slightly worse fit than the asymptotic trait-based model. One possible explanation for this lies with the $\mathbf{G}_{mm}$ term. When all relevant traits have been included, $\mathbf{G}_{mm}$ should theoretically equal $\mathbf{M}\mathrm{G}_{dd}\mathbf{M}^{\mathrm{T}}$ (McGlothlin and Brodie 2009); however, our estimate was roughly equal to $2\mathbf{M}\mathrm{G}_{dd}\mathbf{M}^{\mathrm{T}}$. This suggests that our estimate of this matrix may have been inflated due to factors such as unmeasured traits or an inability to separate maternal additive genetic variance from other sources of maternal variance. It is unknown whether this situation is likely to be common in other data sets.

Surprisingly, accounting for maternal effects when estimating $\mathbf{G}_{dd}$ but ignoring them when calculating response to selection (Model 2) provided a fit similar to that of the variance-components model. This seems to have been the case because the last three genetic terms in the variance-components model, $\frac{1}{2}\mathbf{G}_{dm} + \mathbf{G}_{md} + \frac{1}{2}\mathbf{G}_{mm}$, largely canceled one another out for elements that affected the evolutionary response of days to flower due to the negative direct-maternal correlations we observed. Such negative correlations are common but not universal in nature (Räsänen and Kruuk 2007). In contrast, when maternal effects were completely ignored (Model 1), the genetic variance for days to flower was greatly inflated, causing an overestimation of the response to selection.

Discussion

The success of any quantitative genetic model relies on its ability to predict evolutionary change (Grant and Grant 1995). Evolutionary biologists have long been aware that considering maternal effects is crucial to making such predictions accurately (Dickerson 1947; Willham 1963, 1972; Kirkpatrick and Lande 1989; Mousseau and Fox 1998; Räsänen and Kruuk 2007), and our results strongly support this conclusion. When we tested models that included maternal effects against the standard breeder's equation, maternal effect models consistently made more accurate predictions of the response to artificial selection on days to flower, a maternally influenced trait, across four selection lines. A naïve application of the breeder's equation dramatically overestimated the rate of evolutionary change in each of our selection lines, showing that the consequences of ignoring maternal effects altogether may be quite drastic. When we factored out maternal effects but did not include them in our calculations to predict evolutionary change, treating them as "nuisance parameters" (Räsänen and Kruuk 2007), the breeder's equation made more accurate predictions. This result seems to have been due to

the strongly negative direct-maternal correlations present in our system (Galloway et al. 2009). Negative direct-maternal correlations are common in nature (Räsänen and Kruuk 2007), suggesting such an approximation may often work well, but they are by no means universal, so this approach should be taken only with caution.

The differences among maternal effect models were more subtle. Previously, variance-components and trait-based models of maternal effects have been rather distinct from each other in the literature, and equivalence between their predictive equations has been demonstrated only for a few special cases (Kirkpatrick and Lande 1989; Lande and Price 1989; Hadfield 2012). Our theoretical results demonstrate that two classes of maternal effects models—variance-components and trait-based—make similar predictions under a wide variety of conditions. When selection can be assumed to be uniform across generations and in the absence of cascading maternal effects (traits that both mediate and are influenced by maternal effects), the standard variance-components model and the asymptotic trait-based model were shown to make identical predictions. The two models are nearly equivalent if cascading maternal effects are relatively weak, and diverge from one another as cascading maternal effects become stronger. In this case, the variance-components model will tend to significantly overestimate the response to selection, and the correction factor **K**, which is a simple function of direct genetic variance and direct-maternal covariance, should be applied. When selection changes modestly across generations or when maternal effects are weak, these models also offer a reasonable approximation of the trait-based time-lag model. However, only the latter model is capable of fully incorporating the complexities that arise from maternal effects and is likely to make the most accurate predictions when its parameters are estimable.

Our empirical results supported these theoretical conclusions. Although all maternal effect models we tested made predictions that could be considered reasonably accurate, models varied in their fit to observed response to selection. Specifically, Kirkpatrick and Lande's model (1989) incorporating time lags in evolutionary response made the most accurate predictions, with all other maternal effect models providing a similar, but less accurate fit. As demonstrated by Kirkpatrick and Lande (1989; Lande and Kirkpatrick 1990), maternal effects tend to cause such lags because selection, in addition to changing the genetic composition of a population, alters the distribution of the phenotypes that mediate maternal effects and thus any cross-generational effects associated with those phenotypes. The effect of these time lags is predicted to be more dramatic when selection varies strongly from generation to generation. In our data set, although a consistent selection criterion was applied each generation, that is the earliest or latest 20% (Burgess et al. 2007), phenotypic selection gradients were not equal in each generation and thus the model that accounted for time lags was a better fit. Natural selection is likely to be much more variable than artificial selection (Siepielski et al. 2009), and therefore the greater predictive ability of the trait-based time lag model may be much larger in natural populations.

Although the time-lag model provided the most accurate predictions of evolutionary change in our data set, in some cases it may be desirable to apply a model that does not include time lags. For example, investigators may wish to make predictions about evolution in a natural population based on a single estimate of selection. If it is reasonable to accept the assumption that selection does not vary greatly across generations, both the variance-components and asymptotic trait-based models should provide acceptable predictions. The asymptotic trait-based model and variance-components model provided similarly accurate fits to our observed results, although the fit of the former trait-based model was slightly better. The poorer fit of the variance-components model can be attributed to two causes: first, estimates of maternal genetic variances may have been slightly inflated (perhaps due to an inflation of the maternal variance term); and second, the presence of cascading maternal effects led to a violation of the model's assumptions. Applying the correction factor **K** to the variance-components model slightly increased its accuracy as predicted.

In conclusion, our results emphasize the importance of considering maternal effects when making evolutionary predictions. We recommend fitting trait-based models, particularly those that incorporate time lags, whenever possible to make the most accurate predictions. In doing so, it must be remembered that application of the trait-based framework necessitates a multivariate approach. Accurately estimating the key parameter of the trait-based model, the maternal-effects matrix **M**, requires measurement of the traits of the mother that are hypothesized to underlie maternal effects. By contrast, most studies that have taken the variance-components approach have focused on a single trait or have applied univariate models to several traits (Räsänen and Kruuk 2007).

It is also important to note that as in any multivariate analysis, failing to measure the important maternal traits in trait-based models may significantly reduce the accuracy of predictions. Neglecting traits of importance may cause maternal effects to be attributed to the incorrect mediating phenotype. In many cases, however, it will be possible to use the biology of the study organism to generate strong hypotheses about the identity of important maternal traits. It is also likely that including traits that are relatively well correlated with the causal maternal phenotypes may generate sufficiently accurate predictions. For example, although we detected a strong maternal effect of juvenile size (rosette size) on the same trait in offspring, it is likely

that this effect is causally mediated by another trait of the adult plant.

When it is difficult or impossible to measure enough traits to estimate **M**, our results suggest that the variance-components model may provide a reasonable approximation, especially when cascading maternal effects can be assumed to be absent. Whether such an assumption is likely to be reasonable is an empirical question. We recommend more studies that investigate cascading maternal effects using a trait-based approach to determine whether such cascades often influence the evolution of natural populations.

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Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher's website:

Appendix S1. Derivation of multivariate variance-components model; translation between variance-components and trait-based models.

Table S1. The maternal effects matrix (**M**), recalculated as described in the text from Galloway et al. (2009).

Table S2. Selection gradients (**β**) for ln days to flower for four selection lines (two early flowering, E1 and E2, and two late flowering, L1 and L2) each selected for three generations.

Table S3. Estimate of the additive genetic (co)variance matrix (**G**) for four traits using an animal model (ASReml 3.0) that ignored maternal effects.

Table S4. Estimate of the additive genetic (co)variance matrix (**G**) for four traits calculated using equation (A10b) and results from Table S1 and Galloway et al. (2009; Table 3a).