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Impact of Nonrandom Mating on Genetic Variance and Gene Flow in Populations With Mass Selection

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ABSTRACT

The mechanisms by which nonrandom mating affects selected populations are not completely understood and remain a subject of scientific debate in the development of tractable predictors of population characteristics. The main objective of this study was to provide a predictive model for the genetic variance and covariance among mates for traits subjected to directional selection in populations with nonrandom mating based on the pedigree. Stochastic simulations were used to check the validity of this model. Our predictions indicate that the positive covariance among mates that is expected to result with preferential mating of relatives can be severely overpredicted from neutral expectations. The covariance expected from neutral theory is offset by an opposing covariance between the genetic mean of an individual’s family and the Mendelian sampling term of its mate. This mechanism was able to predict the reduction in covariance among mates that we observed in the simulated populations and, in consequence, the equilibrium genetic variance and expected long-term genetic contributions. Additionally, this study provided confirmatory evidence on the postulated relationships of long-term genetic contributions with both the rate of genetic gain and the rate of inbreeding (ΔF) with nonrandom mating. The coefficient of variation of the expected gene flow among individuals and ΔF was sensitive to nonrandom mating when heritability was low, but less so as heritability increased, and the theory developed in the study was sufficient to explain this phenomenon.

Recent advances in quantitative genetic theory have allowed breeding schemes to consider the management of genetic variation objectively, simultaneously with the maximization of genetic gain. Such advances are highly relevant to breeding practice, not only for commercial schemes but also for those schemes that are orientated toward the conservation of genetic resources. These advances include the development of tractable, deterministic predictors of rates of inbreeding (ΔF), gene flow, and genetic gain (ΔG) for complex selected populations (Woolliams et al. 1999; Woolliams and Bijma 2000), and operational tools for day-to-day selection decisions (Wray and Goddard 1994; Meuwissen 1997; Grundy et al. 1998).

However, the theory underpinning these tools has been developed primarily for random mating of the selected males and females and for a neutral locus where the genotypic frequencies in the offspring display no departure from Hardy-Weinberg (HW) proportions, other than that arising from the partitioning of the gene pool induced by two sexes (Robertson 1965). However, the role of nonrandom mating, where some specific design is placed upon which male is mated to which female, has been less well studied in this context. Although utilizing a mating design to minimize ΔF does not always lead to substantial deviations from HW proportions (Sonesson and Meuwissen 2000), much of the theory on genetic variation and the impact of nonrandom mating has been built up around the concept of departures from HW equilibrium (e.g., Caballero and Hill 1992; Santiago and Caballero 1995; Wang 1996) and the concepts of the avoidance of, or preferential treatment of relatives. The interpretation of the work on nonrandom mating, both its application and its impact, remains a subject of scientific debate. For example, in conservation, accepted practice uses minimum coancestry to minimize ΔF (Caballero et al. 1996; Frankham et al. 2002), yet recent theoretical developments using genetic contributions show that the lowest ΔF with hierarchical matings is achievable when relatives are preferentially mated (Sánchez et al. 2003). In selected populations, there is clear evidence that mating designs are beneficial, although not all these designs define matings through pedigree, e.g., factorial mating (Woolliams 1989). Several articles indicate that attention to the pedigree relationships within a mating design can be advantageous over random-mating schemes (e.g., Santiago and Caballero 1995; Caballero et al. 1996; Sánchez et al. 1999). However, the benefits of these methods have not always been quantified in predictable terms for their joint impact upon genetic gain and rates of inbreeding.

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Moreover, other studies on mating designs (Toro and Pérez-Enciso 1990; Kleive et al. 1994; Fernández and Toro 1999) do not separate out the impact of specifying the matings from the impact of controlling only the overall contribution of each selected individual assuming random mating.

Santiago and Carballero (1995) were successful in producing predictions of the effective population size \(N_e\), defined as \((\Delta F)^{-1}\) in nonrandom mating populations undergoing mass selection, using an approach based upon the variance of allele frequencies. These authors considered nonrandom mating in the form of departures from HW equilibrium achieved through partial full-sib mating. However, Woolliams and Bijma (2000) showed that, for random mating, an approach to predicting \(N_e\) using long-term genetic contributions was capable of extension to more complex selection schemes. To achieve such an extension with nonrandom mating requires an understanding of the expected gene flows of individuals based upon the inheritance of selective advantages, which in turn presupposes an understanding of the behavior of the genetic variation. There appears to be little published information on these topics.

Therefore, the main objective of this study is to advance the theoretical framework for predicting the impact of nonrandom mating for populations undergoing direction selection, providing a predictive model for the genetic variance and covariance among mates. The nonrandom mating is defined solely in terms of departures from HW proportions for neutral alleles, without reference to phenotypes. The impact is measured in terms of genetic parameters, such as genetic variance, expected gene flow, and \(\Delta F\), assuming the infinitesimal model and mass selection. In the course of this article, the opportunity to validate the developments of Woolliams and Bijma (2000) for nonrandom mating is taken. The accuracies of the predictions of \(\Delta F\) and \(\Delta G\) and the validity of the framework are established with the help of stochastic simulations.

**MATERIALS AND METHODS**

**Nonrandom mating and neutral theory:** The correlation between uniting gametes due to the nonrandom mating of parents is an additional factor affecting heterozygosity over and above initial gene frequencies and their accumulated drift. Using the classical \(F\)-statistics of Wright (1969), the expected fractional decrease in the heterozygosity for a given population \((F_1)\) can be related to two further statistics using the relationship \((1 - F_1) = (1 - F_0)(1 - F_0)\), where \(F_0\) is the fractional loss of heterozygosity due to the finiteness of the population census, and \(F_0\) is the loss of heterozygosity due to the nonrandom mating of parents. The \(F_0\) can be seen as a correlation of gene effects between homologous alleles in pairs of mating parents, i.e., the correlation between alleles within infinitely many conceptual offspring derived from each of the pairs of mating parents (often denoted \(\alpha_0\) and hereafter in this study). Whereas, if conceived of as the correlation between alleles within successful offspring (i.e., existing individuals), it measures the actual loss of heterozygosity due to the nonrandomness of the mating of the parents with nonzero contributions in the offspring generation (often denoted as \(\alpha_1\)). Thus the former (\(\alpha_0\)) is a potential correlation of uniting gametes from selected parents, whereas the latter (\(\alpha_1\)) is a realized correlation and will be affected by the finite random sampling of gametes to form the offspring generation and by any artificial and/or natural selection of offspring before reaching the breeding population.

Under the assumption of completely neutral genes \(\alpha_0\) would tend to be equal to \(\alpha_1\). For neutral genes, when nonrandom mating results from a mix of full-sib mating and random mating, \(\alpha_1\) (i.e., \(\alpha_1 = \alpha_0\)) can be related to the proportion of full-sib mating (denoted hereafter \(\phi\)) by \(\alpha_1 = \phi/(4 - 3\phi)\) (Ghai 1969).

To obtain \(\alpha_0\) in a breeding population, let \(\theta\) be the coancestry (kinship) coefficient (Lynch and Walsh 1998) of sire \(i\) and dam \(j\), then following Wright’s (1969) equation \(1 - \alpha_{0ij} = (1 - \theta)/(1 - \theta)\), where \(\theta = F_0\) is the average of all the entries in the matrix of coancestries among the parents \((i.e., i, j, \ldots, \text{and contemporaries})\), including self-coancestries and the reciprocals (Cockerham 1967). Thus \(\alpha_{0ij}\) is defined for any pair of parents in relation to the complete set of selected parents. The term \(\alpha_0\) is the average \(\alpha_{0ij}\) of the selected matings, irrespective of the fitness of the offspring, i.e., as if all matings contribute an equal and large number of offspring to the next generation.

To obtain a summary value of \(\alpha_0\) for a pedigreed population undergoing selection, we follow the same reasoning as above. Note that \(\theta = F_i\) represents the average inbreeding coefficient if the offspring generation had been obtained by complete aggregation of the parental gene pool and sampling at random with replacement. Then for any individual offspring from that set of parents \(\alpha_{0ij} = F_i\) can be defined as \(1 - \alpha_{0ij} = (1 - F(k))/(1 - \theta)\), where \(F(k)\) is the coefficient of inbreeding of individual \(k\), and is equal to \(\theta_{w(i,k/dam(k))}\). For the infinitesimal model, the Mendelian sampling deviation for an offspring \(k\) has a variance equal to

\[
\frac{1}{2} \sigma_{r}^{2}(1 - \frac{1}{2}F(\text{sire}(k)) - \frac{1}{2}F(\text{dam}(k))) = \frac{1}{2} \sigma_{r}^{2}(1 - F(\text{sire}(k))) + \frac{1}{2} \sigma_{r}^{2}(1 - F(\text{dam}(k))) - \frac{1}{2} \sigma_{r}^{2}(\text{sire}(k)) - \frac{1}{2} \sigma_{r}^{2}(\text{dam}(k)).
\]

where \(\sigma_{r}^{2}\) is the initial variance of the breeding values. In the remainder of this study, the term \((1 - \theta)/\theta\) in Equation 1 is omitted for derivations and predictions, analogously to Woolliams et al. (1999) and Woolliams and Bijma (2000). This omission allows the genetic variance to reach an equilibrium. Further details are given in the last section of MATERIALS AND METHODS.

The terms \(\alpha_{0ij}\) are used to define two related, but distinct, summary: (i) \(\alpha_0 = \sum_i \alpha_{0ij}\), where \(\alpha_0\) was the observed contribution of \(k\) to the selected offspring in the next generation, and (ii) \(\alpha_0 = \sum_i \rho_{ij} \alpha_{0ij}\), where \(\rho_{ij}\) was the long-term genetic contribution (described in the following sections) of \(k\). If we assume now that directional selection has taken place among families, then the direct equivalence between \(\alpha_0\) and \(\alpha_1\) (irrespective of whether \(1c\) or \(1r\)) no longer holds for selective genes or neutral genes since selection success will depend on the \(\alpha_1\) of the parents (Caballero et al. 1996).

**Dynamics of genetic (co)variance for a selected trait under nonrandom mating:** In this section, a model is developed to show that the impact of nonrandom mating on covariances between mates for selected traits and neutral traits may be qualitatively different and to describe the circumstances under which this can occur. In particular, it demonstrates that selection induces a negative covariance between true family means and Mendelian sampling terms, not only within individual
selected parents but also between a parent and its mate, thereby reducing genetic variance more than would be predicted by previously existing selection theory.

Consider a population with equal numbers of dams and sires, i.e., a mating ratio of 1, mated in pairs to produce a deviation from HW equilibrium equal to \( \alpha_0 \), on the basis of pedigree information alone. For the trait under selection, assume a heritability of \( h^2 \) when in HW equilibrium in an unselected base generation, with a phenotypic variance \( \sigma^2_P \). It is assumed that the inheritance of the trait under selection can be described by an infinitesimal model and, for simplicity in the derivation of this model, that the nonrandom mating is achieved by managing \( \phi \), the proportion of full-sib matings. Note that this mating scheme does not produce half-sibs. From Ghai (1969), the neutral expectations are \( \alpha_i = \alpha_0 = \alpha \), and \( \phi = 4a/(1 + 3a) \) for large populations.

Let \( P \) denote the phenotype of an individual \( i \) for the selected trait and \( B \) be the breeding value for a neutral trait, then the covariance between breeding values of mates is given by Caballero and Hill (1992) as \( \text{cov}(B_{im}, B_{jm}) = 2\alpha_0\sigma^2_i \), where \( \sigma^2_i \) is the variance of the breeding values in the unselected and randomly mated base population. Now consider \( A \), the breeding value for the selected trait. Then \( A = \frac{1}{2}(A_{im} + A_{jm}) + a_i + a_j \), where \( f_i \) is the true family mean, and \( a_i \) is the Mendelian sampling term. Define \( \sigma^2_{a_i} \) as the variance of the breeding values at time \( t \) with \( \sigma^2_i = \sigma^2_{a_i} + \sigma^2_h \), where \( \sigma^2_h \) is the variance of the true family mean at time \( t \) and \( \sigma^2_h = \frac{1}{2}(1 - \alpha_0)h^2 \) is the variance of the Mendelian sampling terms [note that the term \((1 - \phi)\) in Equation 1 is omitted here, and since \( \sigma^2_{a_i} = 1, h^2 = \sigma^2_{a_i} \)]. For simplicity, the explicit dependence on \( t \) in the notation is neglected. For selection on phenotype \( P \),

\[
\begin{align*}
    f_i &= \frac{\sigma^2_i}{\Phi}P_i + \varepsilon_{i1} \\
    a_i &= \frac{\sigma^2_a}{\phi}P_i + \varepsilon_{i2},
\end{align*}
\]

where \( f_i \) and \( a_i \) are both partitioned into an expectation condition on \( P \) and a residual \( \varepsilon \). Since \( \text{cov}(f_i, a_j) = 0, \varepsilon_{i1}\varepsilon_{j1} = -\sigma^2_{r_{a_i/a_j}} \), following the methods of Bulmer (1980) for selection with the infinitesimal model, let superscript * denote a parameter postselection on \( P \), then \( \text{cov}(f_i, a_j)^* = -\sigma^2_{r_{a_i/a_j}} \). Since \( \sigma^2_h = (1 - \kappa)\sigma^2_h \), where \( \kappa \) is the variance reduction coefficient. This has a direct analogy to linkage disequilibrium, where selection on \( P \) induces negative covariance between the effects of different loci, and where the induction of this covariance is not dependent on mating procedures. The regression of \( a_i \) on \( f_i \) after selection is

\[
    b_{a_i} = -\kappa\sigma^2_{r_{a_i/a_j}}/\sigma^2_h, \tag{3}
\]

where \( \sigma^2_h = \sigma^2(1 - \kappa)\sigma^2_h \) is the variance of true full-sib family means after selection. Note \( b_{a_i} < 0 \), and \( b_{a_i} \neq 0 \) after selection.

When allocating mates \( (i,j) \) using the pedigree alone,

\[
    \text{cov}(A_i, A_j) = \text{cov}(f_i + a_i, f_j + a_j) = \text{cov}(f_i, f_j) + \text{cov}(f_i, a_j) + \text{cov}(f_j, a_i) + \text{cov}(a_i, a_j),
\]

Substituting \( a_i = b_{a_i}f_i + \varepsilon_i \) and analogously for \( a_j \), and using \( \phi \) to estimate the covariance between mates,

\[
    \text{cov}(A_i, A_j) = \phi\sigma^2_h + 2b_{a_i}\phi\sigma^2_h + b_{a_i}^2\phi\sigma^2_h = \phi\sigma^2_h(1 + b_{a_i})^2, \tag{4}
\]

In the absence of selection, this is simply \( \phi\sigma^2_h \). Therefore, with selection, since (i) \( \sigma^2_h < \sigma^2_h \) and (ii) \( b_{a_i} < 0 \), the covariance achieved between the breeding values of mates for the trait of selection is less than that for neutral traits. The implication from Equation 3 is that the covariance between mates for the selected trait may be dramatically reduced below what is expected when \( b_{a_i} \) becomes more strongly negative, when (i) selection intensity is large, since \( \kappa \to 1 \), and when (ii) \( h^2 \) is large, since \( \sigma^2_h/\sigma^2_h \) is large. The term \((1 + b_{a_i})^2 \) is relatively insensitive to \( \alpha \) for mass selection, but is sensitive to \( h^2 \). For \( \kappa = 0.64, \alpha = 0.06, (1 + b_{a_i})^2 \) takes values of 0.87, 0.73, 0.57, 0.38, and 0.18 for \( h^2 = 0, 0.2, 0.4, 0.6, 0.8, \) and 0.99, respectively (from Equation 3 and genetic variances obtained from simulated populations); for \( \alpha = 0.24 \), the values are 0.90, 0.77, 0.62, 0.42, and 0.18.

Since \( \sigma^2_h = \sigma^2_h(1 - \kappa\sigma^2_h/\sigma^2_h) \), \( \sigma^2_h^* = \sigma^2_h + 2\text{cov}(f_i, a_j)^* + \sigma^2_h^* = \sigma^2_h(1 - \kappa h^2) \), and for their offspring \( A_{ij} = \frac{1}{2}(A_i + A_j) + a_{ij} \):

\[
    \sigma^2_{a_{ij}} = \frac{1}{2}((\sigma^2_h^* + \phi(1 + b_{a_i})^2\sigma^2_h^*)) + \sigma^2_h. \tag{5}
\]

This will move to equilibrium over generations so that the effect of selection is counterbalanced by the addition of \( \sigma^2_h \) (analogously to Bulmer 1980, p. 135).

Consequently, for the selected trait, the total observed additive variance may decline even as \( \alpha_0 \) increases (demonstrated in the results), although \( \alpha_0 \) is superficially increasing one component of the variation. This is a phenomenon associated with linkage disequilibrium and arises from (i) a lower Mendelian sampling variance replenishing the genetic variation lost due to selection in each generation and (ii) the induction of negative covariance between the Mendelian sampling term of a parent and the true family mean of its mate.

**Predictions of rate of inbreeding and genetic gain through the concept of long-term genetic contributions:** The genetic contribution of an ancestor \( k \) (denoted \( n_k \)) to a descendant \( j \) is the proportion of genes carried by \( j \) that are derived by descent from the ancestor \( k \). A descendant’s breeding value can be decomposed into a sum of Mendelian sampling deviations from all ancestors, with the weighting for ancestor \( k \)’s Mendelian deviation being \( n_k \). For a mixing population, after a sufficiently large number of generations, \( k \)'s genetic contribution to all individuals within the population approaches the same stable and constant value across generations. In the remainder of the text, the stable genetic contributions from distant ancestors are referred to as “long-term genetic contributions.” The long-term genetic contributions will reflect differences among individual ancestors arising from their respective selective advantages together with cumulative chance factors across generations. Therefore, long-term genetic contributions model the gene flow of individual ancestors through the population.

The asymptotic \( \Delta F \) for nonrandom mating can be derived through its theoretical relationship with the sum of squared long-term genetic contributions,

\[
    \Delta F = \frac{1}{2}(1 - \alpha_0)\sum_i n_i^2. \tag{6}
\]

(Woolliams and Bijma 2000). The rate of genetic gain (\( \Delta G \)) per generation is also related to long-term genetic contributions since sustained genetic gain arises through the generation of covariance between long-term genetic contributions and Mendelian sampling deviations,

\[
    \Delta G = \sum_k n_k a_k. \tag{7}
\]

(Woolliams et al. 1999), where the sum is taken over a generation of ancestors. Therefore, the concept of long-term genetic contribution bridges the loss of heterozygosity and the generation of genetic gain for any deviation from random mating given by \( a_k \).

For mass selection, the selective advantages for an ancestor are its own breeding value and those of its mates. This set of
selective advantages influences not only the breeding success of the resulting offspring from that given ancestor, but also that of subsequent descendants. This dependence of the gene flow on the selective advantage can be expressed as a conditional expectation \( (\mu_k) \), i.e., as a function of the selective advantages. For truncation selection based upon phenotype, \( \mu_k \) can be satisfactorily modeled as a linear relationship between the genetic contribution and the breeding values,

\[
\mu_k = \gamma + \beta_{N,0} (A_k - \overline{A}) + \beta_{N,k} \sum (A_{\text{mates}} - \overline{A})
\]

(Woolliams et al. 1999), where the terms \( \overline{A} \) and \( \overline{A} \) are the mean breeding values of the selected individuals for the sex of \( k \) and its mates’ sex, respectively. For discrete generations,

\[
\gamma = (2N_k)^{-1} + (2N_0)^{-1}
\]

for \( N \) sires and \( N \) dams, respectively, and is independent of \( k \) and \( \alpha \). When \( N_k = N_0 = N \) with no mating hierarchy, \( \gamma_{N,0} = 0 \), and from here onward, we denote this as \( \beta \). Therefore under these two conditions, discrete generations and \( N \) mating pairs, the only parameters varying with the breeding scheme are the slope of the relationship \( \beta \) and the genetic variance among selected individuals derived from \( \sigma_N^2 \) (Woolliams et al. 1999). Equation 8 becomes

\[
\mu_k = \gamma + \beta (A_k - \overline{A}) + (A_{\text{mates}} - \overline{A})
\]

Thus \( \beta \) is the regression coefficient of the long-term contribution of an individual on the sum of its breeding value and that of its mate. The impact of the selective advantage on the gene flow (and, ultimately, on \( \Delta \phi \)) can then be measured by the coefficient of variation (CV) of the conditional expectation:

\[
CV(\mu_k) = 2N\beta^2(\sigma_N^2 + \phi(1 + b_0^2)\sigma_0^2)
\]

Population model and procedures for stochastic simulation:
This section describes the general population model and selection procedures for which predictions and simulations will be compared. The population was reproduced in discrete generations with a constant breeding size of \( N \) sires and \( N \) dams and a mating ratio of dams to sires of 1 in all generations (\( N_k = N_0 = N \)). Each dam mated \( n \) offspring, all full-sibs, and comprising equal numbers of male and female candidates. Selection was upon phenotype \( P \), which was the sum of breeding value \( A \) and an environmental deviation.

For simulation, a noninbred and unrelated base population was generated with \( \sigma_0^2 = 1 \). Each founder’s \( A \) was taken from \( N(0, \sigma_0^2) \), where \( \sigma_0^2 \) is the initial genetic variance (since \( \sigma_0^2 = 1 \), initial heritability \( h_0^2 = \sigma_0^2 \)). In subsequent generations, each new breeding value was the sum of \( 1/2(A_m + A_m) \) and a Mendelian sampling deviation. The latter term was drawn from \( N(0, 1/4\sigma_N^2(1 - 1/2\alpha_{\text{in}} - 1/2\alpha_{\text{out}})) \), where \( \alpha_{\text{in}} \) and \( \alpha_{\text{out}} \) are due to the nonrandom mating between grandparents. An environmental deviation sampled from \( N(0, 1/2\sigma_0^2) \) was added to each individual’s breeding value to obtain \( P \). The simulations omitted the term \( (1 - \overline{b}) \) in Equation 1, as previously indicated in the first section. Consequently, the genetic variance, and hence the variance in the selective advantages, in the simulated populations reached an equilibrium upon which to base stable predictions.

Selected individuals were mated following a mating design with nonrandom mating based upon \( \alpha_0 \) (as defined earlier), which was carried out systematically in all generations except in the base population, where founders were randomly allocated in pairs. The allocation of mates was decided in such a way that \( \alpha_0 \) was as close as possible to a target value \( \alpha_{\text{in}} \). This process involved a search throughout the feasible set of matings, carried out by the simulated annealing technique (Press et al. 1992), to minimize the objective function given by \( (\alpha_0 - \alpha_{\text{in}})^2 \). A random sample of matings was used as a starting point. The maximum feasible value for \( \alpha_0 \) is 1, which can be attained by multiple generations of close inbreeding leading to subling. For the benefit of a more general scheme, the upper limit of \( \alpha_{\text{in}} \) was < 1 in this study. On the other extreme, the lowest possible value of \( \alpha_0 \) in finite populations lies much closer to what is expected for random-mating populations, due to the fact that the avoidance of inbreeding is constrained in the long term by the genetic depletion caused by drift, as pointed out by Caballero and Hill (1992). The values of \( \alpha_{\text{in}} \) used in the simulation were \(-0.03, 0, 0.03, 0.06, 0.12, 0.18, \) and \( 0.24 \).

Long-term genetic contributions were calculated for an ancestral generation born after 20 generations of selection from the unselected base and upon the cohort of descendants born 20 generations after that ancestral generation. This guaranteed attainment of equilibrium of genetic variances in all the cases with \( \alpha_{\text{in}} = 0.12 \). With more extreme \( \alpha_{\text{in}} \) however, a longer period of time was needed before such equilibrium is reached (Santiago and Caballero 1995). For these cases, 20 further generations were bred before establishing the ancestral generation, although it was found unnecessary to extend the period of time for obtaining summary statistics for the converged contributions (i.e., 20 generations from ancestors to descendants). Observed long-term genetic contributions were used to calculate the predictions of \( \Delta F \) and \( \Delta G \) from Equations 6 and 7.

The values of achieved \( \alpha_0, \alpha_{\text{in}}, \alpha_{\text{out}}, \) and \( \sigma_0^2 \) and the genetic covariance among mates were recorded for each generation of the simulated populations, together with the observed \( \Delta F \), \( \Delta G \), \( \Sigma r_{ik} \), and \( \Sigma r_{ik} \) (Equation 7). The observed \( \Delta F \) and \( \Delta G \) were obtained as the average rate of the last 20 generations of the simulated populations. \( \beta \) was obtained by multiple regression of the long-term contribution of ancestors on their own breeding value and that of their mates; as no significant difference in the regression coefficients was found, as predicted, the value used in the text is the average of the two values. The proportion of full-sib matings (\( \phi \)) was also recorded in each simulated population. Results were averaged over 1000 replicates and standard errors derived from the variance between replicates. The values of basic parameters used in the simulations were \( \overline{h} = (0.01, 0.05, 0.1, 0.2, 0.4, 0.6, 0.8, \) and 0.99), \( N = [32, 64, 128] \), and \( n_0 = [4, 8, \) and 16].

RESULTS

Expected vs. observed degree of nonrandom mating:
The degree of nonrandom mating is described in this section, in terms of (i) the two distinct summary \( \phi_1 \)’s (i.e., \( \alpha_0 \) and \( \alpha_0 \)) vs. \( \alpha_{\text{in}} \) and (ii) the expected and observed proportion of full-sib matings (\( \phi_{\text{obs}} \) and \( \phi_{\text{in}} \) respectively). For item i, Table 1 shows that substantial deviations between \( \alpha_0 \) and \( \alpha_0 \), occurred, with \( \alpha_0 < \alpha_0 \), as \( \overline{h} \) increased and \( \alpha_{\text{in}} \) increased. Statistically significant but slight differences with \( \alpha_0 > \alpha_0 \) also occurred with \( \overline{h} = 0.01 \). Where \( \alpha_0 < \alpha_0 \), the substantial difference indicates a negative covariance between the individual’s long-term genetic contribution and \( \alpha_0 \). Thus, those individuals with low values of \( \alpha_0 \), consequently with a relatively greater Mendelian sampling variance in their offspring, had a selective advantage over their contemporaries and, therefore, a greater long-term genetic contribution. This association between long-term genetic contributions and the variation in \( \alpha_0 \) within a scheme became more evident as selection became more intense, through both large \( n_0 \) and/or large mating ratios (i.e., \( N_0 <
Target departures from HW proportions ($\alpha_{\text{obs}}$) vs. observed departures measured as the asymptotic average of $\alpha$, weighted by the observed contribution as parent to the selected offspring in the next generation ($\alpha_{\text{obs}}$) and the asymptotic average of $\alpha$ weighted by the long-term genetic contribution ($\alpha_i$), with phenotypic selection and $N = 32$, for different $\alpha_{\text{obs}}$, family size ($n_0$), and initial heritabilities ($h_0^2$)

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<th>$\alpha_i$</th>
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</tr>
</tbody>
</table>

Standard errors are $<0.25\%$ ($n_0 = 16$) and $0.29\%$ ($n_0 = 4$).

$N_0$, results not shown), since high selection intensity promotes the proliferation of favored lineages.

For item ii, Figure 1 shows that high values of $\alpha_{\text{obs}}$ led to important differences between observed and expected values of $\phi$, with $\phi_{\text{obs}} < \phi_{\text{exp}}$, although a good fit was obtained for intermediate $\alpha_{\text{obs}}$. Note that the simulations were implemented through general algorithms for nonrandom mating so that $\alpha_0$ was attained through multiple sources of nonrandomness rather than through full-sib mating alone, although since $N_i = N_0$ there were no half-sibs. For the lower extreme shown in Figure 1, with $\alpha_{\text{obs}} = 0$, $\phi_{\text{obs}} = 0$ although $\phi_{\text{exp}} = 0$. This should be expected for two reasons: in a small population the probability of a full-sib mating is not vanishingly small as is explicitly assumed in the result of Ghai (1969), and random allocation of males with two sexes will result in a marginally negative $\alpha_0$ (Robertson 1965), requiring some full-sib matings in compensation.

**Effects of nonrandom mating on the genetic (co)variances for the selected trait:** In this section, we describe the effects of nonrandom mating on the selected trait for (i) the genetic covariance among mates and (ii) the genetic variance. Simulated genetic covariance among mates is shown in Figure 2 for a range of $\alpha_{\text{obs}}$ and $h_0^2$ along with the respective neutral expectation under random selection (i.e., $h_0^2 = 0$). The values shown in Figure 2 are $\frac{1}{2}\text{cov}(A, A)/\sigma^2_{\text{obs}}$, since they have an expectation

$\phi$ versus $h_0^2$

**Figure 1.—** Relationship between the proportion of full-sib matings ($\phi$) and the initial heritability ($h_0^2$), for phenotypic selection with different values of $\alpha_{\text{obs}}$. The lines are predicted relationships using $\phi = 4\alpha_{\text{obs}}/(1 + 3\alpha_{\text{obs}})$, and the points are observations from simulated populations ($N = 32$, $n_0 = 16$). Predictions are: zero with $\alpha_{\text{obs}} = 0$; $-\infty$, $\alpha_{\text{obs}} = 0.24$; $-\infty$, $\alpha_{\text{obs}} = 0.06$. Simulations are: $\bigcirc$, $\alpha_{\text{obs}} = 0.24$; $\square$, $\alpha_{\text{obs}} = 0.06$; $\bigtriangledown$, $\alpha_{\text{obs}} = 0$.

**Figure 2.—** Relationship between the covariance between the breeding values of mates ($\text{cov}(A, A)$), scaled by $2\sigma^2_{\text{obs}}$, and $\alpha_{\text{obs}}$ for phenotypic selection with different initial heritabilities ($h_0^2$). The lines are predicted relationships using Equation 4, and the points are observations from simulated populations ($N = 32$, $n_0 = 4$). Predictions are: $-\infty$, $h_0^2 = 0$ (neutral theory); $-\infty$, $h_0^2 = 0.05$; $-\infty$, $h_0^2 = 0.2$; $-\infty$, $h_0^2 = 0.4$. Simulations are: $\bigcirc$, $h_0^2 = 0.05$; $\bigtriangledown$, $h_0^2 = 0.2$; $\square$, $h_0^2 = 0.4$. 

**TABLE 1**
Genetic Variance and Inbreeding
The predictions from Equation 5 tend to overpredict of selection is practiced in randomly mated populations. and its mate) is shown in Figure 5, measured by the CV of the sum of selective advantages of mating pairs and \( N \). Simulations are: ---, \( h_b^2 = 0 \) (neutral theory); ---, \( h_b^2 = 0.05; \) ---, \( h_b^2 = 0.2; \) ---, \( h_b^2 = 0.4 \). Simulations are: \( \circ \), \( h_b^2 = 0.05; \) \( \Delta \), \( h_b^2 = 0.2; \) \( \square \), \( h_b^2 = 0.4 \).

of \( \alpha_{\text{Ofix}} \) for neutral theory. The clear result is that directional selection reduces the covariance of mates from what is expected under neutral theory. Furthermore, this reduction is well predicted using Equation 4 and \( \phi = 4\alpha/(1 + 3\alpha) \) (with \( \alpha \) replaced by \( \alpha_{\text{Ofix}} \)). In the examples shown in Figure 2, the covariance among mates remains approximately linearly related to \( \alpha_{\text{Ofix}} \), but the slope of this relationship becomes lower as the heritability increased from 0 to 0.4. The application of Equation 4 with \( b_{\phi} = 0 \) also results in a lower covariance than that expected from neutral theory, but results in overestimates of the covariance; e.g., for \( h_b^2 = 0.40 \) and \( \alpha_{\text{Ofix}} = 0.18 \), the observed scaled value was 0.050, and Equation 4 predicts 0.082 and 0.057 with and without setting \( b_{\phi} = 0 \), respectively.

Given that the genetic covariance among mates contributes to the genetic variance under nonrandom mating, a reduction in the former component from that predicted by neutral theory will potentially result in a reduction in the latter. This is confirmed in Figure 3 with stochastic simulations and predictions using Equation 5. With selection, the genetic variance in the population can be lower with \( \alpha_{\text{Ofix}} > 0 \) than when comparable selection is practiced in randomly mated populations. The predictions from Equation 5 tend to overpredict the genetic variance by more than is expected from reductions due to finite sample size alone.

Effects of nonrandom mating on the expected gene flow: Figure 4 shows the relationship between the regression coefficient of long-term genetic contributions on the sum of selective advantages of mating pairs and \( \alpha_{\text{Ofix}} \). For a given \( \alpha_{\text{Ofix}} \), for all combinations of \( h_b^2 \) and \( n_0 \) studied, \( \beta \) increased as \( n_0 \) increased (and hence selection intensity) and decreased as \( h_b^2 \) increased. The relationship of \( \beta \) with \( h_b^2 \) and \( n_0 \) is fully consistent with the findings of Woolliams et al. (1999) for random mating.

It may be expected from neutral theory that increasing \( \alpha_{\text{Ofix}} \) would increase the regression on the selective advantage since selected offspring will be more likely to be mated to relatives, so reinforcing the strength or weakness of the inherited selective advantage, i.e., the mean parental breeding value, not only predicts the breeding value of its offspring but also predicts that of its offspring’s mate. This is clearly the case for low \( h_b^2 \); for example, for \( h_b^2 = 0.01 \) and \( n_0 = 16 \), as \( \alpha_{\text{Ofix}} \) increased from 0 to 0.24, \( \beta \) increased more than threefold in a linear relationship with \( \alpha_{\text{Ofix}} \). However, as \( h_b^2 \) increased, the slope of this relationship with \( \alpha_{\text{Ofix}} \) was substantially lower. For \( n_0 = 16 \) and \( h_b^2 = 0.99 \), no increase in \( \beta \) with \( \alpha_{\text{Ofix}} \) was observed (result not shown). This reduction in the slope of the relationship between \( \beta \) and \( \alpha_{\text{Ofix}} \) is directly related to the phenomenon displayed in Figure 2 concerning the covariance between mates as described above: when \( \alpha_{\text{Ofix}} \) and \( h_b^2 \) are large, the covariance is lower than that expected from neutral theory and the selective advantage is poorer than expected at predicting the selective advantage of the offspring’s mate.

The impact of the nonrandom mating on the expected gene flow conditional on the selective advantage (i.e., the sum of the breeding values of an individual and its mate) is shown in Figure 5, measured by the CV of \( \mu_\text{e} \) (see Equation 10). The values presented in Figure 5 use parameters in Equation 10 estimated from the simulations. For \( \alpha_{\text{Ofix}} = 0 \), it is clear that the impact of the selective advantage on gene flow is greatest when \( 0.4 < h_b^2 < 0.6 \), with close to 4-fold impact compared to \( h_b^2 = 0.01 \). The impact of the selective advantage is increased when \( \alpha_{\text{Ofix}} \) increases, but is more sensitive to changes in \( \alpha_{\text{Ofix}} \) when \( h_b^2 \) is low. Therefore, when \( \alpha_{\text{Ofix}} = 0.24 \), the maximum impact is close to \( h_b^2 = 0.2 \) and is only 1.5-fold greater compared to \( h_b^2 = 0.01 \).
Effect of nonrandom mating on predictions of $\Delta F$ and $\Delta G$ based on long-term genetic contributions: The effect of nonrandom mating on $\Delta F$ is shown in Figure 6 and Table 2 contrasts predictions using Equation 6 for two different selection intensities. The pattern of relationship between $\Delta F$ and $h_n^2$ and $\alpha_{\text{Ofix}}$ is very similar to Figure 5, in that the $h_n^2$ with the maximum $\Delta F$ becomes lower as $\alpha_{\text{Ofix}}$ increases, and $\Delta F$ increases very rapidly for small $h_n^2$ when $\alpha_{\text{Ofix}}$ is large.

Predictions of $\Delta F$ using Equation 6 are always underestimated the observed $\Delta F$; but this is expected by a fraction approximately equal to $2\Delta F$ (Woolliams and Bijma 2000). When this is accounted for (as in Table 2), the serious errors occur only when selection intensity and $\alpha_{\text{Ofix}}$ are high. The pattern of these errors is similar to the cases in Table 1, where $\alpha_s$ and $\alpha_r$ show serious discrepancies. The predictions shown use $\alpha_s$ in Equation 6, and not $\alpha_r$, since $\alpha_s$ provided more reliable predictions than $\alpha_r$. Where serious discrepancies occurred between the observed $\Delta F$ and $\Delta F$ predicted from Equation 6, the prediction error could be approximately halved (results not shown) by modifying Equation 6 to be $\Delta F = \frac{1}{2} \sum_f r_{f}^2 (1 - \alpha_{\text{Ofix}})$, so that each individual’s squared contribution was scaled by the individual’s own $\alpha_s$. This partially overcame the covariance that was described above between $\eta_4$ and $\alpha_{\text{Ofix}}$. Finally, predictions of $\Delta G$ (not shown) obtained from Equation 7 were accurate for most of the assessed cases, and often their errors were <5% within the range of parametric settings investigated.

DISCUSSION

This article has provided a novel model for predicting the impact of nonrandom mating on the covariance among mates of populations undergoing selection. Examination of the predictions obtained from this model showed that extrapolating expectations of genetic variance and covariance among mates for a neutral trait with nonrandom mating can be qualitatively wrong, with deviations toward severe overprediction. Deviations were largest when heritability and selection intensity were large and there was a strong preferential mating of relatives. While nonrandom mating had a considerable effect upon the impact of selective advantage for low heritability, as measured by the regression of genetic contributions on the selective advantage and the CV of the expected gene flow conditional on the selective advantage, the phenomenon described by the model substantially reduces this effect for moderate heritabilities. Furthermore, the study showed that high selection intensity can induce a negative covariance between the long-term genetic contribution of an ancestor and its $\alpha_s$, particularly when $\alpha_s$ is large, and suggested that selection acts to attenuate the strong preferential mating of relatives.

A logical starting point for interpreting the results of deviations from neutral expectations is the genetic covariance achieved among mates for a selected trait when nonrandom mating was practiced. Naively, the preferential mating of relatives would be expected to result in a clear positive genetic covariance among breeding values, since for a neutral trait this covariance has an expectation equal to $2\alpha_{\text{Ofix}} r_{f}^2$ (e.g., Caballero and Hill 1992), and this is also shown in our simulations for neutral traits, so provides a methodological validation for our study. However, the predictive model for the covariance among mates showed that inducing such a covariance by using pedigree information during selection will lead to a covariance of opposite sign between the genetic mean of an individual’s family and the Men-
TABLE 2
Simulated vs. predicted rates of inbreeding

<table>
<thead>
<tr>
<th>$h_0^2$ = 0.01</th>
<th>$h_0^2$ = 0.2</th>
<th>$h_0^2$ = 0.4</th>
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<tr>
<td>$n_0$</td>
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</tr>
<tr>
<td>4</td>
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<td>0.59</td>
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<td>1.50</td>
<td>12.9*</td>
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Simulated (Sim) rate of inbreeding ($\times 100$), together with prediction errors from using Equation 6, for phenotypic selection and $N = 32$, different target departures from Hardy-Weinberg proportions ($\alpha_{\text{Oins}}$), family sizes ($n_0$), and heritabilities ($h_0^2$) is shown. * indicates when the difference was > (5DF) × 100. Standard errors of Sim ($\times 100$) were < 0.01, except for $\alpha_{\text{Oins}} = 0.24$ where the standard errors were < 0.03. Prediction errors are expressed as a percentage of deviation (%Prd) = 100 × ([Sim − Prd]/Sim), where Prd comes from Equation 6.

delian sampling term of its mate. Therefore when there is a preferential mating, or avoidance, of relatives the induced covariance is offset by this opposing covariance, which can be substantial. This is in addition to another opposing effect that is directly analogous to Ghai (1980) by which the change in the Mendelian sampling variance with $\alpha$ has an impact on the replenishment of the genetic variation that is lost through selection in each generation.

The mechanism underlying this model was potentiated as the intensity of selection increased and as the heritability increased. In this article where the results presented have been concerned with selection upon phenotype, the heritability represented the squared accuracy of selection and, together with the value of $\alpha$, determined the split in information between the pedigree and the Mendelian sampling term (important in Equations 2, 3, and 5). In more general selection schemes the power of the mechanism would depend on the balance of pedigree information on a candidate and information on its Mendelian components and the use made of such information (e.g., within-family selection should not generate such a mechanism), rather than on the accuracy alone.

While the model provides an explanation of some of the results, it has some limitations. First, while its predictions are more credible than those based on neutral theory, the precision leaves some scope for believing that other mechanisms may be operating. Of greater significance is that the covariance between mates is estimated by assuming that the proportion of full-sib mating was that predicted by Ghai’s (1969) formula. The use of this formula has two problems: (i) it is limited to schemes with equal numbers of males and females since it cannot cope with nonrandomness coming from other sources such as preference/avoidance of half-sibs and (ii) the predictions provided by Ghai while broadly reliable were not without error. In the model, Ghai’s formula was used to translate the desired $\alpha$ to an expected covariance among the true family means of mates in the selected population; consequently, some improvement might arise from a more general approach to this relationship.

The reduction in covariance between mates arising with selection has direct consequences for the additive genetic variance and for the relationship between long-term genetic contributions and the selective advantage. Both are reduced below expectations based upon neutral theory. The impact on genetic variance is sufficient for the equilibrium genetic variance (i.e., where Mendelian sampling variance is not reduced each generation as inbreeding progresses) to be less for preferential mating of relatives than for random mating when $h_0^2$ is high, a qualitative difference. The regression of the long-term genetic contribution on the sum of the ancestral breeding value and the average of its mates would also be expected to increase under neutral theory, since this has a covariance not only with the offspring’s breeding value but also with that of the offspring’s mate. Note that this expectation arises from the nonrandom mating in the offspring generation, not the ancestors: in the ancestor’s generation the nonrandom mating is fully accounted for by regression on both parents. However, if the covariance between mates is reduced then so is the predictive value of the ancestor’s selective advantages.

The impact of $h_0^2$ on the CV of the expected gene flow is similar to the impact of $h_0^2$ on $\Delta F$ that was observed in this study and that of Santiago and Cabal-
lero (1995). This relationship shows a much greater sensitivity to nonrandom mating when the heritability is low than when it is either moderate or high. This can be explained by the behavior of the covariance between mates and its separate consequences for $\beta$ and $\sigma^2_\alpha$ as described, since changes in both parameters are responsive to changes with $\alpha$, when the heritability is low, but decrease in sensitivity as heritability increases. The similarity between $\text{CV}(\mu_r)$ and $\Delta F$ in their relationship with $\alpha$ may be anticipated since in Equation 6, which relates $\Delta F$ to squared contributions, the term $E[\Sigma \hat{r}^2]$ is equivalent to $E[\Sigma (\mu_r^2 + \sigma^2_\hat{r})]$, where $\mu_r$ and $\sigma^2_\hat{r}$ are the mean and variance of the contributions conditional upon the selective advantages. Woolliams and Bijma (2000) showed that $\sigma^2_\hat{r} \approx \mu_r^2$ for random mating, but an analogous relationship has not been established for nonrandom mating, although it has been established that $\sigma^2_\hat{r}$ will depend upon $\alpha$: avoidance of relatives reduces $\sigma^2_\hat{r}$ (e.g., Wang 1997), whereas preferential mating of relatives increases $\sigma^2_\hat{r}$ (e.g., Caballero and Hill 1992).

In conclusion, this study has described mechanisms that influence the covariance observed between mates for a trait that is subject to selection when mating is nonrandom. In particular, the covariance is substantially less than that expected from neutral theory, particularly when the heritability is moderate or high, and this has consequences for the observed additive genetic variance, the scale of expected gene flow that is directly attributable to the selective advantage, and $\Delta F$. The observed sensitivity to nonrandom mating of the latter two phenomena when heritability is low can be explained with reference to neutral theory, and the study shows that it is the lack of sensitivity for moderate to high heritabilities that required the development of theory.

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LITERATURE CITED


