

## SEX-LIMITED MUTATIONS AND THE EVOLUTION OF SEXUAL DIMORPHISM

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**Abstract.**—Although the developmental and genetic mechanisms underlying sex differences are being elucidated in great detail in a number of species, there remains a breach between proximate and evolutionary studies of sexual dimorphism. More precisely, the evolution of sex-limited gene expression at autosomal loci has not been well reasoned using either theoretical or empirical methods. Here, I show that a Mendelian genetic model including elementary details of sexual differentiation provides novel insight into the evolution of sex differences via sex limitation. This model indicates that the nature of allelic effects and the pattern of selection must be known in both sexes to predict the evolution of sex differences. That is, selection interacts with genetic variation for sexual dimorphism to produce unanticipated patterns of trait divergence or convergence between the sexes. Ultimately, this model may explain why previous models for the evolution of sexual dimorphism do not predict the erratic behavior of the sex difference during artificial selection experiments.

**Key words.**—Evolution, population genetics, selection, sex limitation, sexual dimorphism.

Received February 12, 1999. Accepted July 16, 1999.

Darwin proposed that sexual dimorphisms evolve when optimal phenotypes differ between the sexes (Darwin 1874). Yet, divergent evolution between the initially monomorphic sexes is constrained because homologous traits are controlled by the same genes in both sexes (Fisher 1958; Lande 1980). In other words, even when disruptive selection alters allele frequencies between the sexes in one generation, mating restores Hardy-Weinberg equilibrium in zygotes so that males and females again have the same initial allele frequencies (Haldane 1962). Thus, sexual reproduction (i.e., meiosis and syngamy) normally hinders adaptive divergent evolution between the sexes. This paradox has been resolved by the evolution of varied mechanisms of sexual differentiation, including genetic differences between the sexes and autosomal genes with sex-limited effects.

Theoretical models and empirical observations both indicate that genetic differences between the sexes evolve when alleles with antagonistic effects on the sexes accumulate in tight linkage with a new sex-determining gene (Bull 1983; Rice 1992). This process favors suppressed recombination near the sex-determining locus, which leads to genetic differentiation of males and females and the eventual evolution of sex chromosomes (Rice 1994, 1996). However, many genes that underlie sex differences are not sex linked, despite the occurrence of genotypic sex determination and sex chromosomes in diverse taxa (Bull 1983). The evolution of sex-limited (or sex-differential) effects at such loci remains poorly understood because of a general lack of fit between theory and reality. For example, Lande's (1980) quantitative genetic model does not predict, even qualitatively, the evolution of sexual size dimorphism in an extensive artificial selection experiment on *Drosophila melanogaster* (Reeve and Fairbairn 1996). Furthermore, the fit between data and theory was not significantly improved by altering essential aspects of the model (Lande 1980; Cheverud et al. 1985; Reeve and Fairbairn 1996). This lack of fit suggests that some other critical aspect of sexual dimorphism has been overlooked in these models for the evolution of sex differences.

In the model presented here, sex-specific allelic effects are defined for each locus and prove to be essential for under-

standing the evolutionary dynamics of sexual dimorphism. In contrast, the genetic parameters of heritability and genetic correlation in the quantitative genetic models (Lande 1980; Cheverud et al. 1985) do not explicitly address these critical details of gene action and expression. Consequently, the predictions from the population genetic model are more consistent with results from a number of artificial selection experiments than are the predictions from the quantitative genetic models.

In this paper, I develop a population genetic model for the evolution of sexual dimorphism via sex-limited effects at autosomal loci. This model is based on two well-defined traits that demonstrate genetic variation for sex limitation. Although it is unknown whether such genetic variation is typical of individual loci underlying other sexually dimorphic traits in nature, the model is a very general representation of the mechanisms underlying sex-limited gene expression. After illustrating how these sex-specific allelic effects determine sex-specific fitness, I derive recursion equations for allele frequency changes. Finally, I use this model to explore the effect of various patterns of sex-specific selection on the evolution of sexual dimorphism. The predictions of this model are discussed in the context of artificial selection experiments in which the selection regime and the response to selection have been reported for both sexes (Harrison 1953; Korkman 1957; Frankham 1968; Eisen and Hanrahan 1972; Rasmuson 1996; Reeve and Fairbairn 1996; Monteiro et al. 1997).

### MODEL

The particular mechanisms producing sex-limited gene expression vary among as well as within species (Jost 1953; Hodgkin 1990; Cline and Meyer 1996; Goy 1996). However, in general, sexual differentiation simply entails the activation or repression of different genes in females and in males. For example, there are three major alleles of the sex-limited protein in congeneric strains of mice: one allele displays null expression in both sexes, another allele is constitutively expressed in both sexes, and a third allele is androgen-depend-

dent and therefore only expressed in males (Stavenhagen and Robins 1988; Nelson and Robins 1997). Likewise, three major alleles at one autosomal locus control horn development in domestic sheep: one allele causes polledness (lack of horns) in both sexes and is incompletely dominant to the following two alleles, a wild-type allele produces horns in both sexes, and a third allele is androgen dependent and causes horn development in males (Montgomery et al. 1996). Female-limited gene expression in vertebrates involves similar, but estrogen-dependent, gene activation. To represent these possibilities, I hypothesize three different alleles occurring at a single, autosomal locus,  $A$ : the  $A_1$  allele is not expressed in either sex, the  $A_2$  allele is expressed in both sexes, and the  $A_3$  allele is expressed in females only (a perfectly analogous model can be used to simulate the evolution of male-limited effects). The frequencies of the three alleles at the start of generation  $N$  are represented by  $p$ ,  $q$ , and  $r$ , respectively. I further assume an infinitely large and random mating population with discrete generations and no mutation or migration. With these assumptions, the frequencies of the six possible genotypes are given by the terms in the expansion  $(p + q + r)^2$  and they sum to one (see Table 1).

In Table 1, relative sex-specific fitness (i.e.,  $W_{CSEX}$ ) for each of the six genotypes derives from the total count of alleles ( $C = 0, 1$ , or  $2$ ) expressed in each sex ( $M =$  male,  $F =$  female). For example, fitness for the  $A_1A_1$  genotype in females is  $W_{0F}$  because no alleles are expressed in these females. Fitness for the  $A_1A_2$  and  $A_1A_3$  genotypes in females is  $W_{1F}$  because one allele (either  $A_2$  or  $A_3$ ) is expressed in these females. Fitness for the  $A_2A_2$ ,  $A_2A_3$ , and  $A_3A_3$  genotypes in females is  $W_{2F}$  because two alleles (both  $A_2$  and  $A_3$ ) are expressed in these females. Male fitness also depends on the number of alleles expressed for each genotype. However, fitness for the  $A_1A_1$ ,  $A_1A_3$ , and  $A_3A_3$  genotypes in males is  $W_{0M}$  because no alleles are expressed in these males. Fitness for the  $A_1A_2$  and  $A_2A_3$  genotypes in males is  $W_{1M}$  because one allele ( $A_2$ ) is expressed in these males. Finally, fitness for the  $A_2A_2$  genotype in males is  $W_{2M}$  because two alleles are expressed in these males. Mean fitness for each sex ( $W_F$  and  $W_M$ ) is then calculated as the sum of sex-specific genotypic fitness multiplied by the frequency of that genotype:

$$W_F = (W_{0F})p^2 + (W_{1F})2pq + (W_{1F})2pr + (W_{2F})q^2 + (W_{2F})2qr + (W_{2F})r^2 \quad (1)$$

and

$$W_M = (W_{0M})p^2 + (W_{1M})2pq + (W_{0M})2pr + (W_{2M})q^2 + (W_{1M})2qr + (W_{0M})r^2. \quad (2)$$

From these equations, the sex difference in mean fitness ( $W_F - W_M$ ) is equation (1) minus (2):

$$W_F - W_M = [(W_{0F})p^2 - (W_{0M})p^2] + [(W_{1F})2pq - (W_{1M})2pq] + [(W_{2F})q^2 - (W_{2M})q^2] + [(W_{1F})2pr - (W_{0M})2pr] + [(W_{2F})2qr - (W_{1M})2qr] + [(W_{2F})r^2 - (W_{0M})r^2]. \quad (3)$$

When the sex difference in mean fitness is partitioned as

shown in equation (3), it is clear that sex differences in mean fitness can arise from two sources. In the first category (i.e., the first three terms) are fitness differences for the same pattern of gene expression, like  $[(W_{0F})p^2 - (W_{0M})p^2]$  for genotype  $A_1A_1$ . In the second category (i.e., second three terms) are fitness differences for different patterns of gene expression, like  $[(W_{1F})2pr - (W_{0M})2pr]$  for genotype  $A_1A_3$ .

Although genotype frequencies are the same in both sexes at the start of generation  $N$  (Table 1), sex-specific selection changes the frequency of genotypes that contribute gametes to the next generation (see eqs. 1 and 2). Allele frequencies in eggs, that is,  $p_e$ ,  $q_e$ , and  $r_e$ , (or sperm, i.e.,  $p_s$ ,  $q_s$ , and  $r_s$ ) are calculated as the marginal fitness of  $A_1$ ,  $A_2$ , or  $A_3$  alleles in females (or males) weighted by  $p$ ,  $q$ , or  $r$ , divided by mean female fitness  $W_F$  (or male fitness  $W_M$ ) (Table 1). As such, fitness in this model is a composite of all modes of selection from birth to death. Initial genotype frequencies in generation  $N + 1$  are then obtained by cross-multiplication using the frequency of  $A_1$ ,  $A_2$ , and  $A_3$  alleles that are contributed through eggs and sperm. Thus, initial allele frequencies in generation  $N + 1$  are calculated as:

$$p' = p_s p_e + 1/2(p_s q_e) + 1/2(p_e q_s) + 1/2(p_s r_e) + 1/2(p_e r_s), \quad (4)$$

$$q' = q_s q_e + 1/2(p_s q_e) + 1/2(p_e q_s) + 1/2(q_s r_e) + 1/2(q_e r_s), \quad (5)$$

$$r' = 1 - p' - q'. \quad (6)$$

Allele frequencies are once more the same in male and female zygotes of generation  $N + 1$  because the locus is autosomal. Recursion equations for allele frequencies are simply  $\Delta p = p' - p$ ,  $\Delta q = q' - q$ , and  $\Delta r = 1 - \Delta p - \Delta q$ . Substituting equations (4) and (5) for  $p'$  and  $q'$  in the recursion equations, one obtains:

$$\Delta p = p_s p_e + 1/2(p_s q_e) + 1/2(p_e q_s) + 1/2(p_s r_e) + 1/2(p_e r_s) - p \quad (7)$$

and

$$\Delta q = q_s q_e + 1/2(p_s q_e) + 1/2(p_e q_s) + 1/2(q_s r_e) + 1/2(q_e r_s) - q. \quad (8)$$

Setting  $r_e = 1 - p_e - q_e$  and  $r_s = 1 - p_s - q_s$  from Table 1 and simplifying, one obtains:

$$\Delta p = 1/2p_s + 1/2p_e - p \quad (9)$$

and

$$\Delta q = 1/2q_s + 1/2q_e - q. \quad (10)$$

Substituting equations (9) and (10) for  $\Delta p$  and  $\Delta q$ , one obtains:

$$\Delta r = 1 - 1/2p_s - 1/2p_e + p - 1/2q_s - 1/2q_e + q. \quad (11)$$

Equilibrium allele frequencies can be derived by setting changes in allele frequencies of  $p$  and  $q$  to zero; substituting equations from Table 1 for  $p_e$ ,  $q_e$ ,  $p_s$ , and  $q_s$ ; setting  $r = 1 - p - q$ ; and solving simultaneous equations for  $\hat{p}$  and  $\hat{q}$

TABLE 1. Genotypes and their sex-specific fitness, genotype frequencies in males and females before selection conform to Hardy-Weinberg expectations, and allele frequencies in eggs (e) and sperm (s) as a result of sex-specific selection.

Generation	Females						Males						
N Genotype	$A_1A_1$	$A_1A_2$	$A_1A_3$	$A_2A_2$	$A_2A_3$	$A_3A_3$	$A_1A_1$	$A_1A_2$	$A_1A_3$	$A_2A_2$	$A_2A_3$	$A_3A_3$	
Relative sex-specific fitness	$W_{0F}$			$W_{1F}$			$W_{0M}$			$W_{1M}$			
Genotype frequencies	$p^2 + 2pq + 2pr + q^2 + 2qr + r^2$						$p^2 + 2pq + 2pr + q^2 + 2qr + r^2$						= 1
<i>Allele frequencies in gametes</i>	Eggs						Sperm						
	$p_e = \frac{(W_{0F})p^2 + 1/2(W_{1F})(2pq + 2pr)}{W_F}$						$p_s = \frac{(W_{0M})p^2 + 1/2(W_{1M})(2pq) + 1/2(W_{0M})(2pr)}{W_M}$						
	$q_e = \frac{(W_{2F})q^2 + 1/2(W_{1F})(2pq) + 1/2(W_{2F})(2qr)}{W_F}$						$q_s = \frac{(W_{2M})q^2 + 1/2(W_{1M})(2pq + 2qr)}{W_M}$						
	$r_e = 1 - p_e - q_e$						$r_s = 1 - p_s - q_s$						

and finally  $\hat{r} = 1 - \hat{p} - \hat{q}$ . After some tedious algebra, it was determined that equilibrium allele frequencies are a complex function of sex-specific selection *and* the presence of other alleles at the same locus (results not shown). Thus, I use Wright's adaptive landscape to illustrate mean population fitness as a function of different patterns of sex-specific selection and different allele frequencies (Wright 1932). I use the product of the sex-specific mean fitnesses (i.e.,  $W = W_F \times W_M$ ) as the measure of mean population fitness because it is the denominator for all terms on the right hand side of equations (4), (5), and (6). Consequently, this product ( $W_F \times W_M$ ) is analogous to mean population fitness ( $W$ ) in the standard equations for  $p'$ ,  $q'$ , and  $r'$ . I consider eight distinct patterns of sex-specific selection in Figure 1. To facilitate comparison of model predictions with empirical results, these patterns of selection are the same as those found in various artificial selection experiments.

## RESULTS

In general, the adaptive topographies and equilibria in Figure 1 indicate that the sex-limited allele (and sexual dimorphism) increases in frequency when the pattern of sex-specific selection is coincident with the pattern of sex-limited gene expression in at least one sex. In Figure 1A, sexual dimorphism increases because selection is coincident with the pattern of sex-limited gene expression in both sexes (i.e., selection up on females and down on males favors an allele that is expressed only in females). In contrast, in Figure 1B, sexual dimorphism decreases because selection is against the pattern of sex-limited gene expression in both sexes. In Figures 1C and 1D, sexual dimorphism can either increase or decrease with identical selection on both sexes. However, the specific result depends on both the pattern of selection and the nature of the genetic variation present in the population (see discussion below). Single sex selection can also increase or decrease sexual dimorphism, but the result depends upon the pattern of sex-specific selection. Sexual dimorphism increases with selection up in females (Fig. 1E) and selection down in males (Fig. 1H) because sex-specific selection is coincident with the pattern of sex-limited gene expression. Conversely, sexual dimorphism decreases with selection

down in females (Fig. 1F) and selection up in males (Fig. 1G) because selection is against the pattern of sex-limited gene expression. I now present a more detailed description of the model predictions along with results from selection experiments in which both sex-specific selection and the sex-specific response to selection were reported.

With selection up on females and down on males, the sex-limited  $A_3$  allele increases in frequency toward fixation and an adaptive peak (+ in Fig. 1A). The  $A_1$  and  $A_2$  alleles decrease in frequency and are eliminated. When the sex-limited allele is absent, however, there is a saddle point (S in Fig. 1A) with the  $A_1$  and  $A_2$  alleles held in a balanced polymorphism, as described earlier by Haldane (1962). Trivial, nonstable equilibria occur when  $A_1$  or  $A_2$  are fixed (- in Fig. 1A). However, divergent selection equal in magnitude but opposite in direction decreases the frequency of the sex-limited  $A_3$  allele, but increases the frequency of the  $A_1$  and  $A_2$  alleles toward an adaptive peak (+ in Fig. 1B). Again, divergent selection between the sexes, in the absence of suitable genetic variation for sexual dimorphism, maintains a balanced polymorphism (Haldane 1962). Saddle points occur when either the  $A_1$  or the  $A_2$  allele is missing (S in Fig. 1B). A trivial, nonstable equilibrium occurs when the sex-limited  $A_3$  allele is fixed (- in Fig. 1B). These findings suggest that empirical results are variable when the sexes experienced opposing selection because of differences in the nature of genetic variation for sexual dimorphism. Whereas selection for both increased and decreased sexual dimorphism has been successful in some studies (Korkman 1957; Frankham 1968; Eisen and Hanrahan 1972), one study found that selection for enhanced dimorphism was unsuccessful and that selection for decreased dimorphism was effective and actually reversed the normal pattern of sexual dimorphism (Harrison 1953). In yet another experiment, the sex difference increased slightly with one pattern of selection and was reversed with the opposite pattern (Rasmuson 1996).

Identical selection on the sexes can also increase sexual dimorphism, but only when there is a lack of additive genetic variation for the trait. Specifically, the frequency of the sex-limited  $A_3$  allele increases when the  $A_1$  or  $A_2$  allele is missing (S in Figs. 1C,D). This result depends on not only which

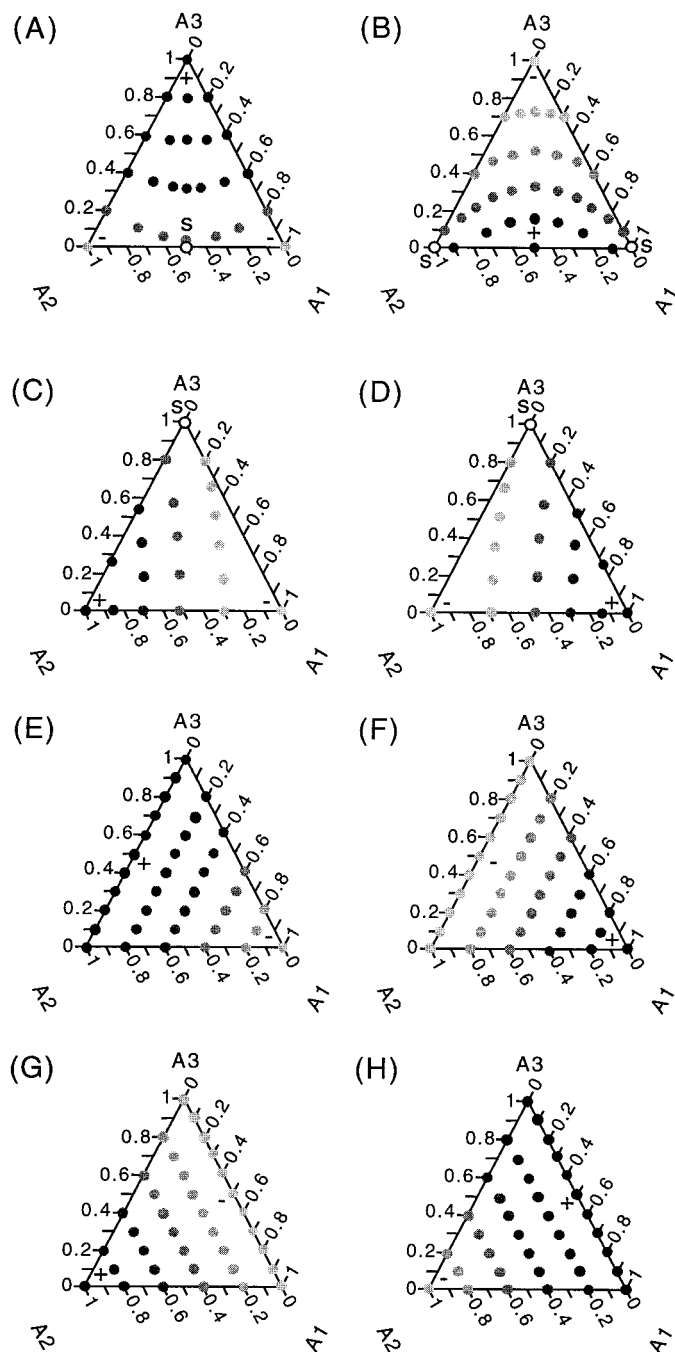


FIG. 1. Ternary plots showing mean population fitness (i.e.,  $W = W_F W_M$ ) as a function of different patterns of sex-specific selection and different allele frequencies. Symbols with the same shading are on contour lines of the adaptive topography at intervals representing 20% of maximum fitness. Within each panel, mean population fitness increases with progressively darker symbols, adaptive peaks are represented by +, saddle points are represented by -, and unstable equilibria are represented by S. Additional symbols in panels A–D represent saddle points that fall between 20% fitness intervals; these extra symbols are shown as open circles. (A) Selection up on females ( $W_{OF} = 0.5$ ,  $W_{IF} = 1$ , and  $W_{2F} = 1.5$ ) and down on males ( $W_{OM} = 1.5$ ,  $W_{1M} = 1$ , and  $W_{2M} = 0.5$ ), (B) selection down on females ( $W_{OF} = 1.5$ ,  $W_{IF} = 1$ , and  $W_{2F} = 0.5$ ) and up on males ( $W_{OM} = 0.5$ ,  $W_{1M} = 1$ , and  $W_{2M} = 1.5$ ), (C) selection up on females ( $W_{OF} = 0.5$ ,  $W_{IF} = 1$ , and  $W_{2F} = 1.5$ ) and up on males ( $W_{OM} = 0.5$ ,  $W_{1M} = 1$ , and  $W_{2M} = 1.5$ ), (D) selection down on females ( $W_{OF} = 1.5$ ,  $W_{IF} = 1$ , and  $W_{2F} = 0.5$ ) and down on males ( $W_{OM} = 1.5$ ,  $W_{1M} = 1$ , and  $W_{2M} = 0.5$ ) and no selection on males ( $W_{OM} = 1$ ,  $W_{1M} = 1$ , and  $W_{2M} = 1$ ), (E) selection up on females ( $W_{OF} = 0.5$ ,  $W_{IF} = 1$ , and  $W_{2F} = 1.5$ ) and no selection on males ( $W_{OM} = 1$ ,  $W_{1M} = 1$ , and  $W_{2M} = 1$ ), (F) selection down on females ( $W_{OF} = 1.5$ ,  $W_{IF} = 1$ , and  $W_{2F} = 0.5$ ) and no selection on males ( $W_{OM} = 1$ ,  $W_{1M} = 1$ , and  $W_{2M} = 1$ ), (G) no selection on females ( $W_{OF} = 1$ ,  $W_{IF} = 1$ , and  $W_{2F} = 1$ ) and selection up on males ( $W_{OM} = 0.5$ ,  $W_{1M} = 1$ , and  $W_{2M} = 1.5$ ), (H) no selection on females ( $W_{OF} = 1$ ,  $W_{IF} = 1$ , and  $W_{2F} = 1$ ) and selection down on males ( $W_{OM} = 1.5$ ,  $W_{1M} = 1$ , and  $W_{2M} = 0.5$ ).

allele coexists with the sex-limited allele, but also the direction of selection (contrast the trivial, nonstable equilibria: in Figs. 1C,D). Thus, sexual dimorphism increases with selection in one direction and decreases with selection in the other direction, given a particular pair of alleles. However, sexual dimorphism decreases when all three alleles are present: the  $A_2$  allele increases in frequency with selection up (+ in Fig. 1C), whereas the  $A_1$  allele increases in frequency with selection down (+ in Fig. 1D). In this case, sexual dimorphism decreases regardless of the direction of selection. Like the model predicts, experiments in which the sexes have been selected in the same direction have produced variable results. Whereas the sex difference has increased with selection in one direction and decreased with selection in the other direction in some studies (Monteiro et al. 1997; also see Reeve and Fairbairn 1996 and references therein), sexual dimorphism has also been observed to decrease with selection in both directions (see Reeve and Fairbairn 1996 and references therein).

Single-sex selection can also increase or decrease sexual dimorphism. With selection up on females and no selection on males, selection does not discriminate between the  $A_2$  and  $A_3$  alleles because they have the same phenotypic effect in females (i.e., the marginal fitness of the two alleles is equivalent). Thus, both alleles increase in frequency at the same rate, which results in a globally stable, neutral equilibrium between the  $A_2$  and the  $A_3$  alleles (+ in Fig. 1E). Although the difference between average male and average female phenotypes increases with this pattern of selection, there is no net increase in sexual dimorphism as measured by the ratio of female to male phenotype. If the sex with the “larger” phenotype is already near its genetic limit for an increase in gene expression (i.e., the  $A_1$  allele is at a low frequency), we would not expect much response to selection in that sex and little change in sexual dimorphism because there is a neutral equilibrium between the  $A_2$  and  $A_3$  alleles. This is just the response observed for body size (Reeve and Fairbairn 1996) and bristle number (Harrison 1953) dimorphism in *Drosophila*. In contrast, sexual dimorphism decreases if we select down on females and impose no selection on males. With this pattern of selection, the  $A_1$  allele increases in frequency toward fixation and an adaptive peak (+ in Fig. 1F) and the frequencies of the sex-limited  $A_3$  allele and the  $A_2$  allele decrease because they are both at a disadvantage in females. Thus, sexual dimorphism decreases, as observed for body size (Reeve and Fairbairn 1996) and bristle number (Harrison 1953) dimorphism in *Drosophila*. When the  $A_1$  allele is missing, however, the sex-limited  $A_3$  allele and the  $A_2$  allele can

coexist in an unstable, neutral equilibrium with no change in dimorphism (– in Fig. 1F).

With selection up on males and no selection on females, the frequency of the  $A_2$  allele increases toward fixation and an adaptive peak because only this allele contributes to trait expression in males (+ in Fig. 1G). The sex-limited  $A_3$  allele and the  $A_1$  allele both decrease in frequency because they are disfavored in males. Such a decrease in sexual dimorphism with single-sex selection has been observed in some experiments (Harrison 1953; Reeve and Fairbairn 1996). The sex-limited  $A_3$  allele and the  $A_1$  allele may coexist in an unstable, neutral equilibrium when the  $A_2$  allele is absent (– in Fig. 1G). If we select down on males and impose no selection on females, sexual dimorphism increases because the sex-limited  $A_3$  allele increases in frequency. In contrast to this prediction, sexual dimorphism for body size decreased slightly in an artificial selection experiment on *Drosophila* (Reeve and Fairbairn 1996). A potential explanation for this result is that selection does not discriminate between the  $A_1$  and  $A_3$  alleles (i.e., the marginal fitness of the two alleles is equivalent). Thus, if these alleles are already at a high frequency in the population, there is a globally stable, neutral equilibrium between  $A_1$  and  $A_3$  (+ in Fig. 1H) and no increase in sexual dimorphism.

#### DISCUSSION

The population genetics model developed here was used to examine the conditions that favor the evolution of sexual dimorphism via sex-limited mutations. In general, the model shows that sexual dimorphism increases when the pattern of sex-specific selection is coincident with the pattern of sex-limited expression in at least one sex. In certain cases, however, this result also depends on the type of genetic variation that is present at the relevant locus. This model not only corroborates earlier studies, but also makes some novel predictions for the evolution of sexual dimorphism.

For instance, the model predicts that a stable polymorphism is maintained when there is sexually antagonistic selection and no genetic variation for sexual dimorphism (i.e., when the sex-limited allele is absent). In essence, this finding confirms Haldane's biallelic model in which he examined the maintenance of genetic polymorphism at autosomal loci by opposing selection on the sexes (Haldane 1962). Not surprisingly, the addition of a sex-limited allele to this model also confirms Fisher's (1958) verbal model for the evolution of sex-limitation. The allele with sex-limited effects increases disproportionately in frequency and becomes fixed when divergent selection on the sexes is in the same direction as the sex difference in allelic expression. However, the sex-limited allele is rapidly eliminated if divergent selection is in the opposite direction.

There are also some unexpected predictions for the evolution of sex-limitation. For example, Fisher (1958) reasoned that sex-limitation would only evolve when "the selective agencies acting on the two sexes oppose each others influence." Yet, the formal model presented here predicts that a sex-limited allele can also increase in frequency under various other patterns of selection. The sex-limited allele can increase in frequency and become fixed with identical selec-

tion on the sexes, but only when additive genetic variation is absent and selection is in a particular direction (see Figs. 1C,D). In addition, selection up on the larger sex, in the absence of selection in the smaller sex, can increase the frequency of the sex-limited allele (see Fig. 1E). Although the latter scenario is not dependent on genetic constraints, increased sexual dimorphism is isometric with average size for this pattern of selection, which could explain isometric increases in sexual dimorphism as a result of increasing body size while controlling for phylogenetic effects (Harrison 1953; Cheverud et al. 1985). Sexual dimorphism can also increase when selection favors a smaller trait value in the smaller sex and there is no selection in the other sex (see Fig. 1H).

Collectively, these results indicate that the pattern of male- and female-specific selection interacts with standing genetic variation to produce unanticipated patterns of trait divergence or convergence between the sexes. Indeed, such interactions between sex-specific selection and the genetic constitution of a population may explain the inconsistent behavior of sexual dimorphism during artificial selection experiments (Harrison 1953; Korkman 1957; Frankham 1968; Eisen and Hanrahan 1972; Rasmuson 1996; Reeve and Fairbairn 1996; Monteiro et al. 1997). Although this explanation is plausible, it remains to be determined if the type of genetic variation hypothesized in this model is typical of sexually dimorphic traits in nature. Despite this caveat, the model is based on real traits with similar allelic effects and a simple pattern of Mendelian inheritance. Consequently, the model is the first to make the mechanism(s) underlying sex differences explicit, thereby illustrating how selection interacts with available genetic variation to influence the evolution of sexual dimorphism. Importantly, this finding casts doubt on the notion that sexually exaggerated traits evolve simply as a result of directional selection on one sex while neglecting (or assuming antagonistic) selection in the other sex.

Many studies of sexual selection also ignore or make assumptions about the genetic basis of sexual dimorphism. In fact, a central assumption of previous quantitative genetic models is that a character is affected by several autosomal genes, with many alleles per locus, which produces a normal distribution of breeding values in males and females. These effects are represented by independent heritability parameters for males and females and by the correlation between additive effects of autosomal genotypes when expressed in males and females. In reality, however, genetic variation for sexual dimorphism is directional in nature and is not normally distributed. To illustrate, realized heritability for increased female size was less than that for decreased female size while male heritability was symmetric in *D. melanogaster* when only one sex was selected (Reeve and Fairbairn 1996). Similar, but male-specific, asymmetric heritability was observed in an artificial selection experiment on sexually dimorphic butterfly eyespots (Monteiro et al. 1997). These results presumably reflect the presence of female-limited and male-limited alleles (and alleles that are similarly expressed in both sexes) in the fruit fly and the butterfly, respectively. However, this information is only evident after selection experiments were completed and was not included in quantitative genetics models a priori. Such results suggest that the underlying ge-

netic architecture of sexual dimorphism is not adequately represented by the standard quantitative genetic parameters.

It will also be important to explore the evolutionary consequences of different modes of gene action. Dominance relationships vary among three autosomal alleles (one allele has androgen-dependent, sex-limited effects) that control horn development in male and female sheep (Montgomery et al. 1996). Interestingly, the effect of alleles at the horn locus can be modified by alleles at another autosomal locus, leading the way to modeling of more complex (i.e., polygenic) sexually dimorphic traits. Although such gene interactions are fundamental to both genetic (Hodgkin 1990; Cline and Meyer 1996) and hormonal (Jost 1953; Goy 1996) mechanisms of sexual differentiation and may be important to consider during the evolution of quantitative traits (Fenster et al. 1997), sex-influenced epistasis (Long et al. 1995; Montgomery et al. 1996) has been completely ignored in genetic models for the evolution of sexual dimorphism (Lande 1980; Cheverud et al. 1985; this study). Thus, extension of the model presented in this paper to sexually dimorphic traits with a polygenic basis appears essential and practical, if alleles at different loci have effects similar to those described above. This is a promising avenue for future work, considering recent advances in the genetic dissection of complex traits (Lander and Shork 1994), the identification of sex-specific quantitative trait loci (Long et al. 1995; Clark et al. 1996; Mackay et al. 1996; Melo et al. 1996; Mogil et al. 1997; Nuzhdin et al. 1997; Gurganus et al. 1998), and the elucidation of molecular mechanisms that produce sex-limited (or sex-differential) gene expression (Hodgkin 1990; Cline and Meyer 1996; Horowitz et al. 1996; Nelson and Robins 1997).

These breakthroughs in molecular genetics, in conjunction with the main finding of the current paper, provide insight into a crucial factor that has been overlooked in previous models for the evolution of sexual dimorphism. Specifically, it is critical to know the nature of individual allelic effects (i.e., the direction of sex-limited effects and the frequency of alleles) to accurately predict divergent (or convergent) evolution between the sexes. Quantitative genetic models do not specify these effects in their genetic parameters (Lande 1980; Cheverud et al. 1985). Similarly, empirical estimates of heritability within and genetic correlations between the sexes provide few, if any, inferences about the mechanisms underlying trait development (Hartl 1988). Thus, assumptions concerning the inheritance of quantitative traits may account for the mediocre predictive power of previous models, even when genetic parameters are accurately estimated (Reeve and Fairbairn 1996). Although sex chromosome mutations and sex-limited mutations on the autosomes (Mackay et al. 1992) may allow sexual dimorphism to evolve relatively freely over much longer periods of time (Wright 1993; Fry et al. 1995), the rate of such mutations remains virtually unknown. Consequently, the evolution of sexual dimorphism may be constrained, even when the genetic correlation between the sexes is less than perfect. In a remarkable example of this point, selection on a female sex-limited character produced a correlated evolutionary response in a male sex-limited character (Land 1973; Diamond 1986). These observations, along with the theoretical predictions of the new model presented here, have important implications for results from

models of sexual selection, most of which disregard pleiotropy between the sexes by assuming sex-limited trait expression (see Lande 1981; Kirkpatrick 1986; Pomiankowski and Iwasa 1998).

#### ACKNOWLEDGMENTS

I am grateful to M. Kirkpatrick for useful suggestions during the development of this model. I also thank J. J. Bull, D. Hall, M. Ryan, M. Wade, and an anonymous reviewer for helpful comments on the manuscript.

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Corresponding Editor: A. Caballero