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12 **Evolvability, Sexual Selection, and Mating Strategies**

Jacqueline L. Sztepanacz, Josselin Clo, and Øystein H. Opedal

This chapter considers how variation in mating systems affects evolvability in populations and how we should estimate it. Most models considered in evolutionary quantitative genetics assume random mating and identical evolvability across sexes. In this chapter, we discuss some ways in which variation in mating systems leads to a violation of these assumptions, and what this means for evolvability. We focus on two major axes of mating system variation: variation in outcrossing rate and variation in reproductive success. We present population and quantitative genetic theory specific to mating systems and review the empirical evidence to support the hypotheses put forth.

12.1 Introduction

Biologists have long been fascinated by the remarkably diverse sexual and mating systems of both plants and animals, especially since Darwin (1871, 1876). In plants, mating systems are highly variable and range from functional asexuality to obligate outcrossing enforced by genetic self-incompatibility systems (Stebbins 1974). A prominent axis of variation in plant mating systems is the outcrossing rate, or the proportion of offspring resulting from mating between genetically distinct individuals (Goodwillie et al. 2005; Moeller et al. 2017). In animals, most species have two distinct sexes and reproduce through obligate outcrossing. Mixed mating systems do occur in some hermaphroditic species, such as certain snails (Jarne and Charlesworth 1993) and nematodes (Picard et al. 2021), but are rarer than in plants. The lack of diversity in outcrossing rate for animal systems compared to plants is well compensated by the diversity of mating strategies and behaviors. The prominent axis of variation in animal mating systems is variation in the reproductive behaviors and success among males and females (Bateman 1948).

Most models considered in evolutionary quantitative genetics (see Hansen, chapter 5)¹ assume random mating and identical evolvability across sexes. In this chapter, we discuss some ways in which variation in mating systems leads to a violation of these assumptions and what this means for evolvability. Through our discussion, we aim to answer the following questions:

1. Is there a universal measuring stick for evolvability that applies meaningfully across mating systems?

1. References to chapter numbers in the text are to chapters in this volume.

2. Does selfing reduce evolvability?
3. Are males and females equally evolvable?
4. Is the heterogametic sex more evolvable than the homogametic sex?
5. How do cross-sex covariances redistribute genetic variation and evolvability?
6. Does sexual selection reduce the effective size of populations and thus impact short-term evolvability?

12.2 Evolvability Defined for Mating Systems

Any measure of evolvability derives its relevance from the theoretical context in which it will function (Houle and Pélabon, chapter 6). Our focus in this chapter is on the evolvability of quantitative traits in populations, *under* directional selection, *over* timescales of tens of generations. While we might expect this constant set of conditions to engender a single best measurement stick for evolvability, as we will see, the same conditions in different mating systems are likely to necessitate different measures.

Under these conditions, the heritable component of phenotypic variation in a population, the additive genetic variance, determines the response to selection, or evolvability, of that population (see Hansen, chapter 5). This is shown by the Lande equation, $\Delta\bar{z} = \sigma_A^2 \beta$, where the predicted response to selection in trait mean ($\Delta\bar{z}$) is equal to the additive genetic variance in the trait (σ_A^2) multiplied by the strength of selection on that trait (β) (Lande 1979). The *under* conditions represented by β implicitly read “under directional selection acting on a randomly mating population,” which may have to be modified under different mating systems. Given the diversity of mating systems across plants and animals, we must also consider whether σ_A^2 will be representative of the true capacity for traits to evolve in a given mating system. In particular, σ_A^2 may not always reflect the genetic variance that would allow a response to selection, and sex-averaged or population-level estimates of σ_A^2 may not capture genetic variation that is entangled between the sexes as a consequence of their largely shared genome. For these reasons, the interpretation of σ_A^2 as a measure of evolvability may differ, depending on the mating system of the population under study.

For additive variance to be a useful measure of evolvability, it also must be scaled in a meaningful way that we can benchmark against a prediction and compare across traits or across populations. The most common scaling of additive variance is heritability (h^2), σ_A^2 as a proportion of total phenotypic variance (σ_P^2). As highlighted by Houle (1992), h^2 is a unitless quantity, but it cannot be meaningfully interpreted or compared without knowing the standard deviation of the trait in the focal population(s). Indeed, due to the strong positive correlations between additive-genetic, nonadditive, and environmental variance components, heritabilities are poorly correlated with the additive genetic variance (Hansen et al. 2011) and thus may be a questionable measuring stick for evolvability in many circumstances. The widespread use of h^2 as a currency of evolutionary potential may be particularly problematic when comparing inbred and outcrossing species (Charlesworth and Charlesworth 1995). Heritabilities confound differences in genetic variance with differences in environmental variance, and for a fixed environmental variance, h^2 scales nonlinearly with increasing σ_A^2 . Genetic variances are expected to decrease under inbreeding, while environmental variances

may increase due to reduced developmental stability of inbred individuals (Fowler and Whitlock 1999; Kelly and Arathi 2003; Noel et al. 2017). Comparing h^2 between the sexes may also be problematic, because males and females can have different environmental variances for the same trait (Wyman and Rowe 2014).

Houle (1992) proposed mean-scaled additive variance as a comparative measure of evolvability, which can be expressed as (Hansen et al. 2003):

$$e = \frac{\sigma_A^2}{\bar{z}^2}, \quad (1)$$

where σ_A^2 is the additive variance, and \bar{z} is the trait mean. This standardization has since been adopted as a predominant metric of evolvability used in quantitative genetics when the trait mean of interest has a meaningful and nonzero value. Evolvability, when quantified in this way, can be interpreted as the proportional change in the trait mean per generation when selection on the trait is as strong as selection on fitness (Hansen et al. 2003, 2011). Comparisons of heritabilities and evolvability for over a thousand published estimates showed no correlation between the two measures (Houle 1992; Hansen et al. 2011), highlighting the importance of choosing a meaningful measure to quantify evolvability. Although heritabilities and evolvabilities may be more closely correlated within specific groups of homogeneous traits, such as livestock (Hoffmann et al. 2016), reanalyses of these data found that correlations are generally less than 0.5 and explain less than 8% of the variation in evolvability (Hansen and Pélabon 2021). Instead of a measuring stick for evolutionary potential, heritability may be better viewed as an indicator of the reliability of estimated breeding values in a population.

12.3 The Effect of Outcrossing Rate on Evolvability

In his influential series of papers on systems of mating, Sewall Wright (1921a–d) laid the foundation for much of the population-genetic theory related to mating systems (see Hill 1996 for a historical perspective). In the classic model of Wright (1921b, 1952), assuming no mutation and no selection on a focal quantitative trait, the genetic variance among groups of inbred individuals increases by a factor of $1+f$, where f is the proportional decrease in heterozygosity due to inbreeding. Hence, a population in which all individuals are completely inbred (with $f=1$) will have twice the genetic variation compared to its ancestral randomly mating population (with $f=0$), assuming that the allele frequencies of ancestral and inbred populations are the same. In natural populations subject to selection and mutation, the situation is more complex. Lande (1977) found that, when explicitly modeling the generation of variation by mutation and loss of variation through stabilizing selection for a quantitative trait, mating systems had no effect on the level of standing genetic variation. This is notably because the increase in variance due to excess homozygosity is canceled out by the more efficient purging of recessive deleterious mutations in inbred populations. In addition, he also showed that the decrease in genetic variance due to linkage disequilibrium in selfing populations is compensated for by the less efficient selection against mutations in linkage disequilibrium. In contrast, with the same assumption of a quantitative trait under stabilizing selection, Charlesworth and Nylin (1995)

found that genetic variation maintained by mutation-selection balance decreased under complete selfing and should be equal to one quarter of the variance maintained in an obligately outcrossing population. These contrasting results were reconciled by Lande and Porcher (2015) and Abu Awad and Roze (2018), who modeled the maintenance of genetic variation for any selfing rate and found that mating system has no or only a weak effect on genetic variance for moderate selfing rates, but that genetic variance declines abruptly for high selfing rates. The mechanism of reduced genetic variance for high selfing rates depends on the mutation rate of the trait under selection (Abu Awad and Roze 2018). If the mutation rate is low, the mutations appear so slowly that purifying selection acts efficiently to remove deleterious mutations, allowing populations to stay close to the phenotypic optimum. Because selfing populations are more efficient at purging the deleterious mutations (because they are recessive at the fitness scale; Manna et al. 2011), these populations maintain less genetic diversity than do outcrossing ones (Abu Awad and Roze 2018; Clo et al. 2020). If the mutation rate is high, however, mutations appear too quickly for purifying selection to purge them efficiently. In such cases, genetic associations emerge between deleterious mutations of opposite signs, thus reducing the deleterious effects of mutations on fitness and allowing populations to remain close to the phenotypic optimum. Due to their reduced effective recombination rates, selfing populations are better at maintaining these genetic associations, which decrease the phenotypic and genetic variance due to the negative contributions of these associations to variation (Lande and Porcher 2015; Abu Awad and Roze 2018; Clo et al. 2020).

12.3.1 Additive Variance Stored in Linkage Disequilibrium

Selfing populations are theoretically expected to be less evolvable than are outcrossing or mixed-mating populations. However, the mechanism of reduced genetic variance should play a key role in determining the short and mid-term evolvability of selfing populations. Indeed, if reduced evolvability of selfing populations is due to more efficient purging of deleterious mutations, and if adaptation depends on this previously deleterious diversity, the capacity of populations to respond to directional selection will necessarily be smaller in selfing populations (Clo et al. 2020). However, if the reduction in genetic variance is due to genetic associations and the associated linkage disequilibrium, the diversity stored within genetic associations can theoretically increase the response to selection (Lande and Porcher 2015; Abu Awad and Roze 2018). Recently, Clo et al. (2020) and Clo and Opedal (2021) showed that recombination events between phenotypically similar but genetically distinct inbred lines, within a population, led to an increase of the additive variance in the early generations of response to directional selection, because the stored diversity becomes expressed in recombining individuals. This increase in genetic diversity allows selfing populations to respond as quickly, and sometimes even quicker than their outcrossing counterparts (Clo et al. 2020; Clo and Opedal 2021). Quantifying the amount of diversity potentially stored in genetic associations in natural populations is complicated. Based on neutral diversity, it is known that selfing populations are organized into sets of repeated multilocus genotypes (Siol et al. 2008; Jullien et al. 2019), reflecting different combinations of alleles for a given quantitative trait (Clo and Opedal 2021). A straightforward way to search for cryptic diversity is to make crosses between these different inbred lines and to look for transgressive segregation in the F_2 generation (the appearance of phenotypes

outside the range of phenotypes that are present in the parental generation). Transgressive segregation has been widely observed in selfing populations (Rieseberg et al. 1999, 2003), suggesting that increased evolvability of highly selfing species during directional selection could be a common phenomenon.

**12.3.2 Limits of Quantitative-Genetics Models:
Integrating Directional Dominance into Mutation-Selection Models**

One limitation of the models reviewed above is that they assume that alleles act additively on the phenotypic scale. This assumption is potentially problematic, because it is well known that dominance contributes to the genetic architecture of quantitative traits, and hence to the genetic variance (Wolak and Keller 2014). When inbreeding and directional dominance (the fact that heterozygotes are, on average, not intermediate to homozygote values) occurs simultaneously, at least three additional terms contribute to the genetic variance (table 12.1; Cockerham and Weir 1984). The genetic variance of a population with an average inbreeding coefficient of f is then equal to

$$\sigma_{G,f}^2 = (1 + f)\sigma_A^2 + (1 - f)\sigma_{DR}^2 + f\sigma_{DI}^2 + 4f\sigma_{ADI} + f(1 - f)H^* \tag{2}$$

where σ_A^2 (the variance of average effects of alleles) and σ_{DR}^2 (the variance of dominance deviations of a randomly mating population) are the terms typically inferred in quantitative genetics. With inbreeding, an individual may have common ancestors through both parental lines, such that nonadditive effects can contribute to the covariance between parents and offspring, which does not occur under random mating. The additional terms arising under partial inbreeding include the variance of dominance deviations of a fully inbred population σ_{DI}^2 , and the covariance between the additive effect of an allele and its homozygous dominance deviation σ_{ADI} (table 12.1). This covariance arises because increased homozygosity in inbred populations increases the probability that an allele occurs in its homozygote state, which creates covariance between the contribution of an allele to the average effect and the dominance deviation of the homozygote genotype (Wolak and Keller 2014). Unlike

Table 12.1
The average effect of alleles (α) and dominance deviations (δ) associated with a genotype and the different components of genetic variance that can be inferred

Term	Symbol	Value
Average effect of allele A	α_A	$p_A G_{AA} + p_B G_{AB} - \mu = -0.42$
Average effect of allele B	α_B	$p_A G_{AB} + p_B G_{BB} - \mu = 0.18$
Dominance deviation of AA	δ_{AA}	$G_{AA} - 2\alpha_A - \mu = -0.98$
Dominance deviation of AB	δ_{AB}	$G_{AB} - \alpha_A - \alpha_B - \mu = 0.42$
Dominance deviation of BB	δ_{BB}	$\delta_{BB} = G_{BB} - 2\alpha_B - \mu = -0.18$
Additive variance	σ_A^2	$p_A 2\alpha_A^2 + p_B 2\alpha_B^2 = 0.15$
Dominance variance	σ_{DR}^2	$p_A^2 \delta_{AA}^2 + p_B^2 \delta_{BB}^2 + 2p_A p_B \delta_{AB}^2 = 0.18$
Inbred dominance variance	σ_{DI}^2	$p_A \delta_{AA}^2 + p_B \delta_{BB}^2 + (p_A \delta_{AA} + p_B \delta_{BB})^2 = 0.15$
Additive-dominance covariance	σ_{ADI}	$p_A \alpha_A \delta_{AA} + p_B \alpha_B \delta_{BB} = 0.13$
Inbreeding depression	H^*	$(p_A \delta_{AA} + p_B \delta_{BB})^2 = 0.18$

Notes: Based on Falconer and Mackay (1996). Consider a locus with two alleles A and B found at frequency $p_A = 0.3$ and $p_B = 0.7$, respectively. The genotypic values are $G_{AA} = 2$, $G_{AB} = 4$ and $G_{BB} = 4$ (B is completely dominant over A). The weighted mean genotypic value of the population is equal to $\mu = 3.82$.

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the other terms in equation (1), this term is a covariance and can thus be negative. The third additional component, H^* , is the squared per-locus inbreeding depression, summed over all loci. While σ_{DR}^2 does not affect the response to selection, the additional dominance components (notably σ_{Di}^2 and σ_{ADI}) contribute to the adaptive potential, because they contribute to the covariance between parents and offspring and thus response to selection (A. Wright and Cockerham 1985; Kelly 1999a,b).

By exploring the effect of directional dominance on a fitness-related trait under stabilizing selection for populations that differ in selfing rates, Clo and Opedal (2021) showed that dominance components can explain a substantial part of the genetic variance of inbred populations. They also showed that ignoring these components leads to an upward bias in the predicted response to selection (notably because the covariance term σ_{ADI} is often substantially negative), and that when considering the effect of directional dominance, the evolutionary potential of populations remains comparable across the entire gradient in outcrossing rates.

The additional variance components discussed above complicates the measurement of evolvability for inbreeding species, and empirical estimates requires complex experimental designs (Shaw et al. 1998; Kelly and Arathi 2003). A reasonable question to ask is: Are these additional dominance terms contributing substantially to the genetic variance of quantitative traits? Given the abovementioned difficulties in estimating all the dominance (co)variance terms, it is not surprising to find very few estimates in the literature. So far, only a handful of studies have estimated all the components of variance for morphological, fitness, and agronomic traits in the plants *Zea mays* (Edwards and Lamkey 2002; Wardyn et al. 2007), *Mimulus guttatus* (Kelly 2003; Kelly and Arathi 2003; Marriage and Kelly 2009), *Nemophila menziesii* (Shaw et al. 1998), *Eucalyptus globulus* (Costa E Silva et al. 2010), and in the animals *Bos taurus* (Hoeschele and Vollema 1993), *Ovis aries* (Shaw and Woolliams 1999) and *Homo sapiens* (Abney et al. 2000). From these studies, it is possible to extract all the components of the genetic variance (ignoring epistasis) for 40 quantitative traits. For each trait, we computed the ratio of the dominance variances (σ_{DR}^2 , σ_{Di}^2 , σ_{AD} , and H^*) over the sum of the additive variance and the focal dominance variance component. As σ_{ADI} can be negative or positive, we used the absolute value of σ_{ADI} . All the ratios are detectably different from zero (table 12.2), suggesting that the dominance terms contribute to the genetic variance but generally to a smaller extent than the additive variance, except for σ_{Di}^2 that on average tends to contribute as much to σ_G^2 as the additive component. Other forms of nonadditive genetic effects, like epistasis, can also contribute to the evolutionary potential of selfing species, but in the same manner as in random mating populations (see Hansen, chapter 5).

Table 12.2

Mean, standard deviation (s.d.), and minimum and maximum values of the ratios of the different nonadditive over additive variance components

Measure	n	Mean (s.d.)	Min	Max
$\sigma_{DR}^2 / (\sigma_A^2 + \sigma_{DR}^2)$	40	0.257 (0.226)	0	0.915
$\sigma_{Di}^2 / (\sigma_A^2 + \sigma_{Di}^2)$	40	0.441 (0.252)	0	0.910
$ \sigma_{ADI} / (\sigma_A^2 + \sigma_{ADI})$	40	0.236 (0.186)	0	0.737
$H^* / (\sigma_A^2 + H^*)$	40	0.347 (0.359)	0	0.915

Note: Data and code for the results presented in the table are available at https://github.com/JosselinCLO/Book_Chapter_Evolvability.

12.3.3 Empirical Relationship between Outcrossing Rate, Heritability, and Evolvability

Charlesworth and Charlesworth (1995) compiled estimates of outcrossing rates, heritabilities, and coefficients of genetic variation from published studies of plants. This first quantitative survey suggested a weak overall relationship between outcrossing rate and heritability. Later, Geber and Griffen (2003) reported lower heritabilities for highly selfing species compared to outcrossing and mixed-mating ones, and Ashman and Majetic (2006) reported lower heritabilities of self-compatible compared to self-incompatible species. Recently, Clo et al. (2019) compiled the largest dataset of mating systems and heritabilities to date; they found that although overall patterns were weak, heritabilities tended to decline with increasing selfing rates. In all these studies, when an effect of the mating system was detected, it always explained limited fractions of the variation in heritabilities (<20% in Geber and Griffen 2003; Clo et al. 2019). In addition, Clo et al. (2019) found that narrow-sense heritabilities of outcrossing and mixed-mating species (selfing rate <0.8) did not differ detectably from broad-sense heritabilities of predominantly selfing species (selfing rate ≥ 0.8), which is expected to be a more accurate predictor of evolutionary potential for this mating category.

Charlesworth and Charlesworth (1995) also analyzed the relationship between outcrossing rates and coefficients of genetic variation. When they restricted the analysis to additive-genetic coefficients of variation, they did detect a weak positive relationship between outcrossing rate and evolvability ($R^2 \approx 9\%$). Opedal et al. (2017) reported a similar pattern for floral traits functionally related to mating systems (figure 12.1).

Although the data shown in figure 12.1 are heterogeneous, which complicates formal analysis, they suggest that the overall relationship between outcrossing rate and evolvability in plants is weak. Most comparative analyses to date have combined population-specific and species-mean outcrossing rates. Because mating systems often differ among populations of mixed-mating species (Whitehead et al. 2018), these naïve analyses could be biased due to the inclusion of species-mean outcrossing rates. Because species-mean outcrossing rates may not be representative for the evolvability measures of the populations, it will lead to a downward bias in the relationship. A more powerful approach to test associations between evolvability and mating system is to compare conspecific populations differing in outcrossing rate. Of the few studies that have attempted this exercise, Bartkowska and Johnston (2009) reported reduced nuclear genetic variance in a highly selfing population compared to mixed-mating populations of *Amsinckia spectabilis*, while the data reported by Herlihy and Eckert (2007) for *Aquilegia canadensis* and by Charlesworth and Mayer (1995) for *Collinsia heterophylla* yield weak negative correlations between population-specific outcrossing rate and evolvability. Although single estimates of outcrossing rates are not necessarily reliable estimates of the mating histories of populations (Opedal 2018), these results underline the apparently weak overall relationship between outcrossing rate and evolvability.

Associations between evolvability and mating system can also be tested by phylogenetic comparative approaches, such as comparing species pairs differing in mating systems. Across four *Oenothera* species pairs, each comprising one sexual and one functionally asexual species, Godfrey and Johnson (2014) found no consistent effect of sexuality on evolvability, although suggestive patterns were detected for some traits.

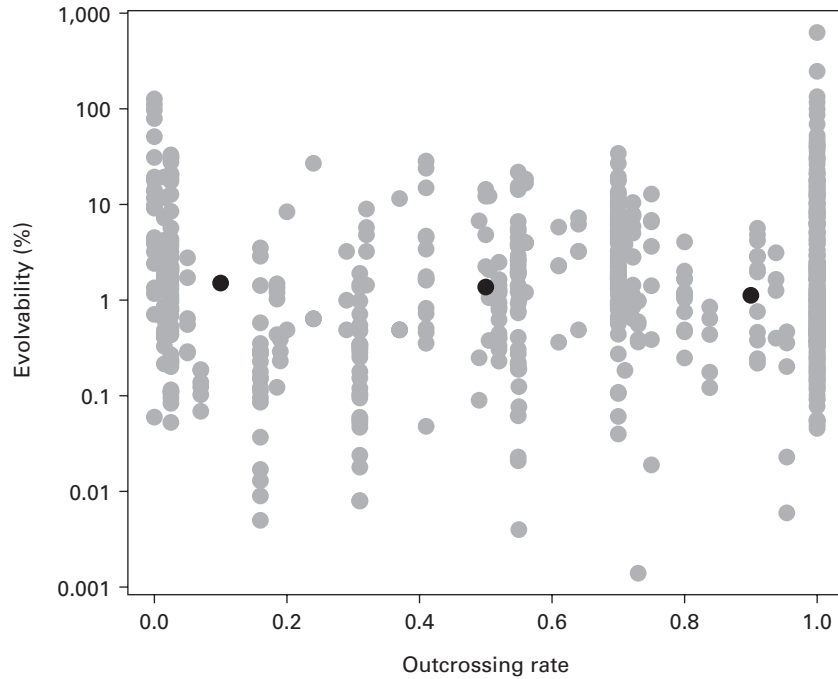


Figure 12.1

An extended version of the data compiled by Opedal et al. (2017), illustrating the apparent lack of a detectable relationship between evolvability and outcrossing rate across 763 single-trait evolvability estimates from 46 species (median $n = 12$ evolvability estimates per species, range = 1–65). Outcrossing rates plotted are population specific when available, and otherwise species means or, for self-incompatible species, assumed to be 1. The solid black symbols indicate the median for selfing (outcrossing rate < 0.2), mixed-mating (outcrossing rate 0.2–0.8), and outcrossing (outcrossing rate > 0.8 or self-incompatible) species. $R^2 < 1\%$ on either logarithmic or arithmetic scale.

12.3.4 Response to Selection as a Function of Outcrossing Rate

The empirical results reviewed above are based on the effect of the selfing rate on the additive variance, for which the effect of mating system is expected to be weak (Clo and Opedal 2021), and which is not an accurate predictor of adaptive potential of inbred populations, because the additional dominance terms contribute to the response to selection (Kelly and Williamson 2000; Clo and Opedal 2021). No trivial measures of the evolvability of populations as a function of their selfing rate are available in the literature (Kelly 1999a,b). One way to estimate the “realized” heritable variance or evolvability of a trait, as a function of the mating system, is to perform directional selection experiments with a known selection differential. Few studies have applied directional selection on quantitative traits for populations differing in their mating systems. However, in a study of the yellow monkeyflower *Mimulus guttatus*, Holeski and Kelly (2006) showed that the mean and variance in response to artificial selection differed among populations maintained under selfing, mixed mating, and outcrossing. Noel et al. (2017) used experimental evolution to generate inbred and outbred lines of the hermaphroditic snail *Physa acuta*, which were subsequently subjected to artificial selection under selfing and outcrossing. Their study provided clear evidence that inbred lines responded more slowly to selection than did outbred lines. Furthermore, when the selected lines were maintained under selfing, response to selection

was initially fast but quickly decayed. Although these experiments yielded important insights into the effect of shifting from outcrossing to selfing on adaptive potential, they did not fully reconcile theory and data concerning the effect of mating system on evolvability. First, in these studies, species that are mixed mating in natural populations were subject to experimental manipulation of their mating system. Shifting from outcrossing to selfing increases the adaptive potential of populations by a factor $1 + f$ (S. Wright 1921b), or higher if dominance contributes to the genetic architecture of the studied trait (Clo and Opedal 2021), explaining why selfing populations generally responded faster in these studies, at least during the first generations of selection. Second, outcrossing and mixed mating prevents the storage of diversity in genetic associations (Clo et al. 2020), and these investigators imposed complete selfing in their study populations, while residual outcrossing is always found in natural populations (Kamran-Disfani and Agrawal 2014). Maintaining a low level of outcrossing in selection experiments may allow a continued selection response by retaining cryptic diversity that is exposed under outcrossing. Directional selection experiments may remain the easiest way to estimate the “realized” evolvability of inbreeding populations, particularly for mixed-mating populations. Studies exploiting natural variation in mating systems would be particularly valuable. If predominantly selfing populations are used, due to their organization into different repeated multilocus genotypes, the immediate response to selection is likely to arise from selection among those natural purely inbred lines. In such a case, the immediate evolvability can be summarized by the among-lines genetic variance. In addition to estimating the realized evolvability for the first generations of response to selection, it seems important to study the potential patterns of transgressive segregations in recombinant lines of fully inbred genotypes. This will determine how selfing populations will evolve in the mid-term. It is nevertheless important to note that the entire variance of transgressive segregation will not predict the response to selection, as the formation of new genotypes based on the diversity stored through linkage is a stochastic process, leading to the formation of more or less well adapted new genotypes (Clo et al. 2020; Clo and Opedal 2021).

12.4 Separate Sexes and Evolvability

Some plants and the vast majority of animals have separate sexes in different individuals and reproduce through obligate outcrossing. Most estimates of additive genetic variation in these populations are obtained for a single sex or are sex-averaged to provide a population-level measure of evolvability. This is potentially problematic, because males and females can differ in the magnitude of their additive genetic variances. Sex-specific genetic variances can arise from differences in the strength and form of selection between the sexes, shaping patterns of genetic variation (Rowe and Houle 1996), sex differences in allele frequencies (Lynch and Walsh 1998; Reinhold and Engqvist 2013), sex-specific mutational effects (Mallet et al. 2012; Sharp and Agrawal 2012), sex-specific dominance (Fry 2010; Grieshop and Arnqvist 2018), sex differences in gene expression (Massouras et al. 2012), and the effect of sex chromosomes on the additive genetic variance (Husby et al. 2013). Therefore, single-sex or sex-averaged estimates of σ_A^2 may yield misleading estimates of evolvability. In the following sections, we discuss how having separate sexes can affect evolvability through the distribution of genetic variation between males and females, and

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through interactions between the sexes that affect how genetic variation evolves and is maintained in populations.

12.4.1 Sexual Conflict

Males and females share most of their genome and must interact in order to reproduce. The evolutionary interests of the sexes, however, are often in conflict (Trivers 1972). Sexual conflict occurs when adaptations arise that are beneficial for one sex but maladaptive for the other (Bonduriansky and Chenoweth 2009), and they may play an important role in the maintenance of genetic variation (Connallon and Clark 2012), directly influencing the evolvability of traits.

There are two mechanistically distinct forms of sexual conflict, both of which are caused by sex differences in selection and may affect evolvability. Interlocus sexual conflict refers to conflict over the outcome of interactions between males and females, such as over optimal mating rates and behaviors (Arnqvist and Rowe 2008). Sexually antagonistic coevolution caused by these interactions often results in sexual “arms races,” which can lead to the rapid evolution of traits involved in the interaction (Arnqvist and Rowe 2008). One clear example is the coevolution between male grasping structures in water striders, which are used to immobilize females during mating, and female spines, which are used to hold the male away (Arnqvist and Rowe 2002a,b). In contrast, intralocus sexual conflict results from sexually antagonistic selection on the same traits expressed in both sexes, whose expression is determined by shared genetics. This form of sexual conflict arises when the direction of selection on a given allele depends on which sex that allele resides in (Arnqvist and Rowe 2013). Many traits are expected to experience intralocus sexual conflict, which may eventually be resolved by the evolution of sexual dimorphism (Bonduriansky and Chenoweth 2009). However, negative genetic covariances for fitness between males and females are often observed (e.g., Foerster et al. 2007; Wolak et al. 2018), suggesting that intralocus sexual conflict remains unresolved in many species.

12.4.2 Sex-Linked Variation

In many species, biological sex is determined by sex chromosomes. There are two primary types of sex-chromosome systems, male (XX/XY) and female (ZW/ZZ) heterogamety. Loci on these chromosomes often encode for both sex-limited and shared traits, some of which are dimorphic in trait expression (Dean and Mank 2014). However, quantitative-genetics methods for estimating σ_A^2 often ignore the potential for sex-linked loci to generate differences in genetic variance between the sexes. Estimates of genetic variation obtained from standard analyses of half-sib breeding designs and implementations of the “animal model” (Kruuk 2004) assume that coefficients of relatedness are the same for relatives of the same degree, irrespective of sex. Consequently, sex-linked effects influence the estimates of additive genetic variation in these models. While it is possible to simultaneously estimate autosomal and sex-linked genetic effects with the animal model (Larsen et al. 2014), few studies have attempted to do so (but see Roulin and Jensen 2015). Consequently, there are few empirical estimates of genetic variation that would allow us to answer the question of whether evolvability tends to be higher for sex-linked or autosomal loci, and for males or females.

Ignoring epistasis, the genetic variance at a sex-linked locus in the heterogametic sex is determined by the additive effects of alleles at that locus. In the homogametic sex,

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however, genetic variation will also depend on intralocus allelic interactions, such as dominance effects. If we assume that sex-linked alleles contribute additively to the phenotype (there is no dominance), and that they have equal hemizygous and homozygous effects on trait expression, then a locus present on the sex chromosome will contribute twice as much variance in the heterogametic compared to the homogametic sex. This has led to the hypothesis that the heterogametic sex will be more genetically more variable than the homogametic sex. Realistically, however, the average effects of alleles are unlikely to be equal in each sex because of dosage compensation, which adjusts the activity of sex-linked loci to equalize gene expression between the sexes (Muller 1932). Variation can either increase or decrease depending on the mechanism of dosage compensation (Cowley et al. 1986), the chromosomal sex-determination system, and their interaction.

There are few empirical tests of the hypothesis that the heterogametic sex has more genetic variance than the homogametic sex. Reinhold and Engqvist (2013) compared coefficients of variation for body size in four animal taxa, two where males are the heterogametic sex and two where females are heterogametic. Consistent with their prediction, the heterogametic sex had more variation in body size in all taxa. However, the authors were only able to look at patterns of phenotypic, and not genetic variation, and in a relatively small dataset. Other studies that have attempted to test this hypothesis have similarly focused on phenotypic variation (e.g., Zajitschek et al. 2020). So far, the best data come from Wyman and Rowe (2014), who compared differences in coefficients of additive genetic variation across heterogametic types. They found no evidence that the heterogametic sex tended to have more genetic variation. Future studies testing this hypothesis may want to carefully consider the mechanism of dosage compensation as well as sex chromosome system. For example, in *Drosophila*, it is the number of X chromosomes that determine whether a fly is female (XX) or male (XY, XO), and the mechanism of dosage compensation is to double the transcription rate of the X chromosome in males. This may enhance the expression of deleterious X-linked mutations in males, leading to stronger purifying selection on males. If this occurs, it could reduce genetic variation and consequently evolvability.

12.4.3 Sex-Specific Autosomal Variation

Males and females may also differ in genetic variation for traits determined by autosomal loci. The total additive genetic variance in sexual dimorphism for traits controlled by autosomal loci is:

$$\sigma_A^2(M - F) = \sigma_A^2(M) + \sigma_A^2(F) - 2\sigma_A(M, F) \quad (3)$$

Where σ_A^2 is the additive genetic variance, and M and F represent males and females, respectively.

Few studies have considered the relationship between sexual dimorphism in σ_A^2 and evolvability (but see Rolff et al. 2005), with most studies focusing on heritabilities (Mousseau and Roff 1989; Gershman et al. 2010; Stillwell and Davidowitz 2010), which for reasons discussed earlier may not be a good measure of evolvability in many contexts. Wyman and Rowe (2014) collated data from 279 male-female pairs of traits from 75 species and asked whether there is a systematic difference in σ_A^2 , expressed as additive genetic coefficients of variation (CV_A), between males and females. The authors failed to detect any difference in the average CV_A between males and females across all trait types

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and species. There was, however, substantial variation in dimorphism of CV_A depending on the trait and species studied, and a difference in the skew of distributions when CV_A was higher for males versus females. When dimorphism in CV_A was male biased (male $CV_A >$ female CV_A), the magnitude of dimorphism in trait-specific means tended to be larger than when CV_A dimorphism was female biased.

Similar results have been found for gene expression traits, which allow us to study phenome-wide differences in σ_A^2 between males and females. Allen et al. (2018) estimated sex-specific genetic variances in gene expression traits in *D. serrata* and found on average that there was no difference in the genetic variance between males and females. However, genes which had male-biased expression had disproportionately higher genetic variance than genes which had female-biased expression. Traits with male-biased expression were also more evolvable regardless of which sex was expressing the trait. In *D. melanogaster*, however, Houle and Cheng (2021) found that genetic variance of male-biased gene-expression traits was higher in males, and genetic variance of female-biased traits was higher in females. Overall, results of higher genetic variance, or faster evolutionary rates, in male-biased gene expression traits has been demonstrated in some studies (e.g., Meiklejohn et al. 2003; Zhang and Parsch 2005; Assis et al. 2012) suggesting that it may be a general pattern. Dutoit et al. (2017) tested whether nucleotide diversity, as a measure of molecular genetic variation, was sexually dimorphic in the collared flycatcher. They found that genes with sex-biased expression had more sequence variation than did unbiased genes, and had a positive relationship between genetic diversity across the genome and sex bias in gene expression. Male-biased genes expressed in the brain also had disproportionately more nucleotide diversity with increasing levels of sex-biased expression than did female-biased genes. In general, there is more evidence for rapid sequence evolution of male-biased genes than of female-biased genes (Meiklejohn et al. 2003; Ellegren and Parsch 2007; Mank et al. 2007), but this does not necessarily imply higher evolvability and could also result from differences in the strength of selection between these gene classes. Male-biased genes do tend to have more tissue-specific expression (Assis et al. 2012; Hansen and Kulathinal 2013), suggesting that they may be less constrained by pleiotropy (Rowe et al. 2018). If this is the case, males may have higher conditional evolvability than females.

The positive relationship between male sex-biased gene expression and evolvability may be explained by at least three nonexclusive mechanisms. Male-biased expression may relax selection operating through females, thus increasing evolvability. Males may be less constrained by pleiotropy than females are, or they may maintain more genetic variation in traits as a side effect of higher genetic variation in fitness. Low-fitness males have been shown to harbor more σ_A^2 for individual and multivariate sexually selected trait combinations than high-fitness males (McGuigan and Blows 2009; Delcourt et al. 2012; Sztepanacz and Rundle 2012). Whether this pattern also extends to females has not been tested. Disentangling the roles of pleiotropy and selection in determining evolvability will be key to understanding these differences.

12.4.4 Cross-Sex Genetic Covariances

Sexually homologous traits in males and females that are determined by the same genetics can be thought of as two traits that genetically covary. When the optimal trait values of males and females differ, cross-sex covariances will determine the extent to which each

sex can reach their phenotypic optimum through the evolution of sexual dimorphism (Lande 1980). Consequently, cross-sex covariances hold a central role in the resolution of intralocus sexual conflict and thus in maintaining population mean fitness.

A homologous trait expressed in both males and females is conceptually equivalent to two genetically correlated traits, and we can therefore use the same tools to study the effects of cross-sex genetic covariances on evolvability that we use to study cross-trait genetic covariances. The evolvability metric e introduced above does not tell the complete story about the evolvability of a single trait when its genetic variance is correlated with other traits. To quantify the independent evolvability of correlated characters, Hansen (2003) developed the concept of conditional evolvability. Conditional evolvability (c) is the amount of genetic variation in a focal trait that is not bound up in correlations with other traits, or in other words, the response per unit directional selection in a focal trait, when a defined set of correlated traits are kept constant (as when they are under infinitely strong stabilizing selection). We may often expect directional selection on males and stabilizing selection on females over longer timescales, which makes the traditional notion of conditional evolvability relevant for assessing the potential for dimorphism evolution on longer timescales. Over shorter timescales, any shared traits may experience divergent selection due to different phenotypic optima, and we would like to know how much of the genetic variance would allow sexually antagonistic versus concordant responses to selection. Sztepanacz and Houle (2019) developed a method for partitioning genetic variation and cross-sex covariation into sexually concordant and sexually antagonistic genetic subspaces. Their partitioning characterizes genetic variation that would allow a response to selection in exactly the same direction between the sexes and in exactly opposite directions. Here, we propose that these genetic subspaces are analogous to a measure of conditional evolvability for dimorphism, and outline how Sztepanacz and Houle's method can be applied to quantify dimorphic evolvability (box 12.1).

12.4.5 Standardized Intersexual Genetic Correlations r_{mf}

Many studies have estimated standardized intersexual genetic correlations, r_{mf} , for single traits. The quantity r_{mf} is the ratio of additive genetic covariance between the sexes to the geometric mean of additive genetic variances of males and females. It can also be expressed

as $r_{mf} = \sqrt{\frac{h_{FD}^2 \cdot h_{MS}^2}{h_{MD}^2 \cdot h_{FS}^2}}$, where h^2 represents heritability estimates based on father-daughter

(FD), mother-son (MS), mother-daughter (MD), and father-son (FS) covariances (Lynch and Walsh 1998). The cross-sex genetic correlation r_{mf} is related to conditional evolvability, because $1 - r_{mf}^2$ is the autonomy of one sex conditional on the other. However, r_{mf} alone cannot tell us much about evolvability as we have defined it, because variances and covariances are what matter, not correlations. For example, high r_{mf} could reflect a high additive genetic covariance between the sexes, or just a low additive variance in one sex.

If we assume that the sexes have equal additive genetic variance for a focal trait, then the additive genetic variance (evolvability) for sexual dimorphism is $2\sigma_A^2(1 - r_{mf})$, where σ_A^2 is the additive genetic variance in the trait (Matthews et al. 2019). As discussed in the previous section, the assumption of equal genetic variance in males and females may be reasonable for many traits, but not for all of them, and in particular, not for sexually selected traits. Poissant et al. (2009) compiled 488 estimates of r_{mf} from more than 100

Box 12.1
Sexually Concordant and Antagonistic Evolvability

The quantitative-genetic framework to simultaneously estimate within- and cross-sex genetic covariances was put forth several decades ago (Lande 1980):

$$\mathbf{G}_{mf} = \begin{bmatrix} \mathbf{G}_m & \mathbf{B}' \\ \mathbf{B} & \mathbf{G}_f \end{bmatrix},$$

where \mathbf{G}_m and \mathbf{G}_f are the symmetric within-sex (co)variances among traits for males and females, respectively, and \mathbf{B} (\mathbf{B}') are the covariances of homologous traits expressed in both males and females. The diagonal elements of \mathbf{B} quantify the amount of genetic variation that is shared between the sexes for the same trait, whereas the off-diagonal elements quantify cross-sex cross-trait covariances. Unlike \mathbf{G}_m and \mathbf{G}_f , \mathbf{B} is not necessarily a symmetric matrix, because the genetic covariance between trait a in males and b in females may not be the same as b in males and a in females.

To quantify the evolvability of males and females under the conditions of sexually concordant and sexually antagonistic selection, we can partition \mathbf{G}_{mf} into sexually concordant and sexually antagonistic genetic subspaces (Sztepanacz and Houle 2019). This partitioning characterizes the genetic variation that would allow a response to selection acting in exactly the same direction between the sexes and selection acting in exactly opposite directions. Therefore, these subspaces of genetic variation reflect sexually concordant and sexually antagonistic evolvability. We illustrate this approach below with a 2-trait numerical example. For a more in-depth mathematical description, see Cheng and Houle (2020).

Our goal is to transform male and female genetic variances and covariances (\mathbf{G}_{mf}) into concordant and antagonistic genetic variances and covariances (\mathbf{G}_{CA}):

$$\mathbf{G}_{mf} = \begin{bmatrix} \mathbf{G}_m & \mathbf{B}' \\ \mathbf{B} & \mathbf{G}_f \end{bmatrix} \rightarrow \mathbf{G}_{CA} = \begin{bmatrix} \mathbf{G}_C & \mathbf{B}'_{CA} \\ \mathbf{B}_{CA} & \mathbf{G}_A \end{bmatrix}$$

The matrix \mathbf{G}_C is genetic variation in the concordant subspace, \mathbf{G}_A in the antagonistic subspace, and \mathbf{B}_{CA} is the genetic covariance that leads to indirect responses in the other space.

Let the 2×2 matrix \mathbf{G}_{mf} be:

		Male		Female	
		trait 1	trait 2	trait 1	trait 2
Male	trait 1	49	5	40	10
	trait 2	5	53	3	49
Female	trait 1	40	3	40	12
	trait 2	10	49	12	70

The first step to defining concordant and antagonistic evolvability is to define a set of orthonormal vectors (\mathbf{S}_m) that spans the concordant and antagonistic subspaces of \mathbf{G}_{mf} . Here, we let this matrix be:

$$\mathbf{S}_m = \frac{1}{\sqrt{2}} \begin{bmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 1 & 0 & -1 & 0 \\ 0 & 1 & 0 & -1 \end{bmatrix} = \frac{1}{\sqrt{2}} \begin{bmatrix} \mathbf{I} & \mathbf{I} \\ \mathbf{I} & -\mathbf{I} \end{bmatrix}$$

where \mathbf{I} is a 2×2 identity matrix. However, any set of vectors that form the basis of a 2×2 matrix would work. The term $\frac{1}{\sqrt{2}}$ scales the concordant and antagonistic axes to unit length,

Box 12.1
(continued)

preserving the size of \mathbf{G}_{mf} . The next step is to project \mathbf{G}_{mf} onto the concordant and antagonistic subspaces defined by \mathbf{S}_m :

$$\mathbf{G}_{CA} = \mathbf{S}_m \mathbf{G}_{mf} \mathbf{S}'_m$$

\mathbf{S}_m is symmetric, so that $\mathbf{S}'_m = \mathbf{S}_m$ and

$$\mathbf{G}_{CA} = \frac{1}{\sqrt{4}} \mathbf{S}_m \mathbf{G}_{mf} \mathbf{S}_m.$$

Working through our example:

$$\mathbf{G}_{CA} = \frac{1}{\sqrt{4}} \begin{bmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 1 & 0 & -1 & 0 \\ 0 & 1 & 0 & -1 \end{bmatrix} \begin{bmatrix} 49 & 5 & 40 & 10 \\ 5 & 53 & 3 & 49 \\ 40 & 3 & 40 & 12 \\ 10 & 49 & 12 & 70 \end{bmatrix} \begin{bmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 1 & 0 & -1 & 0 \\ 0 & 1 & 0 & -1 \end{bmatrix}$$

$$\mathbf{G}_{CA} = \begin{bmatrix} 84.5 & 15 & 4.5 & -7 \\ 15 & 110.5 & 0 & -8.5 \\ 4.5 & 0 & 4.5 & -2 \\ -7 & -8.5 & -2 & 12.5 \end{bmatrix}.$$

The upper right submatrix $\mathbf{G}_C = \begin{bmatrix} 84.5 & 15 \\ 15 & 110.5 \end{bmatrix}$ is the genetic variation in the concordant subspace, which would allow a response to concordant selection. $\mathbf{G}_A = \begin{bmatrix} 4.5 & -2 \\ -2 & 12.5 \end{bmatrix}$ is the genetic variation in the antagonistic subspace, which would allow a response to sexually antagonistic selection, and $\mathbf{B}_{CA} = \begin{bmatrix} 4.5 & 0 \\ -7 & -8.5 \end{bmatrix}$ is the genetic covariance that leads to indirect responses in the other space. The total genetic variance (the trace) of $\mathbf{G}_{CA} = 212$, the same as the trace of \mathbf{G}_{mf} , illustrating that our transformation did not affect the overall size or total evolvability. If we compare the genetic variance in concordant and antagonistic subspaces, we find that there is 11 times more sexually concordant evolvability than there is antagonistic evolvability.

studies to test the prediction that r_{mf} and sexual dimorphism are negatively correlated. They found about half of the estimates of r_{mf} were above 0.8, translating into an autonomy of less than 36%, suggesting that males and females share much of the genetic variation that underlies homologous traits. This appeared to be general across trait types. They found little evidence that r_{mf} differed for different classes of traits, except for fitness components, which tended to have lower intersexual genetic correlations, consistent with other studies (Foerster et al. 2007). A major drawback of this study, in addition to the issues with focusing on correlations, is that only point estimates of r_{mf} were analyzed, with differences in sample size and errors of the estimates not accounted for. Quantitative-genetic estimates of variance and covariance tend to be estimated with substantial error (Sztepanacz and Blows 2017), and cross-sex covariances may be particularly affected because of the lack

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of residual covariances between male and females traits, which may lead to less precise estimates. Unfortunately, the historical lack of reporting of standard errors for genetic variances and covariances reduces our ability to thoroughly assess the potential issue.

Whether positive cross-sex genetic correlations increase or decrease evolvability depends on whether selection is sexually concordant or antagonistic. Positive correlations will increase evolvability under sexually concordant selection and decrease it when selection is sexually antagonistic. Morrissey's (2016) meta-analysis of 424 selection estimates for 89 traits and 34 species compiled by Cox and Calsbeek (2009) found a strong and positive correlation between male and female selection gradients: $(r(\beta_m, \beta_f) = 0.794 [0.666, 0.928])$, showing that sexually antagonistic selection was rare and not highly antagonistic. A historical emphasis on intralocus sexual conflict, and studies focusing on highly sex-dimorphic traits that typically experience sexually antagonistic selection has led to a general view that intersexual genetic correlations are an evolutionary constraint. However, the data showing many positive r_{mf} estimates and frequent sexually concordant selection suggests that intersexual genetic correlations may often increase evolvability. An analysis of published data in a model that quantified the costs of evolving sexual dimorphism also showed that only 10% of traits are associated with large costs of selection for sexual dimorphism, while the rest have modest or small costs (Matthews et al. 2019). In general, genetic correlations are often viewed from the perspective of evolutionary constraints rather than evolvability, although they may increase evolvability as often as they constrain it (Agrawal and Stinchcombe 2009). While they are two sides of the same coin, recasting our perspective from evolutionary constraints to evolvability may lead to more balanced insights.

12.4.6 Multivariate Cross-Sex Covariances

In addition to the issues of correlation-focused analyses discussed above, we also know that bivariate correlations rarely reflect the higher-dimensional distribution of genetic variation across multivariate trait combinations (Walsh and Blows 2009). There are fewer studies that quantify multivariate cross-sex covariances (i.e., the **B** matrix), and some suffer from the same issues of scaling discussed above, which complicate inferences about the relationship between evolvability and **B**. The majority of studies have tended to focus on noticeably dimorphic (Lewis et al. 2011; Gosden et al. 2012; Ingleby et al. 2014; Cox et al. 2017; Kollar et al. 2021) and sexually-selected traits (Gosden et al. 2012; Ingleby et al. 2014; Cox et al. 2017). In these cases, **B** was most often found to limit the magnitude (Lewis et al. 2011; Ingleby et al. 2014; Cox et al. 2017) and direction (Lewis et al. 2011; Gosden et al. 2012) of the predicted response to estimated selection gradients or to random skewers. The effect of **B** on evolvability under random or concordant selection has been quantified less frequently. Cox et al. (2017) reported that **B** had little effect on the predicted response to selection in random directions, while Holman and Jacomb (2017) and Sztepanacz and Houle (2019) showed that **B** facilitated the response to sexually concordant selection.

A few studies have already used the recent approach of Sztepanacz and Houle (2019) (see box 12.1) to sort genetic variation into sexually concordant and antagonistic genetic subspaces. Sztepanacz and Houle (2019) found that concordant evolvability was much higher than antagonistic evolvability for wing shape in *Drosophila melanogaster*. Kollar et al. (2021) found more antagonistic genetic variance for morphology and physiology

traits in the moss *Ceratodon purpureus* and more concordant evolvability for growth and development traits. However, the confidence intervals of their estimates were large and often overlapping. Finally, Houle and Cheng (2021) reanalyzed published data on gene expression (Ayroles et al. 2009), and cuticular hydrocarbon traits (Ingleby et al. 2014) in *D. melanogaster*; and they found more concordant than antagonistic genetic variation.

Asymmetry appears to be a common feature of \mathbf{B} (Steven et al. 2007; Barker et al. 2010; Lewis et al. 2011; Gosden and Chenoweth 2014; Ingleby et al. 2014; Walling et al. 2014), but its effects have been rarely quantified. Gosden and Chenoweth (2014) found that asymmetry accounted for 10–50% of the variance in \mathbf{B} , and that asymmetry was positively associated with population divergence. One limitation of recasting \mathbf{G}_{mf} into concordant and antagonistic genetic subspaces is that it does obviously show sex differences in multivariate evolvability that arise from asymmetry in \mathbf{B} . One way to more clearly show these differences is to compare the predicted response to random (Cheverud et al. 1983) or known selection vectors using an observed versus modified \mathbf{G}_{mf} (e.g., Cox et al. 2017; Holman and Jacomb 2017; Sztepanacz and Houle 2019). \mathbf{G}_{mf} can be modified in a variety of ways, depending on the question being addressed. To determine the effect of asymmetries in \mathbf{B} on the predicted response, \mathbf{B} could be made symmetric. To quantify the effect of the modified covariances, we can use the metric $R = e_{mf}/e^*$, the ratio of the evolvabilities for observed \mathbf{G}_{mf} and modified \mathbf{G}^* (Agrawal and Stinchcombe 2009; Holman and Jacomb 2017). Values of $R < 1$ indicate that the covariances that were modified constrain predicted responses, whereas $R > 1$ suggests they facilitate it. Using this approach, Sztepanacz and Houle (2019) found that, on average, predicted responses to random sexually concordant and antagonistic selection vectors were biased away from the selection gradient more in females than in males. Their data suggest that females have reduced evolvability under directional selection compared to males.

12.5 The Effect of Sexual Selection on Evolvability

Males and females not only share the majority of their genome, but they also must interact during reproduction. These interactions lead to sexual selection, which is known to drive the evolution of extravagant ornamental traits, complex behaviors, and to have an important role in population persistence, divergence, and speciation. Ultimately, sexual selection arises from variation in reproductive success among individuals, which affects evolvability through its effects on the evolution and maintenance of genetic variation. There are many nonexclusive mechanisms that cause variation in reproductive success, such as intrasexual competition for access to mates or resources, pre- or post-copulatory mate choice exerted by the opposite sex, and gamete (sperm or pollen) competition. In the following sections, we first discuss how variation in reproductive success can affect evolvability by reducing the effective size of populations. We then discuss the effect of mate preferences on evolvability.

12.5.1 Reduction in Effective Population Size Due to Sexual Selection

The effective size of a population, N_e , determines the rate at which drift purges genetic variation from populations through the fixation of random alleles (see Pélabon et al., chapter 13). Sexual selection increases variation in reproductive success compared to an ideal (Wright-Fisher) population, which has the potential to reduce the effective size (N_e)

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of a population below its census size (N). The effective size of a population is maximized when the effective sizes of the sexes are equal (S. Wright 1931). In most sexual systems, the reproductive success of males, including the number of males who fail to reproduce, is affected by sexual selection to a larger extent than that of females (Bateman 1948; Collet et al. 2012). This difference is expected to lead to the divergence of N_e between males and females and potentially reduce evolvability through the increasing effects of drift in the population.

The effect of sexual selection on N_e and its consequent effects on evolvability are difficult to investigate empirically, because estimating the mean and variance in reproductive success is often a challenge. Using an experiment in *D. melanogaster*, Pischedda et al. (2015) showed that sexual selection had minimal impact on the effective population size in lab-adapted populations. They found that strong sexual selection was operating in their population, with variance in reproductive success ~ 14 times higher in males than in females. However, inducing high rates of random offspring mortality reduced the effect of sexual selection on N_e compared to N by balancing the effective population sizes of males and females. Overall, their results showed that very strong sexual selection can have minimal effect on N_e in populations with high offspring mortality. Experimental work in *D. pseudoobscura* has also shown that sexual selection may not affect N_e . Snook et al. (2009) estimated N_e in populations undergoing experimental evolution with different intensities of sexual selection. They estimated N_e with both a census-based estimator and a genetic estimator based on molecular markers from two sampling events that took place 26 generations apart. Both genetic and census-based estimates of N_e showed that it did not differ among sexual-selection treatments, and that the ratio $\frac{N_e}{N}$ also did not differ.

Genetic analyses of other systems that experience strong sexual selection have also shown nearly equal ratios of effective and census population sizes (Broquet et al. 2009). Together these data suggest that sexual selection may not have a large effect on N_e , at least for short-lived fecund species that experience high offspring mortality. In longer-lived species or those with lower rates of offspring mortality, this may not be the case (Gagne et al. 2018).

Even if sexual selection does reduce N_e , it does not necessarily mean that evolvability will be reduced. Although none of the studies discussed above make a direct link between N_e and evolvability, there is relatively little empirical evidence, in general, to suggest that N_e has a major role in evolvability on short timescales, given a sufficient effective population size (Pélabon et al., chapter 13).

12.5.2 The Lek Paradox

The evolution of conspicuous male sexual displays generated much of the historical and current interest in sexual selection research, beginning with Darwin (1871), who struggled to reconcile how exaggerated male traits, which would otherwise reduce survival, could evolve and be maintained in populations. Darwin argued that the survival cost of bearing such traits is compensated by the increase in reproductive success that they engender, either through benefits in intrasexual competition or because they make their bearers more sexually attractive.

In many systems, females exert strong preferences to mate with certain males where there are no apparent benefits to their choice (Andersson 1994). The leading hypothesis

to explain the evolution of female preferences and male displays in the absence of direct benefits is that display traits reflect the genetic quality of a male, and females are choosing to gain indirect fitness benefits for their offspring (Kirkpatrick and Ryan 1991). One of the major difficulties in understanding this “good-genes” hypothesis of sexual selection is that additive genetic variation in the sexually selected traits and their fitness benefits should be rapidly exhausted in the population through the process of sexual selection itself, negating any benefits of choice. This is the so-called lek paradox (Borgia 1979). Resolving the lek paradox, or how evolvability is maintained in the face of strong sexual selection, is a central focus of sexual-selection research.

The assumption that sexual selection depletes additive genetic variation (and therefore evolvability) appeared to be supported by the observation that life-history traits (i.e., components of fitness) had lower heritabilities than morphological traits (Mousseau and Roff 1987; Roff and Mousseau 1987). As we have emphasized throughout this chapter, however, heritability is not necessarily a good indicator of the magnitude of additive genetic variation or evolvability of a trait. Indeed, individual sexually-selected (Pomiankowski and Møller 1995) and life-history (Houle 1992) traits have been shown to have higher additive genetic variance and evolvability than do morphological traits.

12.5.3 The Maintenance of Genetic Variance under Sexual Selection

Various mechanisms have been proposed to explain how additive genetic variation is maintained under sexual selection (for a comprehensive review, see Radwan 2007). However, their relative importance remains unclear. The genic-capture hypothesis proposed by Rowe and Houle (1996) suggests that the expression of sexually-selected traits is costly and therefore depends on an individual’s condition. Condition is controlled by many loci, and consequently, collects mutations that occur across a large part of the genome, allowing additive genetic variation to be maintained in the face of strong sexual selection. Although some empirical studies have found evidence for condition-dependent expression of male sexual displays (e.g., Hill 1990; Bonduriansky and Rowe 2005; Delcourt and Rundle 2011), many have not, and even fewer have investigated whether there is genetic variance in condition dependence (Cotton et al. 2004).

Genetic compatibility provides a different avenue by which evolvability could be maintained or even increased by sexual selection. It posits that offspring fitness depends on the allelic combinations of mothers and fathers (Trivers 1972) and hence on dominance and epistatic effects (Tregenza and Wedell 2000; Neff and Pitcher 2008). Interest in the genetic-compatibility hypothesis arose as a mechanism to explain polyandry and the costs associated with multiple mating. Early verbal models relied on post-copulatory genetic incompatibilities to discriminate between genetically compatible sires and provide females with fitness benefits for their offspring (Zeh and Zeh 1996), although females can also exercise precopulatory choice on the basis of genetic compatibility or dissimilarity (Mays and Hill 2004). However, one of the major theoretical difficulties of the genetic-compatibility model is how preference for nonadditive benefits can evolve when the nonadditive benefits are not heritable (Lehmann et al. 2007). Empirical studies of genetic compatibility are most extensive with respect to the major histocompatibility complex (MHC), which is a locus of polymorphic genes that control immunological function and self-recognition in vertebrates. Genetic identity of the MHC can be distinguished through odors (Penn 2002), enabling pre-copulatory choice

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based on this locus. Humans, mice, and fish (reviewed in Tregenza and Wedell 2000) have all been shown to prefer odor samples of males that have genetically dissimilar MHC genotypes.

Falling between the “good-genes” and “genetic compatibility” hypotheses is mate preference for heterozygosity. Females choose males that have high heterozygosity across many loci, because they will have a greater likelihood of producing genetically compatible offspring (Brown 1997), or because heterozygosity increases male fitness, contributing direct benefits to females and their offspring. Models suggest that preferences for heterozygous mates can evolve and be maintained in populations in the absence of direct benefits (Fromhage et al. 2009), and there is empirical evidence to support preference for heterozygosity in some circumstances (Landry et al. 2001; Garcia-Navas et al. 2009). For each of the three mechanisms discussed in this section, we can point to specific examples of where they appear to be operating in a population or species. However, the empirical data do not provide support for any of them as a general mechanism to maintain additive genetic variation in populations.

12.5.4 Multivariate Sexual Selection and Trade-Offs

Many, if not most, sexual displays are complex and comprise many individual traits, such as different components of wing song in crickets (Brooks et al. 2005) or *Drosophila* (Hoy et al. 1988), pheromone profiles comprising several different chemical compounds (Blows and Allan 1998), or complex color patterns (Butler et al. 2007). In these cases, additive genetic variation in the individual component traits of the display will likely tell us little about their evolvability (Blows et al. 2004). Fitness trade-offs between sexually and naturally selected traits and/or between males and females are likely to arise because of the action of sexual selection and maintain genetic variation that is beneficial for one trait type (or sex) and detrimental for the other. Radwan et al. (2016) hypothesized that stronger sexual selection is associated with increased genetic variation in sexually-selected and ecological traits as a consequence of these trade-offs. However, there is limited evidence to support this hypothesis or others that predict increased genetic variance associated with sexual selection (e.g., Petrie and Roberts 2006). Multivariate studies of sexual selection often find that multivariate sexual-selection gradients are orthogonal to the major axes of genetic variance in sexual displays (Hine et al. 2004; Van Homrigh et al. 2007). These data support the prediction that sexual selection reduces evolvability of targeted traits, and the current data also suggest that the genetic variance that is maintained is a consequence of antagonistic pleiotropy, which is another variance-maintaining mechanism (Connallon and Clark 2012). High-fitness males have less genetic variance in sexual displays than low-fitness males, suggesting that the genetic variance underlying sexual displays is under apparent stabilizing selection (McGuigan et al. 2011; Delcourt et al. 2012; Sztepanacz and Rundle 2012). Therefore, the genetic variance in multivariate sexual displays may not be relevant to evolvability under a scenario of directional sexual selection.

12.5.5 Conclusions for Sexual Selection

The effect of sexual selection on evolvability is complex. On one hand, we might expect sexual selection to reduce evolvability by reducing effective population sizes and the genetic variation among successful reproducers. On the other hand, high evolvability is

observed in many individual sexually-selected traits. Despite the substantial theoretical and empirical attention given to solving this paradox of the lek, we still do not have a clear understanding of how to resolve it. The most general explanation is that antagonistic pleiotropy resulting from multivariate trade-offs maintains segregating variation in sexually-selected traits. Whether this variation is relevant to evolvability will depend on the direction and form of selection operating in the population.

12.6 Conclusion

In this chapter, we have considered how two major axes of mating-system variation affect evolvability: variation in outcrossing rate, and variation in the mating strategies and behaviors that lead to variation in reproductive success. We have shown that estimating the evolvability of quantitative traits may be difficult when properly accounting for the effect of mating system. The main challenges are the rigorous decomposition of genetic variance into additive and nonadditive components, the recasting of population-level evolvability into sexually concordant and antagonistic subspaces, and finally the consideration of linkage disequilibrium on short- and mid-term evolvability and the stochasticity associated with it. Our review of the theoretical and empirical evidence has led us to the following conclusions:

- There is no universal measure of evolvability is meaningful across mating systems.
- Selfing does not necessarily reduce evolvability, and variation in outcrossing rate has no systematic effect on the evolvability of populations.
- There is no empirical evidence that the heterogametic sex is more evolvable than the homogametic sex.
- There is no systematic difference in evolvability between males and females, but there are often differences in evolvability in particular populations.
- Within populations, when males are more evolvable, the difference in evolvability between the sexes tends to be more extreme than when females are more evolvable.
- There is more sexually concordant than antagonistic evolvability.
- In general, sexual selection does not reduce the effective size of populations and consequently may have little impact on short-term evolvability.
- Antagonistic pleiotropy may be the most important mechanism maintaining genetic variation in sexually selected traits, but this variation may not be relevant for evolvability under sexual selection.
- A multivariate view of genetic variation and selection is necessary to understand the evolvability of most traits, including those that experience sexual selection.



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