

ELIMINATION OF A GENETIC CORRELATION BETWEEN THE SEXES VIA ARTIFICIAL CORRELATIONAL SELECTION

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Genetic correlations between the sexes can constrain the evolution of sexual dimorphism and be difficult to alter, because traits common to both sexes share the same genetic underpinnings. We tested whether artificial correlational selection favoring specific combinations of male and female traits within families could change the strength of a very high between-sex genetic correlation for flower size in the dioecious plant *Silene latifolia*. This novel selection dramatically reduced the correlation in two of three selection lines in fewer than five generations. Subsequent selection only on females in a line characterized by a lower between-sex genetic correlation led to a significantly lower correlated response in males, confirming the potential evolutionary impact of the reduced correlation. Although between-sex genetic correlations can potentially constrain the evolution of sexual dimorphism, our findings reveal that these constraints come not from a simple conflict between an inflexible genetic architecture and a pattern of selection working in opposition to it, but rather a complex relationship between a changeable correlation and a form of selection that promotes it. In other words, the form of selection on males and females that leads to sexual dimorphism may also promote the genetic phenomenon that limits sexual dimorphism.

KEY WORDS: Between-sex genetic correlation, dioecious, response to selection, sexual dimorphism.

Sexual dimorphism is enigmatic because males and females share a common genetic architecture, yet may express very different traits (Fisher 1930; Lande 1980; Fairbairn 2007). Although selection may favor different values of characters in each sex, how much dimorphism actually evolves depends on the genetic independence of male and female phenotypes. Genes that are sex specific in their expression allow for independent evolution of the sexes, but genes that are expressed in both sexes contribute to

similarities between males and females, and constrain the evolution of differences between the sexes (Lande 1980). The degree to which similarities in male and female phenotypes are co-inherited is quantified by between-sex genetic correlations, which are typically very high for homologous traits of males and females (Poissant et al. 2010). In fact, traits that are the most strongly genetically correlated between the sexes are the least sexually dimorphic across a range of taxa, which supports the widely held premise that these correlations constrain the evolutionary divergence of the sexes (Reeve and Fairbairn 2001; Bonduriansky and Rowe 2005; McDaniel 2005; Poissant et al. 2010).

The extent to which between-sex genetic correlations represent constraints over evolutionary time depends on their magnitude and perturbability. Genetic correlations can and do evolve through drift and selection, but the constancy of genetic correlations in general is a controversial question, and depends on aspects

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of genetic architecture that are largely unknown for any system (Arnold et al. 2008; Eroukhmanoff 2009). Multivariate stabilizing selection may help to maintain genetic correlations by favoring combinations of traits (Lande 1984; Brodie 1992). Selection is not expected to act on combinations of traits expressed simultaneously in both sexes, suggesting that the value of between-sex correlations may be less constrained to be stable over evolutionary time (Barker et al. 2010). However, in the case of a single trait expressed in both sexes, genetic correlations are expected to be strong and largely inescapable consequences of genetics and development. Particularly in the early stages of the evolution of sexual dimorphism, polymorphic loci expressed in both sexes are expected to cause a strong between-sex genetic correlation (Lande 1980; Bonduriansky and Chenoweth 2009). A reduction in this correlation requires the appearance of sex-specific alleles at a locus or changes in modifier loci that act in only one sex (Mackay 2001; Rhen 2007; Mank et al. 2008; Connallon and Clark 2010), or in differential epistasis affecting intersex pleiotropy (Pavlicev et al. 2008; Wagner et al. 2007). The shared genetic basis and evolutionary history of a trait expressed in both sexes leads to the prediction that between-sex genetic correlations will be large and static, and represent substantial limitations to the evolution of sex differences (Price and Burley 1993; Merilä et al. 1998; Poissant et al. 2010).

To evaluate the evolutionary stability of between-sex genetic correlations, and thereby their importance as genetic constraints to sexual dimorphism, we tested whether artificial selection could lower the strength of a between-sex genetic correlation in flower size, as measured by calyx width, in *Silene latifolia*. Sexual dimorphism in flower size occurs in this, as well as many other dioecious species (Darwin 1877; Bell 1985; Delph et al. 1996). Flower size dimorphism in *S. latifolia*, in which flowers on females are larger than flowers on males, is likely the result of past disruptive or sex-specific selection that occurred after the evolution of dioecy from hermaphroditism within the lineage (Desfeux et al. 1996). Of the three dioecious species from this lineage (all of which shared a common dioecious ancestor), *S. latifolia* expresses the highest degree of sexual dimorphism in flower size (L. Delph, unpubl. data), indicating that some of the difference between the sexes evolved after *S. latifolia* emerged as a separate species. As described above, genes controlling flower size in the ancestral hermaphrodite would have been initially shared by both sexes, and sexual dimorphism would have subsequently evolved via the spread of sex-specific gene expression. However, previous estimates of the between-sex genetic correlation for flower size in *S. latifolia* are close to 1.0, indicating that some of these genes remain polymorphic and expressed in both sexes. This correlation has been demonstrated in two ways: via a cross-classified breeding design (Steven et al. 2007), and via artificial directional selection on flower size in one

sex (sex-specific selection), which consistently led to a significant correlated response in the other (Meagher 1999, Delph et al. 2004). Hence, the between-sex genetic correlation for flower size remains high, despite past disruptive or sex-specific selection for flower size to differ between males and females.

We conducted two separate artificial selection experiments in which we first attempted to lower the between-sex genetic correlation for flower size, and second directly tested the efficacy of the first experiment. In the first experiment, we challenged the stability of the between-sex genetic correlation and attempted to gain insight into its makeup. If the shared history of a between-sex trait has led to a correlation maintained by shared loci, selection should alter the correlation slowly, if it all. A rapid change in a genetic correlation, regardless of the kind of selection employed, suggests that the correlation is a consequence of more transient genetic mechanisms. The disruptive or sex-specific selection experienced in nature clearly has left a high correlation intact, suggesting that artificial-selection programs of that kind are not likely to change the correlation. Previous studies have selected on correlated traits within a single sex by selecting points on one side of the major axis defining the correlation, but while such selection changes the means of the traits (moving the line defining the correlation up or down), the correlation itself remains unaltered (e.g., Bell and Burris 1973; Frankino 2007). To have the greatest chance of lowering the genetic correlation and therefore most accurately assess its stability, we developed a novel form of selection, which we refer to as artificial correlational selection because the selection involved a breeding design structured to change the correlation itself without altering the means (Fig. 1). Although the correlation remained high in two control lines and one of the selection lines, we were able to significantly lower the genetic correlation in two of the three selection lines. If the observed reduction in the between-sex genetic correlation is important in an evolutionary sense, then selection on flower size in one sex should generate at most a limited correlated response in the other sex. Hence, we followed up the first experiment with a second one that used one control line and the selection line with the lowest between-sex genetic correlation. In this experiment, we performed sex-specific selection to reduce flower size in females. We predicted a strong correlated response in males in the former control line and a significantly weaker correlated response in males in the selection line with the reduced correlation.

Materials and Methods

EXPERIMENTAL PROCEDURES

Silene latifolia (Caryophyllaceae) is a dioecious, weedy, short-lived perennial native to Europe (Baker 1948). The flowers are fragrant, open at night, and are pollinated primarily by night-flying moths that prefer plants with large floral displays (Shykoff

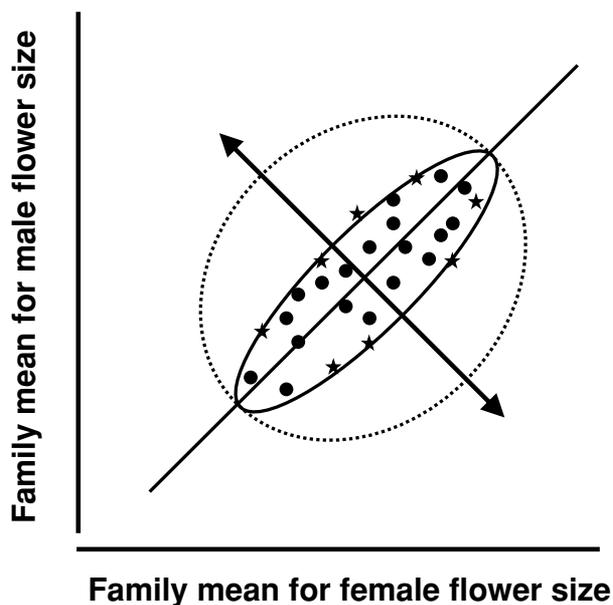


Figure 1. In this depiction of our approach to family-level, artificial correlational selection, we show the eight families with the largest values (four positive and four negative, indicated by stars) along the minor principal components axis (the line with arrowheads), which were selected as parents for the next generation. This selection was undertaken in an attempt to decrease the correlation between males and females (as indicated by the dotted ellipse) without causing selection on mean flower size.

and Bucheli 1995). Sexual dimorphism exists in over 40 traits, ranging across floral, leaf, growth, life-historical, and physiological traits (Delph 2007; Delph et al. 2010). With respect to flowers, males make flowers that are smaller in size (calyx width, calyx length, petal-limb length), mass, and nutrient content compared to flowers on females, and because of a genetically based size/number trade-off, males produce many times more flowers than females (Meagher 1999; Delph et al. 2004).

SELECTION TO REDUCE THE BETWEEN-SEX GENETIC CORRELATION

Single fruits were collected from 103 female plants growing in a wild population in Giles County, Virginia. Seeds from these fruits were germinated, and crosses were made as described in Steven et al. (2007) to create 150 full-sibling families nested within both maternal and paternal half-sibling relationships. These families were used as the base generation for the experiment, from which we set up a total of five lines: three “selection” lines to reduce the correlation (S1, S2, and S3) and two control lines (C1 and C2).

In the first round of selection, we chose families to serve as founders for the three selection lines and begin selection for a reduced correlation between the calyx width of males and females.

To select eight families for each of three lines, we calculated family means for the calyx width of flowers from males and females and plotted the means for females against the means for males. Because the first and second principal components of this plot are analogous to the major axis of the correlation and its perpendicular minor axis, respectively, we performed a principal-component analysis using the statistical program JMP and selected families with the largest minor axis values (and therefore the greatest deviation from the major axis of the correlation). In an attempt to spread variation along the second principal component evenly among the lines, we first identified the families with the three smallest second principal-component values and the three largest second principal-component values, and assigned each to one of the three selection lines. We then did the same with the next group of the three most extreme values until we had four families that were very negative on the minor axis and four that were very positive in each of the three selection lines (Fig. 1). We avoided putting half-siblings in the same lines and checked that the means of the lines were similar to the overall population mean.

For the later rounds of selection, we were restricted to the families already in a line; in this case, we chose the four families that were most negative and the four that were the most positive on the minor axis in each line. For each of the two control lines, eight families were chosen randomly from all 150 families in the base generation such that families chosen for the next generation fell randomly along the major axis. Families in the control line in subsequent generations were also selected randomly.

Once eight families in the base generation were chosen for each line, a male and a female plant from each family were chosen to contribute to the first generation after selection. Each family was crossed to each other family once, and a family provided either a maternal or paternal parent for each cross but not both; in other words, a nonreciprocal half-diagonal crossing design was used. Each of the eight families parented seven crosses, giving a total of 28 crosses per line. To generate the first three generations, we used a half-diagonal crossing design rather than a full-crossing design because of greenhouse-space constraints. A full-crossing design with fully reciprocal crosses was employed at the end of generations 3 and 4 to create generations 4 and 5, respectively, to have more power to detect cross-generational changes in the genetic correlations. In this crossing design, each family provided a maternal and a paternal parent for one cross, to give 56 crosses per line.

Plants were reared in a greenhouse at Indiana University. In each generation, two seeds per family were sown directly into 4" square plastic pots containing one part sterilized soil to one part Metro-mix (Scotts-Sierra Horticultural products, Marysville, OH), and thinned to one seedling per pot after germination, resulting in six to eight seedlings per cross. We always kept the

most central seeding to prevent a timing-of-germination bias. All individual plants from all lines were randomly intermixed on six greenhouse benches. Seedlings were provided with a 16 h light/8 h dark supplemented daylight regime with timer-controlled high-intensity metal-halide overhead lamps. Plants were watered and treated with pesticides as needed and fertilized every 10 days using half-strength, all-purpose 20:20:20 (J. R. Peters, Inc., Allentown, PA). For each generation, the number of plants, respectively, was 1075 (base generation), 772, 979, 961, 2384, and 2244.

We recorded the sex of each plant, and measured the calyx width of the third, fourth, and fifth flower produced on each plant in all generations. Measurements were performed in this way to minimize the effect of within-plant variation and/or plant architecture on calyx width. These three measures were averaged to give a mean calyx width for each individual plant.

To assess the effectiveness of artificial selection to reduce the between-sex correlation for calyx width, we used ASReml version 2.0 (VSN International Ltd., Hemel Hempstead, UK) to estimate the genetic variance, covariance, and correlation for male and female calyx width in every generation of each line. ASReml uses a model with individuals, rather than families, as a unit of observation and estimates genetic parameters using a restricted maximum likelihood approach, which allowed us to include all pedigree relationships and estimate heritabilities and between-sex covariances and correlations. We treated male and female calyx width as separate traits in the model. To determine if genetic correlations differed significantly from 0 or 1, we generated a null model in ASReml by constraining the covariance, and then compared the null model to the unconstrained model using the log-likelihood ratio statistic (Shaw et al. 1995). All statistical tests were labeled as significant if $P < 0.05$.

To determine whether artificial selection on the between-sex correlation caused a change in trait means, we compared the mean calyx width among all lines in generation 5 within each sex using analysis of variance (ANOVA), and used the Tukey–Kramer test to conduct pairwise comparisons among means. We used t -tests to compare each line in generation 5 with the base population. Within each sex, comparisons of additive genetic variance between the base population and each line in generation 5 were conducted using log-likelihood ratios. We mean-standardized the data for these tests to minimize scaling effects. Within each generation and line, the additive genetic variance of females was compared to the additive genetic variance of males, also using log-likelihood ratios and mean-standardized data. To determine whether selection and/or crossing program generated differences in inbreeding between the control and selection lines, we used the program VCE (Neumaier and Groeneveld 1998) to calculate inbreeding coefficients from all pedigree data within a line, and found no significant differences (data not shown).

SELECTION TO TEST THE REALIZED BETWEEN-SEX GENETIC CORRELATION

To evaluate whether our selected, lower correlation eliminated constraints in dimorphic response to selection, we conducted a generation of sex-specific directional selection to reduce flower size in females, using Control 1 (C1) and Selection 3 (S3) (hereafter “founding lines”). Responses to selection were evaluated relative to control lines established for each experimental line, as follows. A total of four new lines were generated from the preceding experiment by creating (1) a selection line to reduce calyx width in females and (2) a control line, for both the C1 and S3 lines. For each of the two founding lines used, seeds from the crosses made to produce generation 5 were planted for 24 families (each of the eight females per line, each crossed to three different males) and grown as above. Ten seeds from each of these 48 families were planted and grown as above and calyx width was measured on 420 individuals. In the selection lines, selection to reduce calyx width in females was performed by choosing the six to seven families with the lowest mean calyx width for females, without regard to the mean for males. Control lines were created by randomly selecting six to seven families. In both cases, one female and one male from each of these families were crossed to all individuals of the opposite sex not from the same family, generating a total of 30 families per line. Twelve seeds from each of these crosses were planted and grown as above and calyx width was measured for a total of 1384 individuals. To determine whether a response for females and a correlated response for males occurred, two-way ANOVAs were performed separately for the two founding lines, with calyx width as the dependent variable and selection type (selection vs. control), sex (female vs. male), and the selection type by sex interaction as fixed effects. Post-hoc Tukey’s comparisons of least squares means were used to compare males and females across the two selection types.

Results

SELECTION TO REDUCE THE BETWEEN-SEX GENETIC CORRELATION

Although the between-sex genetic correlation for flower size (calyx width) did not change in the two control lines, artificial correlational selection reduced the between-sex genetic correlation in two of the three selection lines (Fig. 2). The loss of the genetic correlation was sudden and complete in S3; the correlation dropped from 0.92 to 0.10 between generations 2 and 3, and remained not significantly different from zero thereafter. S2 also experienced a dramatic reduction from a starting correlation of 0.87 in the base generation (not significantly different from 1.0), to a low of 0.32 in generation 4. Selection did not have a consistent effect on mean flower size; the two control lines (C1, C2) had both the highest and lowest means at the end of the experiment

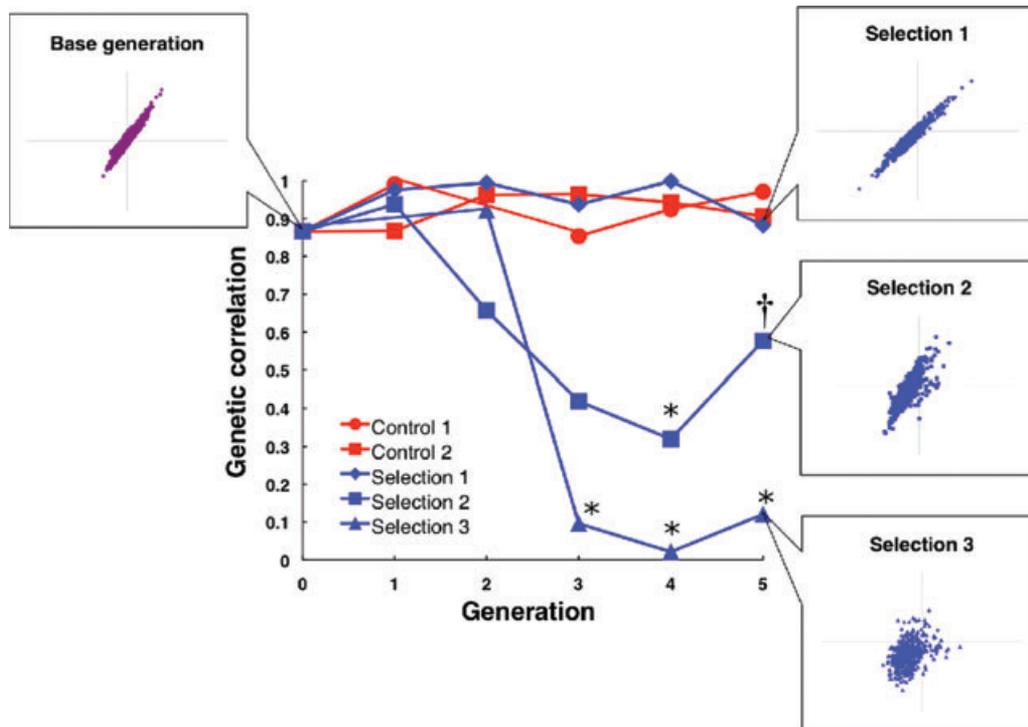


Figure 2. The genetic correlations between male and female flower size are shown for the control and selection lines over five generations of family-level, artificial correlational selection to reduce the genetic covariance between the sexes in *Silene latifolia*. Estimates of the between-sex correlation for flower size were made using restricted maximum likelihood (REML), with the plant as the unit of observation and male and female flower size as separate traits. Analysis of generation 2 in control line 1 and generation 1 in selection line 3 did not converge on an accurate estimate, and those points are not included in the figure. Boxes show the male flower size Best Linear Unbiased Predictors (BLUPs) (x axis) plotted against the female flower size BLUPs (y-axis) for each individual within the indicated lines, as estimated by REML. Based on log likelihoods from the appropriate null model and the log-likelihood ratio statistic, points marked with "*" are not significantly greater than 0 and are significantly less than 1. The point marked with "†" is significantly less than 1 and significantly greater than 0. All other points are not significantly less than 1.

Table 1. Mean (standard error) of flower size, heritability, and variance parameters after five generations of correlational selection. Within each sex, means that do not share a letter are significantly different from each other. In all lines and both sexes in generation 5, flowers were significantly smaller than in the base generation. Within each line, females marked with * have greater additive genetic variation than males. Within each sex, additive genetic variation estimates marked with † are significantly greater than the base generation. All significance testing was conducted on mean-standardized data, using comparisons of constrained and unconstrained models, log-likelihood ratio statistics, and a P-value of 0.05.

	Mean flower size (mm)		Heritability of flower size		Phenotypic variation for flower size		Additive genetic variation for flower size		Genetic covariance between males and females for flower size
	Males	Females	Males	Females	Males	Females	Males	Females	
Base generation	7.52 (0.05)	11.33 (0.05)	0.40 (0.11)	0.83 (0.10)	0.81 (0.06)	1.36 (0.11)	0.32	1.13	0.52
Generation 5									
Control 1	6.20 ^a (0.06)	9.51 ^a (0.06)	0.69 (0.12)	0.91 (0.12)	1.15 (0.15)	1.41 (0.20)	0.78	1.28	0.98
Control 2	7.09 ^b (0.07)	10.66 ^d (0.07)	0.66 (0.13)	0.91 (0.10)	0.83 (0.11)	1.46 (0.19)	0.55	1.32	0.77
Selection 1	7.09 ^b (0.11)	10.37 ^c (0.07)	0.54 (0.15)	0.84 (0.12)	1.97 (0.27)	2.17 (0.30)	1.06†	1.83†	1.23
Selection 2	6.97 ^b (0.06)	10.61 ^{cd} (0.07)	0.57 (0.18)	0.91 (0.14)	1.19 (0.18)	1.85 (0.30)	0.68	1.67*	0.62
Selection 3	6.93 ^b (0.06)	10.08 ^b (0.07)	0.72 (0.16)	0.82 (0.16)	1.21 (0.19)	1.98 (0.34)	0.86	1.63	0.14

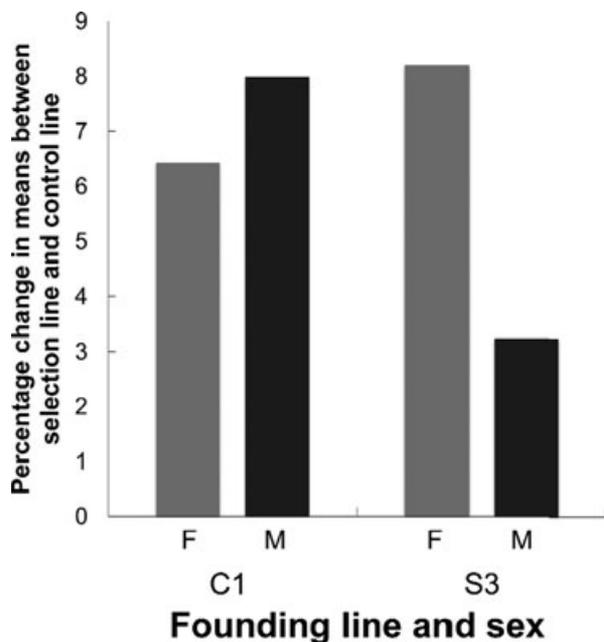


Figure 3. The absolute percentage change in female (F) and male (M) flower size as a consequence of directional selection to reduce flower size in females is shown. Two lines generated in the correlational selection experiment were used as founding populations: Control 1 (C1) and Selection 3 (S3). Within each founding line, we established a control line in which parents were selected at random for one generation and a selection line in which we imposed one generation of selection to decrease calyx width in females, and then calculated the percent change of the selection line relative to the control line.

(Table 1). Consistent with previous studies, males had smaller calyx widths and lower heritabilities than females. This pattern was found in both the base generation and generation 5 in all selection lines. There was no decrease in heritability of flower size for either sex after five generations, and additive genetic variation for calyx width was greater in the final generation as compared to the base generation for all selection and control lines (but the difference is only statistically significant in S1, Table 1). Additive genetic variation was significantly different between the sexes in S2.

SELECTION TO TEST THE REALIZED BETWEEN-SEX GENETIC CORRELATION

In the selection experiment in which females were selected to have smaller flowers, the selection differential for females was 1.59 mm for the C1 founding line and 1.71 mm for the S3 founding line, and selection on males was negligible (0.06 mm and 0.07 mm for C1 and S3, respectively). As expected given a between-sex genetic correlation close to 1.0, selection in C1 resulted in a significant and equivalent change in flower size for both sexes despite the fact that selection was only on females (Fig. 3). This finding confirms that the presence of a strong genetic correlation does in fact result in coupled evolutionary responses in both

sexes (see also Delph et al. 2004). In contrast, directional selection on flower size in females in the S3 line, with a genetic correlation of 0.12, resulted in a negligible correlated change in flower size in males. Consequently, in an analysis of variance within each founding line, while both selection type and sex were statistically significant predictors of flower size in the generation after selection, the interaction between sex and selection type was statistically significant only in S3 (Table 2).

Discussion

We were able to greatly reduce the high between-sex genetic correlation for flower size in *S. latifolia* in fewer than five generations in two of three selection lines by selecting directly to alter the correlation rather than mean flower size. Moreover, selection on females in the line with the greatest reduction in the correlation resulted in the expected lower response in males, relative to the response seen in a control line whose correlation remained high. Hence, the estimates of the between-sex genetic correlations from the first experiment had the predicted evolutionary consequences for correlated responses to selection.

The finding that selection can so dramatically reduce a strong genetic correlation in such a short number of generations is surprising, especially for a single trait expressed in two sexes. Genetic correlations between the sexes are summary statistics of genetic architecture that comprise the accumulated effects of pleiotropy, physical linkage, gametic-phase disequilibrium, allelic effects, and allele frequencies (Lynch and Walsh 1998). Although the results of this study cannot determine the genetic cause of rapidly evolving genetic correlations, some insight into underlying mechanisms can be gleaned from the patterns observed.

Only mechanisms capable of rapid change can explain the disappearance of a correlation in so few generations. The appearance and spread of new sex-specific alleles or mutations in modifier loci is unlikely in such a short time (Connallon and Clark 2010), which suggests that whatever mechanism underlies the change was already present and influencing variation in the population before selection was applied. Large changes in the frequencies of alleles acting in only one sex as a result of selection or drift (which could be strong within artificial-selection lines) could reduce the strength of correlations relatively rapidly. Correlations should be strongest when alleles with major effects in both sexes are segregating at intermediate frequencies, so fixation or loss of some alleles might alter correlations within a few generations (Agrawal et al. 2001). If this mechanism is responsible for the dramatic change in between-sex correlations, it implies that the genetic variation present in the population before selection encompasses not only flower size per se, but also varying degrees of sex-limited expression, and possibly variation in epistatic effects among shared and sex-limited loci.

Table 2. Two-way ANOVA comparing flower size among selection type (selection to decrease female calyx width vs. randomly mated control) and sex (female vs. male) after one generation, from parents in the Control 1 and Selection 3 founding lines. Parameter estimates for indicated selection type (C = control) and sex (F = female) are included to provide a measure of effect sizes.

Source	Parameter estimates	df	Sum of Squares	F ratio	P
Control 1 founding line					
Selection type	0.34 (C)	1,1	74.92	74.64	<0.0001
Sex	1.68 (F)	1,1	1807.57	1800.81	<0.0001
Selection type × sex	0.02 (C*F)	1,1	0.36	0.36	0.54
Error		674	676.53		
Selection 3 founding line					
Selection type	0.32 (C)	1,1	63.44	72.33	<0.0001
Sex	1.55 (F)	1,1	1507.94	1719.22	<0.0001
Selection type × sex	0.18 (C*F)	1,1	19.87	22.65	<0.0001
Error		664	582.40		

The difficulty for this explanation is that loci involved must affect the strength of the correlation between traits without affecting the value of each trait. Loci that express differential epistasis (i.e., “relationship QTL” or rQTL) are plausible candidates because they interact with other loci to generate variable patterns of pleiotropy (Pavlicev et al. 2008, 2011; Wagner et al. 2007). Spread of alternative rQTL alleles is predicted to alter the pattern of genetic covariance between traits without causing changes to the trait means. Changes in rQTL frequencies also are expected to inflate the variance of only one of the two traits involved in the correlation as observed in QTL studies of mouse body size and shape (Pavlicev et al. 2008). Although we observed increases in genetic variation in a few of our lines (Table 1), the results are not fully consistent with the differential epistasis model because the changes were not restricted to the selection lines in which genetic correlations were reduced. For example, females had greater variance than males in S2, a line in which the genetic correlation decreased, but genetic variation for both sexes was greater in S1, a line in which correlations stayed close to 1. The loss of genetic covariance is also not caused simply by the loss of genetic variance in one sex; S3, the line in which the covariance is smallest, had genetic variances larger than the control lines in both sexes. Although rQTLs may be present and acting in our selection lines, they are likely not the only element of change involved in altering genetic correlations.

Genetic correlations caused by gametic-phase disequilibrium might erode at rates up to 50% each generation in the absence of the assortative mating that generates it (Tallis and Leppard 1988; Conner 2002). Selection of the form practiced in this experiment should quickly alter patterns of gametic-phase disequilibrium, although separate loci must already influence the flower size expressed in the two sexes for change to occur. However, several lines of evidence argue against this explanation for the change

in the between-sex genetic correlation in this study. First, the presence of such sex-specific loci would not promote the strong correlation seen in the population before selection unless they were closely physically linked. Physical linkage disequilibrium is not expected to decay rapidly. Second, the control lines showed little of the change in the correlation after random mating for five generations that would be expected to accompany the breakdown of gametic-phase disequilibrium in unlinked loci. The differences among lines in the effectiveness of selection (one out of the three showed no measurable change in the correlation) further suggest a role of chance and variation in starting allele frequencies in the process, similar to results of other selection lines on correlated traits (Bell and Burris 1973; Scheiner and Istock 1991; Shaw et al. 1995). However, if allele-frequency changes for genes of major effect do explain the rapid reduction in the correlation, we also should see altered heritabilities and means of traits (Agrawal et al. 2001). Instead, we observed no statistically significant change in heritabilities, only minor reductions in mean flower size, and means in the selection lines did not change more than those of the controls.

Although the precise genetic mechanism that permits the rapid loss of a correlation remains unclear, the apparent liability of between-sex genetic correlations nevertheless requires a conceptual shift in understanding the forces that limit the phenotypic differentiation of the sexes. Strong genetic correlations do result in coupled evolutionary change of males and females, as confirmed in our second experiment. However, the fundamental cause of these correlations may have less to do with the inflexibility of underlying shared genetic mechanisms, and more to do with the form of selection that acts in nature.

A high between-sex genetic correlation for flower size may be maintained because of selection for dimorphism in the trait, not despite it. The selective pattern so effective at breaking the

correlation in our experiment is not likely to occur in a natural population. Such selection would have to simultaneously favor families that produce large-flowered males and small-flowered females and families with small-flowered males and large-flowered females. Correlational selection is more likely to occur on traits that are simultaneously expressed in the same individual, which leads to the prediction that nonlinear selection should increase stability of within-sex correlations more than between-sex correlations (Barker et al. 2010). Sexually antagonistic directional selection on flower size should be the strongest force for increasing dimorphism in the wild (Lande 1980). Even sex-specific selection (selection only on one sex or the other, but not both) preserves a high between-sex genetic correlation in this species (Delph et al. 2004) and may be the most common pattern in nature (Cox and Calsbeek 2009). Either form of directional selection would favor families at the tips of the major axis of variation, which would work to preserve a strong positive genetic correlation between the sexes. Thus, the very selection that favors sexual dimorphism may promote the genetic phenomenon that limits it.

Regardless of the mechanisms that underlie them, between-sex genetic correlations constrain the evolution of sexual dimorphism. Our findings suggest that these constraints come not from a simple conflict between an inflexible genetic architecture and a pattern of selection working in opposition to it, but rather a complex relationship between a changeable genetic correlation and a pattern of selection that promotes it.

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