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The X chromosome is a hot spot for sexually antagonistic fitness variation

Jonathan R. Gibson[1,2], Adam K. Chippindale[1] and William R. Rice[1*]

[1]*Department of Ecology, Evolution and Marine Biology, University of California at Santa Barbara, Santa Barbara, CA 93106-9610, USA*
[2]*Department of Biology, University of California at Santa Cruz, Santa Cruz, CA 95064, USA*

Sexually antagonistic alleles are selected discordantly between the sexes. Experimental evidence indicates that sexually antagonistic fitness variation is abundant in the genome of *Drosophila melanogaster*. Theory predicts that the X chromosome will be enriched with this type of variation. To test this prediction in *D. melanogaster*, we sampled, and cytogenetically cloned, 20 X chromosomes and compared their fitness variation to genome-wide levels. At the juvenile stage, in which gender roles are most similar, the X chromosome made no detectable contribution to genome-wide fitness variation. At the adult stage, in which gender roles diverge, the X chromosome was estimated to harbour 45% of the genome-wide fitness variation and 97% of the genome-wide sexually antagonistic variation. This genomic structure has important implications for the process of sexual selection because X-linked sexually antagonistic variation contributes to negative intersexual heritability for fitness, i.e. high-fitness males (females) produce, on average, low-fitness daughters (sons).

Keywords: X chromosome; sex chromosomes; intersexual conflict; intersexual ontogenetic conflict; sexual dimorphism; *Drosophila*

1. INTRODUCTION

Experimental studies have revealed sexually antagonistic fitness variation in the genomes of both plants and animals (for example, Sherman 1977; Endler 1980; Meagher 1992; Rice 1992, 1998; Kohorn 1994; Forsman 1995; Chippindale *et al.* 2001), but its chromosomal distribution has not been assessed. Comparative studies indicate that the X chromosome is enriched with genes associated with sex and reproduction (Reinhold 1998; Hurst & Randerson 1999; Saifi & Chandra 1999; Ritchie 2000; Wang *et al.* 2001), yet its contribution to fitness variation is unknown. Theory addresses both of these empirical patterns by predicting that the X chromosome will be exceptionally polymorphic for sexually antagonistic fitness variation (Rice 1984; Rice & Chippendale 2001).

To illustrate why X-linkage facilitates polymorphism for sexually antagonistic alleles, consider a rare recessive mutation that has a large disadvantage in females and a small advantage in males (assumed to be the heterogametic sex with hemizygous expression of X-linked genes). When averaged across the sexes, the mutation is not favoured by selection and it would not accumulate at an autosomal locus. If X-linked, however, it will initially accumulate because it is expressed far more commonly in males (in which there is no masking by dominance) compared with females. The degree of male-biased expression declines as the allele accumulates, which enables counterselection in females to eventually halt the spread of the allele. Next, consider a dominant mutation that benefits females more than it harms males. At an autosomal locus, the mutation would fix because it has a net advantage when averaged across the sexes. However, with X-linkage, as the mutation accumulates it masks its own expression in heterozygous females, but not in hemizygous males. This asymmetry is magnified as the mutation accumulates, reducing its net selective advantage in females relative to its disadvantage in males. Eventually, the frequency gain of the mutation in females is exactly matched by its decline in males and polymorphism is established. In general, this pattern of frequency-dependent, differential gene expression in the two sexes promotes stable polymorphism at X-linked loci over a wide range of detriment/benefit ratios (figure 1).

Outside the context of sexually antagonistic variation, X-linkage can hinder polymorphism. The effective population size of an X-linked locus is reduced by its smaller number of genes ($3N$ at an X-linked locus versus $4N$ at an autosomal locus, where N is population size), and this reduction is expected to decrease polymorphism compared with an autosomal locus (Wright 1933; but there is also a countervailing effect due to a reduced influence of sexual selection on X-linked genes (Charlesworth 1996; Hedrick & Parker 1997)). In addition, the efficiency of natural selection can be increased at X-linked loci because recessive alleles are not masked by dominance in males (Charlesworth *et al.* 1987), and this can further reduce polymorphism due to more frequent selective sweeps (Maynard Smith & Haigh 1974; Kaplan *et al.* 1989; Wiehe & Stephan 1993; Begun & Whitley 2000).

There have been many experimental studies of *Drosophila melanogaster* that measured fitness (total or its components) of the X chromosome or autosomes (for example, Sved 1975; Curtsinger 1984; Eanes *et al.* 1985; Mackay 1986). These studies did not estimate normal levels of standing genetic variation within an outbred population because they suffer from one or more of the following limitations: fitness was not measured under (i) the environmental conditions or (ii) the genetic back-

* Author for correspondence (rice@lefesci.ucsb.edu).

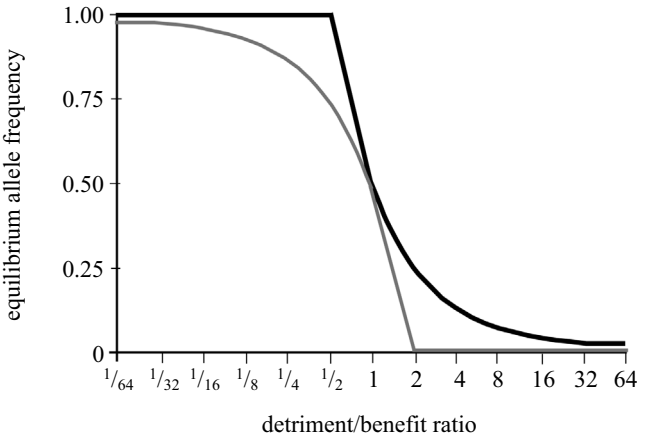

Figure 1. The equilibrium frequency of an X-linked sexually antagonistic allele in relation to the ratio of fitness gain to one sex and the harm to the other sex. The black curve refers to a recessive male-benefit allele and the grey curve to a dominant female-benefit allele. Polymorphism is expected over a wide range of the parameter space. The detriment/benefit ratio = $-t/s$, where t is the negative selection coefficient in one sex and s is the positive selection coefficient in the other sex, relative to an alternative allele that has equal fitness in both sexes. The effect of incomplete dominance, and the theory used to generate the curves, are described in Rice (1984).

grounds to which the chromosomes were adapted; fitness of chromosomes from outbred populations was (iii) measured in the homozygous state or (iv) in only one or a few genetic backgrounds; (v) activation of transposable elements may have produced artificially elevated levels of standing genetic variance; and (vi) sex-specific fitness could not be determined. Our experimental design ensures that none of these problems apply to the fitness assays reported here.

Empirical studies of molecular variation have demonstrated that the X chromosome of *D. melanogaster* (and its close relative, *Drosophila simulans*) has substantially reduced genetic variation compared with the autosomes (Langley *et al.* 1981; Moriyama & Powell 1996; Begun & Whitley 2000). The level of X-linked fitness variation, however, cannot be determined directly from molecular data. To test the prediction that the X chromosome is enriched with sexually antagonistic fitness variation, we first developed two benchmarks for comparison.

The first benchmark was the level of genome-wide fitness variation within each sex, and the covariation between the sexes. Recent studies demonstrated that *D. melanogaster* carries substantial genome-wide genetic variance for fitness when assayed under competitive conditions with natural levels of heterozygosity (Fowler *et al.* 1997; Chippindale *et al.* 2001; Chippindale & Rice 2001). To determine how much of this variation is sexually antagonistic (i.e. intersexual negative covariance for fitness), we measured the fitness of the same 40 genomes (i.e. genomic haplotypes consisting of the X chromosome and the two major autosomes) in both males and females (Chippindale *et al.* 2001). Fitness was measured under natural levels of heterozygosity and partitioned into its juvenile and adult components. Juvenile fitness (i.e. egg-to-adult viability measured under competitive conditions) accounted for *ca.* 15% of genetic variance in total fitness. This fitness component contained no detectable sexual antagonism, as demonstrated by (i) a strong positive correlation for fitness when the same genomes were expressed in males versus females (i.e. positive intersexual covariance), (ii) substantial intersexual-additive variation (measures consistent effects on fitness of the same genome across the sexes), and (iii) no intersexual-interactive variation (measures inconsistent effects on fitness of the same genome across the sexes).

Adult fitness (i.e. male reproductive success and female fecundity, both measured under competitive conditions) accounted for *ca.* 85% of genetic variation in total fitness. It was typified by antagonistic selection between the sexes, as demonstrated by (i) a negative correlation for fitness when the same genomes were expressed in males versus females (i.e. negative intersexual covariance); (ii) no measurable intersexual-additive variation; and (iii) substantial intersexual-interactive variation.

The second benchmark is the expected proportion of genome-wide fitness variance and covariance that is X-linked, on the null hypothesis that the X chromosome is not enriched with sexually antagonistic variation. The most parsimonious expectation is that the amount of fitness variation and covariation residing on the X chromosome will be proportional to its size, which is *ca.* 20% of the euchromatic genome (Adams *et al.* 2000). A benchmark of 20% X-linked fitness variation, however, assumes that fitness combines additively across chromosomes, and it does not adjust for any special characteristics of the X chromosome, such as its distinctive effective population size (Wright 1933; Charlesworth 1996; Hedrick & Parker 1997; Charlesworth *et al.* 1987) and the observed depressed levels of X-linked molecular variation (Langley *et al.* 1981; Moriyama & Powell 1996; Begun & Whitley 2000).

We control for these confounding factors that affect X-linked loci by contrasting fitness variation on the X chromosome between juvenile and adult life-history stages. Our previous study (Chippindale *et al.* 2001) of genome-wide fitness variation found no evidence for sexually antagonistic variation at the juvenile life-history stage, in which gender roles are most similar, so theory does not predict that the X chromosome will harbour excess fitness variation for juvenile fitness. However, our earlier study found substantial sexually antagonistic variation for the adult life-history stage, in which gender roles diverge strongly, so here an excess of X-linked fitness variation is predicted. A comprehensive null hypothesis, that controls for the distinctiveness of the X chromosome, is that it will code for the same, or similar, proportions of genetic variation in both the juvenile and adult stages. The alternative hypothesis is that the X chromosome will code for proportionately more genetic variation for adult fitness, in which sexually antagonistic variation is common, compared to juvenile fitness, in which it is more rare or absent.

The data that we collected were bivariate measures of fitness when the same X chromosomes were expressed in males versus females. Fitness was measured at both the juvenile and adult life-history stages (see § 2). To assess the proportional contribution of the X chromosome to fitness, these data were compared to the same measures

for entire genomes that had been measured previously (Chippindale *et al.* 2001).

Four specific predictions were tested. The first two predictions concern genetic variation for fitness when the two sexes are analysed independently. The second two predictions concern how fitness combines across the sexes when the same genetic material (X chromosome or entire haploid genome) is expressed in both sexes. The predictions were (i) when measuring fitness in females, the proportion of genome-wide fitness variation that is X-linked will be larger for the adult stage (in which sexually antagonistic variation is common) compared with the juvenile stage (in which it is rare or absent); (ii) as prediction (i) but applied to males; (iii) the proportion of genome-wide fitness variation that resides on the X chromosome will be greater for the intersexual-interaction variance observed in adults, compared to the intersexual-additive variance observed in juveniles; and (iv) the proportional contribution of the X chromosome to genome-wide intersexual covariation for fitness will be greater for the negative covariance observed in adults, compared to the positive covariance observed in juveniles.

2. MATERIAL AND METHODS

The assay commenced with 20 X chromosomes, randomly selected from a large outbred laboratory population (LH_M, described in Chippindale *et al.* (2001)). Each X chromosome was cloned and amplified (using cytogenetic techniques, figure 2*a*), and then its fitness was measured independently in females (figure 2*b*) and males (figure 2*c*). The fitness of each X chromosome was measured in a large number of random heterozygous genetic backgrounds (an average of 225 genetic backgrounds per X chromosome per sex) and under the same environmental conditions to which the base population had adapted for over 200 generations. In males, each X chromosome was measured in the hemizygous state, and in females, in the heterozygous state. The protocols for cloning and measuring fitness were the same as those described in Chippindale *et al.* (2001), with the exception that only the X chromosome, rather than a full X/autosome genomic haplotype, was cloned and measured (figure 2).

Genetic variance of fitness was calculated by first scaling the data so that the average fitness of the fittest of the 20 X chromosomes (or 40 genomes) was equal to 1.0. A random-effects ANOVA was next used to calculate the proportion of the phenotypic variance in fitness that was additive genetic variance (i.e. additive across different genetic backgrounds) by using the 'variance components estimates' routine within the JMP statistical package (SAS Institute, Cary, NC). Genetic covariance of fitness between the sexes was calculated from the correlation of mean fitness of X chromosomes in males and females. Additional details can be found in Chippindale *et al.* (2001) and Chippindale & Rice (2001).

The statistical significance of the hypothesis that the X chromosome is especially polymorphic for sexually antagonistic fitness variation was assessed by bootstrap analysis of the data collected for the X chromosome alone and the data collected for entire genomes. For each of 10 000 bootstraps, the original two datasets were randomly resampled with replacement, the genetic variances (or covariances) were calculated, and then the proportion of genetic variance (or covariance) on the X chromosome was compared to that for the entire genome. These calculations were carried out for both juvenile and adult fitness components.

3. RESULTS

In the adult stage, significant X-linked genetic variation for fitness was observed in both females (ANOVA, $F_{19,152} = 2.515$ and $p = 0.001$) and males (ANOVA, $F_{19,152} = 1.676$ and $p = 0.0459$), but no significant genetic variation was observed for the juvenile stage (ANOVA, $p > 0.54$ for both sexes). Adult fitness for the same X chromosome depended strongly on the sex in which it was expressed (figure 3*a*, ANOVA, genotype × gender interaction, $F_{19,320} = 2.331$ and $p = 0.0015$), and there was a negative genetic correlation for fitness between the sexes (figure 3*b*, Pearson's correlation test, $F_{1,18} = 3.903$ and $p = 0.031$).

In evaluating the correspondence of the data (i.e. levels of X-linked versus genome-wide fitness variation) to theoretical predictions, we first focus on the patterns of the point estimates of the variance components, and then consider the statistical significance of these patterns. In all comparisons, the X chromosome was estimated to contribute substantially more to adult, compared to juvenile, fitness. In adult females, the estimated additive genetic variance for fitness on the X chromosome was 39% of the value for entire genomic haplotypes, whereas in the juvenile stage it was 0% (figure 4*a*). In the assay of male fitness the same pattern was found, i.e. the X chromosome was estimated to carry 50% of the genome-wide variance in adult fitness and 0% in juvenile fitness (figure 4*b*).

Pooling data for the fitness of the same genomes, or X chromosomes, in males and females allowed us to measure how fitness combines across sexes. The degree of gender-specific selection was quantified by comparing intersexual-additive and intersexual-interactive variance components. Gender-dependent fitness effects are estimated by the intersexual-interaction genetic variance, and gender-independent fitness effects are estimated by the intersexual-additive genetic variance. The pattern of intersexual-additive and intersexual-interaction variance displayed by the X chromosome was qualitatively similar to that found earlier for whole genomes (Chippindale *et al.* 2001), but it differed quantitatively (figure 4*c*,*d*). Out of the total genetic variation produced by entire genomic haplotypes, the X chromosome was estimated to contribute 0% to the intersexual-additive genetic variance for juvenile fitness (concordant fitness effects between the sexes, figure 4*c*) compared to 47% of intersexual-interaction variance for adult fitness (discordant fitness effects between the sexes, figure 4*d*). Last, the X chromosome was estimated to contribute predominantly (97%, figure 4*e*) to the genome-wide negative genetic covariance for adult fitness compared to its negligible estimated contribution to the positive genetic covariance for juvenile fitness (0%, figure 4*e*).

The statistical significance of the hypothesis that the X chromosome is especially polymorphic for sexually antagonistic fitness variation was assessed by bootstrap analysis of the data displayed in figure 4. There were four relevant contrasts: the relative contribution of the X chromosome to (i) the intrasexual-additive genetic variation in juvenile versus adult fitness in females (figure 4*a*), (ii) this same

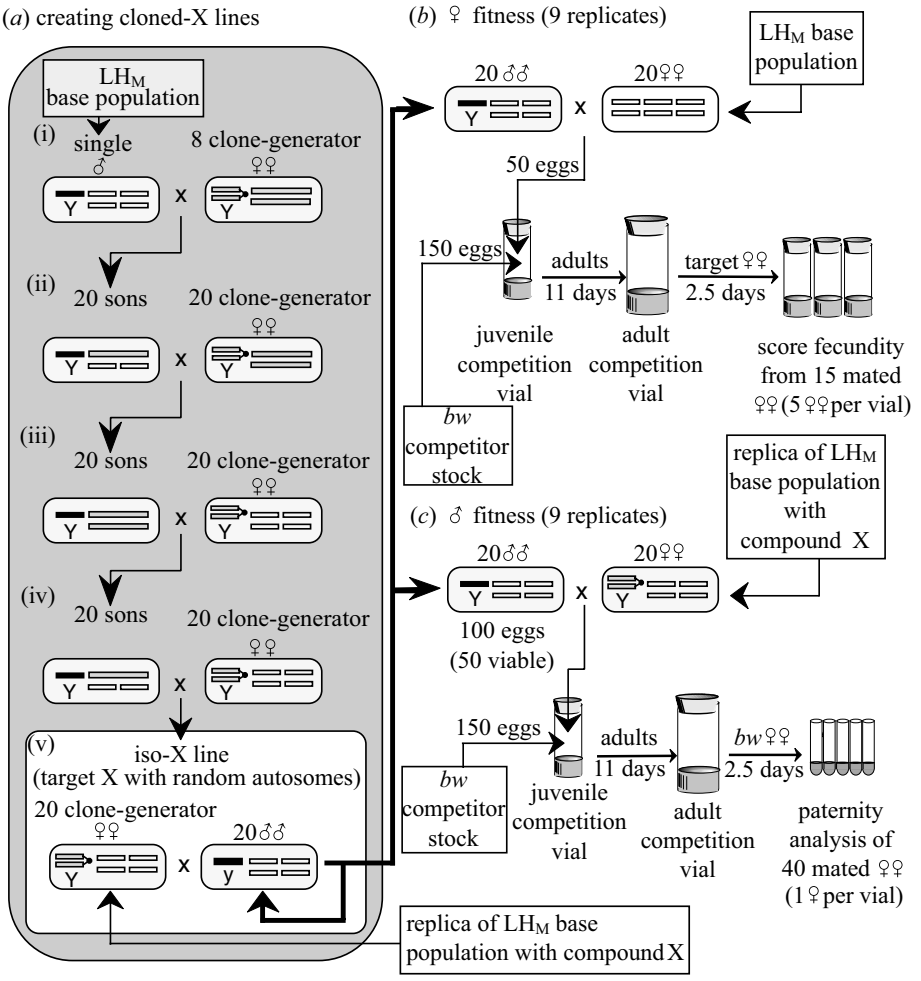

Figure 2. The crosses used to clonally amplify an X chromosome and then measure its fitness in males and females. (*a*) An X chromosome is randomly sampled (step i), separated from its original genetic background (steps ii–iii), and then used to begin an iso-X stock (steps iii–v). The iso-X stock was continuously backcrossed to a compound X stock that carried autosomes derived from the base population (step v). The juvenile and adult fitness of the X chromosome were measured in (*b*) females and (*c*) males. The protocol was applied independently to 20 different X chromosomes. Each X chromosome was assayed nine times independently (step *b* or *c*) in each sex. Details of the cytogenetic cloning technique, cytogenetic constructs and fitness assay protocol are provided in Chippindale *et al.* (2001).

contrast when measured independently in males (figure 4*b*), (iii) the intersexual-interaction variances of adult fitness versus the intersexual-additive variance of juvenile fitness, when data for the sexes are combined (figure 4*c,d*), and (iv) negative genetic covariance of adult fitness versus the positive genetic covariance of juvenile fitness (figure 4*e*). An excess in the percentage of X-linked genetic variance/covariance for adult compared to juvenile fitness had bootstrap support of 95% or higher for contrasts (i), (iii) and (iv). Although the pattern observed in contrast (ii) was consistent with an excess of X-linked variation for adult fitness, it was not evaluated via bootstrap analysis because significant additive genetic variance in the juvenile stage was not found for the X chromosome or entire genomic haplotypes.

4. DISCUSSION

Collectively, these results suggest that, as predicted from surveys of molecular variation, the X chromosome has a minor role in coding for fitness variation and covariation at the juvenile stage, in which gender roles are similar and in which data for entire genomes indicated no evidence for sexually antagonistic fitness variation. This finding of low variation for juvenile fitness on the X chromosome was similar to a previous study (Eanes *et al.* 1985) that reported no significant additive genetic variation for egg-to-adult viability in a wild *D. melanogaster* population from northeastern North America. These researchers did find significant genetic variation in a second North American population, but it was potentially a consequence of dysgenic crosses that would have augmented the standing genetic variance. In sharp contrast, the X chromosome has a major role in coding for fitness variation and covariation at the adult stage, in which gender roles diverge and in which data for entire genomes provide evidence for substantial sexually antagonistic fitness variation.

The finding of frequent strong reversals in the fitness of X chromosomes (and entire genomes), when expressed in males compared with females, is consistent with previous studies of quantitative trait loci (QTL). It is common for the same QTL to have markedly different effects in males compared with females (for example, Long *et al.* 1995;

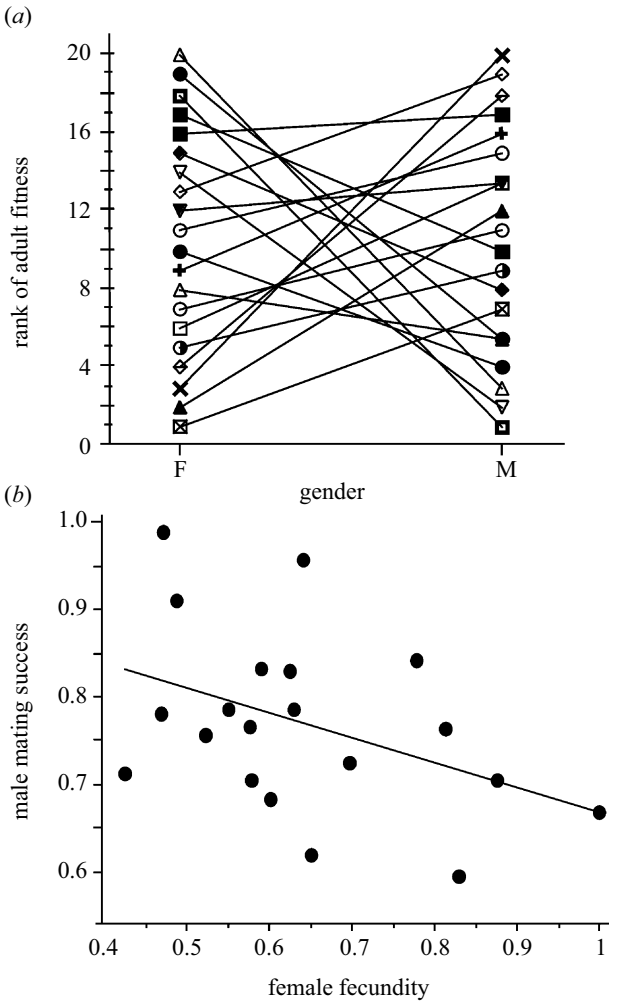

Figure 3. Adult fitness changes substantially when the same X chromosomes are expressed in males (M) and females (F). (*a*) Interaction plot of the rank of adult fitness (female fecundity and male reproductive success; measures are described in detail in Chippindale *et al.* (2001)) produced by the same X chromosome in males versus females (ANOVA, genotype × gender interaction, $F_{19,320} = 2.331$ and $p = 0.0015$). (*b*) Negative correlation between adult fitness of males and females (Pearson's correlation test, $F_{1,18} = 3.903$ and $p = 0.031$).

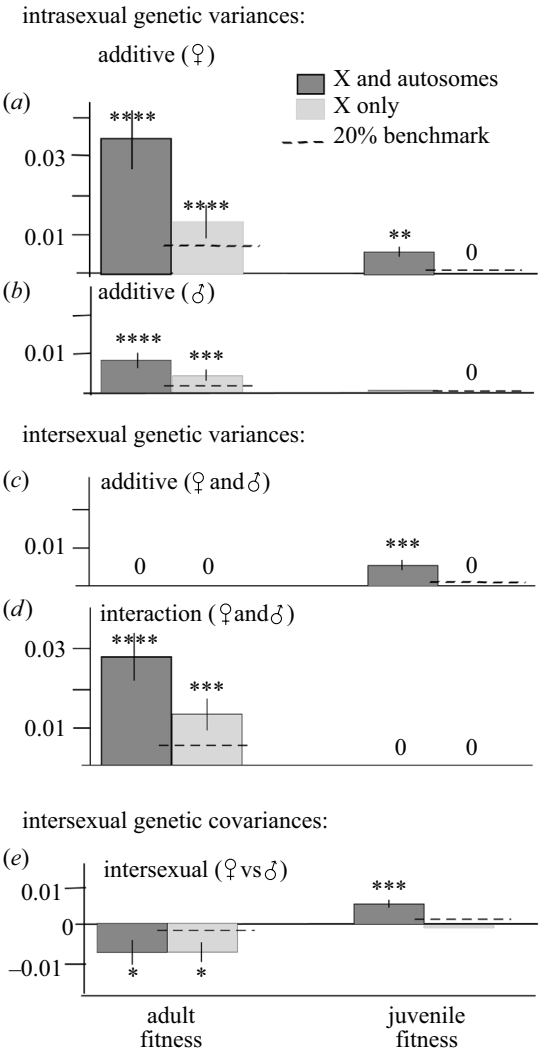

Figure 4. The observed genetic variance and covariance of a sample of 20 X chromosomes compared to the same measures for a sample of 40 entire haploid genomes. (*a*,*b*) Intrasexual genetic variances. (*a*) The additive genetic variance among X chromosomes or genomic haplotypes when they were expressed in females, i.e. the genetic variance associated with genotype, as estimated from a one-way random-effects ANOVA model: fitness = genotype (statistical procedures described in Chippindale *et al.* (2001) and Chippindale & Rice (2001)). (*b*) The same measure in males when data are pooled for the same X chromosomes (or genomic haplotypes) that were expressed in both males and females. (*c*,*d*) Intersexual genetic variances. (*c*) The intersexual-additive genetic variances for fitness (i.e. the variance among genotypes estimated from the mixed-effects model: fitness = genotype + gender + gender × genotype). (*d*) The intersexual-interaction genetic variance for fitness (i.e. the genotype × gender interaction variance in the preceding model). (*e*) The intersexual covariance for fitness (i.e. the covariance estimated from the regression of mean male fitness versus mean female fitness). The scale of the *y*-axis is the same for all histograms. The 20% benchmark represents the percentage of the euchromatic genome (haploid) that is X-linked. Error bars, s.d.; asterisks above histograms denote statistical significance of the null hypothesis: $\sigma^2_G = 0$; $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.005$, $^{****}p < 0.0001$. Dark grey columns, X chromosome and autosomes; light grey columns, X chromosome only; dashed line, 20% benchmark.

Mackay *et al.* 1996; Nuzhdin *et al.* 1997). This difference in expression of the same gene, or tightly linked genes, in the two sexes can lead to sexually antagonistic selection, but only when the direction of the sex-specific effect is maladaptive. This interaction between a gene and its sexual environment is in no way required for sexual antagonism because identical expression of the same gene in both sexes will be sexually antagonistic whenever it moves one sex toward its phenotypic optimum and the other sex away from its optimum.

Our results for intersexual covariance for adult fitness indicate that the X chromosome codes for an excess of sexually antagonistic fitness variation. We estimate that nearly all of the genome-wide sexually antagonistic fitness variation is X-linked. This estimate has a large standard deviation, however, and additional assays with larger sample sizes will be necessary to determine the degree to which sexually antagonistic fitness variation is limited to the X chromosome.

The observed high variation in fitness for the sample of 20 X chromosomes may have some bearing on the number of contributing loci and the size of their effects. If the X chromsome carries a large number of sexually antagonistic loci of small effect, then these numerous beneficial and harmful effects would tend to cancel out within each sex and the standing variance among chromosomes should be small—which it is not. This suggests at least two possibilities. The X chromosome may carry a predominance of alleles that favour one sex at the expense of the other. In this case, as the number of contributing loci increases so too does the variance in fitness among X chromosomes. If most new gain-of-function mutations show substantial dominance, then this might produce an asymmetry that produces a predominance of female-benefit sexually antagonistic alleles. Alternatively, there may be a relatively small number of loci with large effects on fitness. In this case, the high variance in fitness among X chromosomes would be expected without a requisite excess in alleles that favour one sex.

One of the interesting patterns from this study, and our previous study of entire genomes (Chippindale *et al.* 2001), is that males consistently display less standing genetic variance in fitness compared with females. A major part of this difference results from a genetic interaction between the Y and the X chromosomes and autosomes. These strong epistatic interactions were found to reduce additive genetic variation in males (Chippindale & Rice 2001).

The influence of the X chromosome as a hot spot for sexually antagonistic variation in our study of *D. melanogaster* may be unusually large because of the relatively large X chromosome of this species (20% of the genome) and because, in natural environments, the contribution of juvenile fitness (egg-to-adult viability) to total fitness may be larger than in the laboratory. Nonetheless, our study demonstrates that asymmetries in the chromosomal distribution of genome-wide fitness variation can be important in understanding fundamental evolutionary processes such as sexual selection.

When X-linked sexually antagonistic fitness variation is substantial, as theory (Rice 1984), past experiments (for example, Sherman 1977; Endler 1980; Meagher 1992; Kohorn 1994; Forsman 1995) and the data we present suggest, it will contribute to a negative intersexual heritability for fitness. Males (assuming male heterogamety) only pass their X chromosome to their daughters. As a consequence, X-linked sexually antagonistic variation that contributes to high-fitness sires cannot be transmitted to their sons (causing the sire–son X-linked heritability to be zero), but will be transmitted to daughters, in which sexually antagonistic alleles will lower their fitness (causing the sire–daughter X-linked heritability to be negative). Females pass their X chromosome to both sons and daughters. X-linked sexually antagonistic variation will contribute to high-fitness females producing low-fitness sons (the dam–son X-linked heritability is negative) and better than average daughters (the X-linked dam–daughter heritability is positive). In birds, and other species that have female heterogamety, males do pass X chromosomes to their sons, and this should substantially improve heritability of fitness between fathers and their sons, and thereby facilitate the sexual selection process. Genomic structure may thus substantially influence the dynamics of sexual selection.

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REFERENCES

Adams, M. D. (and 194 others) 2000 The genomic sequence of *Drosophila melanogaster*. *Science* **287**, 2185–2195.

Begun, D. J. & Whitley, P. 2000 Reduced X-linked nucleotide polymorphism in *Drosophila simulans*. *Proc. Natl Acad. Sci. USA* **97**, 5960–5965.

Charlesworth, B. 1996 Background selection and patterns of genetic diversity in *Drosophila melanogaster*. *Genet. Res.* **68**, 131–149.

Charlesworth, B., Coyne, J. A. & Barton, N. H. 1987 The relative rates of evolution of sex-chromosomes and autosomes. *Am. Nat.* **130**, 113–146.

Chippindale, A. K. & Rice, W. R. 2001 Y chromosome polymorphism is a strong determinant of male fitness in *Drosophila melanogaster*. *Proc. Natl Acad. Sci. USA* **98**, 5677–5682.

Chippindale, A. K., Gibson, J. R. & Rice, W. R. 2001 Negative genetic correlation for adult fitness between sexes reveals ontogenetic conflict in *Drosophila*. *Proc. Natl Acad. Sci. USA* **98**, 1671–1675.

Curtsinger, J. W. 1984 Frequency dependent selection in *Drosophila*: estimation of net fitness in pseudohaploid populations. *Evolution* **44**, 857–869.

Eanes, W. F., Hey, J. & Houle, D. 1985 Homozygous and heterozygous viability variation of the X chromosome of *Drosophila melanogaster*. *Genetics* **111**, 831–844.

Endler, J. A. 1980 Natural selection on color patterns in *Poecilia reticulata*. *Evolution* **34**, 76–91.

Forsman, A. 1995 Opposing fitness consequences of color pattern in male and female snakes. *J. Evol. Biol.* **8**, 53–70.

Fowler, K., Semple, C., Barton, N. H. & Partridge, L. 1997 Genetic variation for total fitness in *Drosophila melanogaster*. *Proc. R. Soc. Lond.* B **264**, 191–199.

Hedrick, P. W. & Parker, J. D. 1997 Evolutionary genetics and genetic variation of haplodiploids and X-linked genes. *A. Rev. Ecol. Syst.* **28**, 55–83.

Hurst, L. D. & Randerson, J. P. 1999 An eXceptional chromosome. *Trends Genet.* **15**, 383–385.

Kaplan, N. L., Hudson, R. R. & Langley, C. H. 1989 The hitchhiking effect revisited. *Genetics* **123**, 887–899.

Kohorn, L. U. 1994 Shoot morphology and reproduction in jojoba: advantages of sexual reproduction. *Ecology* **75**, 2384–2394.

Langley, C. H., Voelker, R. A., Brown, A. J. L., Ohnishi, S., Dickson, B. & Montgomery, E. 1981 Null allele frequencies at allozyme loci in natural populations of *Drosophila melanogaster*. *Genetics* **99**, 151–156.

Long, A. D., Mullaney, S. L., Reid, L. A., Fry, J. D., Langley, C. H. & Mackay, T. F. C. 1995 High resolution mapping of genetic factors affecting abdominal bristle number in *Drosophila melanogaster*. *Genetics* **139**, 1273–1291.

Mackay, T. F. C. 1986 A quantitative genetic-analysis of fitness and its components in *Drosophila melanogaster*. *Genet. Res.* **47**, 59–70.

Mackay, T. F. C., Hackett, J. B., Lyman, R. F., Wayne, M. L. & Anholt, R. R. 1996 Quantitative genetic variation of odor-guided behavior in a natural population of *Drosophila melanogaster*. *Genetics* **144**, 727–735.

Maynard Smith, J. & Haigh, J. 1974 Hitch-hiking effect of a favorable gene. *Genet. Res.* **23**, 23–35.

Meagher, T. R. 1992 The quantitative genetics of sexual dimorphism in *Silene latifolia* (Caryophyllaceae). 1. Genetic variation. *Evolution* **46**, 445–457.

Moriyama, E. N. & Powell, J. R. 1996 Intraspecific nuclear DNA variation in *Drosophila*. *Mol. Biol. Evol.* **13**, 261–277.

Nuzhdin, S. V., Pasyukova, E. G., Dilda, C. L., Zeng, Z.-B. & Mackay, T. F. C. 1997 Sex-specific quantitative trait loci affecting longevity in *Drosophila melanogaster*. *Proc. Natl Acad. Sci. USA* **94**, 9734–9739.

Reinhold, K. 1998 Sex linkage among genes controlling sexually selected traits. *Behav. Ecol. Sociobiol.* **44**, 1–7.

Rice, W. R. 1984 Sex chromosomes and the evolution of sexual dimorphism. *Evolution* **38**, 735–742.

Rice, W. R. 1992 Sexually antagonistic genes: experimental evidence. *Science* **256**, 1436–1439.

Rice, W. R. 1998 Male fitness increases when females are eliminated from gene pool: implications for the Y chromosome. *Proc. Natl Acad. Sci. USA* **95**, 6217–6221.

Rice, W. R. & Chippindale, A. K. 2001 Intersexual ontogenetic conflict. *J. Evol. Biol.* **14**, 685–693.

Ritchie, M. G. 2000 The inheritance of female preference functions in a mate recognition system. *Proc. R. Soc. Lond.* B **267**, 327–332.

Saifi, G. M. & Chandra, H. S. 1999 An apparent excess of sex- and reproduction-related genes on the human X chromosome. *Proc. R. Soc. Lond.* B **266**, 203–209.

Sherman, P. W. 1977 Nepotism and evolution of alarm calls. *Science* **197**, 1246–1253.

Sved, J. A. 1975 Fitness of third chromosome homozygotes in *Drosophila melanogaster*. *Genet. Res.* **66**, 197–200.

Wang, P. J., McCarrey, J. R., Yang, F. & Page, D. C. 2001 An abundance of X-linked genes expressed in spermatogonia. *Nature Genet.* **27**, 422–426.

Wiehe, T. H. E. & Stephan, W. 1993 Analysis of a genetic hitchhiking model, and its application to DNA polymorphism data from *Drosophila melanogaster*. *Mol. Biol. Evol.* **10**, 842–854.

Wright, S. 1933 Inbreeding and homozygosis. *Proc. Natl Acad. Sci. USA* **19**, 411–420.

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