Fitness consequences of the selfish supergene *Segregation Distorter*

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Abstract

Segregation distorters are selfish genetic elements that subvert Mendelian inheritance, often by destroying gametes that do not carry the distorter. Simple theoretical models predict that distorter alleles will either spread to fixation, or stabilise at some high intermediate frequency. However, many distorter alleles are less common than expected, suggesting that key evolutionary forces remain undiscovered. Here, we measured the fitness of *Drosophila melanogaster* adults and juveniles carrying zero, one or two copies of three different variants of the naturally-occurring supergene *Segregation Distorter* (*SD*), in order to investigate why *SD* remains relatively rare despite its strong distortion. First, we show that the three variants differ in the severity and dominance of the fitness costs they impose on carrier individuals. Second, *SD*-carrying parents sometimes produce less fit offspring, suggesting that *SD* alleles have non-genetic, transgenerational costs. Third, we found parent-of-origin-specific effects of *SD* on the offspring sex ratio, perhaps due to off-target effects of *SD* on the sex chromosomes. Finally, we used a theoretical model to investigate how transgenerational and sex ratio effects alter the population genetics of distorter alleles; accounting for these additional costs can explain why real-world meiotic drive alleles are much rarer than predicted by earlier models.

Keywords: gene drive, meiotic drive, population genetic model, selfish genes, *t* paradox.

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Introduction

Segregation distorters are genetic elements that manipulate meiosis or gametogenesis such that they are present in more than the usual 50% of the gametes (Burt and Trivers 2006; Lindholm et al. 2016). Because of this bias in transmission, segregation distorters are predicted to spread rapidly to fixation assuming that individuals carrying the distorter are equally fit as non-carriers (Bruck 1957). Even if a distorter allele reduces the fitness of individuals that carry it, it can still be favoured by selection provided that its individual-level fitness costs are outweighed by the within-individual advantage conferred by segregation distortion (Lindholm et al. 2016). For this reason, there is currently great interest in using natural or artificially-created segregation distorters to spread human-beneficial alleles through wild populations, for example to introduce malaria resistance alleles into wild mosquito populations (Gantz et al. 2015). In addition to their promise for applied science, the study of segregation distorters has led to multiple advances in our understanding of evolution, genetics, and speciation (Rice 2013; Lindholm et al. 2016; Manser et al. 2017; Lin et al. 2018; Verspoor et al. 2018). The best-studied naturally-occurring distorter alleles are the *t* allele in mice (Carroll and Potts 2007), and the *Segregation Distorter* (*SD*) allele of *Drosophila melanogaster* (Larracuente and Presgraves 2012), both of which caused biased tranmission in heterozygous males by preventing the development of gametes that did not inherit the distorter.

The '*t* paradox' (Carroll and Potts 2007) is a long-standing evolutionary puzzle. The paradox is named after the mouse *t* allele, though the same problem applies to many other segregation distorters. In many species, distorter alleles are quite rare within populations; for example, the *t* allele occurs at frequencies of 5-14% depending on the population (Ardlie 1998), and *SD* occurs at frequencies of 0-8% (Brand et al. 2015). The paradox is that these frequencies are substantially lower than predicted by simple population genetic models (Bruck 1957; Lewontin 1968; Charlesworth and Hartl 1978; Taylor and Jaenike 2002; Holman et al. 2015). Taking the mouse *t* allele as an example, we know that *t* is transmitted to a fraction k of the offspring of heterozygous males where $k \approx 0.95$, and that individuals homozygous for *t* are usually sterile or non-viable (Ardlie 1998). Assuming that *t* has no other effects on fitness or inheritance, the segregation distorter is expected to reach an equilibrium allele frequency of $\frac{1}{2} - \sqrt{(k(1-k))}/2k$ (Bruck 1957), which is 38.5% for $k = 0.95$. The fact that the expected frequency is much higher than the allele frequencies observed for *t*, and other distorters with similar properties such as *SD*, is the *t* paradox. This discrepancy indicates that one or more key biological details about distorter alleles remained to be discovered, and so several subsequent models sought to resolve the puzzle by incorporating additional biological details missing from Bruck's model. For example, Lewontin (1962) argued that population structure can reduce the equilibrium frequency of a distorter allele (see also Bull et al. 2019), and Lewontin (1968) showed that strong, partially recessive fitness costs can reduce the equilibrium frequency of the distorter allele. Additionally, males carrying segregation distorters often perform worse in sperm competition due to the loss of half their gametes, which can affect the evolution of the distorter under certain conditions (Taylor and Jaenike 2002; Holman et al. 2015; Lindholm et al. 2016).

Here, we attempt to explain the puzzling rarity of *Segregation Distorter* (*SD*) in *D. melanogaster*. Similar to *t* in mice, *SD* is a gene complex or 'supergene' (Thompson and Jiggins 2014) composed of several linked loci on an autosome (chromosome 2). *SD* causes strong segregation distortion in heterozygous males by disrupting the development of non-*SD*-carrying spermatids (reviewed in Larracuente and Presgraves 2012). The *SD* supergene contains an 'insensitive' allele at the *Responder* locus (*Rsp*), while most chromosomes that lack *SD* carry a 'sensitive' *Rsp* allele that makes them susceptible to distortion. Chromosomal inversions in the *SD* region help to keep the component loci in linkage by suppressing recombination, which prevents the creation of recombinant 'suicide chromosomes' in which the insensitive *Rsp* allele linked to *SD* is replaced by a sensitive allele. The threat of suicide chromosomes appears to have selected for reduced recombination, and indeed the *SD* locus is usually embedded in a very large non-recombining region (*c.* 10% of the genome; Presgraves et al. 2009) that contains deleterious mutations that have hitchhiked alongside *SD* (Temin and Marthas 1984; Larracuente and Presgraves 2012; Brand et al. 2015). All *SD* alleles are thought to descend from a single common ancestor that appeared around 38,000 years ago (Brand et al. 2015), though *SD* has since diversified into multiple variants of *SD* that differ in their inversions and in their load of deleterious mutations (Presgraves et al. 2009; Larracuente and Presgraves 2012; Brand et al. 2015). In some populations, *SD* chromosomes are present at low, stable frequencies that suggest balancing selection (e.g. 0-8% in 14 populations; Brand et al. 2015), although high and unstable allele frequencies have also been reported: one *SD* variant increased in frequency from 17% to 98% over 23 years in Wisconsin (1984).

The evolutionary dynamics of distorter alleles such as *SD* depend strongly on the fitness of drive-carrying individuals (e.g. Lewontin 1968). Negative frequency-dependent selection is of particular interest, because it can maintain a balanced polmorphism of distorting and non-distorted alleles. If selection on the distorter is not negatively frequency-dependent, the distorter will eventually fix or go extinct (Holman et al. 2015). Recessive fitness costs provide a likely source of negative frequency-dependent selection, because recessive costs are expressed more often when the distorter allele (and thus distorter homozygotes) is common. However, some distorter alleles have no obvious fitness cost in homozygotes (Temin and Marthas 1984; Price et al. 2012), meaning that recessive costs cannot provide a complete answer to the *t* paradox. Additionally, models (e.g. Bruck 1957; Lewontin 1968) demonstrate that homozygote lethality is insufficient to explain the low allele frequencies of strong distorters like *SD* or *t*. For these two reasons, we also tested whether *SD* has additional fitness costs besides being harmful in homozygous form.

Here, we focus on the three best-studied variants of *SD*, which are named *SD-5*, *SD-72*, and *SD-Mad* (all originally collected in Wisconsin; Sandler et al. 1959). *SD-5* carries a different set of inversions from the other two and is thought to be homozygous lethal (Larracuente and Presgraves 2012), while some *SD-72*- and *SD-Mad*-type alleles are reportedly fit as homozygotes (Temin and Marthas 1984). To our knowledge, the relative fitness of *SD* heterozygotes has never been measured, although this parameter is crucial to the evolutionary dynamics of *SD* (Lewontin 1968). We therefore measured the fitness costs of carrying either 1 or 2 copies of *SD*, for larvae as well as male and female adults. We also investigated older reports (Hiraizumi and Nakazima 1967; Denell et al. 1969) that the offspring sex ratio of

males carrying *SD* deviates from the usual 50:50. If autosomal distorter alleles like *SD* alter the sex ratio in addition to their other effects, there would be presumably be evolutionary consequences (Fisher 1930) with ramifications for the *t* paradox; therefore, we also wrote a model to predict how sex ratio bias would affect allele frequencies of *SD*. Lastly, we tested whether *SD* has non-genetic, transgenerational fitness effects, e.g. mediated by parental effects or genomic imprinting, and use models to investigate how *SD* evolves in the presence of such transgenerational effects. Our empirical and theoretical findings have implications for the evoluton of *SD* (and other natural and human-engineered distorter alleles), and help to resolve the *t* paradox.

Methods

Fly stocks

All flies were reared at 25°C under natural light (*c.* 14h day length) in 25mm plastic vials containing food medium (yeast-soy-cornmeal-agar-corn syrup). All stocks were obtained from the Bloomington *Drosophila* Stock Centre unless otherwise stated (SD stock numbers: 64322, 64324, and 64323).

In order to generate a non-SD reference allele which also allowed us to visually distinguish flies carrying 0, 1 or 2 copies of *SD*, we created a stock carrying an isogenic copy of chromosome 2 that carried one recessive and one dominant phenotypic marker. The recessive marker was a mutant allele of *bw* encoding brown eye colour (obtained from a teaching laboratory in Melbourne; unknown origin), while the dominant marker was the transgene *Ubi-GFP* (stock 5826), which expresses green fluorescent protein (GFP) throughout the body. To recombine these markers, we crossed F1 *bw/Ubi-GFP* females to *bw* males and collected male progeny expressing brown eyes and GFP. From these recombinants, we selected a single male and crossed it to a female carrying wild-type X chromosomes (one from the *bw* stock and one from the *SD-72* stock) as well as the balancer chromosome *SM5*, collected +/+; *bw-GFP/SM5* progeny, and crossed them to create what we hereafter call the *bw-GFP* stock.

In the adult fitness assays, we used opposite-sex *bw* individuals as mates, and *Gla/CyO* individuals (stock 44227) as same-sex competitors. The offspring of *Gla/CyO* flies express a dominant mutant phenotype, distinguishing them from the offspring of the focal flies.

Lastly, the three SD-bearing Bloomington stocks had different balancer chromosomes (*SD-5* used *CyO*, *SD-72* used *SM5*, and *SD-Mad* was not balanced), so we first re-balanced the three SD stocks to use the *CyO* balancer (from the *Gla/CyO* stock) to remove this potential confounding effect. We then crossed *SD/CyO* progeny to the *bw-GFP* stock to create *SD/bw-GFP* individuals.

Experiment 1

Experimental crosses

We performed four types of experimental crosses for each of the three *SD* alleles (Figure 1). In Cross 1, we mated two *SD/bw-GFP* flies, yielding offspring carrying 0, 1 or 2 *SD* alleles. In Cross 2, we mated *SD/bw-GFP* females to *bw* males, yielding offspring carrying 0 or 1 *SD* alleles. Cross 3 was the reciprocal of Cross 2: a *bw* mother and *SD/bw-GFP* father. Lastly, to measure the baseline fitness of the *bw-GFP* allele, we mated two *bw-GFP* flies (Cross 4).

All of these crosses were performed in parallel on a common cohort of flies under identical conditions in a randomised order, minimising confounding effects. We ran all four crosses (and their associated fitness assays; see below) in each of three experimental blocks, with equal representation of crosses within blocks. We measured three components of fitness: survival rate from first-instar larva (hereafter 'L1 larvae') to adult, adult male competitive fertilisation success, and adult female fecundity following social interaction. For brevity, we term these juvenile, male, and female fitness. We also recorded the adult sex ratio produced by each cross.

Juvenile fitness and sex ratio assays

Mated females from the four experimental crosses were placed separately onto egg collection plates (grape-agar medium with live yeast) for 24h, then removed. We waited 24h, then collected L1 larvae and sorted them by GFP phenotype. The reason for beginning the assay with L1 larvae, not eggs, was that we could correctly classify the GFP phenotype of L1 larvae (100/100 successes in a pilot) but not eggs. We placed the sorted larvae in fresh vials in groups of up to 100. It was difficult to obtain 100 larvae for every class of progeny because some progeny classes are rare due to segregation distortion and/or mortality in the embryonic stage. We subsequently quantified juvenile fitness and the sex ratio by counting, sexing, and phenotyping the adults that eclosed from these vials.

Adult female and male fitness assays

Flies that survived to adulthood in the juvenile fitness assay were sorted by phenotype/genotype into single-sex vials, left to mature for 48-72h, and then used in adult fitness assays.

To measure female fitness, we placed 5 same-genotype females in an 'interaction vial' with 15 *bw* males and 10 *Gla/CyO* females (all flies were 48- to 72-hour-old virgins), and allowed them to interact for 48h to facilitate mating, courtship, behavioural interactions, and competition for food. We then recorded the number of surviving focal females, and moved them as a group to a new yeasted food vial (without the non-focal flies), where they oviposited for 24h. We then removed the females and counted the number of larvae eclosing from their eggs, and used this as our measure of female fitness. Thus, our measure of female fitness measure is the

product of female fecundity, the proportion of eggs that are fertilised, and offspring survival in the zygote-to-L1 stage.

To measure male fitness, we placed 5 same-genotype males in an interaction vial with 15 *bw* females and 10 *Gla/CyO* males (again, all flies were 48- to 72-hour-old virgins), where they interacted and mated for 48h. We then moved all surviving individuals (focal and non-focal) to a new food vial where they continued to interact and oviposit for 24h. We then removed all adults and allowed their offspring to develop to adulthood, then counted the number of progeny sired by the focal males and the competitor *Gla/CyO* males. We used the proportion of progeny sired by the focal males as a measure of adult male fitness. This fitness measure encompasses pre- and post-copulatory sexual selection, as well as the survival rate of focal males' offspring relative to those of *Gla/CyO* males.

Limitations of Experiment 1's juvenile fitness assay

Upon phenotyping adult flies emerging from Crosses 1-4, we observed unexpected recombination between the *bw* and *Ubi-GFP* loci for the *SD-72* and *SD-Mad* (but not *SD-5*) chromosomes (we had assumed that *SD* chromomes would be largely non-recombining in light of previous data; e.g. Presgraves et al. 2009). Specifically, in Cross 2, some GFP-negative larvae developed brown eyes, and some GFP-positive ones developed red eyes, indicating recombination in the *SD/bw-GFP* mother (recombinants were never seen in Cross 3, because there is no recombination in male *Drosophila*; this shows that phenotyping errors cannot explain the results). The proportion of recombinant adults in Cross 2 was 3.6% (95% CIs: 2.4-4.9%) for *SD-5*, 36.1% (33-39%) for *SD-72*, and 32.8% (30-36%) for *SD-Mad*. The *bw* locus is at the terminal end of the right arm of chromosome 2 (2R), and *SD-5* is distinguished from the other two variants by an additional inversion on 2R; we therefore hypothesise that the *Ubi-GFP* transgenic insertion lies somewhere on 2R between the *SD* complex and *bw*, probably close to the *SD-5*-specific inversion (Figure 1 in Larracuente and Presgraves 2012). As a consequence of this unexpected recombination, we cannot be certain how many larvae of each genotype were present at the start of the juvenile fitness assay for Cross 2, at least for *SD-72* and *SD-Mad* – we simply removed the recombinant individuals from the dataset, and made the simplistic assumption that all of the larvae that did not reach adulthood were non-recombinants. We interpret the relevant part of the Results in light of the resulting bias. This limitation is offset by data from Experiment 2 (which does not rely on these markers, and uses a non-recombining balancer chromosome), as well as data from Cross 3 (since there is no recombination in male *Drosophila*).

Additionally, for Cross 1, individuals carrying 0 or 1 *SD* chromosomes were phenotypically indistinguishable until they reached adulthood and developed eyes, and so we simply the measured the survival rate of a mixed pool of larvae carrying either 0 or 1 *SD* alleles. The great majority of larvae in this pool will caryy 1 *SD* allele, rather than 0, because of segregation distortion. Specifically, the proportion of *SD* progeny in the pool will be $1/(k + 2(1 - k))$, or 95.2% for $k = 0.95$. This limitation is offset by data from Crosses 2 and 3 and Experiment 2.

Experiment 2

Experiment 2 was designed to measure the direct and transgenerational effects of *SD* on sex-specific larval survival, and to address the limitations of Experiment 1. Experiment 2 used the transgenic construct *P{Sxl-Pe-EGFP.G}G78b* (extracted from stock 24105, backcrossed into the w^{1118} genotype for 5 generations, and made homozygous), which allows discrimination of males and females at the egg stage (female-destined embryos express GFP while males do not; Thompson et al. 2004). We conducted six types of crosses using parents bred at standardised density: in each cross, one parent was *SD/CyO* and the other was homozygous for *P{Sxl-Pe-EGFP.G}G78b*; we performed this cross with the three *SD* variants, with either the mother or the father providing *SD* (10-24 replicates per cross). We then collected embryos of both sexes (mean: 48 embryos per sex per cross), placed them in single-sex vials to develop, and then counted and phenotyped the eclosing adults to infer the survival rates of different progeny classes.

Statistical analysis

We analysed Experiment 1 using Bayesian hierarchical models implemented in the R package `brms` (Bürkner 2017). The data on juvenile fitness, male fitness, and adult sex ratio were treated as binomially distributed, and we fit 'vial' as a random effect to account for nonindependence among individuals from the same vial. Female fitness was modelled using the negative binomial distribution, since the data were overdispersed counts. We verified model fit using posterior predictive checks (Gelman and Hill 2006).

For hypothesis testing, we calculated the posterior differences between between pairs of means for contrasts that we deemed informative for this study. For example, we calculated the posterior difference between the mean fitnesses of individuals with 0 or 1 *SD* allele, or individuals that received *SD* from their father versus their mother, and thereby tested for genetic and parental effects respectively. We also calculated the posterior probability that the group with the larger posterior mean actually has a smaller mean than the other group; this provides a metric with a similar interpretation to the p-value (contrasts for which >95% of the posterior lies on one side of zero were considered notable). It is not necessary to correct for multiple testing when calculating these pairwise differences, since the contrasts are all calculated using the posterior from the same model and thus are not independent tests.

The aim of Experiment 2 is to estimate the proportion of *SD* and non-*SD* male and female larvae that survive to adulthood. However, because the genotype of larvae could not be visually determined at the start of Experiment 2, we had to estimate the initial numbers of larvae belonging to each genotype in order to calculate a survival rate. For example, if we placed 50 larvae in a vial and 20 non-SD and 20 *SD* individuals reached adulthood, we inferred the genotypes of the 10 dead ones in order to estimate the relative survival rates of *SD* and non-*SD* individuals. This unmeasured variable depends on the gametes produced by the *SD/CyO* parent. Because *SD* is well-documented to only cause distortion in males (Larracuente and Presgraves 2012), we assumed that the *SD/CyO* mothers transmitted *SD* to 50% of their progeny. We also assumed 50% transmission in *SD/CyO* fathers (i.e. $k = 0.5$),

in light of evidence that *CyO* carries an insensitive allele of *Rsp* that makes it immune to segregation distortion (Ganetzky 1977). We then used a binomial random number generator with $p = 0.5$ to 'guess' the genotypes of the dead larvae. Our sample size was sufficiently large that generating a new set of random numbers and re-running the model gave near-identical results, thanks to the law of large numbers. We also re-ran the model under the assumption that there is some segregation distortion in *SD/CyO* fathers (i.e. $k > 0.5$, contradicting the evidence in Ganetzky 1977), and found that all the key results did not change (Figure S1).

Population genetic model

Our experiments suggested that some *SD* variants have parent-of-origin-specific effects on fitness and/or cause SD-carrying males to produce a biased offspring sex ratio. We therefore constructed a simple one-locus, two-allele population genetic model to examine the effect of these two factors on the evolution of *SD*.

The model considers the spread of an autosomal segregation distorter in an infinitely large, panmictic population with discrete generations. We assume that individuals carrying two wild type alleles have a relative fitness of 1, while other genotypes potentially have relative fitness between 0 and 1. We tracked the parental origin of the *SD* allele in heterozygotes, to allow heterozygotes with a maternally-inherited *SD* to have a different fitness than heterozygotes with a paternally-inherited *SD*, and thereby allow for the possibility that *SD* has a parent-of-origin-specific effect on fitness. We assumed that male heterozygotes transmit *SD* to a fraction $(1 + K)/2$ of their offspring (where $0 < K < 1$), and produce a fraction $(1 + s)/2$ female offspring ($-1 < s < 1$), while all other genotypes were assumed to show normal Mendelian inheritance and a 50:50 offspring sex ratio. For example, a mating between a wild-type female and a male *SD* heterozygote produces $(1 + K)(1 - s)/4$ heterozygote sons, $(1 + K)(1 + s)/4$ heterozygote daughters, $(1 - K)(1 - s)/4$ wild-type sons, and $(1 - K)(1 + s)/4$ wild-type daughters. Note that for convenience, the model uses capital K (range: 0-1, where 0 indicates no distortion and 1 complete distortion), rather than the lowercase k discussed earlier (where 0.5 indicates no distortion and 1 complete distortion).

For each parameter space, we determined the evolutionary fate of an *SD* allele in a starting population with 1% *SD* alleles at Hardy-Weinberg genotype frequencies. We calculated the equilibrium allele frequencies numerically, since the analytical solution would be unwieldy. In each generation, we first multiplied the frequency of each genotype by its relative fitness (representing the combined action of natural and sexual selection across all life stages) and then renormalised the genotype frequencies to sum to one. We then determined the frequency of each of the possible mating types as the product of each possible pair of maternal and paternal genotype frequencies. From these, we determined the offspring genotype frequencies, and replaced the parental generation with the offspring. The simulation ran for 10,000 generations to ensure that *SD* had reached equilibrium, though it was terminated early if *SD* went extinct (defined as reaching 0.001% frequency) or fixed (>99%).

Results

Experiment 1

Posterior estimates of mean fitness for each group are plotted in Figure 1. Table 1 lists notable pairwise differences between groups, Tables S1-S4 give sample sizes and summary statistics, and Tables S6-S9 give results for all the contrasts we examined.

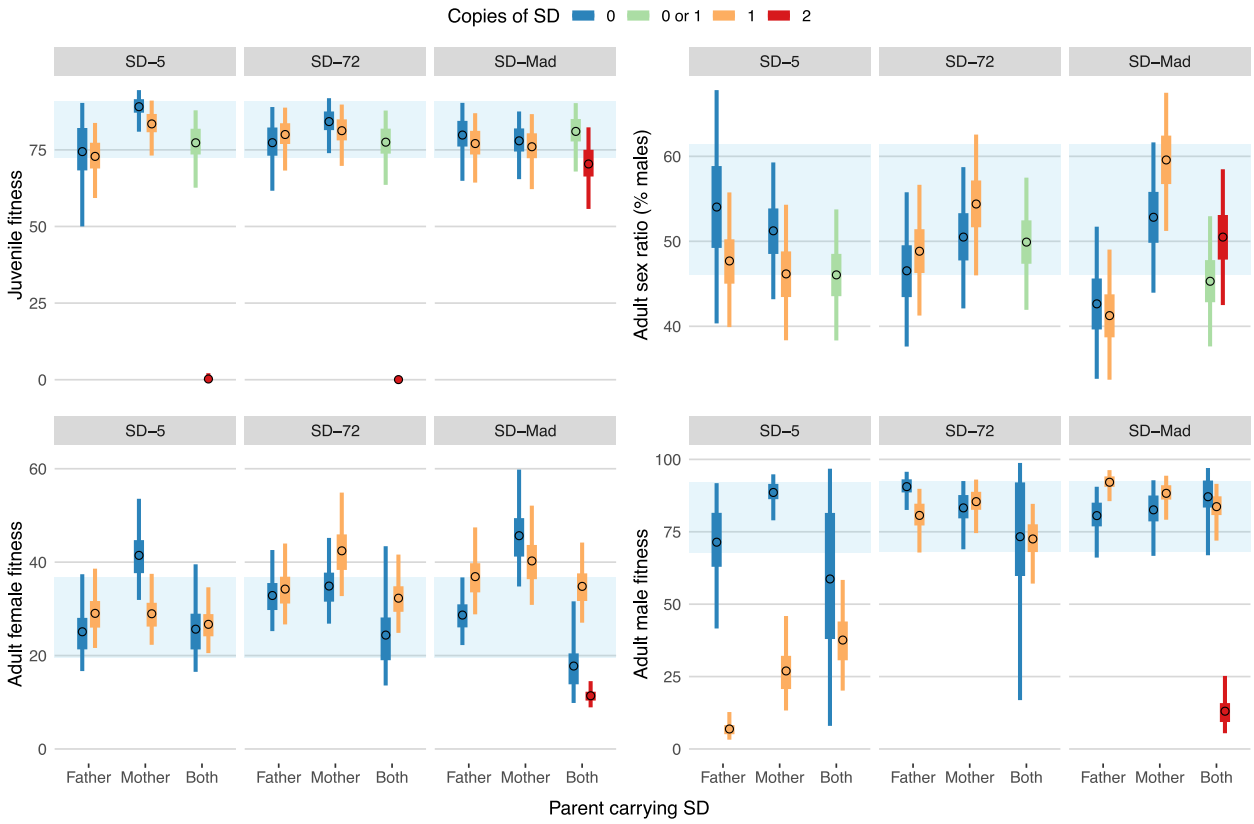

Figure 1: Posterior estimates of the group means for the four different response variables in Experiment 1, for each type of cross (x-axis), *SD* variant (panels), and genotype (colours). Juvenile fitness was measured as % L1 larva-to-adult survival, adult sex ratio refers to the number of males and females among the individuals that reached adulthood, female fitness is the estimated number of progeny produced per female, and male fitness as the siring success relative to competitior males. The thicker inner bar shows the region containing 50% of the posterior, the outer bar covers 95% of the posterior, and the circle marks the median. Tables S6-S9 give the accompanying statistcal results. Points labelled as carrying "0 or 1" *SD* allele refer to cases where the genotype of the offspring could not be ascertained due to the brown eye marker not being expressed in larvae; most of these individuals probably carried 1 *SD* allele because of segregation distortion.

Juvenile fitness

When collecting larvae we observed 40 L1 larvae homozygous for SD-5, and over 600 carrying two copies of SD-72, but none of these larvae survived to adulthood. The smaller number for

Table 1: List of the all the notable differences between groups in Experiment 1 (posterior probability, p, <0.05; see Tables S6-S9 for test results that did not meet this arbitrary cutoff). For each contast, we give the parent carrying SD (neither, mother, father, or both) and the number of SD alleles carried by the offspring. The difference in means is expressed as % larvae surviving, % male larvae, per-female progeny production, or % offspring sired, and the parentheses give 95% credible intervals. The difference is positive when the first-listed mean is larger than the second-listed mean, and negative otherwise.

SD	Trait	Comparison	Difference (95% CI)	p	Implication
SD-5	Larval survival	Both parents, 0 or 1 → Both parents, 2	77.1 (62.2 to 87.8)	0.0	SD is more costly when
SD-5	Female fitness	Neither, 0 → Mother, 0	-14.4 (-28.6 to -0.4)	0.0	Parental effect or genor
SD-5	Female fitness	Mother, 0 → Father, 0	16.4 (1.0 to 31.0)	0.0	Parental effect or genor
SD-5	Female fitness	Mother, 0 → Mother, 1	12.5 (-0.2 to 26.1)	0.0	SD is costly when heter
SD-5	Male fitness	Mother, 1 → Father, 1	20.0 (5.5 to 39.2)	0.0	Parental effect or genor
SD-5	Male fitness	Mother, 0 → Mother, 1	61.6 (41.0 to 77.7)	0.0	SD is costly when heter
SD-5	Male fitness	Father, 0 → Father, 1	64.5 (34.6 to 85.6)	0.0	SD is costly when heter
SD-72	Larval survival	Both parents, 0 or 1 → Both parents, 2	77.5 (63.6 to 87.8)	0.0	SD is more costly when
SD-Mad	Sex ratio	Neither, 0 → Father, 0	11.1 (-0.8 to 23.0)	0.0	Parental effect or genor
SD-Mad	Sex ratio	Mother, 1 → Father, 1	18.3 (7.1 to 29.7)	0.0	Parental effect or genor
SD-Mad	Female fitness	Neither, 0 → Mother, 0	-18.7 (-34.7 to -3.8)	0.0	Parental effect or genor
SD-Mad	Female fitness	Mother, 0 → Father, 0	17.0 (3.2 to 32.6)	0.0	Parental effect or genor
SD-Mad	Female fitness	Both parents, 1 → Both parents, 2	23.4 (15.0 to 33.1)	0.0	SD is more costly when
SD-Mad	Male fitness	Father, 0 → Father, 1	-11.5 (-26.7 to 0.6)	0.0	SD is costly when heter
SD-Mad	Male fitness	Both parents, 1 → Both parents, 2	70.6 (54.2 to 82.6)	0.0	SD is more costly when

SD-5 indicates that most *SD-5* homozygotes died before hatching, while *SD-72* homozygotes tended to die between hatching and adulthood. By contrast, many larvae homozygous for *SD-Mad* reached adulthood, and there was no detectable fitness effect of *SD-Mad* on juvenile fitness even in homozygotes.

The limitations of this assay (see Methods) mean that Figure 1 might underestimate the survival rate of individuals carrying a maternally-inherited *SD* allele, for *SD-72* and *SD-Mad*. Therefore, we cannot be certain that there is really no difference in juvenile fitness between individuals with an *SD* mother versus an *SD* father for *SD-72* and *SD-Mad*.

Sex ratio among individuals reaching adulthood

For crosses in which the father carried *SD-Mad*, the sex ratio of the emerging adults was significantly more female-biased than for crosses in which the mother carried *SD-Mad*, irrespective of offspring genotype. The results did not replicate earlier findings that the non-*SD* offspring of *SD* heterozygote fathers show a female-biased sex ratio (Hiraizumi and Nakazima 1967; Denell et al. 1969); indeed, there was a nonsignificant trend in the opposite direction for *SD-5* (the posterior median % male offspring was 54% among the non-*SD* offspring and 48% male among the *SD* offspring; Figure 1).

Adult female fitness

Females homozygous for *SD-Mad* had low fitness. Additionally, females were fitter if their mother, as opposed to their father, carried *SD-5* or *SD-Mad*, irrespective of whether the offspring inherited *SD*.

Adult male fitness

Males homozygous for *SD-Mad* had low fitness. We again observed evidence for non-genetic effects: for *SD-5*, males with a paternally-inherited *SD* chromosome were substantially less fit than males with a maternally-inherited *SD* chromosome. There was also a strong fitness cost of inheriting an *SD-5* allele from either parent. Interestingly, males with an *SD-Mad* father were fitter if they inherited *SD-Mad* rather than the non-*SD* allele.

Experiment 2

Experiment 2 also suggested that *SD* chromosomes can have both direct and transgenerational effects on L1 larva-to-adult survival (Figure 2; Table 2; full results in Tables S5 and S10). Male larvae with an *SD-5/CyO* mother were significantly less likely to survive than those an *SD-5/CyO* father, irrespective of whether the larva actually inherited *SD-5* (the same was not true for the other *SD* variants, suggesting that *SD-5* not *CyO* mediates this effect). Additionally, female larvae who inherited *SD-5* from the mother survived less well than did females who inherited *CyO*, suggesting that a single copy of *SD-5* reduces survival more than a single copy of *CyO*. The same effect was not observed for males, or for crosses in which *SD-5* came from the father, possibly indicating that *SD-5* has a sex- or parent-of-origin-specific effect on survival (we lack the sample size to be certain). By contrast, male larvae whose father carried *SD-Mad* were fitter if they inherited *SD-Mad* rather than *CyO*, suggesting that *SD-Mad* is less harmful than *CyO*. Lastly, we observed some significant sex differences in survival for all three *SD* chromosomes, with female larvae surviving better than male larvae. We did not find any evidence that the direct genetic effect of *SD* on larval survival is sex-specific: the difference in survival rate for *SD* and *CyO* individuals was similar for males and females (Figure 2).

Figure 2: Posterior estimates of % L1 larva-to-adult survival in Experiment 2 for each combination of offspring sex and genotype (x-axis), *SD* variant (panels), and whether the mother or father had the genotype *SD*/*CyO* ('cross'; colours). The thicker inner bar shows the region containing 50% of the posterior, the outer bar covers 95% of the posterior, and the circle marks the median. See Tables 2 and S10 for associated hypothesis tests. The model underlying this plot assumed fair meiosis ($k = 0.5$) in *SD*/*CyO* males; see Figure S1 for equivalent plots made using different assumed values of k.

Table 2: List of the all the notable differences between groups in Experiment 2 (posterior probability, p, <0.05; see Table S10 for test results that did not meet this arbitrary cutoff). For each group, we list the sex of the focal larvae, their genotype (*SD* or *CyO*), and the parent that carried *SD* (mother or father). The difference in means is expressed in % larvae surviving; other details are as in Table 1.

SD	Comparison	Difference (95% CI)	p	Implication
SD-5	Daughters, CyO, mother → Daughters, SD, mother	4.6 (-0.6 to 10.0)	0.0	SD lowers survival compared
SD-5	Sons, CyO, mother → Daughters, CyO, mother	-10.7 (-19.4 to -2.0)	0.0	Sons have lower survival than
SD-5	Sons, CyO, mother → Sons, CyO, father	-10.7 (-19.8 to -1.5)	0.0	Parental effect or genomic im
SD-5	Sons, SD, mother → Daughters, SD, mother	-9.1 (-18.7 to 0.4)	0.0	Sons have lower survival than
SD-5	Sons, SD, mother → Sons, SD, father	-9.7 (-19.4 to -0.1)	0.0	Parental effect or genomic im
SD-72	Sons, CyO, father → Daughters, CyO, father	-7.0 (-15.5 to 1.0)	0.0	Sons have lower survival than
SD-72	Sons, CyO, mother → Daughters, CyO, mother	-11.0 (-17.9 to -4.3)	0.0	Sons have lower survival than
SD-72	Sons, SD, mother → Daughters, SD, mother	-9.9 (-15.8 to -4.2)	0.0	Sons have lower survival than
SD-Mad	Daughters, CyO, mother → Daughters, SD, mother	5.4 (1.2 to 9.9)	0.0	SD lowers survival compared
SD-Mad	Sons, CyO, mother → Daughters, CyO, mother	-9.4 (-16.3 to -2.7)	0.0	Sons have lower survival than
SD-Mad	Sons, CyO, mother → Sons, CyO, father	-7.7 (-15.6 to 0.6)	0.0	Parental effect or genomic im

Population genetic model

We first assumed that the *SD* allele had no direct or transgenerational fitness costs (top left, Figure 3), which allowed *SD* to invade even if segregation distortion (K) was very weak. However, if the *SD* allele caused males carrying it to produce a highly biased sex ratio (unrealistically high, based on our data), *SD* required a higher K to invade. The reason that this sex ratio bias hinders the spread of *SD* is that autosomal loci usually maximise their fitness by producing a 50:50 sex ratio, due to 'Fisherian' selection on the sex ratio, which disfavours alleles causing unequal production of sons and daughters (Fisher 1930). In cases where the *SD* allele was able to invade, it generally went to fixation: a balanced polymorphism of *SD*- and non-*SD* alleles was seldom observed. There was a small zone of polmorphism when drive was very weak and sex ratio bias was very strong (both of which are unrealistic for any known distorter alleles). This polymorphism results from the frequency-dependent selection on alleles that affect the sex ratio: over-producing one sex is especially costly if that sex is over-represented in the population.

Secondly, when we assumed that all individuals with at least one *SD* allele had a relative fitness of 0.8 (dominant costs, top second left of Figure 3), the *SD* allele could still invade, though it needed a substantially higher transmission bias K to do so. When *SD* could invade, it again proceeded to fixation, except under unrealistically weak drive and extreme sex ratio bias. Notably, invasion was more difficult (i.e. a higher K was required) when we assumed that *SD* heterozygote males produce a female-biased rather than male-biased sex ratio; this is because *SD* can only bias segregation in males. *SD* invaded slightly more easily when *SD* heterozygote males produced >50% sons, but invasion was still harder than when *SD* did not bias the sex ratio (due to Fisherian sex ratio selection against *SD*).

Thirdly, when we assumed that *SD* is recessive-lethal but cost-free in heterozygotes (top second right, Figure 3), the *SD* allele stabilised at high, intermediate frequencies for realistic (i.e. high) values of K (as expected; Bruck 1957). This is because recessive fitness costs create negative frequency-dependent selection on *SD*, halting the spread of the *SD* allele once homozygotes become common enough to cancel out the effect of segregation distortion (Holman et al. 2015). A female-biased sex ratio reduced the equilibrium frequency of *SD* while a male-biased sex ratio had little effect, due to the opposing effects of Fisherian selection and the benefits of producing more sons (i.e. the sex in which distortion occurs).

Fourthly, we modelled a recessive-lethal *SD* that reduces the relative fitness of heterozygotes to 0.8 (top right, Figure 3 - this assumption is probably the most realistic so far, based on our empirical findings). Here, the *SD* allele only invaded when K was high, and it stabilised at medium-high frequencies. Interestingly, *SD* alleles that induced a male-biased sex ratio invaded for substantially lower K and reached a higher equilibrium frequency for any given K than those that did not affect the sex ratio. Presumably this occurred because when *SD* is kept rare by its direct fitness costs, the population sex ratio stays close to 50:50, and so Fisherian sex ratio selection against *SD* remains weak (while the benefits of extra transmission bias stay the same).

For all four of these scenarios, we produced similar graphs under the additional assumption

that offspring suffer an additional cost when the *SD* allele is inherited from a particular parent. In the middle row of Figure 3, genotypes carrying a paternally-inherited *SD* allele have their fitness reduced by an additional 0.2, while in the bottom row, the same applies to genotypes with a maternally-inherited *SD*. Comparison of the three rows shows that these trans-generational costs further hamper the spread of *SD*, and that paternal costs are worse than maternal costs, because the *SD* allele is inherited from fathers more often than mothers due to its male-limited distortion. By combining recessive lethality with some mixture of heterozygote fitness costs, sex ratio bias, or transgenerational costs, we could get *SD* chromosomes to persist at low, stable frequencies as they often do in nature (e.g. the middle right panel of Figure 3 near $K = 0.95$, which approximates the costs and K value for *SD-5*).

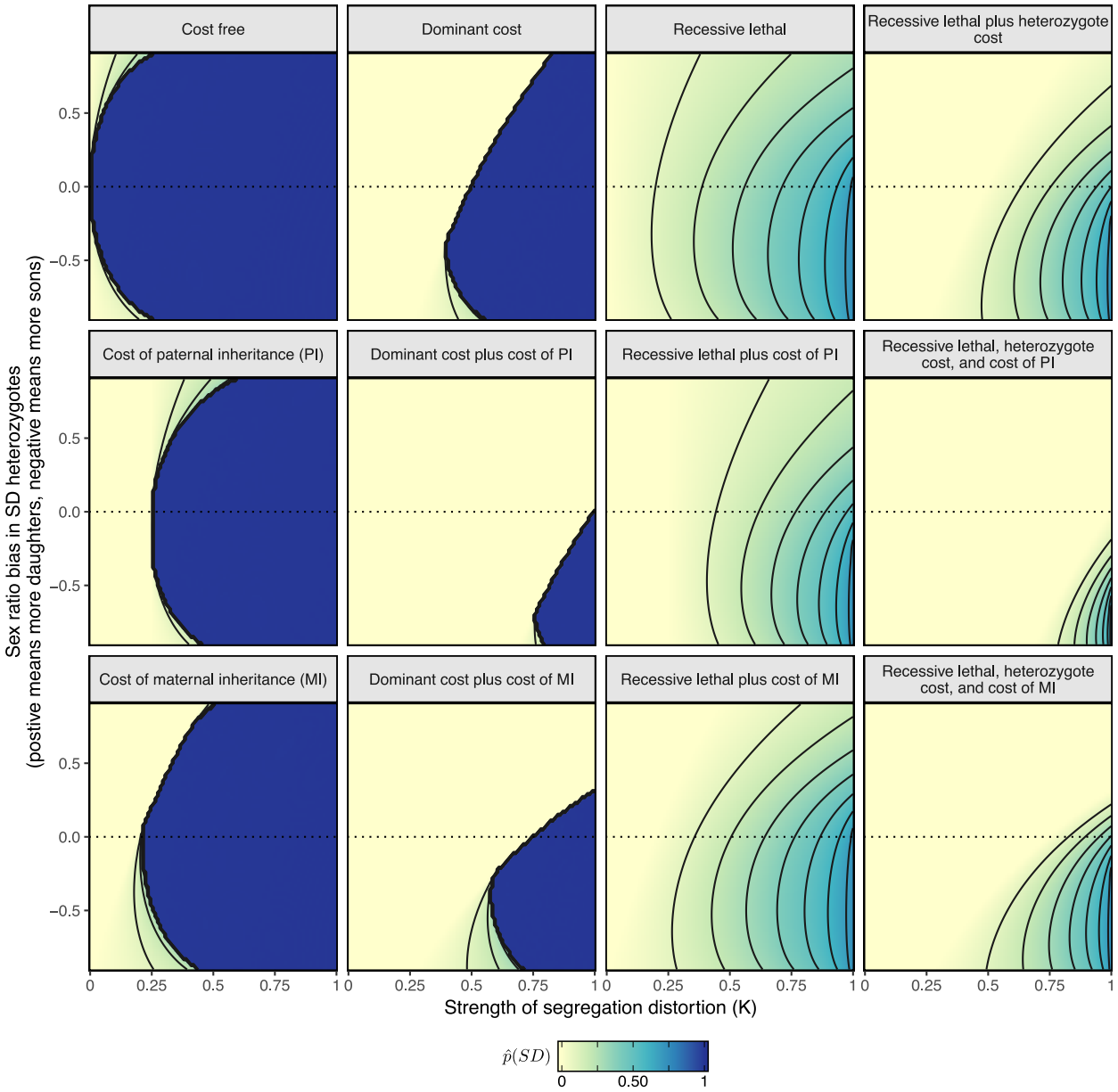

Figure 3: The equilibrium frequency reached by the *SD* allele, $\hat{p}(SD)$, depends on the strength of segregataion distortion ($K = 0$ indicates fair meiosis, $K = 1$ denotes complete distortion), as well as the direction and strength of sex ratio bias in the progeny of *SD* heterozygote males. The four columns make different assumptions about the fitness costs to individuals carrying the *SD* allele, while the three rows assume either that *SD* has no parent-of-origin-specific effects on fitness (top row), or that *SD* is especially costly when paternally inherited (middle row) or maternally inherited (bottom row). In the 'Dominant costs' column and the fourth column, individuals with one copy of *SD* had a relative fitness of 0.8, while 'Recessive lethal' means that *SD* homozygotes had zero fitness.

Discussion

Our study reaffirmed that *SD-5* and *SD-72* are homozygous lethal. Most *SD-5* homozygotes died while still in the egg, while *SD-72* homozygotes died after hatching but before adulthood. Although cultures of *SD-Mad* homozygotes can survive in the lab, we found that male and female *SD-Mad* homozygotes had much lower fitness than their *bw-GFP* competitors, suggesting that *SD-Mad* homozygotes would have close to zero fitness in a natural population. The fitness costs to male adults were dominant for *SD-5* but recessive for *SD-72* and *SD-Mad*. By contrast, the fitness costs to female adults were recessive for all three *SD* variants, illustrating that the dominance of the cost differs between sexes as well as between *SD* variants. Although we did not observe any *SD* variants that had high fitness as homozygotes, it is possible that such variants exist; an *SD* variant with inversions characteristic of *SD-72* or *SD-Mad* was reportedly found in 98% of individuals in a population in Wisconsin (Temin and Marthas 1984).

Interestingly, we found some evidence for costly non-genetic transgenerational effects associated with all three *SD* variants, which might represent either parental effects (i.e. non-genetic effects of the parent's phenotype on the offspring phenotype; Badyaev and Uller 2009) or genomic imprinting (i.e. when the effect of an allele depends on which parent it came from; Holman and Kokko 2014). Firstly, female fitness was reduced among the non-*SD* offspring of *SD-5* or *SD-Mad* heterozygote fathers. One possible mechanism is that non-*SD*-carrying chromosomes that escape segregation distortion are epigenetically modified in ways that affect adult fitness; this mechanism is plausible because *SD* is thought to function by altering the chromatin of sensitive chromosomes (Larracuente and Presgraves 2012). Secondly, *SD-5* was especially harmful to adult male fitness when paternally inherited, hinting at either genomic imprinting or a genotype-dependent paternal effect of *SD-5*. Thirdly, in Experiment 2, we found that male larvae whose mother carried *SD-5* were less likely to reach adulthood than were male larvae whose father carried *SD-5*, irrespective of whether the larva inherited *SD-5*. This result again suggests that *SD-5* has a transgenerational effect on offspring fitness, though puzzlingly the harmful effect was associated with mothers rather than fathers this time (possibly because Experiments 1 and 2 used a different non-*SD* reference chromosome and genetic background). To our knowledge, all previous theoretical models of segregation distorters implicitly assume that transgenerational effects are absent, motivating us to allow *SD* alleles to have parent-of-origin-specific effects on fitness in our model. The model showed that non-genetic transgenerational costs of *SD* can reduce the invasion probability and equilibrium frequency of *SD* (this is an example of indirect genetic effects affecting evolution; Wolf et al. 1998). Thus, if segregation distorters commonly have transgenerational costs in addition to their direct cost to the individual carrying them, transgenerational costs may help to explain the puzzling rarity of *SD* (Brand et al. 2015) and other autosomal distorters such as the *t*-haplotype (Carroll and Potts 2007).

We also observed that fathers heterozygous for *SD-Mad* produced an excess of daughters, while *SD-5* and *SD-72* parents produced a similar sex ratio to controls. Our results thus differ from earlier studies of *SD-5* and *SD-72*, which found an excess of daughters but only among the non-*SD* progeny (Hiraizumi and Nakazima 1967; Denell et al. 1969). Larracuente

and Presgraves (2012) proposed that Y-bearing spermatids might be eliminated in *SD* males as a result of 'collateral damage' arising because of sequence homology between Y-linked loci and *Responder*, which could explain the observed shortage of sons in crosses where the father carries *SD*. As an alternative or complement to this hypothesis, we speculate that *SD* might cause a parental effect that affects the relative survival rates of male and female progeny, for example by inducing epigenetic modifications that are more harmful to males than females. Our modelling results suggest that *SD* alleles invade less easily, and reach a lower equilibrium frequency, when they cause male heterozygotes to produce a female-biased sex ratio. There are two reasons for this result: firstly, autosomal alleles that skew the sex ratio away from 50:50 are usually disfavoured by selection (Fisher 1930), and secondly, *SD* alleles can only distort segregation in sons. The model also showed that producing a male-biased sex ratio was disadvantageous for *SD* alleles, except in populations where *SD* was kept rare by its fitness costs. When *SD* is rare, the population-wide sex ratio remains close to 50:50, reducing the Fisherian cost to *SD* of producing extra sons. Assuming that other autosomal segregation distorters also cause imbalanced sex ratios, this finding may be relevant to resolving the *t*-paradox for other species' distorter alleles.

Future studies could compete *SD* alleles with differing costs, and differing cost dominance, in population cages. We predict that *SD* alleles with dominant costs will either fail to spread (if the costs are sufficiently high relative to the strength of segregation distortion, k), or will sweep to fixation, while alleles with recessive costs will potentially reach an evolutionary equilibrium. Similarly, we predict that the stability and allele frequencies of *SD* chromosomes in natural populations will correlate with their fitness costs in homozygotes and heterozygotes. In line with this prediction, *SD-5* is more costly, has more dominant costs, and was rarer than other the other two variants in the original Wisonsin population (Temin and Marthas 1984), and it would be interesting to see if the frequencies of competing *SD* variants can be similarly explained in other populations. Our results also have implications for the design of artificial gene drives, or attempts to use natural gene drives to deliver human-beneficial 'payloads' such as a malaria resistance allele for mosquitos (Lindholm et al. 2016). For example, we suggest considering the fitness of drive-carrying individuals' offspring (not just the fitness of the carriers themselves) when testing a newly-designed gene drive in the lab, since our model shows that transgenerational costs can strongly influence the invasion success of the gene drive.

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Availability of data and code

All raw data and R code is available at https://lukeholman.github.io/fitnessCostSD/.

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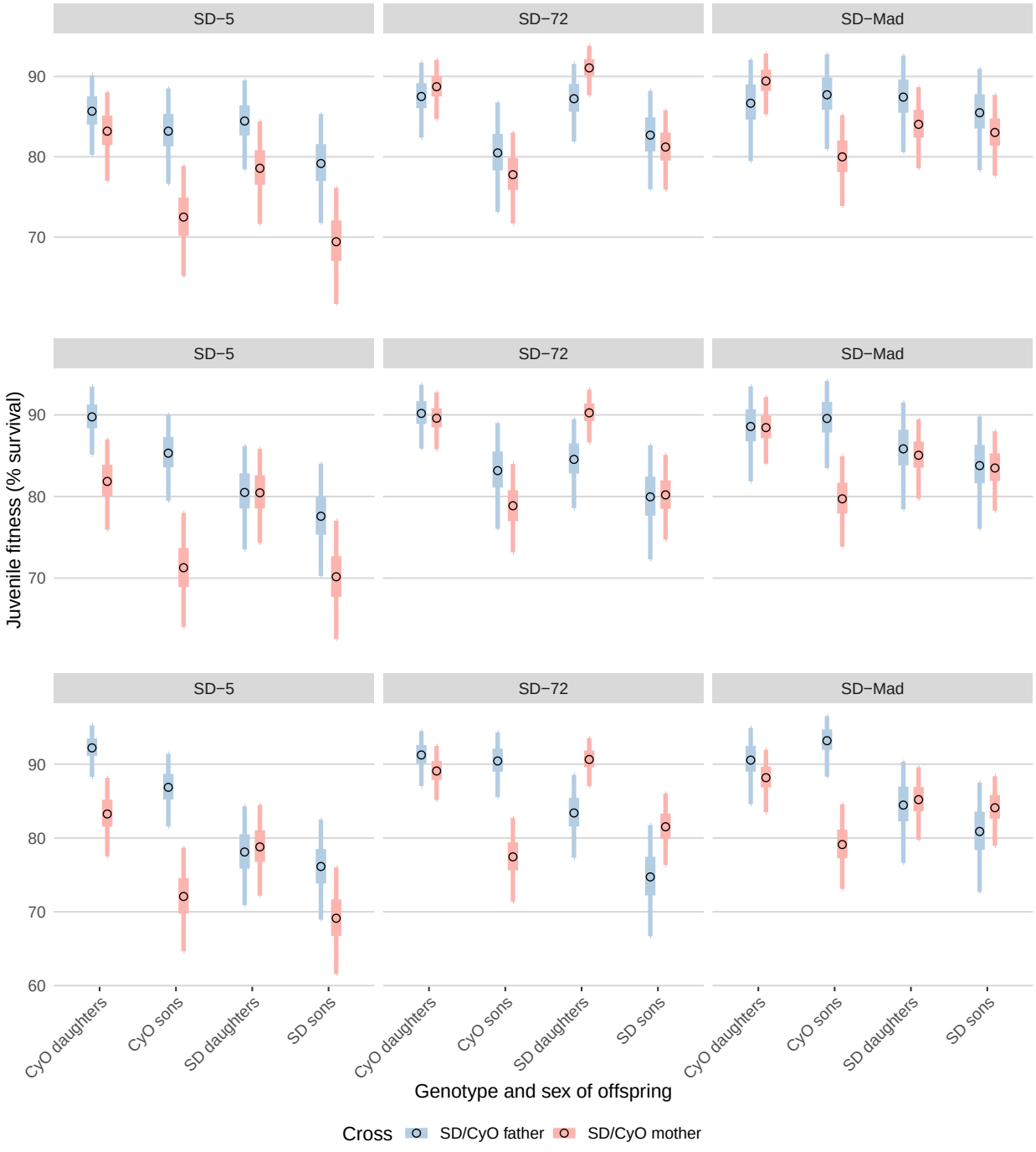
Online Supplementary Material

Fitness consequences of the selfish supergene *Segregation Distorter*

The figures and tables in this document, along with the with the R code used to generate them, can also be viewed online:
https://lukeholman.github.io/fitnessCostSD/statistics.html

Supplementary figures



Supplementary Figure 1: Equivalent plots to Figure 2, under the assumption that meiosis is fair ($k = 0.5$, top row, same as Figure 2), slightly biased ($k = 0.6$, middle row), and more strongly biased ($k = 0.7$, bottom row). Note that the significant results for Figure 2 mostly stay the same or increase in magnitude, suggesting that they are genuine and are not sensitive to our assumptions about the data.

Supplementary tables

Supplementary Table 1: Number and percentage of L1 larvae surviving to adulthood for each SD genotype and cross type.

SD	Copies of SD	Parent with SD	Number larvae counted	n survivors	% surviving
No SD chromosome	0	Neither parent	600	495	82.5
SD-5	0	Father	113	89	78.8
SD-5	0	Mother	459	408	88.9
SD-5	0 or 1	Both parents	700	520	74.3
SD-5	1	Father	563	412	73.2
SD-5	1	Mother	494	415	84.0
SD-5	2	Both parents	40	0	0.0
SD-72	0	Father	287	226	78.7
SD-72	0	Mother	396	333	84.1
SD-72	0 or 1	Both parents	700	542	77.4
SD-72	1	Father	600	477	79.5
SD-72	1	Mother	423	342	80.9
SD-72	2	Both parents	600	0	0.0
SD-Mad	0	Father	296	239	80.7
SD-Mad	0	Mother	371	279	75.2
SD-Mad	0 or 1	Both parents	700	558	79.7
SD-Mad	1	Father	600	462	77.0
SD-Mad	1	Mother	436	320	73.4
SD-Mad	2	Both parents	585	413	70.6

566 **Supplementary Table 2**: Number and percentage of male and female adults emerging
567 from the juvenile fitness assay vials.

SD	Copies of SD	Parent with SD	n males	n females	n total	% male
No SD chromosome	0	Neither parent	267	228	495	53.9
SD-5	0	Father	48	41	89	53.9
SD-5	0	Mother	206	202	408	50.5
SD-5	0 or 1	Both parents	239	281	520	46.0
SD-5	1	Father	196	216	412	47.6
SD-5	1	Mother	193	222	415	46.5
SD-5	2	Both parents	0	0	0	NaN
SD-72	0	Father	105	121	226	46.5
SD-72	0	Mother	169	164	333	50.8
SD-72	0 or 1	Both parents	272	270	542	50.2
SD-72	1	Father	233	244	477	48.8
SD-72	1	Mother	186	156	342	54.4
SD-72	2	Both parents	0	0	0	NaN
SD-Mad	0	Father	102	137	239	42.7
SD-Mad	0	Mother	145	134	279	52.0
SD-Mad	0 or 1	Both parents	253	305	558	45.3
SD-Mad	1	Father	190	272	462	41.1
SD-Mad	1	Mother	184	136	320	57.5
SD-Mad	2	Both parents	209	204	413	50.6

568 **Supplementary Table 3**: Average relative fitness of adult males for each SD genotype and
569 cross type, expressed as the average proportion of offspring sired. The last two columns give
570 the sample size in terms of number of vials (each of which contained 5 focal males), and
571 number of males.

SD	Copies of SD	Parent with SD	Average relative fitness	SE	n vials	n males
No SD chromosome	0	Neither parent	0.79	0.040	13	65
SD-5	0	Father	0.68	0.147	5	25
SD-5	0	Mother	0.82	0.045	17	85
SD-5	0	Both parents	0.59	NA	1	5
SD-5	1	Father	0.14	0.055	18	90
SD-5	1	Mother	0.32	0.072	12	60
SD-5	1	Both parents	0.39	0.074	13	65
SD-72	0	Father	0.88	0.027	16	80
SD-72	0	Mother	0.77	0.054	13	65
SD-72	0	Both parents	0.79	NA	1	5
SD-72	1	Father	0.76	0.045	18	90
SD-72	1	Mother	0.80	0.039	17	85
SD-72	1	Both parents	0.67	0.051	19	95
SD-Mad	0	Father	0.75	0.055	14	70
SD-Mad	0	Mother	0.75	0.069	11	55
SD-Mad	0	Both parents	0.82	0.078	5	25
SD-Mad	1	Father	0.87	0.028	18	90
SD-Mad	1	Mother	0.81	0.037	17	85
SD-Mad	1	Both parents	0.75	0.053	18	90
SD-Mad	2	Both parents	0.19	0.072	14	70

572 **Supplementary Table 4**: Average fecundity of adult females for each SD genotype and
573 cross type. The last two columns give the sample size in terms of number of oviposition vials
574 (each of which contained up to 5 focal females), and number of males.

SD	Copies of SD	Parent with SD	Average fecundity	SE	n vials	n females
No SD chromosome	0	Neither parent	26.55	3.874	10	48
SD-5	0	Father	25.06	8.127	6	28
SD-5	0	Mother	41.13	3.700	15	71
SD-5	0	Both parents	24.95	3.767	5	22
SD-5	1	Father	28.88	3.337	12	55
SD-5	1	Mother	29.74	3.118	16	69
SD-5	1	Both parents	26.83	2.583	15	67
SD-72	0	Father	32.68	3.258	14	65
SD-72	0	Mother	35.10	3.023	15	68
SD-72	0	Both parents	22.53	6.671	3	15
SD-72	1	Father	33.97	2.743	16	77
SD-72	1	Mother	41.90	3.792	14	68
SD-72	1	Both parents	31.85	2.885	15	73
SD-Mad	0	Father	28.25	3.769	16	79
SD-Mad	0	Mother	44.71	3.723	13	65
SD-Mad	0	Both parents	16.50	1.762	3	14
SD-Mad	1	Father	36.85	3.968	16	77
SD-Mad	1	Mother	40.58	4.602	14	64
SD-Mad	1	Both parents	34.88	3.478	16	76
SD-Mad	2	Both parents	11.26	1.631	17	83

575 **Supplementary Table 5**: Number and percentage of L1 larvae surviving to adulthood in
576 Experiment 2, for each SD genotype, cross type, and offspring sex.

SD	Parent with SD	Offspring sex	% surviving SD larvae	% surviving CyO larvae	n larvae counted	n crosses
SD-5	Father	Female	83.4	83.8	763	16
SD-5	Father	Male	79.0	79.3	727	17
SD-5	Mother	Female	76.4	81.9	871	18
SD-5	Mother	Male	70.8	67.8	972	20
SD-72	Father	Female	85.5	85.9	744	16
SD-72	Father	Male	81.0	78.6	615	15
SD-72	Mother	Female	90.2	87.4	1123	23
SD-72	Mother	Male	78.9	76.8	1186	24
SD-Mad	Father	Female	87.2	83.9	457	10
SD-Mad	Father	Male	87.8	83.1	480	11
SD-Mad	Mother	Female	84.4	85.7	942	20
SD-Mad	Mother	Male	82.3	78.4	1010	21

Supplementary Table 6: The results of hypothesis tests computed using the model of larval survival in Experiment 1. Each row gives the posterior estimate of a difference in means, such that the estimate is positive if mean 1 is larger than mean 2, and negative otherwise (expressed in % larval survival). The mean 1 and mean 2 columns list the parent which had SD (mother, father, or both), followed by the number of SD alleles present in the offspring (0, 1 or 2). The Posterior probability column gives the probability that the mean with the smaller point estimate is actually larger than the other mean, analagously to a one-tailed p-value. The Evidence ratio (ER) column gives the ratio of evidence, such that ER = 5 means that it is 5 times more likely that the mean with the smaller point estimate really is the smaller one. Asterisks highlight rows where the posterior probability is less than 0.05.

SD	Comparison	Difference	Error	Posterior probability
SD-5	Neither, 0 - Father, 0	8.9 (-11.6 to 34.9)	11.8	0.225
SD-72	Neither, 0 - Father, 0	6.0 (-10.5 to 24.3)	8.9	0.246
SD-Mad	Neither, 0 - Father, 0	3.5 (-12.5 to 21.0)	8.4	0.341
SD-5	Neither, 0 - Mother, 0	-5.8 (-18.1 to 5.3)	5.9	0.156
SD-72	Neither, 0 - Mother, 0	-0.9 (-14.0 to 12.1)	6.6	0.444
SD-Mad	Neither, 0 - Mother, 0	5.4 (-9.3 to 20.0)	7.3	0.218
SD-5	Mother, 0 - Father, 0	14.7 (-2.8 to 39.3)	10.7	0.057
SD-72	Mother, 0 - Father, 0	6.9 (-9.6 to 25.0)	8.8	0.214
SD-Mad	Mother, 0 - Father, 0	-1.9 (-18.1 to 15.9)	8.6	0.399
SD-5	Mother, 1 - Father, 1	10.6 (-4.4 to 26.4)	7.8	0.080
SD-72	Mother, 1 - Father, 1	1.2 (-13.1 to 15.4)	7.2	0.429
SD-Mad	Mother, 1 - Father, 1	-1.0 (-17.9 to 15.2)	8.4	0.449
SD-5	Mother, 0 - Mother, 1	5.6 (-5.2 to 17.4)	5.7	0.156
SD-72	Mother, 0 - Mother, 1	3.0 (-10.2 to 16.9)	6.8	0.326
SD-Mad	Mother, 0 - Mother, 1	1.9 (-14.4 to 19.4)	8.6	0.413
SD-5	Father, 0 - Father, 1	1.6 (-25.5 to 23.4)	12.5	0.415
SD-72	Father, 0 - Father, 1	-2.7 (-21.5 to 15.1)	9.3	0.394
SD-Mad	Father, 0 - Father, 1	2.8 (-16.7 to 20.4)	9.2	0.366
SD-5	Both parents, 0 or 1 - Both parents, 2	77.1 (62.2 to 87.8)	6.5	0.000
SD-72	Both parents, 0 or 1 - Both parents, 2	77.5 (63.6 to 87.8)	6.1	0.000
SD-Mad	Both parents, 0 or 1 - Both parents, 2	10.6 (-6.7 to 27.7)	8.7	0.105

Supplementary Table 7: The results of hypothesis tests computed using the model of adult sex ratio in Experiment 1. Each row gives the posterior estimate of a difference in means, such that the estimate is positive if mean 1 is larger than mean 2, and negative otherwise (expressed in % males). The mean 1 and mean 2 columns list the parent which had SD (mother, father, or both), followed by the number of SD alleles present in the offspring (0, 1 or 2). The Posterior probability column gives the probability that the mean with the smaller point estimate is actually larger than the other mean, analagously to a one-tailed p-value. The Evidence ratio (ER) column gives the ratio of evidence, such that ER = 5 means that it is 5 times more likely that the mean with the smaller point estimate really is the smaller one. Asterisks highlight rows where the posterior probability is less than 0.05.

SD	Comparison	Difference	Error	Posterior probability
SD-5	Neither, 0 - Father, 0	-0.3 (-15.9 to 15.7)	8.1	0.482
SD-72	Neither, 0 - Father, 0	7.2 (-4.9 to 19.1)	6.1	0.114
SD-Mad	Neither, 0 - Father, 0	11.1 (-0.8 to 23.0)	6.0	0.034
SD-5	Neither, 0 - Mother, 0	2.5 (-9.0 to 13.7)	5.7	0.323
SD-72	Neither, 0 - Mother, 0	3.2 (-7.9 to 14.5)	5.7	0.284
SD-Mad	Neither, 0 - Mother, 0	0.9 (-11.0 to 12.4)	5.9	0.437
SD-5	Mother, 0 - Father, 0	-2.8 (-18.4 to 13.4)	8.1	0.362
SD-72	Mother, 0 - Father, 0	4.0 (-8.5 to 16.1)	6.3	0.260
SD-Mad	Mother, 0 - Father, 0	10.2 (-2.7 to 22.6)	6.3	0.056
SD-5	Mother, 1 - Father, 1	-1.5 (-13.0 to 9.9)	5.7	0.391
SD-72	Mother, 1 - Father, 1	5.6 (-5.8 to 17.0)	5.7	0.159
SD-Mad	Mother, 1 - Father, 1	18.3 (7.1 to 29.7)	5.7	0.001
SD-5	Mother, 0 - Mother, 1	5.1 (-6.2 to 16.6)	5.8	0.187
SD-72	Mother, 0 - Mother, 1	-3.9 (-15.7 to 7.9)	6.0	0.251
SD-Mad	Mother, 0 - Mother, 1	-6.7 (-18.6 to 5.0)	6.0	0.128
SD-5	Father, 0 - Father, 1	6.3 (-9.9 to 22.4)	8.1	0.208
SD-72	Father, 0 - Father, 1	-2.3 (-13.8 to 9.5)	6.0	0.343
SD-Mad	Father, 0 - Father, 1	1.4 (-10.2 to 13.2)	5.9	0.410
SD-Mad	Both parents, 1 - Both parents, 2	-5.2 (-16.1 to 5.9)	5.5	0.164

Supplementary Table 8: The results of hypothesis tests computed using the model of female fitness in Experiment 1. Each row gives the posterior estimate of a difference in means, such that the estimate is positive if mean 1 is larger than mean 2, and negative otherwise (expressed as the number of offspring produced). The mean 1 and mean 2 columns list the parent which had SD (mother, father, or both), followed by the number of SD alleles present in the offspring (0, 1 or 2). The Posterior probability column gives the probability that the mean with the smaller point estimate is actually larger than the other mean, analagously to a one-tailed p-value. The Evidence ratio (ER) column gives the ratio of evidence, such that ER = 5 means that it is 5 times more likely that the mean with the smaller point estimate really is the smaller one. Asterisks highlight rows where the posterior probability is less than 0.05.

SD	Comparison	Difference	Error	Posterior probability
SD-5	Neither, 0 - Father, 0	1.9 (-12.3 to 14.7)	6.9	0.368
SD-72	Neither, 0 - Father, 0	-5.8 (-18.5 to 6.5)	6.2	0.161
SD-Mad	Neither, 0 - Father, 0	-1.7 (-12.7 to 9.9)	5.8	0.371
SD-5	Neither, 0 - Mother, 0	-14.4 (-28.6 to -0.4)	7.0	0.022
SD-72	Neither, 0 - Mother, 0	-7.9 (-20.5 to 4.5)	6.4	0.105
SD-Mad	Neither, 0 - Mother, 0	-18.7 (-34.7 to -3.8)	7.8	0.006
SD-5	Mother, 0 - Father, 0	16.4 (1.0 to 31.0)	7.6	0.019
SD-72	Mother, 0 - Father, 0	2.0 (-10.9 to 14.7)	6.4	0.371
SD-Mad	Mother, 0 - Father, 0	17.0 (3.2 to 32.6)	7.5	0.009
SD-5	Mother, 1 - Father, 1	-0.1 (-11.5 to 10.8)	5.7	0.500
SD-72	Mother, 1 - Father, 1	8.2 (-5.5 to 22.8)	7.2	0.125
SD-Mad	Mother, 1 - Father, 1	3.4 (-10.5 to 17.7)	7.2	0.321
SD-5	Mother, 0 - Mother, 1	12.5 (-0.2 to 26.1)	6.6	0.027
SD-72	Mother, 0 - Mother, 1	-7.5 (-22.5 to 6.9)	7.4	0.146
SD-Mad	Mother, 0 - Mother, 1	5.4 (-10.9 to 22.3)	8.5	0.255
SD-5	Father, 0 - Father, 1	-3.9 (-16.9 to 10.1)	6.8	0.264
SD-72	Father, 0 - Father, 1	-1.4 (-13.9 to 11.4)	6.3	0.412
SD-Mad	Father, 0 - Father, 1	-8.2 (-20.4 to 3.4)	6.0	0.080
SD-Mad	Both parents, 1 - Both parents, 2	23.4 (15.0 to 33.1)	4.6	0.000

Supplementary Table 9: The results of hypothesis tests computed using the model of male fitness in Experiment 1. Each row gives the posterior estimate of a difference in means, such that the estimate is positive if mean 1 is larger than mean 2, and negative otherwise (expressed in % offspring sired). The mean 1 and mean 2 columns list the parent which had SD (mother, father, or both), followed by the number of SD alleles present in the offspring (0, 1 or 2). The Posterior probability column gives the probability that the mean with the smaller point estimate is actually larger than the other mean, analagously to a one-tailed p-value. The Evidence ratio (ER) column gives the ratio of evidence, such that ER = 5 means that it is 5 times more likely that the mean with the smaller point estimate really is the smaller one. Asterisks highlight rows where the posterior probability is less than 0.05.

SD	Comparison	Difference	Error	Posterior probability
SD-5	Neither, 0 - Father, 0	10.9 (-13.9 to 42.5)	14.6	0.238
SD-72	Neither, 0 - Father, 0	-8.3 (-23.7 to 4.4)	7.2	0.110
SD-Mad	Neither, 0 - Father, 0	1.7 (-15.5 to 19.4)	8.9	0.420
SD-5	Neither, 0 - Mother, 0	-6.2 (-22.2 to 7.6)	7.5	0.195
SD-72	Neither, 0 - Mother, 0	-0.9 (-18.2 to 16.6)	8.6	0.452
SD-Mad	Neither, 0 - Mother, 0	-0.2 (-18.2 to 18.0)	9.2	0.483
SD-5	Mother, 0 - Father, 0	17.2 (-5.8 to 47.4)	13.9	0.091
SD-72	Mother, 0 - Father, 0	-7.3 (-22.6 to 4.7)	7.0	0.133
SD-Mad	Mother, 0 - Father, 0	2.0 (-16.1 to 19.3)	8.9	0.394
SD-5	Mother, 1 - Father, 1	20.0 (5.5 to 39.2)	8.8	0.003
SD-72	Mother, 1 - Father, 1	4.8 (-9.6 to 19.9)	7.4	0.254
SD-Mad	Mother, 1 - Father, 1	-3.8 (-13.8 to 5.1)	4.7	0.201
SD-5	Mother, 0 - Mother, 1	61.6 (41.0 to 77.7)	9.4	0.000
SD-72	Mother, 0 - Mother, 1	-2.2 (-18.4 to 12.7)	7.8	0.399
SD-Mad	Mother, 0 - Mother, 1	-5.7 (-23.0 to 8.5)	7.8	0.229
SD-5	Father, 0 - Father, 1	64.5 (34.6 to 85.6)	13.5	0.000
SD-72	Father, 0 - Father, 1	9.9 (-2.2 to 23.9)	6.7	0.055
SD-Mad	Father, 0 - Father, 1	-11.5 (-26.7 to 0.6)	6.9	0.032
SD-Mad	Both parents, 1 - Both parents, 2	70.6 (54.2 to 82.6)	7.2	0.000

Supplementary Table 10: Complete version of Table 2, showing all the contrasts that were tested in Experiment 2.

SD	Comparison	Difference	Error	Posterior probability	Notable
SD-5	Daughters, CyO, father - Daughters, SD, father	1.2 (-3.5 to 6.3)	2.5	0.310	
SD-5	Daughters, CyO, mother - Daughters, CyO, father	-2.5 (-9.8 to 4.8)	3.7	0.245	
SD-5	Daughters, CyO, mother - Daughters, SD, mother	4.6 (-0.6 to 10.0)	2.7	0.041	*
SD-5	Daughters, SD, mother - Daughters, SD, father	-5.9 (-14.6 to 2.5)	4.2	0.078	
SD-5	Sons, CyO, father - Daughters, CyO, father	-2.5 (-10.4 to 4.9)	3.9	0.260	
SD-5	Sons, CyO, father - Sons, SD, father	4.0 (-1.8 to 10.0)	3.0	0.087	
SD-5	Sons, CyO, mother - Daughters, CyO, mother	-10.7 (-19.4 to -2.0)	4.5	0.008	*
SD-5	Sons, CyO, mother - Sons, CyO, father	-10.7 (-19.8 to -1.5)	4.6	0.010	*
SD-5	Sons, CyO, mother - Sons, SD, mother	3.1 (-2.8 to 9.0)	3.0	0.149	
SD-5	Sons, SD, father - Daughters, SD, father	-5.3 (-14.5 to 3.7)	4.5	0.118	
SD-5	Sons, SD, mother - Daughters, SD, mother	-9.1 (-18.7 to 0.4)	4.8	0.028	*
SD-5	Sons, SD, mother - Sons, SD, father	-9.7 (-19.4 to -0.1)	5.0	0.025	*
SD-72	Daughters, CyO, father - Daughters, SD, father	0.3 (-4.4 to 5.0)	2.4	0.449	
SD-72	Daughters, CyO, mother - Daughters, CyO, father	1.2 (-4.7 to 7.4)	3.0	0.340	
SD-72	Daughters, CyO, mother - Daughters, SD, mother	-2.3 (-5.9 to 1.1)	1.8	0.088	
SD-72	Daughters, SD, mother - Daughters, SD, father	3.8 (-1.6 to 9.9)	2.9	0.085	
SD-72	Sons, CyO, father - Daughters, CyO, father	-7.0 (-15.5 to 1.0)	4.2	0.045	*
SD-72	Sons, CyO, father - Sons, SD, father	-2.2 (-8.8 to 3.8)	3.2	0.243	
SD-72	Sons, CyO, mother - Daughters, CyO, mother	-11.0 (-17.9 to -4.3)	3.5	0.001	*
SD-72	Sons, CyO, mother - Sons, CyO, father	-2.7 (-11.4 to 6.3)	4.5	0.274	
SD-72	Sons, CyO, mother - Sons, SD, mother	-3.4 (-8.1 to 1.2)	2.4	0.074	
SD-72	Sons, SD, father - Daughters, SD, father	-4.5 (-12.7 to 3.3)	4.1	0.134	
SD-72	Sons, SD, mother - Daughters, SD, mother	-9.9 (-15.8 to -4.2)	3.0	0.000	*
SD-72	Sons, SD, mother - Sons, SD, father	-1.5 (-9.3 to 6.4)	4.1	0.354	
SD-Mad	Daughters, CyO, father - Daughters, SD, father	-0.8 (-6.9 to 5.2)	3.1	0.409	
SD-Mad	Daughters, CyO, mother - Daughters, CyO, father	2.8 (-4.3 to 10.7)	3.8	0.236	
SD-Mad	Daughters, CyO, mother - Daughters, SD, mother	5.4 (1.2 to 9.9)	2.2	0.007	*
SD-Mad	Daughters, SD, mother - Daughters, SD, father	-3.4 (-11.0 to 4.9)	4.0	0.196	
SD-Mad	Sons, CyO, father - Daughters, CyO, father	1.1 (-7.8 to 9.8)	4.5	0.413	
SD-Mad	Sons, CyO, father - Sons, SD, father	2.2 (-4.1 to 8.7)	3.2	0.232	
SD-Mad	Sons, CyO, mother - Daughters, CyO, mother	-9.4 (-16.3 to -2.7)	3.5	0.002	*
SD-Mad	Sons, CyO, mother - Sons, CyO, father	-7.7 (-15.6 to 0.6)	4.1	0.034	*
SD-Mad	Sons, CyO, mother - Sons, SD, mother	-3.0 (-8.0 to 1.9)	2.5	0.112	
SD-Mad	Sons, SD, father - Daughters, SD, father	-1.9 (-10.9 to 6.7)	4.6	0.335	
SD-Mad	Sons, SD, mother - Daughters, SD, mother	-1.0 (-8.0 to 6.1)	3.6	0.385	
SD-Mad	Sons, SD, mother - Sons, SD, father	-2.5 (-10.3 to 6.3)	4.1	0.258	