

Sexual selection and the population genetics of a selfish gene

Supplementary material

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Click **here** to view the HTML report, which serves as online supplementary material for the associated manuscript (DOI here if accepted. . .), submitted to *Proceedings of the Royal Society B*. The report is split into two parts. The first documents our empirical analysis, while the second provides an in-depth explanation for how we coded our population genetic model. Together, the report includes all supplementary figures and tables, the R script required to produce the analysis, figures and tables, and the raw data.

In an attempt to future proof the availability of our supplementary material, we also include Table S1-12 and Figures S1-8 in this document. Additionally, our data will also be deposited in the Dryad database **here** (this link will be supplied if the manuscript is accepted).

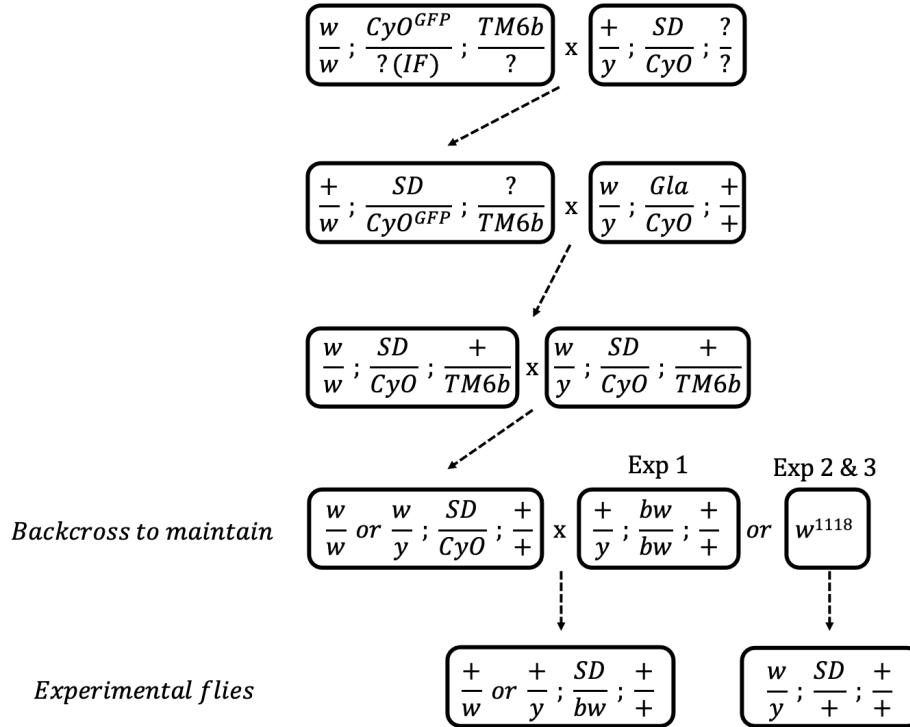


Figure S1. Crossing scheme used to standardise the genetic background across the *SD-5/+*, *SD-72/+*, *SD-Mad/+* and *SD+/+* lines. The *SD+/+* line was created in identical fashion except that we substituted the *SD* bearing chromosome with chromosome 2 from the *w¹¹¹⁸* isogenic line. Note that at step four there are three possible options 1) the leftmost genotype can be backcrossed to maintain it in the laboratory, 2) the leftmost genotype can be crossed to a *bw* stock to produce the experimental flies used in Experiment 1

or 3) the leftmost genotype can be crossed to w^{1118} to create the experimental flies used in Experiments 2 and 3.

Table S1: recipe for food medium used in our experiment. The provided quantities make ~ 1 litre of food.

Ingredients	Quantity
Soy flour	20 g
Cornmeal	73 g
Yeast	35 g
Dextrose	75 g
Agar	6 g
Water	1000 mL
Tegosept	17 mL
Acid mix (4 mL orthophosphoric acid, 41 mL propionic acid, 55 mL water to make 100 mL)	14 mL

Table S2: the percentage of female offspring that inherited a *SD* allele from a heterozygous parent k , split by the sex of the parent. *SD* only drives when present in males. $n = 14-15$ for all groups.

Variant carried	Sex	k - the estimated inheritance (%)	Est.Error	Q2.5	Q97.5
SD-5	Female	47.31	5.39	36.99	58.11
SD-72	Female	47.7	5.47	36.96	58.38
SD-Mad	Female	45.78	5.46	35.26	56.7
W1118	Female	49.51	5.25	39.17	59.63
SD-5	Male	94.13	1.47	90.88	96.61
SD-72	Male	90.72	2.24	85.7	94.54
SD-Mad	Male	84.7	3.1	77.96	90.04
W1118	Male	53.65	5.5	42.72	64.28

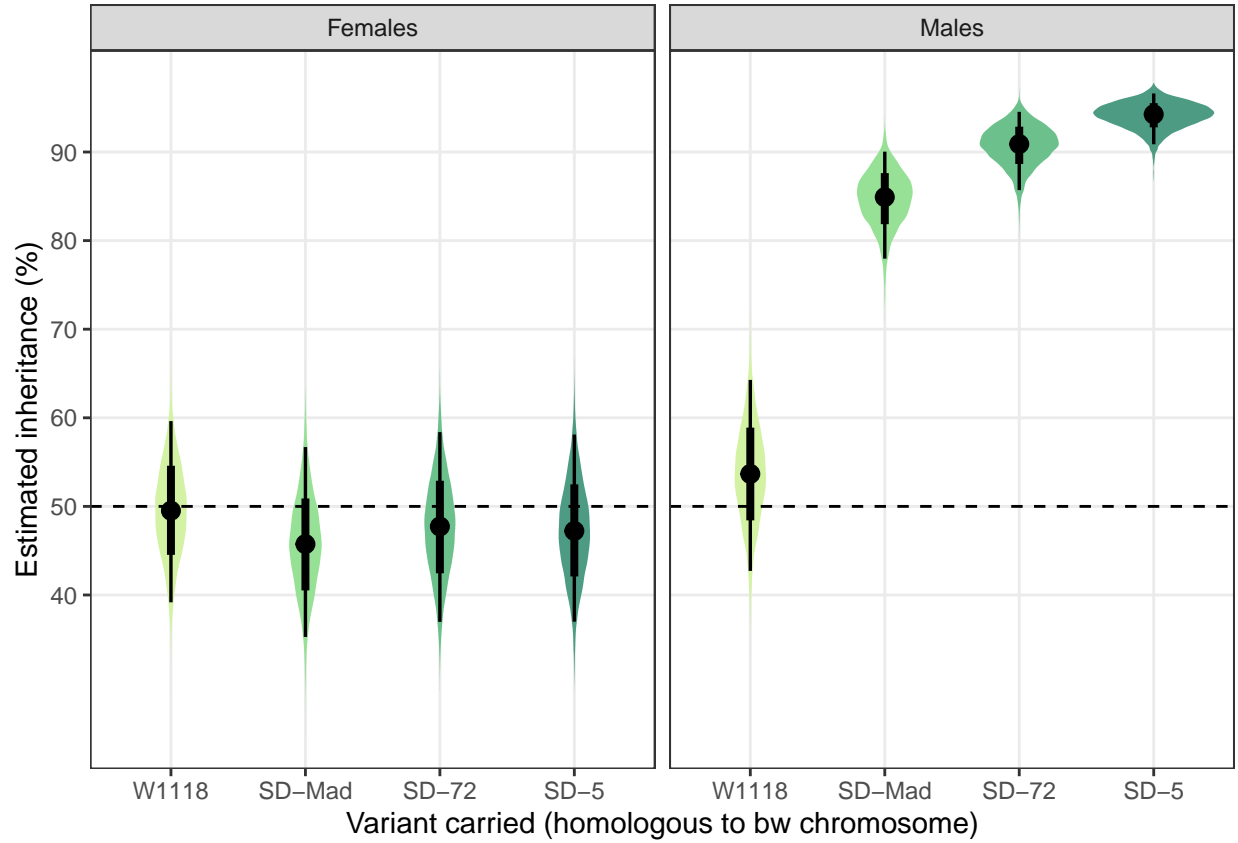


Figure S2: The estimated percentage of female offspring that inherited a *SD* allele from a heterozygous parent, split by the sex of the parent. Black points indicate the estimated mean with associated 66 and 95% uncertainty intervals, while coloured area shows the posterior distribution. The dotted line indicates 50% inheritance; the expectation in the absence of segregation distortion.

Table S3: the viability corrected inheritance (following Temin, 1991) of each *SD* variant and the control allele from a *SD/+* (or *+/+*) male.

Variant carried	k corrected for viability costs	Q2.5%	Q97.5%
SD-5	0.944	0.818	0.985
SD-72	0.909	0.724	0.975
SD-Mad	0.868	0.634	0.963
W1118	0.542	0.397	0.682

Table S4a: the estimated percentage of *SD/+* or control males that successfully mated with a female when competing with a single *Lbw* male.

Variant carried	Estimated % of males mating	2.5%	97.5%
W1118	36.6	21.73	54.01
SD-Mad	41.5	25.18	58.79
SD-72	43.28	26.04	62.52

Table S4b: the mating success of $SD/+$ males relative to the w^{1118} control males. A value of 2 means that $SD/+$ males were twice as successful as w^{1118} control males.

SD-variant	Mating success relative to w1118	2.5%	97.5%
SD-72	1.24	0.64	2.25
SD-Mad	1.19	0.61	2.08

Table S5a: the mean time taken for $SD/+$ or control males to start mating with a LH_m female.

Variant carried	Estimated time to mating (mins)	2.5%	97.5%
W1118	47	28	81
SD-Mad	24	15	41
SD-72	29	17	49

Table S5b: the mean mating latency of males that successfully mated with LH_m females when competing against Lbw males, relative to the w^{1118} control males. A value of 0.5 means that males mated in half the time of w^{1118} males.

SD-variant	Mean mating latency relative to w1118	2.5%	97.5%
SD-72	0.66	0.3	1.27
SD-Mad	0.56	0.26	1.09

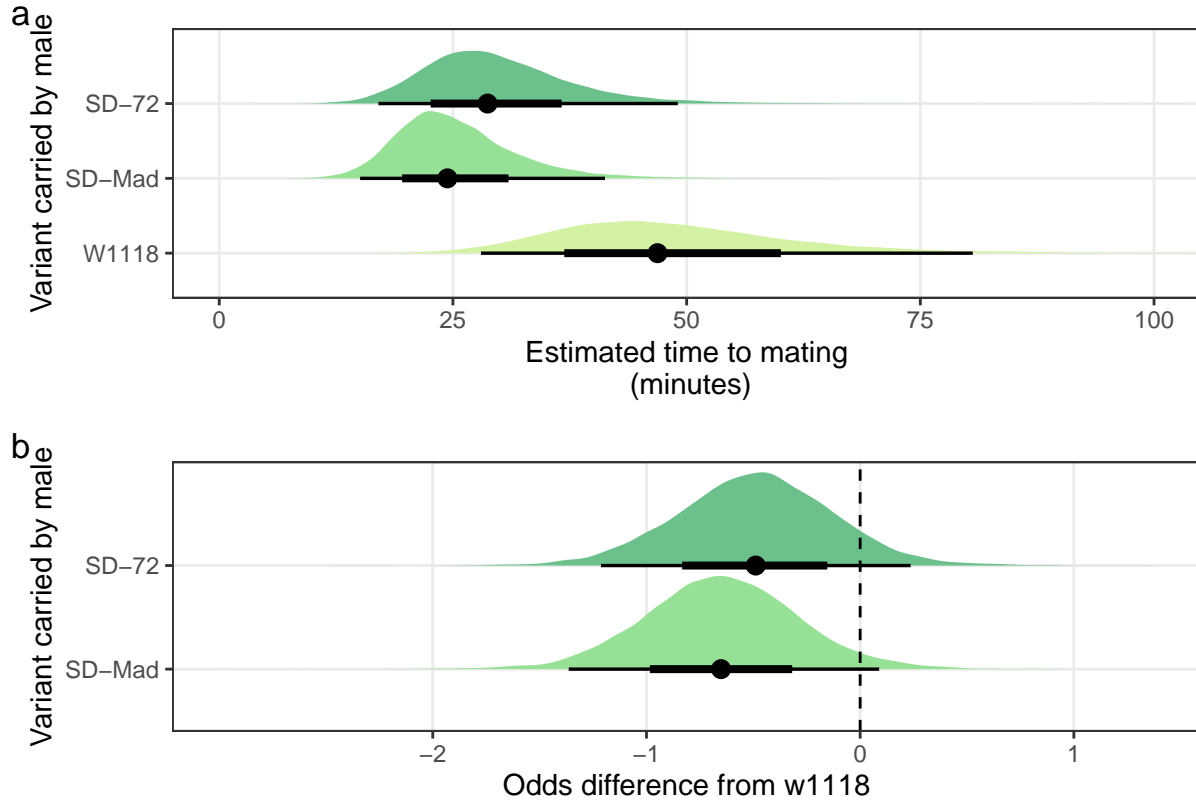


Figure S3: the mean time required for an $SD/+$ male to start mating with a LH_m female and how this compares to w^{1118} control males. Panel **a** shows the estimated mating latency for $SD/+$ and control males. Panel **b** shows effect sizes on the odds scale for the SD variants. Negative values indicate that $SD/+$ males mated faster than w^{1118} control males. Black points indicate the estimated mean with associated 66 and 95% uncertainty intervals, while coloured area shows the posterior distribution.

Table S6a: the mean copulation duration when a $SD/+$ or control mated with a LH_m female.

Variant carried	Estimated copulation duration (mins)	2.5%	97.5%
W1118	21.8	19.5	24.4
SD-Mad	21.6	19.3	24.1
SD-72	21.6	19.4	24.2

Table S6b: the mean mating latency of $SD/+$ males that successfully mated with LH_m females when competing against Lbw males, relative to the w^{1118} control males. A value of 0.5 means that males mated in half the time of w^{1118} males.

SD-variant	Mean copulation duration relative to w1118	2.5%	97.5%
SD-72	0.993	0.849	1.162
SD-Mad	0.995	0.851	1.157

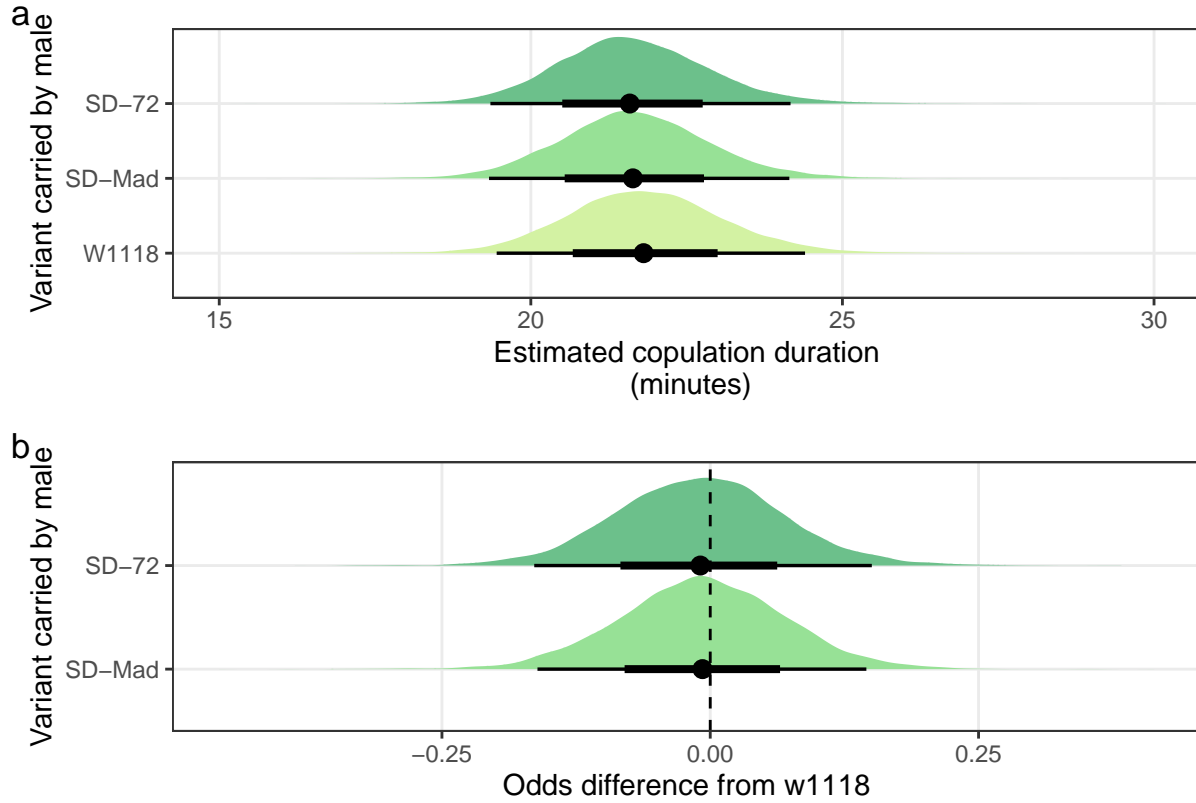


Figure S4: no difference in the duration of mating between a $SD/+$ male and a LH_m female, compared to w^{1118} control males. Panel **a** shows the estimated copulation duration for $SD/+$ and control males. Panel **b** shows effect sizes on the odds scale for the SD variants. Positive values indicate that $SD/+$ males mated for longer than w^{1118} control males. Black points indicate the estimated mean with associated 66 and 95% uncertainty intervals, while coloured area shows the posterior distribution.

Table S7a: the estimated percentage of offspring sired by $SD/+$ or control males, when they mated first.

Variant carried	Estimated % of offspring sired	2.5%	97.5%
W1118	8.17	0.99	44.4
SD-Mad	1.83	0.17	16.28
SD-72	2.15	0.21	16.97
SD-5	0.78	0.08	5.79

Table S7b: the mean proportion of offspring sired by each SD variant relative to the w^{1118} control, when these males mated with LH_m females first. A value of 0.5 means that the proportion of offspring sired was half that of w^{1118} males.

SD-variant	Mean proportion of offspring sired relative to w1118	2.5%	97.5%
SD-5	0.15	0.02	0.6

SD-variant	Mean proportion of offspring sired relative to w1118	2.5%	97.5%
SD-72	0.43	0.05	1.65
SD-Mad	0.39	0.04	1.7

Table S8a: the estimated percentage of offspring sired by $SD/+$ or control males, when they mated second.

Variant carried	Estimated % of offspring sired	2.5%	97.5%
W1118	97.9	91.61	99.7
SD-Mad	99.52	97.61	99.94
SD-72	97.63	90.34	99.65
SD-5	93.16	74.51	98.91

Table S8b: the mean proportion of offspring sired by each SD variant relative to the w^{1118} control, when these males mated with LH_m females second. A value of 0.5 means that the proportion of offspring sired was half that of w^{1118} males.

SD-variant	Mean proportion of offspring sired relative to w1118	2.5%	97.5%
SD-5	0.945	0.855	0.997
SD-72	0.997	0.969	1.027
SD-Mad	1.019	1.002	1.049

Table S9a: the estimated percentage of females that remated that were first mated to a $SD/+$ or control male.

Variant carried	Block	Estimated % of mates remating	2.5%	97.5%
W1118	1	30.36	14.97	51.05
W1118	2	16.22	7.473	29.98
W1118	3	48.62	30.85	66.63
SD-Mad	1	42.93	22.99	65.09
SD-Mad	2	24.9	11.75	43.87
SD-Mad	3	61.8	41.97	78.74
SD-72	1	42.54	23.09	64.14
SD-72	2	24.72	11.72	43.59
SD-72	3	61.53	41.95	78.84
SD-5	1	75.46	55.54	89.24
SD-5	2	57.68	39.09	75.63
SD-5	3	86.97	74.02	94.58

Table S9b: the mean proportion of mates remating with LH_m^{UBI} males for $SD/+$ males relative to the w^{1118} control males. A value of 2 means that remating was twice as likely when females initially mated with a $SD/+$ male compared with a w^{1118} male.

SD-variant	Mean proportion of mates remating relative to w1118	2.5%	97.5%
SD-5	2.61	1.52	4.66
SD-72	1.47	0.79	2.65
SD-Mad	1.48	0.77	2.65

Table S10a: the estimated time taken for females to remate, when provided with an opportunity, four days after initially mating with a *SD/+* or control male.

Variant carried	Block	Estimated time to remating (mins)	2.5%	97.5%
W1118	1	115	64.8	212.8
W1118	2	218.3	127.4	402.6
W1118	3	104.6	65.5	169.7
SD-Mad	1	92.4	53.6	172.1
SD-Mad	2	176.1	100.4	332.5
SD-Mad	3	84.3	53.2	136.9
SD-72	1	99.4	57.4	182.4
SD-72	2	188.9	114.9	332.9
SD-72	3	90.5	55.2	149.7
SD-5	1	58.1	36.6	94.6
SD-5	2	110.6	71.2	176
SD-5	3	52.9	33.6	81.9

Table S10b: the mean remating latency of females that initially mated with *SD/+* males, relative to the w^{1118} control males. A value of 0.5 means that females remated in half the time of females that initially mated with a w^{1118} male.

SD-variant	Mean remating latency relative to w1118	2.5%	97.5%
SD-5	0.52	0.28	0.88
SD-72	0.91	0.47	1.6
SD-Mad	0.85	0.43	1.5

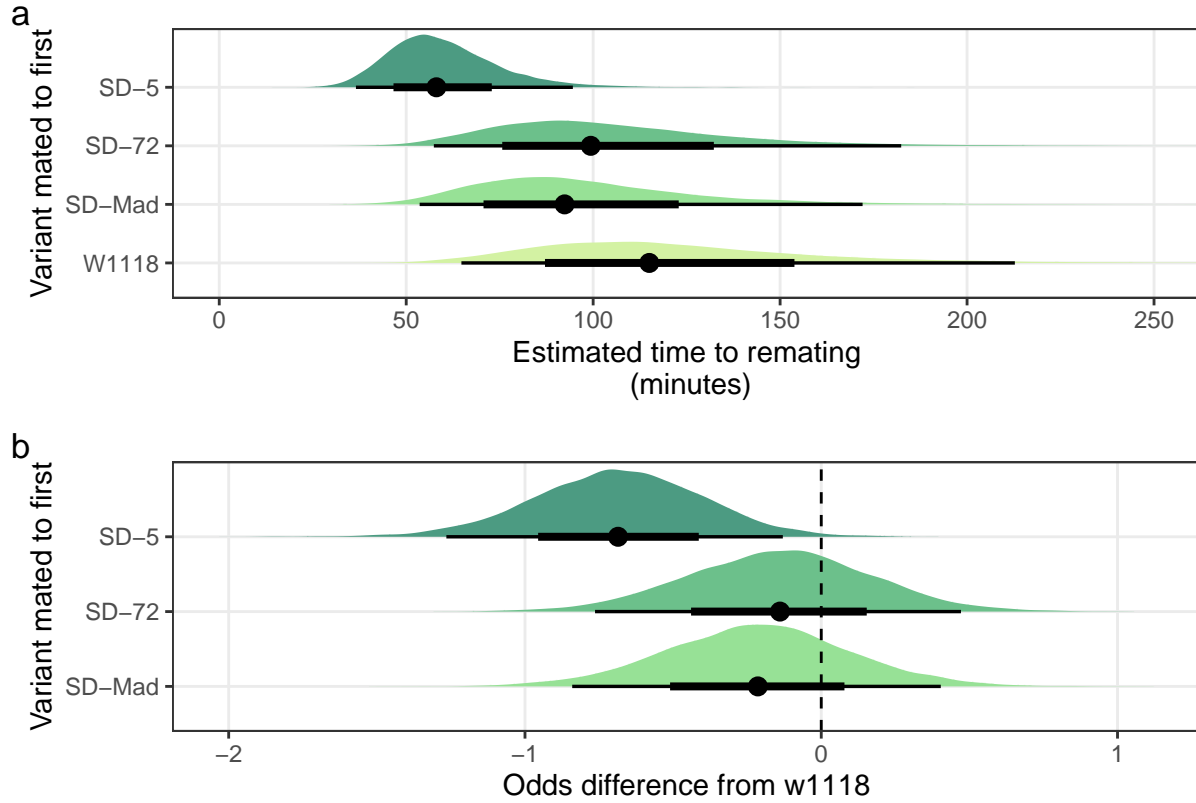


Figure S5: the effect that *SD/+* males have on female remating latency and how this compares to *w¹¹¹⁸* control males. Panel **a** shows the estimated remating latency for females exposed to *LH_m^{UBI}* males over a three-hour period, that had mated with a *SD/+* or control male four days earlier. Panel **b** shows effect sizes on the odds scale for the *SD* variants. Negative values indicate that the mates of *SD/+* males remated faster than the mates of *w¹¹¹⁸* control males. Black points indicate the estimated mean with associated 66 and 95% uncertainty intervals, while coloured area shows the posterior distribution.

Table S11a: the mean copulation duration when a *SD/+* male mated with a *LH_m* female in the first mating role.

Variant carried	Estimated copulation duration (mins)	2.5%	97.5%
W1118	19.3	16	23.2
SD-Mad	20.1	16.4	24
SD-72	22	18.3	26.5
SD-5	21.5	18	25.3

Table S11b: the mean copulation duration for *SD/+* males that mated with a *LH_m* female in the second mating role, relative to the *w¹¹¹⁸* control males. A value of 0.5 means that males mated for half the time of *w¹¹¹⁸* males.

SD-variant	Mean copulation duration relative to w1118	2.5%	97.5%
SD-5	1.118	0.936	1.314
SD-72	1.145	0.946	1.371

SD-variant	Mean copulation duration relative to w1118	2.5%	97.5%
SD-Mad	1.044	0.857	1.253

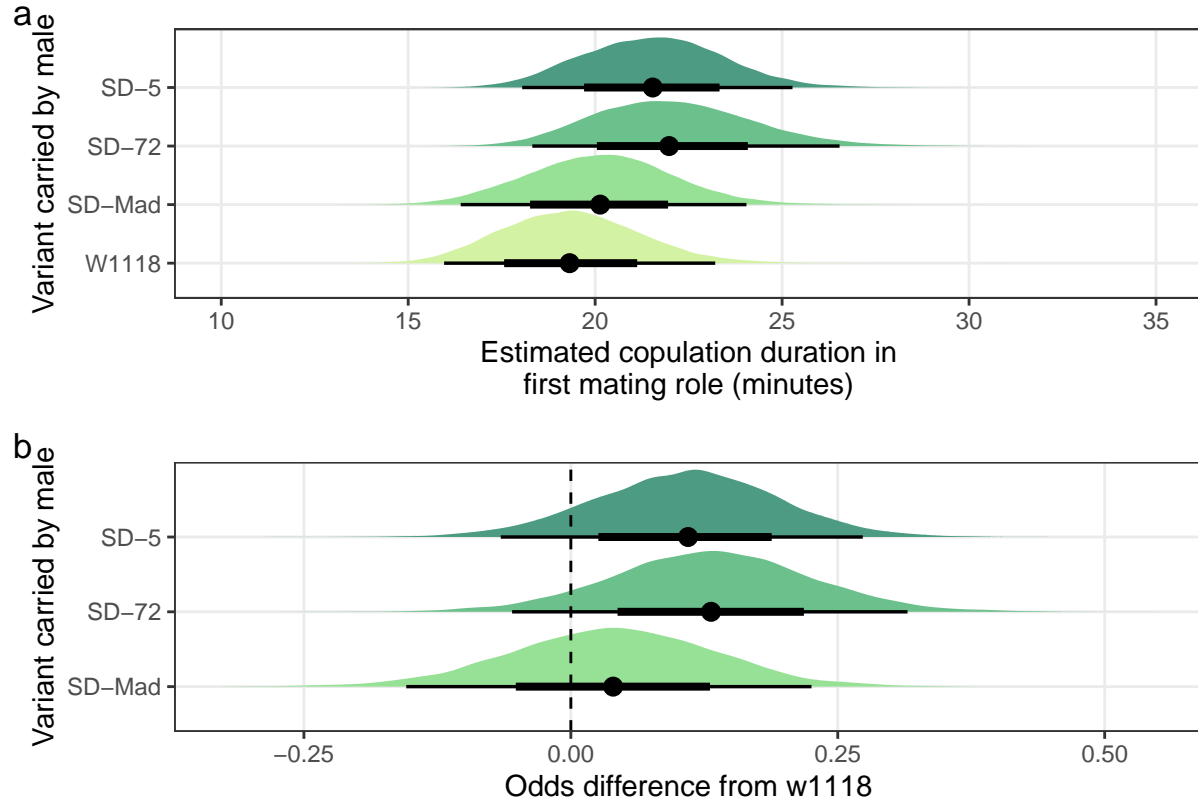


Figure S6: no difference in the duration of mating between a *SD/+* male and a *LH_m* female, compared to *w¹¹¹⁸* control males, when the *SD/+* (or control) male mated first. Panel **a** shows the estimated copulation duration for *SD/+* and control males. Panel **b** shows effect sizes on the odds scale for the *SD*-variants. Positive values indicate that *SD/+* males mated for longer than *w¹¹¹⁸* control males. Black points indicate the estimated mean with associated 66 and 95% uncertainty intervals, while coloured area shows the posterior distribution.

Table S12a: the mean copulation duration when a *SD/+* male mated with a *LH_m* female in the second mating role.

Variant carried	Estimated copulation duration (mins)	2.5%	97.5%
W1118	18.4	14.5	23.7
SD-Mad	20.4	15.8	26.4
SD-72	24.6	19.1	31.6
SD-5	19.4	15.1	25.1

Table S12b: the mean copulation duration for $SD/+$ males that mated with a LH_m female in the second mating role, relative to the w^{1118} control males. A value of 0.5 means that males mated for half the time of w^{1118} males.

SD-variant	Mean copulation duration relative to w1118	2.5%	97.5%
SD-5	1.063	0.795	1.392
SD-72	1.351	1.002	1.764
SD-Mad	1.119	0.833	1.47

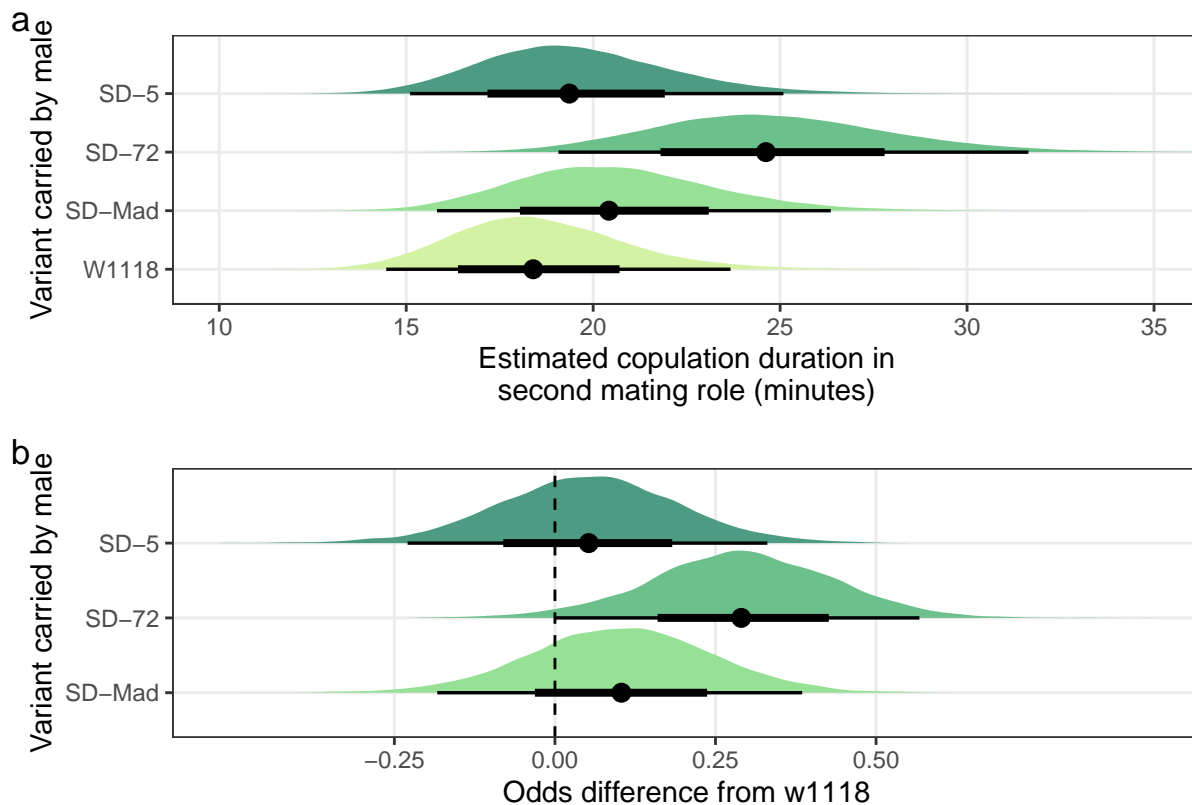


Figure S7: mating duration between a $SD/+$ male and a LH_m female, compared to w^{1118} control males, when the $SD/+$ (or control) male mated second. Panel **a** shows the estimated copulation duration for $SD/+$ and control males. Panel **b** shows effect sizes on the odds scale for the SD variants. Positive values indicate that $SD/+$ males mated for longer than w^{1118} control males. Black points indicate the estimated mean with associated 66 and 95% uncertainty intervals, while coloured area shows the posterior distribution.

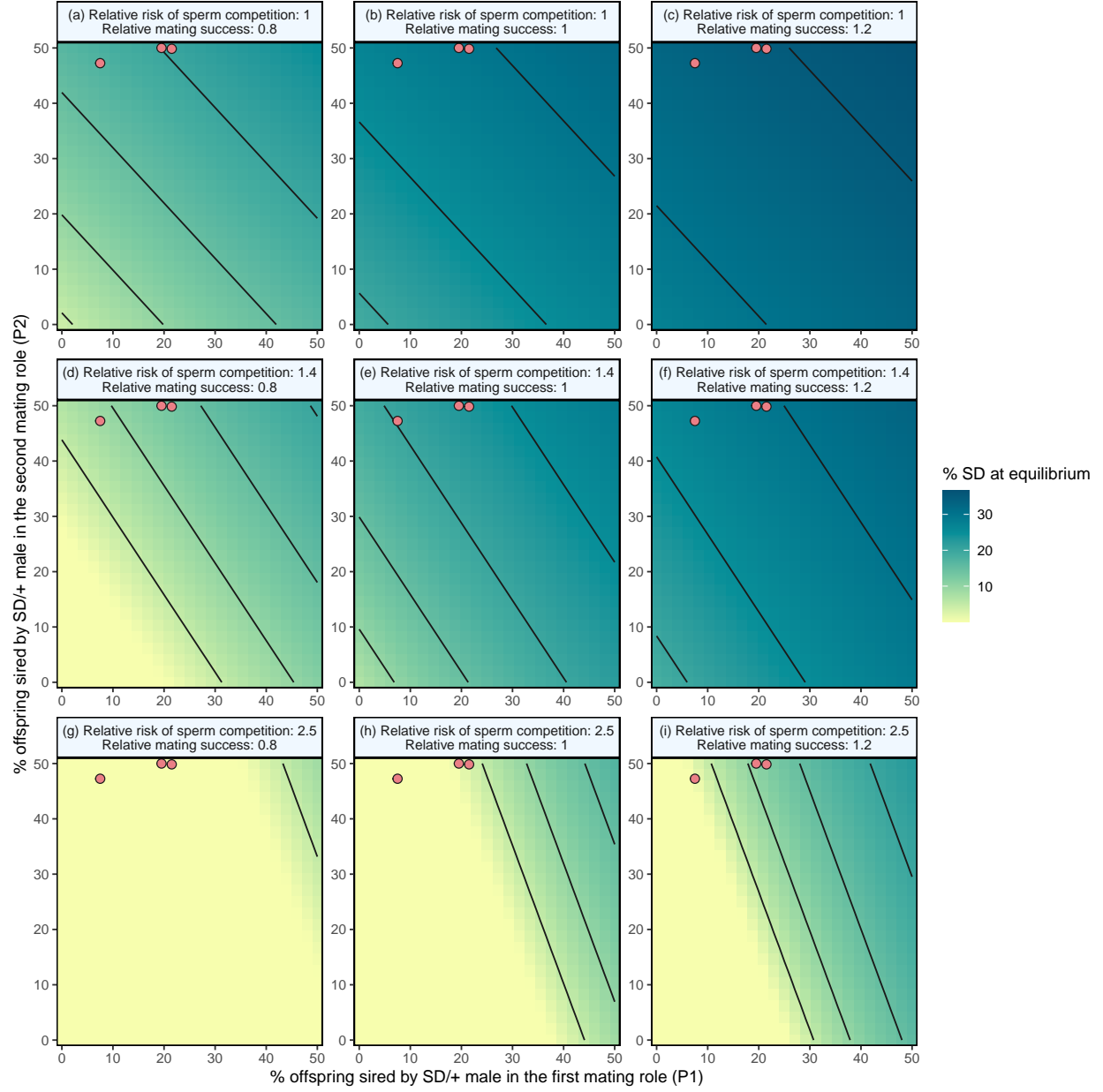


Figure S8: predicted equilibrium frequency of the *SD* allele, calculated from the population genetic model. The plot depicts the interaction between the P1 (x-axis) and P2 (y-axis) costs suffered by *SD/+* males in their effects on the equilibrium frequency of *SD* (shown by the colour scale and 5% contour lines). The plot is split into nine panels, with varying levels of *SD/+* male mating success across the rows and increasing likelihoods of a female remating after first mating to an *SD/+* male, $p_{SD/+}$, down the columns. The three orange points in each panel represent males carrying the *SD-5* (leftmost point), and *SD-72* and *SD-Mad* (rightmost points) alleles; these points show where males carrying these alleles fall in the figure's parameter space, as measured in Experiment 2. In the parameter space presented here, $k = 0.944$ (our highest estimated value), $P1_{normal} = 0.5$, *SD* homozygotes are non-viable and *SD* heterozygotes suffer no fitness costs outside of mating success and sperm competition.