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Supplementary Information 1:

Analyses of sex-biased dispersal

1. The relationship between sex-biased dispersal and sex determination in reptiles

A possible behavioural reason for biased adult sex ratio (ASR) could be sex-specific dispersal, because members of the sex with longer dispersal distance may suffer higher rate of mortality during their movements. Thus, if sex-biased dispersal is associated with the type of genetic sex determination (GSD), this could potentially generate a spurious relationship between ASR and GSD.

To test for a relationship between sex bias in dispersal and GSD, we conducted a preliminary literature search of published studies on sex differences in dispersal in amphibians and reptiles with known GSD. We found sufficient dispersal data for both XY and ZW species only for reptiles (28 species, data presented in Table SI 1.1). In these species we determined the sex dispersing farther on the basis of explicit statements of the source papers; we treat dispersal unbiased or variable when no statistical differences were found between the sexes or the direction of bias was inconsistent between samples, respectively. Out of 10 species with XY-type sex determination, 80% has male-biased dispersal and 20% shows no or variable sex bias in dispersal. Similarly, out of 18 species with ZW-type sex determination, 67% has male-biased dispersal, whereas 5% and 28% has female-biased and unbiased or variable dispersal, respectively. In this sample GSD is not associated with sex bias in dispersal (categorized as male-biased versus not male-biased; Pagel's Discrete Method[19], LR = 1.64, $P = 0.801$). This finding that reptiles tend to have male-biased dispersal is consistent with the conclusions of recent studies on sex-specific dispersal in snakes[58] and in lizards[22]. Thus, available data suggest that sex bias in dispersal and GSD are not associated in reptiles.

Table SI 1.1 Data on sex-biased dispersal in 28 reptile species, and their sources.

Family	Species	GSD*	Sex bias in dispersal	Reference for dispersal data
Iguanidae	Amblyrhynchus cristatus	XY	male	[59]
Iguanidae	Anolis limifrons	XY	male	[60]
Iguanidae	Anolis oculatus	XY	male	[61]
Iguanidae	Anolis roquet	XY	male	[62]
Iguanidae	Anolis sagrei	XY	male	[63]
Iguanidae	Crotaphytus collaris	XY	no or variable	[64]
Iguanidae	Ctenosaura pectinata	XY	male	[65]
Iguanidae	Sceloporus occidentalis	XY	male	[66]
Iguanidae	Uta stansburiana	XY	male	[67]
Scincidae	Egernia whitii	XY	no or variable	[68]
Acrochordidae	Acrochordus arafurae	ZW	female	[69]
Agamidae	Phrynocephalus przewalskii	ZW	male	[70]
Agamidae	Phrynocephalus vlangalii	ZW	male	[71]

Boidae	Boa constrictor	ZW	male	72
Colubridae	Cerberus schneiderii	ZW	no or variable	73
Colubridae	Coronella austriaca	ZW	male	74
Colubridae	Stegonotus cucullatus	ZW	male	75
Colubridae	Thamnophis atratus	ZW	male	76
Colubridae	Thermophis baileyi	ZW	male	77
Elapidae	Aipysurus laevis	ZW	no or variable	78
Elapidae	Cryptophis nigrescens	ZW	male	79
Elapidae	Hoplocephalus bungaroides	ZW	no or variable	80, 81
Elapidae	Laticauda laticaudata	ZW	no or variable	82
Elapidae	Laticauda saintgironsi	ZW	no or variable	82
Gekkonidae	Gehyra variegata	ZW	male	83
Lacertidae	Lacerta agilis	ZW	male	84
Lacertidae	Lacerta vivipara	ZW	male	85, 86
Lacertidae	Podarcis sicula	ZW	male	87

*Genetic sex-determination system (source: see Supplementary Data[34, 36, 37])

2. Sex-biased dispersal and ASR in birds

We directly tested whether ASR bias is related to sex-biased dispersal using birds where published data[88] on sex-specific dispersal distances (in meters) were available for 21 species from our ASR data set (Table SI 1.2). For this analysis we calculated sex bias in dispersal distance as $\log_{10}$(female dispersal distance / male dispersal distance). We used ASR as response variable and sex bias in dispersal distance as predictor variable in the phylogenetic model. This analysis shows that sex bias in dispersal distance is not significantly associated with ASR in birds (phylogenetic generalized least squares [PGLS][18]: b ± s.e.m. = 0.083 ± 0.06, t= 1.42, P = 0.171).

Table SI 1.2 Data on sex bias in dispersal distance in birds.

Family	Species	ASR	Male dispersal distance (m)	Female dispersal distance (m)	Sex bias in dispersal distance
Accipitridae	Accipiter gentilis	0.481	27741	15588	-0.250
Accipitridae	Accipiter nisus	0.47	9660	18340	0.278
Accipitridae	Circus cyaneus	0.338	6300	5680	-0.045
Anatidae	Branta canadensis	0.501	15200	3100	-0.690
Anatidae	Cygnus olor	0.584	12859	7754	-0.220
Cinclidae	Cinclus cinclus	0.49	3090	6450	0.320
Corvidae	Aphelocoma coerulescens	0.537	387	1165	0.479
Corvidae	Pica pica	0.58	358	465	0.114
Emberizidae	Melospiza melodia	0.505	110	127	0.062
Emberizidae	Passerculus sandwichensis	0.491	262	309	0.072

Emberizidae	Zonotrichia leucophrys	0.5	555	614	0.044
Falconidae	Falco peregrinus	0.58	58000	83000	0.156
Hirundinidae	Hirundo rustica	0.585	6375	8125	0.105
Maluridae	Malurus splendens	0.576	100	200	0.301
Muscicapidae	Saxicola rubetra	0.52	500	500	0.000
Phasianidae	Centrocercus urophasianus	0.278	7400	8800	0.075
Phasianidae	Lagopus lagopus	0.525	1000	2900	0.462
Phasianidae	Lagopus leucura	0.579	1250	4000	0.505
Phasianidae	Tetrao tetrix	0.61	1500	8000	0.727
Picidae	Melanerpes formicivorus	0.6	220	530	0.382
Troglodytidae	Troglodytes aedon	0.524	608	674	0.045

3. The effect of sex-determination system on ASR in models that control for sex-biased dispersal

We used the subset of species that overlaps between our ASR data set (Supplementary Data) and the available dispersal data sets (Tables SI 1.1 and 1.2, plus 6 amphibians we found by searching the literature [see section 1. above], and 3 mammalian species from Ref. 88) to investigate whether the relationship between sex-determination system and ASR remains significant when the influence of sex-biased dispersal is taken into account in multi-predictor models. In these analyses sex-biased dispersal was included as a binary trait with 'male-biased' and 'not male-biased' states, the latter including species with female-biased, unbiased and variable dispersal. All data and the sources of sex-biased dispersal are shown in Table SI 1.3.

First, we constructed two conservative models that include the GSD-uniform snakes, birds, and mammals as a single datum each (corresponding to models in the main analyses, see lines 490-506 in main text and Extended Data Table 1), because our data set is strongly biased toward birds (21 of 40 species). In these models dispersal was included for snakes as male-biased (see section 1, above), for birds as not male-biased, and for mammals as male-biased. We found that ASRs are significantly more male-biased in species with ZW sex-determination system than in species with XY sex-determination system when sex-bias in dispersal is controlled for (Model 1 in Table SI 1.4). This result is not sensitive to the dispersal categorisation of the snakes since the significant effect of sex-determination system on ASR remains when snakes are included as not male-biased instead of male-biased (effect of GSD in PGLS: b (± s.e.m.) = 0.10 (± 0.04), t = 2.828, $P = 0.013$, n = 17). The effect of sex-determination system on ASR also tends to be significant when all confounding variables (body size, sexual size dimorphism, breeding latitude and sex-biased dispersal) were included in the model (Model 2 in Table SI 1.4). Note that sample size is small relative to the number of predictors in this latter model. Finally, GSD predicts the ASR significantly even when we use all species (including snakes, birds and mammals) as individual data points (Model 3 in Table SI 1.4).

These results, together with those presented in sections 1 & 2 above, consistently show that the relationship between sex determination and ASR is not confounded by the influence of sex-biased dispersal.

Table SI 1.3 ASR and sex-biased dispersal in tetrapods, and data sources.

Taxon	Species	ASR*	GSD*	Sex-bias in dispersal	Dispersal reference	Body size*	Sexual size dimorphism*	Latitude*
Amphibians	Bufo bufo	0.75	ZW	not male	[89]	66.16	-0.081	51.64
Amphibians	Hyla arborea	0.55	XY	male	[90]	43.90	-0.013	46.53
Amphibians	Rana catesbeiana	0.47	XY	not male	[91]	131.96	-0.032	44.02
Amphibians	Rana lessonae	0.51	XY	not male	[92]	59.65	0.033	52.00
Amphibians	Rana ridibunda	0.44	XY	male	[92]	70.06	-0.013	49.58
Amphibians	Triturus alpestris	0.49	XY	male	[93]	50.83	-0.066	48.20
Reptiles	Acrochordus arafurae	0.56	ZW	not male	[77]	870.00	-0.119	-12.61
Reptiles	Anolis sagrei	0.44	XY	male	[63]	42.95	0.086	25.59
Reptiles	Boa constrictor	0.53	ZW	male	[72]	1925.00	-0.056	-31.83
Reptiles	Cerberus schneiderii	0.51	ZW	not male	[73]	407.55	0.009	1.45
Reptiles	Egernia whitii	0.49	XY	not male	[68]	85.15	-0.018	-35.88
Reptiles	Gehyra variegata	0.46	ZW	male	[83]	51.40	0.009	-31.63
Reptiles	Lacerta agilis	0.48	ZW	male	[84]	71.60	-0.027	50.90
Reptiles	Lacerta vivipara	0.45	ZW	male	[85, 86]	51.16	-0.042	48.16
Reptiles	Podarcis sicula	0.57	ZW	male	[87]	64.20	0.037	45.51
Reptiles	Uta stansburiana	0.44	XY	male	[67]	47.00	0.037	36.63
Birds	Accipiter gentilis	0.48	ZW	male	[88]	---	-0.204	43.74
Birds	Accipiter nisus	0.47	ZW	not male	[88]	---	-0.286	48.71
Birds	Aphelocoma coerulescens	0.54	ZW	not male	[88]	96.75	0.025	28.00
Birds	Branta canadensis	0.5	ZW	male	[88]	631.93	0.061	51.91
Birds	Centrocercus urophasianus	0.28	ZW	not male	[88]	---	0.275	43.89
Birds	Cinclus cinclus	0.49	ZW	not male	[88]	113.00	0.063	48.22
Birds	Circus cyaneus	0.34	ZW	male	[88]	229.35	-0.183	50.08
Birds	Cygnus olor	0.58	ZW	male	[88]	1181.90	0.086	49.75
Birds	Falco peregrinus	0.58	ZW	not male	[88]	269.75	-0.174	10.88
Birds	Hirundo rustica	0.59	ZW	not male	[88]	98.40	-0.014	16.80
Birds	Lagopus lagopus	0.53	ZW	not male	[88]	262.05	0.058	61.16
Birds	Lagopus leucura	0.58	ZW	not male	[88]	---	0.010	51.39
Birds	Malurus splendens	0.58	ZW	not male	[88]	50.90	0.043	-27.70
Birds	Melanerpes formicivorus	0.6	ZW	not male	[88]	119.50	0.02	23.58
Birds	Melospiza melodia	0.51	ZW	not male	[88]	57.17	0.029	40.78
Birds	Passerculus sandwichensis	0.49	ZW	not male	[88]	73.07	0.000	45.11
Birds	Pica pica	0.58	ZW	not male	[88]	163.20	0.030	43.08
Birds	Saxicola rubetra	0.52	ZW	not male	[88]	71.20	-0.005	54.13
Birds	Tetrao tetrix	0.61	ZW	not male	[88]	308.00	0.116	55.06
Birds	Troglodytes aedon	0.52	ZW	not male	[88]	66.65	-0.042	1.97
Birds	Zonotrichia leucophrys	0.54	ZW	not male	[88]	---	0.054	52.01
Mammals	Helogale parvula	0.48	XY	not male	[88]	---	---	-7.04
Mammals	Lycaon pictus	0.59	XY	male	[88]	---	---	-2.74
Mammals	Ursus americanus	0.33	XY	male	[88]	---	---	47.57

* sources: see Supplementary Data

Table SI 1.4 The relationships between adult sex ratio, sex-determination system, dispersal, and other confounding factors in phylogenetically corrected multi-predictor analyses.

	Model 1 (n = 17)			Model 2* (n = 17)			Model 3 (n = 32 species)		
	b (± s.e.m.)	*t*	*P*	*b* (± s.e.m.)	*t*	*P*	*b* (± s.e.m.)	*t*	*P*
Sex-determination system	0.115 (± 0.04)	3.17	0.007	0.072 (± 0.04)	1.93	0.080	0.092 (± 0.04)	2.52	0.018
Sex bias in dispersal	0.063 (± 0.03)	2.23	0.043	0.060 (± 0.04)	1.52	0.157	0.068 (± 0.02)	2.87	0.008
Body size	---	---	---	0 (± 0)	-0.52	0.614	0 (± 0)	1.17	0.251
Breeding latitude	---	---	---	0 (± 0)	-0.11	0.913	0 (± 0)	-0.66	0.516
Sexual size dimorphism	---	---	---	-0.627 (± 0.39)	-1.27	0.232	0.352 (± 0.18)	2.01	0.055

Results of phylogenetic generalized least squares (PGLS) [18]. ASR is included in the models as response variable. Models 1 and 2 include snakes, birds and mammals as a single data point each; Model 3 includes all species as individual data. For sex-determination system, *b* is the estimated difference in ASR between ZW and XY species. For sex bias in dispersal, *b* is the estimated difference in ASR between the 'not male-biased' and the 'male-biased' group. *In Model 2 we used Pagel's gradual branch lengths because the model does not converge with Nee's branch lengths[54].

References

58. Myers, E. A., Rodriguez-Robles, J. A., Denardo, D. F., Staub, R. E:, Stropoli, A., Ruane, S., Burbink, F. T. Multilocus phylogeographic assessment of the California Mountain Kingsnake (Lampropeltis zonata) suggests alternative patterns of diversification for the California Floristic Province. Molecular Ecology. 22, 5418–5429, (2013).

59. Rassmann, K., Tautz, D., Trillmich, F. & Gliddon, C. The microevolution of the Galápagos marine iguana Amblyrhynchus cristatus assessed by nuclear and mitochondrial genetic analyses. *Molecular Ecology* **6**, 437 - 452 (2003)

60. Losos, J. B. Lizards in an Evolutionary Tree: Ecology and Adaptive Radiation of Anoles. University of California Press, (2009)

61. Stenson A.G., Malhotra A. & Thorpe R. S. Population differentiation and nuclear gene flow in the Dominican anole (Anolis oculatus). *Molecular Ecology*, **11**, 1679–1688, (2002)

62. Johansson H., Surget-Groba Y. & Thorpe R. S. Microsatellite data show evidence for male-biased dispersal in the Caribbean lizard Anolis roquet. *Moecular Ecology*, **17**, 4425–4432, (2008)

63. Calsbeek R. Sex-specific adult dispersal and its selective consequences in the brown anole, Anolis sagrei, *Journal of Animal Ecology* **78**, 617-624 (2009)

64. Hranitz, J. M. & Baird, T. A. Effective population size and genetic structure of a population of collared lizards, Crotaphytus collaris, in central Oklahoma. *Copeia*. **2000**, 786-791 (2000)

65. Zarza, E., Reynoso, V. H. & Emerson, B. C. Discordant patterns of geographic variation between mitochondrial and microsatellite markers in the Mexican black iguana (Ctenosaura pectinata) in a contact zone. *Journal of Biogeography*, **38**, 1394–1405 (2011)

66. Massot, M., Huey, R. B., Tsuji, J. & van Berkum, F. H. Genetic, prenatal, and postnatal correlates of dispersal in hatchling fence lizards (Sceloporus occidentalis). *Behavioral Ecology*, **14**, 650–655 (2003)

67. Doughty, P., Sinervo, B. & Burghardt, G. M. Sex-biased dispersal in a polygynous lizard, Uta stansburiana. *Animal Behaviour* **47**, 227–229 (1994)

68. Chapple D. G. & Keogh J. S. Complex mating system and dispersal patterns in a social lizard, Egernia whitii. *Molecular Ecology*, **14**, 1215–1227 (2005)

69. Houston, D. & Shine, R. Movements and activity patterns of Arafura filesnakes (Serpentes: Acrochordidae) in tropical Australia. *Herpetologica,* **50**, 349-357 (1994)

70. Urquhart, J., Wang, Y. & Fu, J. Historical vicariance and male-mediated gene flow in the toad-headed lizards Phrynocephalus przewalskii. *Molecular Ecology*, **18**, 3714–3729 (2009)

71. Qi, Y., Yang, W., Lu, B. & Fu, J. Genetic evidence for male-biased dispersal in the Qinghai toad-headed agamid Phrynocephalus vlangalii and its potential link to individual social interactions. *Ecol Evol*. **3**, 1219–1230 (2013)

72. Rivera, P. C., Gardenal, C. N. & Chiaraviglio, M. Sex-biased dispersal and high levels of gene flow among local populations in the argentine boa constrictor, Boa constrictor occidentalis. *Austral Ecology*, **31**, 948–955 (2006)

73. Chim, C. K. & Diong, C. H. A mark-recapture study of a dog-faced water snake Cerberus schneiderii (Colubridae: Homalopsidae) population in Sungei Buloh wetland reserve, Singapore. *The Raffles Bulletin of Zoology*, **61**(2), 811–825, (2013)

74. Pernetta, A. P., Allen, J. A., Beebee, T. J. C. & Reading, C. J. Fine-scale population genetic structure and sex-biased dispersal in the smooth snake (Coronella austriaca) in southern England. *Heredity*, **107**, 231–238 (2011)

75. Dubey, S., Brown, G. P., Madsen, T. & Shine, R. Male-biased dispersal in a tropical Australian snake (Stegonotus cucullatus, Colubridae). *Molecular Ecology,* **17**, 3506–3514 (2008)

76. Welsh, H. H., Wheeler, C. A. & Lind, A. J. Spatial ecology of the Oregon gartersnake, Thamnophis atratus hydrophilus, in a free-flowing stream environment. *Copeia*, **2010**(1), 75-85 (2010)

77. Hofmann, S., Fritzsche, P., Solhøy, T., Dorge, T. & Miehe, G. Evidence of sex-biased dispersal in Thermophis baileyi inferred from microsatellite markers. *Herpetologica*, **68**(4), 514-522 (2012)

78. Lukoschek, V., Waycott, M. & Keogh, J. S. Relative information content of polymorphic microsatellites and mitochondrial DNA for inferring dispersal and population genetic structure in the olive sea snake, Aipysurus laevis. *Molecular Ecology*, **17**, 3062–3077 (2008)

79. Keogh, J. S., Webb, J. K. & Shine, R. Spatial genetic analysis and long-term mark–recapture data demonstrate male-biased dispersal in a snake. *Biology Letters*, **3**, 33–35, (2007)

80. Webb, J. K. & Shine, R. A field study of spatial ecology and movements of a threatened snake species, Hoplocephalus bungaroides. *Biological Conservation* **82**, 203-217 (1997)

81. Croak, B. M., Crowther, M. S., Webb, J. K. & Shine, R. Movements and habitat use of an endangered snake, Hoplocephalus bungaroides (Elapidae): Implications for conservation. *PLoS ONE* **8**(4), e61711. doi:10.1371/journal.pone.0061711, (2013)

82. Lane, A. & Shine, R. Intraspecific variation in the direction and degree of sex-biased dispersal among sea-snake populations. *Molecular Ecology* **20**, 1870–1876 (2011)

83. Gruber, B. & Henle, K. Analysing the effect of movement on local survival: a new method with an application to a spatially structured population of the arboreal gecko Gehyra variegata. *Oecologia,* **154**, 679–690 (2008)

84. Olsson, M., Gullberg, A. & Tegelström, H. Malformed offspring, sibling matings, and selection against inbreeding in the sand lizard (Lacerta agilis). *J. Evol. Biol,* **9**, 229–242, (1996)

85. Clobert, J. *et al*. Determinants of dispersal behavior: the common lizard as a case study. In: Vitt, L., Pianka, E., *editors*. Lizard Ecology: Historical and Experimental Perspectives. Princeton, *Princeton Univ. Press*; pp. 183–206 (1994)

86. Hofmann, S. Who is sitting next to me? Relatedness between next neighbours in common lizards. *Amphibia-Reptilia,* **29**, 19-24 (2008)

87. Vignoli, L., Vuerich, V. & Bologna, M A. Experimental study of dispersal behaviour in a wall lizard species (Podarcis sicula) (Sauria Lacertidae). *Ethology Ecology & Evolution*, **24**(3), 244-256 (2012)

88. Mabry, K. E., Shelley, E. L., Davis, K. E., Blumstein, D. T., Van Vuren, D. H. Social mating system and sex-biased dispersal in mammals and birds: a phylogenetic analysis, *PLoS ONE,* **8**(3), e57980. doi:10.1371/journal.pone.0057980 (2013)

89. Schlupp, I. & Podloucky, R. Changes in breeding site fidelity: A combined study of conservation and behaviour in the common toad Bufo bufo. *Biological Conservation,* **69**(3), 285-291 (1994)

90. Vos, C. C., Ter Braak, C. J. F., & Nieuwenhuizen, W. Incidence function modelling and conservation of the Tree Frog Hyla arborea in the Netherlands. *Ecological Bulletins*, **48**, 165-180 (2000)

91. Austin, J. D., Dávila, J. A., Lougheed, S. C. & Boag, P. T. Genetic evidence for female-biased dispersal in the bullfrog, Rana catesbeiana (Ranidae). *Molecular Ecology,* **12**(11), 3165–3172 (2003)

92. Holenweg Peter, A-K. Dispersal rates and distances in adult water frogs, Rana lessonae, R. ridibunda, and their hybridogenetic associate R. esculenta. *Herpetologica*, **57**(4), 449-460 (2001)

93. Perret, N., Pradel, R., Miaud, C., Grolet, O. & Joly, P. Transience, dispersal and survival rates in newt patchy populations. *Journal of Animal Ecology*, **72**(4), 567–575 (2003)

Supplementary Information 2

This Supplementary Information presents population genetic models of the effect that genetic sex determination systems may have on the adult sex ratio. Section 1 develops results for deleterious mutations, and Section 2 for sex-antagonistic selection.

All the models assume that populations are sufficiently large that the effects of drift can be neglected and the loci evolve independently. We expect the results will give good approximations for loci where the magnitude of the selection coefficient s is larger than $1/N_e$, where N_e is the effective population size of the sex chromosome under consideration.

These models do not capture the effects of several stochastic processes thought to be important to sex chromosomes because of their reduced effective population sizes[23]. One is Muller's ratchet, in which deleterious mutations drift to fixation on nonrecombining sex chromosomes. A second is the fixation of deleterious mutations that hitchhike with beneficial mutations that sweep to fixation at linked loci. While those processes could also contribute to biased adult sex ratios, they are complex, and an adequate analysis of their effects on the ASR is beyond what is possible here. In any event, the deterministic results developed here are a necessary foundation for more complex models.

1. Deleterious mutations

This section develops a simple model to estimate the impact that deleterious mutation may have on the adults sex ratio (ASR), which we define as the proportion of males in the adult population. If the sex ratio is unbiased at conception, the adult sex ratio will be

$$\mathrm{ASR} \;=\; \frac{\overline{W}_m}{\overline{W}_f \;+\; \overline{W}_m} \tag{1}$$

where $\overline{W}_m$ and $\overline{W}_f$ are the relative rates of survival to adulthood of males and females. For concreteness, we develop the model assuming XY sex determination, and at the end we generalize the results to ZW systems. For simplicity, the model assumes the loci are completely sex-linked, and that loci carried on one type of sex chromosome (e.g. the X) have no homologue on the other type (e.g. the Y) that might mask the fitness effects of deleterious mutations. Intuitively, we expect that loci in the pseudoautosomal region will have a smaller impact on the ASR.

Begin by considering X-linked loci. We assume that fitness effects are multiplicative across loci. The mean fitnesses of females and males are approximately

$$\overline{W}_f \;\approx\; \prod_i (1 - h_i\, s_i^f\, p_i) \;\approx\; \exp\left\{-\sum_i h_i\, s_i^f\, p_i\right\} \tag{2}$$

$$\overline{W}_m \;\approx\; \prod_i (1 - s_i^m\, p_i) \;\approx\; \exp\left\{-\sum_i s_i^m\, p_i\right\} \tag{3}$$

where s_i^f and s_i^f are the selection coefficients for the deleterious allele at locus i, p_i is that allele's frequency, and h_i is the dominance coefficient in females. These approximations hold when linkage disequilibrium is weak, mutation is weak relative to selection, and $s_i^m,\ h_i\, s_i^f << 1$. At a mutation-selection equilibrium,

$$p_i \;\approx\; \mu_i \Big/ \left(\frac{2}{3} h_i\, s_i^f \;+\; \frac{1}{3} s_i^m\right). \tag{4}$$

where μ_i is the mutation rate to the deleterious allele at locus i. The form of the denominator is a result of the fact that deleterious mutations spend 2/3 of their evolutionary time in females and 1/3 in males. So we have

$$\overline{W}_f \;\approx\; \exp\left\{-3 \sum_i \left(\frac{\mu_i\, h_i\, s_i^f}{2\, h_i\, s_i^f \;+\; s_i^m}\right)\right\} \tag{5}$$

$$\overline{W}_m \;\approx\; \exp\left\{-3 \sum_i \left(\frac{\mu_i\, s_i^m}{2\, h_i\, s_i^f \;+\; s_i^m}\right)\right\} \tag{6}$$

Now assume that deleterous mutations are nearly or completely recessive in females ($h_i << 1$). Then

$$\overline{W}_f \;\approx\; 1 \tag{7}$$

$$\overline{W}_m \;\approx\; \exp\{-3\, U_X\} \tag{8}$$

where U_X is the total mutation rate for X-linked genes (that is, the sum across loci of the mutation rates to deleterious alleles per gamete per generation).

These results are consistent with the well-known result that the genetic load (that is, the loss in population mean fitness) from deleterious mutation is simply equal to the mutation rate and is independent of selection coefficient[94]. The factor of 3 appears because recessive mutations at X-linked loci experience selection in males in only one of every three generations.

The second class of loci we consider are genes that are carried on the Y but absent from the X. The genetic load principal applies directly to this case, and so

$$\overline{W}_f \approx 1 \tag{9}$$

$$\overline{W}_m \approx \exp\{-U_Y\} \tag{10}$$

where U_Y is the total rate of deleterious mutation for loci in this first class.

Combining the effects of X-linked and Y-linked genes (Eqs. (7) - (9)), we have

$$\overline{W}_f \approx 1 \tag{11}$$

$$\overline{W}_m \approx \exp\{-3\,U_X - U_Y\}. \tag{12}$$

If the total mutation rates are small (U_X, $U_Y << 1$), the fitness of males relative to the fitness of females is:

$$\overline{W}_m \approx 1 - 3\,U_X - U_Y. \tag{13}$$

We can now find the ASR resulting from deleterious mutation by multiplying the fitness effects of X-linked and Y-linked genes (Eqs. (9) - (12)), which gives:

$$\mathrm{ASR} \approx \frac{\exp\{-3\,U_X - U_Y\}}{1 + \exp\{-3\,U_X - U_Y\}}. \tag{14}$$

This result simplifies further when the total mutation rates, U_X and U_Y, are much smaller than 1:

$$\mathrm{ASR} \approx \frac{1}{2} - \frac{3}{4}U_X - \frac{1}{4}U_Y. \tag{15}$$

A parallel argument for ZW sex determination systems gives

$$\overline{W}_f \approx \exp\{-3\,U_Z - U_W\}. \tag{16}$$

$$\overline{W}_m \approx 1 \tag{17}$$

$$\mathrm{ASR} \approx \frac{1}{1 + \exp\{-3\,U_Z - U_W\}} \tag{18}$$

$$\approx \frac{1}{2} + \frac{3}{4}U_Z + \frac{1}{4}U_W \tag{19}$$

where in Eq. (19) we again assume that the total mutation rates are much smaller than 1.

Sex chromosomes show bewildering variation across animals and plants[17], which makes it difficult to make general statements about what the empirical implications of these calculations might be. To get some sense, consider the following crude estimates for U_X and U_Y in humans. The human X carries about 5% of the genes in the genome[95], and the Y carries about 0.3 % of the genes[96]. The genome-wide rate of mutation to deleterious alleles is estimated to be about 1 per haploid genome per generation[97], suggesting $U_X \approx 0.05$ and $U_Y \approx 0.003$. Using those values and Eq. (13), the equilibrium adult sex ratio is ASR = 0.46.

This calculation is very rough. The parameter estimates are crude and they neglect important factors such as sex-biased mutation. Further, we have made restrictive assumptions (e.g. that deleterious mutations are fully recessive). It seems unlikely, however, that refining the parameter estimates and generalizing the assumptions would lead to a sex ratio that deviates from 1/2 by more than a few percent for humans

(and likely other eutherian mammals). The conclusion could be very different in other species, however, particularly if values for U_X and U_Y are much larger.

2. Sex-antagonistic selection

Sex-antagonistic selection occurs when alleles have opposing fitness effects on females and males. When this type of selection acts on sex-linked loci (on X or Z chromosomes), either fixation or polymorphism can result.

Fixation

Fixation is the typical outcome when dominance effects are weak and the relative fitness effects of the alleles within males are approximately equal in magnitude but opposite in sign to their relative fitnesses in females. In that case, the allele that is favored in the homogametic sex fixes because it experiences selection in the homogametic sex twice as often as in the heterogametic sex.

This outcome, however, does not automatically lead to a prediction about which sex will have higher mortality. That is because it is the evolutionary outcome depends on the relative fitnesses *within* each sex, and is independent of how much each allele affects females versus males. (We are very grateful to a reviewer for pointing this out.) This point may become clearer with a simple numerical example. Consider an X-linked locus in an XY sex determination system with two alleles, a and A. First consider the case where the viabilities are

	Allele	
	a	A
Males:	0.9	1

	aa	Aa	AA
Females:	1	0.9	0.8

The female-beneficial allele a will fix, which leads to a female-biased sex ratio. Now consider a second case in which the viabilities are

	Allele	
	a	A
Males:	0.9	1

	aa	Aa	AA
Females:	0.8	0.7	0.6

In this case, the female-beneficial allele again fixes, but the outcome is a male-biased sex ratio. These two examples illustrate the basic point that fixation of the allele that is favored in the homogametic sex does not necessarily lead to higher viability for that sex.

We are, however, able to make a general statement by introducing an additional assumption. Again assuming approximately equal relative allelic effects within each sex and weak or no dominance, and assume further that the optimal genotype for males has the same viability as the optimal genotype for females. (The first case above is an example.) The outcome is that female-favorable alleles fix in XY systems, causing the ASR to decrease. Conversely, male-favorable alleles will tend to fix in ZW systems, leading to an increase in the ASR.

When selection is stronger in the hemizygous sex, the allele favorable to that sex can fix. That would increase the ASR in XY systems and decrease it in ZW systems.

In sum, there are limited situations in which we can predict how fixation of alleles under sex-antagonistic selection will impact the ASR.

Stable polymorphism

Another possible outcome of sex-antagonistic selection is a stable polymorphism. In this case, there does not seem to be any simple generalization that can be made the direction in which the ASR will be biased. The range of parameters that support a stable polymorphism is fairly limited[98], however, so this may not often be an important factor in the evolution of the ASR.

To make these statements more quantitative, we consider a model for sex-antagonistic selection analyzed by Bennett[98]. There are two alleles, A and a, that are X-linked. The relative viability scheme that we use here is:

Males:	a	A	
	1	$1 + s_m$	
Females:	aa	Aa	AA
	$1 + s_{aa}$	1	$1 - s_{AA}$

For concreteness here we assume all the $s \geq 0$, which means allele A is favored in males and allele a in females, and that heterozygotes have intermediate fitness in females.

Bennett found that a stable polymorphism occurs if and only if:

$$s_{aa} > \frac{s_m}{2} \text{ and } s_{AA} < \frac{s_m}{2(1 + s_m)} \tag{20}$$

When those conditions are met, the equilibrium frequency of A in eggs is

$$\hat{p}_f = \frac{2 s_{aa} - s_m}{2(s_{aa} - s_{AA}(1 + s_m))}, \tag{21}$$

and in sperm it is

$$\hat{p}_m = \frac{(1 + s_m)(s_m - 2 s_{aa})}{s_m^2 - 2 s_{aa}(1 + s_m) + 2 s_{AA}(1 + s_m)}. \tag{22}$$

When there is no dominance in females ($s_{aa} = s_{AA}$), one can show that the female favorable allele a will fix if:

$$\frac{s_m}{2} \leq s_{aa} = s_{AA}. \tag{23}$$

That result is the basis of the earlier statement that the female-favorable allele will generally fix when fitness effects in the two sexes are of comparable magnitude and opposite in sign, and heterozygotes have intermediate viability. The conclusion is reversed for ZW systems: there Z chromosomes spend more of their evolutionary histories in males, and so male-favorable alleles will tend to fix.

When there is a stable polymorphism, we can calculate the ratio of female to male fitness:

$$R_W = \frac{(s_{AA}(1 + s_m) - s_{aa})\left(1 + (2 - 4(1 + s_{aa})(1 - s_{AA}))(1 + s_m) + (1 + s_m)^2\right)}{\left(1 - 2(1 + s_{aa} - s_{AA})(1 + s_m) + (1 + s_m)^2\right)^2} \tag{24}$$

Here are two numerical examples. In the first, females have higher viability than males ($R_W > 1$), while in the second example the males have higher viability ($R_W < 1$):

s_m	s_{aa}	s_{AA}	$\hat{p}_f$	$\hat{p}_m$	R_W
0.205	0.1	0.1	0.12	0.14	1.09
0.22	0.1	0.1	0.45	0.50	0.91

These examples illustrate the point made earlier that there are no robust generalizations about which sex will have higher viability when sex-antagonism results in a polymorphism.

References for Supplementary Information 2

94. Haldane, J.M.S. The effect of variation on fitness. *American Naturalist* **71**: 337-349 (1937).

95. Ross, M.T., *et al*. The DNA sequence of the human X chromosome. *Nature* **434**: 325-337 (2005).

96. Skaletsky, H., *et al*. The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. *Nature* **423**: 825-837 (2003).

97. Keightley, P.D. Rates and fitness consequences of new mutations in humans. *Genetics* **190**: 295-304 (2012).

98. Bennett, J.H. Selectively balanced polymorphism at a sex-linked locus. *Nature* **180**: 1363-1364 (1957).