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The genetic sex-determination system predicts

adult sex ratios in tetrapods

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Adult sex ratio (ASR) has critical effects on behaviour, ecology and population dynamics[1–3], but the causes of variation in ASRs are unclear[4,5]. Here we assess whether the type of genetic sex determination influences ASR using data from 344 species in 117 families of tetrapods. We find that taxa with female heterogamety have a significantly more male-biased ASR (mean proportion of males: 0.55 ± 0.01 SE) than taxa with male heterogamety (0.43 ± 0.01). The genetic sex-determination system explains 24% of interspecific variation in ASR in amphibians and 36% in reptiles. We consider several genetic factors that could contribute to this pattern, including meiotic drive and sex-linked deleterious mutations, but further work is needed to quantify their effects. Regardless of the mechanism, the effects of the genetic sex-determination system on the adult sex ratio are likely to have profound impacts on the demography and social behaviour of tetrapods.

Adult sex ratio (ASR) varies widely in nature, ranging from populations that are heavily male-biased to ones composed only of adult females[5–8]. Birds and schistosome parasites tend to have male-biased ASR, for example, while mammals and copepods usually exhibit female-biased ASR[5]. Extreme bias occurs among marsupials (Didelphidae and Dasyuridae): males die after the mating season, so there are times when the entire population consists of pregnant females[9]. Understanding the causes and consequences of ASR variation is an important goal in evolutionary biology, population demography and biodiversity conservation because ASR impacts behaviour, breeding systems, and ultimately population fitness[1,2,10–13]. It is also a significant issue in social sciences, human health and economics, since unbalanced ASRs have been linked to violence, rape, mate choice decisions and spread of diseases like HIV[14–16]. The causes of ASR variation in wild populations, however, remain obscure[5,13,17].

43

One factor that could impact the ASR is the genetic sex-determination system[7,8,18]. Taxa

such as mammals and fruit flies have XY sex determination (males are heterogametic),

whereas taxa such as birds and butterflies have ZW sex determination (females are

heterogametic). Sex-determination systems could affect the ASR in several ways. A

skewed ASR might result from an unbalanced sex ratio at birth caused by sex ratio

distorters[19]. Alternatively, a biased ASR could develop after birth if sex chromosomes

contribute to sex differences in mortality[8,18,20,21]. Differential postnatal mortality is likely

to be the main driver of biased ASR in birds and mammals, since birth sex ratios in these

classes tend to be balanced[7].

53

Here we use data from the four major clades of tetrapods (amphibians, reptiles, birds, and

mammals) to assess whether adult sex ratios differ between taxa with XY and ZW sex

determination (Fig. 1; Supplementary Table 1). While mammals and birds are fixed for

XY and ZW sex determination, respectively, reptiles and amphibians provide particularly

attractive opportunities for this study since transitions between sex-determination systems

have occurred many times within these clades[22,23]. We compiled published data on adult

sex ratios in wild populations and their sex-determination systems (Supplementary Table

1). To control for phylogenetic effects, we used phylogenetic generalized least squares

(PGLS)[24] to test for differences in ASRs between XY and ZW taxa, and Pagel's discrete

method (PDM)[25] to test whether XY and ZWsystems are evolutionarily associated with

female-biased and male-biased sex ratios, respectively. Phylogenies were taken from

recent molecular studies (see Methods for details).

66

67   Both the ASR and the sex-determination system are highly variable across tetrapods (Fig.

68   1, Supplementary Table 1). We find that ASR and sex determination are correlated.

69   Before controlling for phylogenetic effects, we find that ASRs are significantly more

70   male-biased in species with ZW sex determination than in those with XY sex

71   determination (Fig. 2, Table 1, Extended Data Table 1). Similarly, the proportion of

72   species with male-biased ASRs is greater among ZW than among XY species (Fig. 1,

73   Table 1). These differences are significant within amphibians, within reptiles, and across

74   tetrapods as a whole (Table 1, Extended Data Table 1).

75

76   The pattern remains significant after controlling for phylogenetic effects. Both the mean of

77   ASR across species (analyzed using PGLS) and the proportion of species with male-

78   biased sex ratios (analyzed using PDM) are significantly different between XY and ZW

79   systems within amphibians, within reptiles, and across tetrapods as a whole (Table 1,

80   Extended Data Table 1). The effect is strong in clades with variation in sex determination:

81   the type of genetic sex determination explains up to 24% of the interspecific variance in

82   ASR among amphibians and 36% in reptiles (estimated using PGLS, Extended Data Table

83   2). The results remain significant when we treat three large clades with invariant sex-

84   determination systems as a single datum each (snakes, ZW; birds, ZW; mammals, XY;

85   Extended Data Table 1), when we make different assumptions about branch lengths in the

86   phylogeny (Extended Data Table 2), and when we use arc-sine transformed ASR values

87   and control for variance in sample size (see Methods).

88

89   Body size and breeding latitude correlate with life-history traits in many organisms and

90   these traits could affect ASR[26–28]. Sexual size dimorphism is linked to differential sexual

91   selection acting on males and females and thus influences sex-specific mortality, and has

4

92   been suggested to drive the evolution of genetic sex-determination systems[29].

93   Nevertheless, we find that neither body size nor breeding latitude explains the ASR in

94   phylogenetically controlled multi-predictor analyses (Table 2). Sexual size dimorphism is

95   significantly associated with ASR in reptiles and across tetrapods as a whole, but the

96   effect of the genetic sex-determination system remains significant when size dimorphism

97   is included in the analysis (Table 2).

98

99   Sex differences in dispersal may also result in biased ASRs. However, dispersal is

100   unlikely to explain the relationship between ASR and sex-determination systems. First,

101   male-biased dispersal is typical in reptiles regardless of sex-determination system

102   (Supplementary Material 1)[30,31]. Second, there is no relationship between ASR and sex

103   bias in dispersal distance in birds (Supplementary Material 1). Finally, the relationship

104   between sex determination and ASR remain significant when the influence of sex-biased

105   dispersal is controlled for in multi-predictor models in tetrapods (Supplementary Material

106   1).

107

108   The sex-determination system may affect the ASR in the directions seen in the data in a

109   number of ways. First, sexual selection can fix mutations that increase male mating

110   success and decrease male survival. They will accumulate on Y but not W chromosomes,

111   and will accumulate more readily on X than Z chromosomes if they tend to be recessive.

112   Second, biased ASRs could result from recessive mutations at loci carried on the X (or Z)

113   but absent from the Y (or W) chromosome since they are not masked in the heterogametic

114   sex (the "unguarded sex chromosome" hypothesis)[7,8,18], and from deleterious mutations

115   carried on the Y (or W) but not on the X (or Z). At loci carried on both sex chromosomes,

116   alleles on the Y (or W) can show partial degeneration[32]. Population genetic models

5

117   suggest deleterious mutation pressure alone may not be adequate to explain ASR biases as

118   large as those observed (Supplementary Material 2), but the models do not include factors

119   that could be important, notably degeneration of Y and W chromosomes by genetic drift[32].

120   A third hypothesis is imperfect dosage compensation, which may be deleterious to the

121   heterogametic sex[33]. Fourth, distorted sex ratios can result from meiotic drive acting on

122   sex chromosomes[34,35]. Drive more often produces female-biased sex ratios in XY systems

123   at birth[36]. There is little data on drive in ZW systems, but if it operates in a symmetric

124   fashion then we expect it to cause male-biased sex ratios. Fifth, Y and W chromosomes

125   might degenerate during the lifespan, for example by telomere shortening or loss of

126   epigenetic marks, more rapidly than X and Z chromosomes. A final possibility is that sex-

127   antagonistic selection acting on sex-linked loci could lead to biased sex ratios, but unlike

128   the preceding hypotheses there does not seem to be a robust prediction about the direction

129   of the ASR bias it will produce (see Supplementary Material 2).

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131   The limited data that are available do not provide clear support for any of these

132   hypotheses, although critical tests are lacking. For instance, the meiotic drive process

133   predicts biased sex ratios at birth. Although a recent comparative analysis in birds

134   suggests that sex ratios at birth are unrelated to biased ASRs[10], offspring sex ratios have

135   not been compared between different sex-determination systems. Additional insight might

136   come from study of dioecious plants with biased sex ratios[37], but their skewed ASR could

137   result from selection on the gametophytic stage that is absent from animals[38].

138   Evolutionary feedbacks from the ASR to the sex-determination system are also possible:

139   for example, the ASR could influence sexual size dimorphism and sexual conflict, which

140   in turn could trigger transitions in sex determination[29,39,40].

141

142　In conclusion, we demonstrate strong and phylogenetically robust associations between

143　genetic sex-determination systems and a demographic property of populations, ASR.

144　Although the mechanisms that drive this association need further theoretical and empirical

145　analyses, the observed pattern is biologically important for two reasons. First, changes in

146　sex-determination systems are expected to have knock-on effects on social behaviour.

147　Theory suggests that ASR affects violence, pair bonds, infidelity and parental care[1,41], and

148　field-based studies support these predictions[4,13,15,16]. For instance, female-biased ASRs co-

149　occur with polygyny and female care, whereas male-biased ASRs tend to co-occur with

150　polyandry and male care in birds[4]. Second, sex-determination systems may have important

151　demographic consequences through skewed birth sex ratios and sex-biased survival. Such

152　biases may not only impact upon the productivity and growth of populations, but also their

153　genetic composition and viability. Further theoretical, experimental, and comparative

154　studies are clearly needed to understand the linkages between sex determination,

155　demography, and social behaviour.

156

157　**Methods Summary**

158　We collected ASR data for 39 amphibian, 67 reptile, 187 bird and 51 mammal species

159　from the literature. When more than one estimate was available for a species we used their

160　mean. Because genetic sex-determination systems of amphibians vary between closely

161　related species[42], we used only those species in which sex determination was characterized

162　at the species level[22,43]. Sex determination is evolutionarily less labile in reptiles, thus we

163　included all species for which sex determination was known either at the family level or,

164　in variable families, at the species level[22,44,45]. Breeding latitude was calculated as the

165　distance from the Equator in latitudinal degrees (averaged if multiple records were

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166 available for a species). Sexual dimorphism in body size was calculated as $\log_{10}$(male

167 size) - $\log_{10}$(female size). All data and their sources are given in Supplementary Table 1.

168

169 We controlled for phylogenetic effects in two ways. First, we tested whether ASR bias

170 (female- or male-biased) is evolutionary associated with the type of sex determination

171 using Pagel's discrete method (PDM)[25] as implemented in *BayesTrait*. Second, we tested

172 for differences in ASR with phylogenetic generalized least squares (PGLS)[24] using the R

173 package *caper*[46]. We used recently published phylogenies for amphibians[47], reptiles[48–50],

174 birds[51], and mammals[52,53]. The branching topology between these four major clades was

175 based on recent tetrapod phylogenies[54,55] (Fig. 1).

176

177 We developed simple population genetic models of the effects that deleterious mutation

178 and sex-antagonistic selection can have on the ASR (Supplementary Material 2). The

179 results regarding deleterious mutations reported in the text assume the mutations are

180 largely or entirely recessive and have multiplicative fitness effects across loci, that the loci

181 are in linkage equilibrium, and that selection is strong relative to mutation and drift. The

182 loci are assumed to be fully sex-linked, and those carried on the one type of sex

183 chromosome (e.g. the X) are assumed to have no homologue on the other type (e.g. the Y)

184 that could otherwise mask a deleterious mutation. Fitness effects of mutations in

185 hemizygotes and homozygotes are assumed equal. In our models of sex-antagonistic

186 selection the loci are fully sex-linked and carried on an X or Z chromosome. The models

187 for both deleterious mutation and sex-antagonistic selection are deterministic. They

188 therefore do not account for stochastic processes (such as "Muller's ratchet") that are

189 thought important to sex chromosome evolution[32]. It is possible that the conclusions

190 would change qualitatively if the models were extended to include those additional effects.

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312 **Supplementary Information** is linked to the online version of the paper at

313 www.nature.com/nature.

314

Author Contributions

325   T.S., A.L. and V.B. designed the study. I.P., V.B., P.F.D. and A.L. collected the reptile,

326   amphibian, mammal and bird data, respectively. I.P., V.B. and A.L. conducted the analyses.

327   M.K. developed the population genetic models. All authors wrote the paper.

328

Table 1. The effect of the sex-determination system on the adult sex ratio.

Taxon	Number of species	Mean ASR				% species with male-biased ASR		
		XY	ZW	*t*-test[†]	PGLS[†]	XY	ZW	PDM[†]
Amphibians	39	0.51	0.61	**	**	42.9	90.9	*
Reptiles	67	0.45	0.57	***	***	24.2	76.5	*
Birds	187	--	0.55	--	--	--	76.5	--
Mammals	51	0.37	--	--	--	9.8	--	--
Tetrapods	344	0.43	0.55	***	***	22.3	77.2	***

* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, -- no data or not tested

[†]Detailed results of the statistical analyses are presented in Extended Data Table 1.

Mean adult sex ratios (ASR, proportion of males in the population), *t*-tests and percentage of species with male-biased ASRs represent species-level statistics and analyses, while phylogenetic generalized least squares (PGLS)[24] and Pagel's discrete method (PDM)[25] were used for phylogenetically corrected analyses of the difference in ASR between XY and ZW species.

Table 2. The relationships between adult sex ratio, sex-determination system and other

factors in phylogenetically corrected multi-predictor analyses.

	Amphibians (n = 39)			Reptiles (n = 67)			Tetrapods (n = 259)		
	b (± SE)	t	P	b (± SE)	t	P	b (± SE)	t	P
Sex-determination system	0.10 (± 0.03)	3.38	0.002	0.10 (± 0.02)	4.56	<0.001	0.10 (± 0.02)	5.23	<0.001
Body size	0. (± 0)	1.41	0.166	0 (± 0)	0.78	0.440	0 (± 0)	0.05	0.962
Breeding latitude	0 (± 0)	0.13	0.898	0 (± 0)	0.04	0.966	0 (± 0)	0.24	0.811
Sexual size dimorphism	-0.32 (± 0.34)	0.92	0.363	-0.31 (± 0.15)	2.17	0.034	-0.38 (± 0.07)	5.57	<0.001

Results of phylogenetic generalized least squares (PGLS)[24]. Separate models were

constructed for amphibians, reptiles and tetrapods, that included ASR as response variable.

For sex determination, b is the estimated difference in ASR between ZW and XY species.

352 **Figure 1. Phylogenetic distribution of adult sex ratio (ASR) and genetic sex-**

353 **determination systems across tetrapods.** Inner band shows the type of sex determination

354 (red: XY, blue: ZW) and the outer band shows the ASR bias for each species included in the

355 study (red: ≤ 0.5, blue: > 0.5). Sample sizes: 39 species for amphibians, 67 species for

356 reptiles, 187 species for birds and 51 species for mammals (see Supplementary Table 1).

357

358 **Figure 2. Variation in adult sex ratio as a function of the sex-determination system in**

359 **amphibians, reptiles, mammals and birds, and tetrapods (all four clades combined).**

360 Central dots and solid whiskers are means ± 1 SE, horizontal bars are medians, and boxes and

361 dashed whiskers show the interquartile ranges and data ranges, respectively, based on species

362 values. Numbers of species are at the bottom of each panel. See Table 1 and Extended Data

363 Table 1 for statistical results and Extended Data Figure 1 for phylogenetically corrected

364 graphs.

365

Methods

Data collection

We collected data on ASR (proportion of males in the adult population) in amphibians and reptiles from literature published by December 2013, by searching in Google Scholar and Web of Science with the key words "sex ratio" and "reptile" or "amphibian" or the scientific names of species. We also used reviews to identify additional data sources[43,56]. ASR data for mammals[7] were obtained from a similar search finished in 2007; and we used avian ASR estimates from our existing data set (Supplementary Information of Liker et al.[13]).

We specifically collected ASR data for amphibians and reptiles from studies that aimed to obtain representative estimates for the population composition and thus provide reliable sex ratio data[57]. These include either long-term demographic studies applying mark-recapture or sacrificing methods (i.e. each individual was counted only once) with similar capture probabilities for the sexes, or total population counts. When more than one measure was available, we used the total counts of individually marked animals over the study period because this may best approximate the overall ASR. We excluded studies in which the authors explicitly stated or speculated that their data may not represent the population-level ASR, or when the methods were not described in enough detail to assess the reliability of the ASR estimate. Moreover, we tested whether ASR estimates differ between sampling (hand-capture, trap, other) and marking (mark-recapture, sacrifice) methods, and we found no such differences (linear mixed-effects model with species as random factor, sampling: $F_{(3, 105)} = 0.50$, $P = 0.683$; marking: $F_{(2, 105)} = 2.18$, $P = 0.118$; n = 234 records). When more than one estimate of ASR was available for the same population (e.g. from several yearly counts at the same location) we took their mean weighted by sample size. When more than one independent record was available for a species from different populations or studies, we used

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391   their simple mean. Weighted and non-weighted mean ASRs were highly correlated

392   (amphibians: Pearson's r = 0.973, $P < 0.001$, n = 35 species; reptiles: r = 0.995, $P < 0.001$, n =

393   60 species); we used non-weighted averages because not all studies reported sample size.

394

395   We categorized the genetic sex-determination (GSD) systems of the species from published

396   sources either as male-heterogametic (XY) or female-heterogametic (ZW). For amphibians,

397   only species with known GSD system were included[22,43], because GSD is an evolutionarily

398   labile trait in amphibians; species within a genus or even populations within a species can

399   differ in GSD[42]. For reptiles, we included all species for which GSD was known either at the

400   family level, or at the species level if both XY and ZW systems were reported in the

401   family[22,44,45]. Our result for reptiles is not changed qualitatively by restricting our analyses to

402   those species for which GSD is known at species level[22], i.e. when species for which we

403   assumed GSD based on other species in the family were excluded (difference between XY

404   and ZW reptile species, phylogenetic generalized least squares model (PGLS)[24,58]: b ± SE =

405   0.11 ± 0.02; t = 4.70, $P < 0.001$, n = 26; R^2 = 0.479). All birds were assigned to ZW, and all

406   mammals to XY sex-determination systems[22].

407

408   We also collected data on three additional ecological and behavioural variables to control for

409   their known correlation with ASR and so reduce potential confounding effects in multi-

410   predictor analyses. First, we used body size (in mm) which was measured as snout to vent

411   length for amphibians and squamates, and carapace length for the two turtle species, where

412   possible from the same population for which ASR was reported. Head-body length was used

413   for mammals (n = 36)[59]. Since head-body length is not available for the vast majority of birds,

414   we calculated this from the total body length by extracting bill and tail length (n = 133;

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415   Supplementary Table 1). Where we had sex-specific data, the mean of male and female head-

416   body length was used as body size variable in the analyses.

417

418   Second, we estimated sexual size dimorphism (SSD) as $\log_{10}$(male body size) - $\log_{10}$(female

419   body size). For birds, we used body mass dimorphism (data available for n =181 species)[60]

420   due to the lack of sex-specific body length data. The results of the multivariate PGLS model

421   of tetrapods presented in Table 2 remain qualitatively the same when wing length dimorphism

422   (data available for n =153 species) is used for birds instead of body mass dimorphism (effect

423   of sex determination: b ± SE = -0.10 ± 0.02, t = 4.97, P < 0.001; body size: b ± SE = 0 ± 0, t =

424   0.06, P = 0.949; latitude: b ± SE = 0 ± 0, t = 0.223, P = 0.823; size dimorphism: b ± SE = -

425   0.52 ± 0.12, t = 4.33, P < 0.001; n = 248 species).

426

427   Third, we included breeding latitude as the geographic coordinates of the ASR studies for

428   amphibians and reptiles, taking absolute values to represent distance from the Equator in

429   latitudinal degree. When the authors did not report latitude, we used Google Earth to estimate

430   it on the basis of the description of the study site. For birds and mammals, we used the

431   latitudinal midpoint of the breeding range of the species (n = 182 and 44 species, for birds and

432   mammals, respectively; sources: V. Remes, A. Liker, R. Freckleton and T. Székely

433   unpublished data for birds, and the PanTHERIA database for mammals[61], respectively). Mean

434   values of these variables were used if multiple data of body size, latitude or size dimorphism

435   per species were available.

436

437   Other possible confounding factors include the lifespan of individuals and sex-specific

438   dispersal distances. First, longer average lifespan may lead to exaggeration of ASR bias.

439   However, in species with available data[62], lifespan is unrelated to ASR (PGLS, birds: b ± SE

440 $= 0 \pm 0$, t $= 0.196$, $P = 0.845$, n $= 71$ species; mammals: b $\pm$ SE $= 0 \pm 0$, t $= 0.751$, $P = 0.457$,

441 n $= 35$ species) and also to the absolute deviation of ASR from 0.5 (i.e. when assuming that

442 longer lifespan can exaggerate ASR bias in either direction; birds: b $\pm$ SE $= 0 \pm 0$, t $= 1.543$, P

443 $= 0.127$, n $= 71$ species; mammals: b $\pm$ SE $= 0 \pm 0$, t $= 0.180$, $P = 0.858$, n $= 35$ species).

444 Second, sex-specific dispersal can bias ASR due to the higher mortality in the sex with longer

445 dispersal distances. However, we found no evidence of a relationship of sex bias in dispersal

446 either with GSD in reptiles, or with ASR in birds (Supplementary Material 1). For these

447 reasons, as well as because data on lifespan and/or sex-specific dispersal are not available for

448 most species in our ASR data set, we did not include these variables in the main multi-

449 predictor models (see Supplementary Material 1 for additional models including dispersal).

450

451 Our final dataset comprises data on 39 amphibian species and 67 reptile species (in total n =

452 229 ASR records from different populations), 187 bird species and 51 mammalian species (a

453 total of 344 species). We could not find body size and latitude data for some species, thus

454 sample sizes were reduced in multi-predictor models. All species-level data and their sources

455 are given in Supplementary Table 1.

456

457 **Data analysis**

458 To assess the reliability of the amphibian and reptile ASR estimates, we calculated the

459 repeatability of ASR as the intraclass correlation coefficient (ICC) following Lessells &

460 Boag[63], using only those species for which we had at least two ASR estimates from different

461 populations. These analyses show a moderate repeatability of ASR, and that a significant part

462 of ASR variation is interspecific (amphibians: ICC $= 0.559$, $F_{(22,96)} = 7.27$, $P < 0.001$, n $= 23$

463 species, n $= 120$ records; reptiles: ICC $= 0.524$, $F_{(13,26)} = 4.11$, $P = 0.001$, n $= 14$ species, n $=$

464 40 records). For birds, our earlier analyses showed that nearly half (44%) of the ASR

465 variation was interspecific, and that the direction of ASR (i.e. male- or female-biased) was

466 highly conserved: in 44 species out 55 (80%), the direction of ASR bias was the same for all

467 repeated estimates[5]. For mammals, we did not find enough multiple ASR data within species

468 to estimate repeatability.

469

470 In the comparative analyses we used the topology of Pyron & Wiens[47] for amphibians, a

471 composite phylogeny for reptiles[48–50], Jetz et al.[51] for birds[13], the family-level relationships

472 of Meredith et al.[52] and the genus/species level relationships of Fritz et al.[53] for mammals.

473 For analyses across tetrapods, the branching topology between these four major clades

474 was based on recent tetrapod phylogenies[54,55] (Fig. 1). Since we did not have branch

475 length information for these composite phylogenies, we ran the analyses using arbitrary

476 gradual branch lengths according to Nee's method[64]. However, our results remained

477 consistent when we repeated the analyses with other branch length assumptions (Pagel's

478 method and unit branch lengths[64]; Extended Data Table 2).

479

480 To test the association between ASR bias (male- versus female-biased) and GSD (XY versus

481 ZW) in phylogenetically corrected analyses, we used Pagel's discrete method[25] as

482 implemented in *BayesTrait*[65]. We used maximum likelihood methods to fit independent and

483 dependent models for transitions in ASR bias and GSD states, and compared the fit of these

484 two models by a likelihood ratio test[25]. To test the ASR difference between XY and ZW

485 species, we used PGLS models with maximum likelihood estimates of Pagel's lambda

486 values[24] using the R[66] package *caper*[46, 58]. ASR was the response variable in all models, and

487 genetic sex-determination system was fitted as the predictor (Table 1, Extended Data Table

488 1). The parameter estimate *b* shows the difference in ASR (proportion of males in the

489 population) between ZW and XY species. To test the robustness of the bivariate results, we

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490   added body size, breeding latitude and SSD as predictors in multi-predictor models to control

491   for their potential confounding effects (Table 2). As in earlier ASR studies[5,7], the distribution

492   of ASR values did not deviate significantly from normal in the four clades separately as well

493   as in tetrapods as a whole; our results remain qualitatively identical when ASR is arc-sine

494   transformed before PGLS analyses (amphibians: $b \pm SE = 0.10 \pm 0.03$, $t_{37} = 3.44$, $P = 0.001$, n

495   = 39; reptiles: $b \pm SE = 0.12 \pm 0.02$, $t_{65} = 5.95$, $P < 0.001$, n = 67; tetrapods: $b \pm SE = 0.11 \pm$

496   0.02, $t_{342} = 5.24$, $P < 0.001$, n = 344).

497

498   The difference between XY and ZW systems for tetrapods is not sensitive to the inclusion of

499   large clades with uniform sex-determination systems (snakes and birds are all ZW, mammals

500   are all XY) since it remains unchanged when each of these clades is reduced to a single datum

501   of its mean ASR (PGLS: $b \pm SE = 0.10 \pm 0.02$, $t = 5.07$, $P < 0.001$, $R^2 = 0.232$, n = 87).

502   Furthermore, our result is also robust to between-species differences in sample size: when we

503   added log(no. individuals) to the previous model, the effect of sex determination remained

504   significant ($b \pm SE = 0.15 \pm 0.07$, $t = 2.08$, $P = 0.041$) while sample size had no significant

505   effect on ASR ($b \pm SE = 0 \pm 0.01$, $t = 0.35$, $P = 0.72$, n = 78). Furthermore, sample size was

506   not a significant predictor of ASR when we added it as a fourth confounding variable in the

507   full PGLS model ($b \pm SE = 0 \pm 0.01$, $t = 1.16$, $P = 0.250$, n = 78), and the effect of other

508   predictors remained qualitatively the same as in Table 2. Finally, the results do not change

509   when we only used the most reliable ASR data (based on mark-recapture or sacrifice

510   methods): sex-determination system is significantly related to ASR in amphibians, reptiles

511   and tetrapods (PGLS results, amphibians: $b \pm SE = 0.09 \pm 0.03$, $t = 3.07$, $P = 0.004$, n = 35

512   species; reptiles: $b \pm SE = 0.11 \pm 0.03$, $t = 3.974$, $P < 0.001$, n = 22; tetrapods with snakes,

513   birds and mammals included as single data points: $b \pm SE = 0.10 \pm 0.02$, $t = 4.23$, $P < 0.001$, n

514   = 55).

Population genetic models

We developed population genetic models of the effects that deleterious mutation and sex-antagonistic selection might have on the ASR (Supplementary Material 2). The models assume that deleterious mutations are largely or entirely recessive, that they have multiplicative fitness effects across loci, that the loci are fully sex-linked and in linkage equilibrium, that mutation is not sex-biased, and that selection is strong relative to mutation and drift. Fitness effects of mutations in hemizygotes and homozygotes are assumed equal. Full details of the models are given in Supplementary Material 2. Here we summarize key results.

When deleterious alleles reach a mutation-selection balance, with X-Y sex determination the mean viability of males relative to females is

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

where U_X and U_Y are the total rates of mutation to deleterious alleles across all loci on the X and Y chromosomes. With Z-W sex determination, the mean viability of females to males is

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

where U_Z and U_W are the total rates of mutation to deleterious alleles across all loci on the Z and W chromosomes. Using very rough estimates for rates of deleterious mutations appropriate for human sex chromosomes, we estimate that mutation-selection balance might bias the ASR by a few percent. This degree of bias is substantially less than what is

540 seen in our data. We emphasize that the conclusion could be quite different using other

541 parameter values, or if the model was extended to include stochastic effects.

542 The second hypothesis to explain biased ASRs that we explored with models is sex-

543 antagonistic selection, the situation in which alleles are selected differently in females and

544 males[67]. In Supplementary Material 2, we use numerical examples to show that under both

545 XY and ZW sex determination, either a female-biased or male-biased ASR can result.

546 Thus there does not seem to be a robust generalization about how sex-antagonistic

547 selection will bias the ASR.

548

549 **Methods References**

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Extended Data titles and legends

Extended Data Table 1. Detailed analyses of the effect of sex-determination system on the adult sex ratio.

These are extensions of Table 1 in the text showing details of the phylogenetically uncorrected (t-tests) and phylogenetically corrected analyses (PGLS[24] and PDM[25]). Birds and mammals were not tested with phylogenetic control because there is no variation in the type of sex-determination system within birds and mammals.

Extended Data Table2. Phylogenetically controlled analyses of the relationship between adult sex ratio and genetic sex-determination system using different branch length assumptions.

These are results of phylogenetic generalized least squares models (PGLS)[24] as implemented in the R package 'caper'[46]. The models assume gradual branch lengths calculated either by Nee's or by Pagel's method, or unit branch lengths[61].

Extended Data Figure 1. Phylogenetically corrected mean and standard error of adult sex ratio in clades with different sex-determination systems.

Parameter estimates for means and the associated standard errors were calculated by phylogenetic generalized least squares models (PGLS)[24] presented in Extended Data Table 2 (with branch lengths estimated by Nee's method).