

# The genetic sex-determination system predicts adult sex ratios in tetrapods

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**The adult sex ratio (ASR) has critical effects on behaviour, ecology and population dynamics<sup>1,2</sup>, but the causes of variation in ASRs are unclear<sup>3,4</sup>. Here we assess whether the type of genetic sex determination influences the ASR using data from 344 species in 117 families of tetrapods. We show that taxa with female heterogamety have a significantly more male-biased ASR (proportion of males:  $0.55 \pm 0.01$  (mean  $\pm$  s.e.m.)) than taxa with male heterogamety ( $0.43 \pm 0.01$ ). The genetic sex-determination system explains 24% of interspecific variation in ASRs 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 effects on the demography and social behaviour of tetrapods.**

The adult sex ratio (ASR) varies widely in nature, ranging from populations that are heavily male-biased to those composed only of adult females<sup>4–6</sup>. Birds and schistosome parasites tend to have male-biased ASRs, for example, whereas mammals and copepods usually exhibit female-biased ASRs<sup>4</sup>. 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<sup>7</sup>. Understanding the causes and consequences of ASR variation is an important goal in evolutionary biology, population demography and biodiversity conservation because the ASR affects behaviour, breeding systems and ultimately population fitness<sup>1,2,8–10</sup>. It is also an important issue in social sciences, human health and economics, since unbalanced ASRs have been linked to violence, rape, mate choice decisions and the spread of diseases such as HIV<sup>11,12</sup>. The causes of ASR variation in wild populations, however, remain obscure<sup>4,8,13</sup>.

One factor that could affect the ASR is the genetic sex-determination system<sup>5,6,14</sup>. Taxa such as mammals and fruitflies (*Drosophila*) 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<sup>15</sup>. Alternatively, a biased ASR could develop after birth if sex chromosomes contribute to sex differences in mortality<sup>6,14,16</sup>. Differential postnatal mortality is likely to be the main driver of biased ASRs in birds and mammals, since birth sex ratios in these classes tend to be balanced<sup>5</sup>.

Here we use data from the four major clades of tetrapods (amphibians, reptiles, birds and mammals) to assess whether ASRs, measured by convention as the proportion of males in the population, differ between taxa with XY and ZW sex determination (Fig. 1 and Supplementary Data). 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<sup>17</sup>. We compiled published data on adult sex ratios in wild populations and their sex-determination systems (Supplementary Data). To control for phylogenetic effects, we used phylogenetic generalized least squares (PGLS)<sup>18</sup> models to test for differences in ASRs between XY and ZW taxa, and Pagel's discrete method (PDM)<sup>19</sup> to test whether XY and ZW systems are evolutionarily associated with female-biased and male-biased sex ratios, respectively. Phylogenies were taken from recent molecular studies (see Methods for details).

Both the ASR and the sex-determination system are highly variable across tetrapods (Fig. 1 and Supplementary Data). We find that the ASR and sex determination are correlated. Before controlling for phylogenetic effects, we find that ASRs are significantly more male-biased in species with ZW sex determination than in those with XY sex determination (Fig. 2, Table 1 and Extended Data Table 1). Similarly, the proportion of species with male-biased ASRs is greater among ZW than XY species (Fig. 1 and Table 1). These differences are significant within amphibians, within reptiles, and across tetrapods as a whole (Table 1 and Extended Data Table 1).

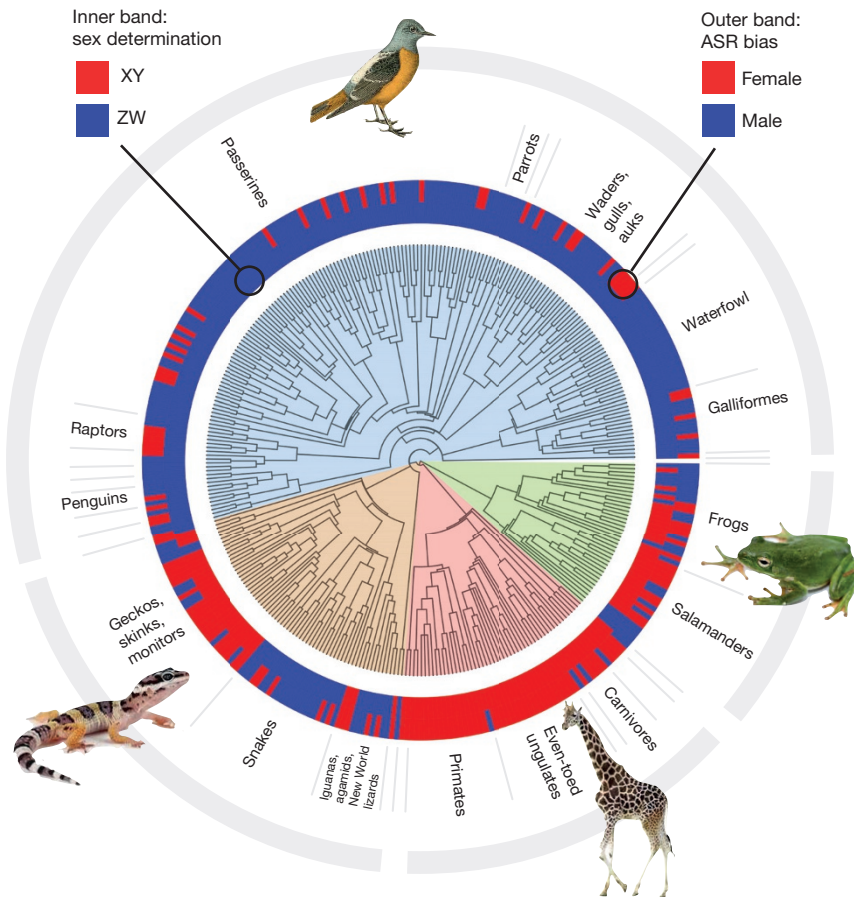
The pattern remains significant after controlling for phylogenetic effects. Both the mean of ASR across species (analysed using PGLS) and the proportion of species with male-biased sex ratios (analysed using PDM) differ significantly between XY and ZW systems within amphibians, within reptiles, and across tetrapods as a whole (Table 1 and Extended Data Table 1). The effect is strong in clades with variation in sex determination: the type of genetic sex determination explains up to 24% of the interspecific variance in the ASR among amphibians and 36% in reptiles (estimated using PGLS; Extended Data Table 2). The results remain significant when we treat three large clades with invariant sex-determination systems as a single datum each (snakes, ZW; birds, ZW; mammals, XY; Extended Data Table 1), when we make different assumptions about branch lengths in the phylogeny (Extended Data Table 2), and when we use arc-sine-transformed ASR values and control for variance in sample size (see Methods).

Body size and breeding latitude correlate with life-history traits in many organisms and these traits could affect ASR<sup>20</sup>. Sexual size dimorphism is linked to differential sexual selection acting on males and females and thus influences sex-specific mortality, and has been suggested to drive the evolution of genetic sex-determination systems<sup>21</sup>. Nevertheless, we find that neither body size nor breeding latitude explains significant variation in the ASR in phylogenetically controlled multi-predictor analyses (Table 2). Sexual size dimorphism is significantly associated with ASR in reptiles and across tetrapods as a whole, but the effect of the genetic sex-determination system remains significant when size dimorphism is included in the analysis (Table 2).

Sex differences in dispersal may also result in biased ASRs. However, dispersal is unlikely to explain the relationship between ASR and sex-determination systems. First, male-biased dispersal is typical in reptiles

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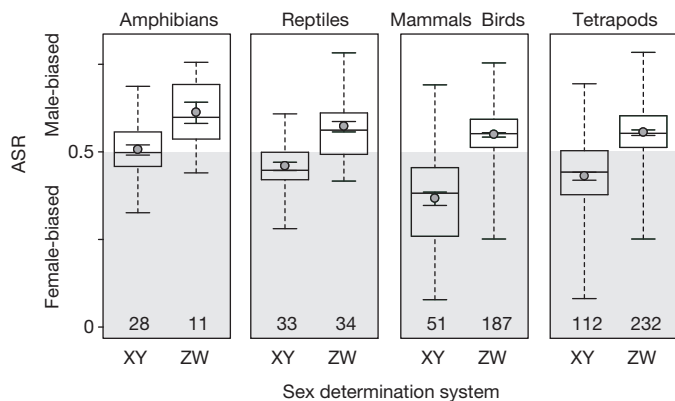
**Figure 1 | Phylogenetic distribution of the ASR and genetic sex-determination systems across tetrapods.** Inner band shows the type of sex determination (red: XY, blue: ZW), and the outer band shows the ASR bias for

each species included in the study (red:  $\leq 0.5$ , blue:  $> 0.5$  proportion of males). Sample sizes: 39 species for amphibians, 67 species for reptiles, 187 species for birds and 51 species for mammals (see Supplementary Data).

regardless of the sex-determination system<sup>22</sup> (Supplementary Information 1). Second, there is no relationship between the ASR and sex bias in dispersal distance in birds (Supplementary Information 1). Finally, the relationship between sex determination and the ASR remains significant when the influence of sex-biased

dispersal is controlled in multi-predictor models in tetrapods (Supplementary Information 1).

The sex-determination system may affect the ASR in the directions seen in the data in several ways. First, sexual selection can fix mutations that increase male mating success and decrease male survival. These will accumulate on Y but not on W chromosomes, and will accumulate more readily on X than on Z chromosomes if they tend to be recessive. Second, biased ASRs could result from recessive mutations at loci carried on the X (or Z) chromosome but absent from the Y (or W) chromosome since they are not masked in the heterogametic sex (the ‘unguarded sex chromosome’ hypothesis)<sup>5,6,14</sup>, and from deleterious mutations carried on the Y (or W) but not on the X (or Z) chromosome. At loci carried on both sex chromosomes, alleles on the Y (or W) can show partial degeneration<sup>23</sup>. Population genetic models suggest that deleterious mutation pressure alone may not be adequate to explain ASR biases as large as those observed (Supplementary Information 2), but the models do not include factors that could be important, notably the degeneration of Y and W chromosomes by genetic drift<sup>23</sup>. A third hypothesis is imperfect dosage compensation, which may be deleterious to the heterogametic sex<sup>24</sup>. Fourth, distorted sex ratios can result from meiotic drive acting on sex chromosomes<sup>25</sup>. Drive more often produces female-biased sex ratios in XY systems at birth<sup>26</sup>. There is little data on drive in ZW systems, but if it operates in a symmetrical fashion then we expect it to cause male-biased sex ratios. Fifth, the Y and W chromosomes might degenerate during the lifespan, for example by telomere shortening or loss of epigenetic marks, more rapidly than the X and Z chromosomes. A final possibility is that sex-antagonistic selection acting on sex-linked loci could lead to biased



**Figure 2 | Variation in the ASR as a function of the sex-determination system in amphibians, reptiles, mammals and birds, and across tetrapods (all four clades combined).** Adult sex ratio is the proportion of males in all adults. Central dots and solid whiskers are mean  $\pm$  s.e.m., horizontal bars are medians, and boxes and dashed whiskers show the interquartile ranges and data ranges, respectively, based on species values. Numbers of species are at the bottom of each panel. See Table 1 and Extended Data Table 1 for statistical results, and Extended Data Fig. 1 for phylogenetically corrected graphs.

**Table 1 | The effect of the sex-determination system on the ASR**

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	73.5	*
Birds	187	—	0.55	—	—	—	76.5	—
Mammals	51	0.37	—	—	—	9.8	—	—
Tetrapods	344	0.43	0.55	***	***	22.3	77.2	***

Mean ASR (proportion of males in the population), t-tests and the percentage of species with male-biased ASRs represent species-level statistics and analyses, while PGLS<sup>18</sup> and PDM<sup>19</sup> were used for phylogenetically corrected analyses of the difference in ASR between XY and ZW species.

\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; '—' denotes no data or not tested.

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

**Table 2 | Phylogenetically corrected multi-predictor analyses of ASR variation**

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

Relationships between the ASR, sex-determination system and other factors in phylogenetically corrected multi-predictor analyses using PGLS models<sup>18</sup>. Separate models of ASR were constructed for amphibians, reptiles and all tetrapods combined. For sex determination,  $b$  is the estimated difference in ASR between ZW and XY species.

sex ratios, but unlike the preceding hypotheses there does not seem to be a robust prediction about the direction of the ASR bias it will produce (Supplementary Information 2).

The limited data available do not provide clear support for any of these hypotheses, although critical tests are lacking. For instance, the meiotic drive process predicts biased sex ratios at birth. Although a recent comparative analysis in birds suggests that sex ratios at birth are unrelated to biased ASRs<sup>8</sup>, offspring sex ratios have not been compared between different sex-determination systems. Further insight might come from the study of dioecious plants with biased sex ratios<sup>27</sup>, but their skewed ASRs could result from selection on the gametophytic stage that is absent from animals<sup>28</sup>. Evolutionary feedbacks from the ASR to the sex-determination system are also possible: for example, the ASR could influence sexual size dimorphism and sexual conflict, which in turn could trigger transitions in sex determination<sup>21,29,30</sup>.

In conclusion, we demonstrate strong and phylogenetically robust associations between genetic sex-determination systems and a demographic property of populations, the ASR. Although the mechanisms that drive this association need further theoretical and empirical analyses, the observed pattern is biologically important for two reasons. First, changes in sex-determination systems are expected to have knock-on effects on social behaviour. Theory suggests that the ASR affects violence, pair bonds, infidelity and parental care<sup>1</sup>, and field-based studies support these predictions<sup>3,10,12</sup>. For instance, female-biased ASRs co-occur with polygyny and female care, whereas male-biased ASRs tend to co-occur with polyandry and male care in birds<sup>3</sup>. Second, sex-determination systems may have important demographic consequences through skewed birth sex ratios and sex-biased survival. Such biases may not only affect the productivity and growth of populations, but also their genetic composition and viability. Further theoretical, experimental and comparative studies are clearly needed to understand the linkages between sex determination, demography and social behaviour.

**Online Content** Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper; references unique to these sections appear only in the online paper.

Received 19 February; accepted 5 August 2015.

Published online 7 October 2015.

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**Supplementary Information** is available in the online version of the paper.

**Acknowledgements** M. Pennell and G. Imreh helped construct the phylogeny figure. We thank T. H. Clutton-Brock, S. P. Otto, D. Bachtrog and K. Reinhold for suggestions, and R. P. Freckleton for advice on analyses. We were supported by the European Union (TÁMOP-4.2.2.B-15/1/KONV-2015-0004), and by the US National Science

Foundation (DEB-0819901 to M.K.). T.S. was supported by a Humboldt Award and MTA-DE 'Lendület' grant in projects that lead to the current work. A.L. was supported by the Hungarian Scientific Research Fund (OTKA K112838) and a Marie Curie Intra-European Fellowship.

**Author Contributions** T.S. and A.L. conceived the study. T.S., A.L. and V.B. designed the analyses. I.P., V.B., P.F.D. and A.L. collected the reptile, amphibian, mammalian and bird data, respectively. I.P., V.B. and A.L. conducted the analyses. M.K. developed the population genetic models. All authors wrote the paper.

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## METHODS

**Data collection.** We collected data on the ASR (expressed by convention as the 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<sup>31,32</sup>. ASR data for mammals<sup>5</sup> were obtained from a similar search finished in 2007; and we used avian ASR estimates from our existing data set (supplementary information of ref. 10). We aimed to collect all ASR data that were available for amphibian and reptile species with known sex determination, so no statistical methods were used to pre-determine sample sizes. During the collection of ASR data for amphibians and reptiles, investigators were blinded to the type of sex determination. ASR data for birds and mammals were collected before the initiation of the current study, and for different purposes.

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<sup>33</sup>. These include either long-term demographic studies applying mark-recapture or culling methods (that is, 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 differed between sampling (hand-capture, trap, other) and marking (mark-recapture, culling) 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 the ASR was available for the same population (for example, 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 their simple mean. Weighted and non-weighted mean ASRs were highly correlated (amphibians: Pearson's  $r = 0.973$ ,  $P < 0.001$ ,  $n = 35$  species; reptiles:  $r = 0.995$ ,  $P < 0.001$ ,  $n = 60$  species); we used non-weighted averages because not all studies reported sample size.

We categorized the genetic sex-determination (GSD) systems of the species from published sources either as male-heterogametic (XY) or female-heterogametic (ZW). For amphibians, only species with known GSD systems were included<sup>31,34</sup>, because GSD is an evolutionarily labile trait in amphibians; species within a genus or even populations within a species can differ in GSD system<sup>35</sup>. For reptiles, we included species for which the GSD was known either at the family level or at the species level if both XY and ZW systems were found in the family<sup>34,36,37</sup>. Our result for reptiles is not changed qualitatively by restricting our analyses to those species for which the GSD is known at species level<sup>34</sup>, that is, when species for which we assumed the GSD based on other species in the family were excluded (difference between XY and ZW reptile species, PGLS model<sup>18,38</sup>:  $b \pm \text{s.e.m.} = 0.11 \pm 0.02$ ;  $t = 4.70$ ,  $P < 0.001$ ,  $n = 26$ ;  $R^2 = 0.479$ ). All birds were assigned to ZW, and all mammals to XY sex-determination systems<sup>34</sup>.

We also collected data on three additional ecological and behavioural variables to control for their known correlation with the ASR and so reduce potential confounding effects in multi-predictor analyses. First, we used body size, which was measured as snout-to-vent length (in mm) for amphibians and squamates, and carapace length for the two turtle species, where possible from the same population for which ASR was reported. Head-body length was used for mammals ( $n = 36$ ) (Encyclopedia of Life, <http://www.eol.org>). Since head-body length is not available for the vast majority of birds, we calculated this from the total body length by subtracting bill and tail length ( $n = 133$ ; Supplementary Data). Where we had sex-specific data, the mean of male and female head-body length was used as body size variable in the analyses.

Second, we estimated sexual size dimorphism as  $\log_{10}(\text{male body size}) - \log_{10}(\text{female body size})$ . For birds, we used body mass dimorphism (data available for  $n = 181$  species)<sup>39</sup> owing to the lack of sex-specific body length data. The results of the multivariate PGLS model of tetrapods presented in Table 2 remain qualitatively the same when wing length dimorphism (data available for  $n = 153$  species) is used for birds instead of body mass dimorphism (effect of sex determination:  $b \pm \text{s.e.m.} = -0.10 \pm 0.02$ ,  $t = 4.97$ ,  $P < 0.001$ ; body size:  $b \pm \text{s.e.m.} = 0 \pm 0$ ,  $t = 0.06$ ,  $P = 0.949$ ; latitude:  $b \pm \text{s.e.m.} = 0 \pm 0$ ,  $t = 0.223$ ,  $P = 0.823$ ; size dimorphism:  $b \pm \text{s.e.m.} = -0.52 \pm 0.12$ ,  $t = 4.33$ ,  $P < 0.001$ ;  $n = 248$  species).

Third, we included breeding latitude<sup>40,41</sup> as the geographic coordinates of the ASR studies for amphibians and reptiles, taking absolute values to represent distance from the Equator in latitudinal degree. When the authors did not report latitude, we used Google Earth to estimate it on the basis of the description of the

study site. For birds and mammals, we used the latitudinal midpoint of the breeding range of the species ( $n = 182$  and 44 species, for birds and mammals, respectively; sources: V. Remes, A. Liker, R. Freckleton & T. Székely unpublished data for birds, and the PanTHERIA database for mammals<sup>42</sup>, respectively). Mean values of these variables were used if multiple data of body size, latitude or size dimorphism per species were available.

Other possible confounding factors include the lifespan of individuals and sex-specific dispersal distances. First, longer average lifespan may lead to exaggeration of ASR bias. However, in species with available data<sup>43</sup>, lifespan is unrelated to the ASR (PGLS, birds:  $b \pm \text{s.e.m.} = 0 \pm 0$ ,  $t = 0.196$ ,  $P = 0.845$ ,  $n = 71$  species; mammals:  $b \pm \text{s.e.m.} = 0 \pm 0$ ,  $t = 0.751$ ,  $P = 0.457$ ,  $n = 35$  species) and also to the absolute deviation of the ASR from 0.5 (that is, when assuming that longer lifespan can exaggerate ASR bias in either direction; birds:  $b \pm \text{s.e.m.} = 0 \pm 0$ ,  $t = 1.543$ ,  $P = 0.127$ ,  $n = 71$  species; mammals:  $b \pm \text{s.e.m.} = 0 \pm 0$ ,  $t = 0.180$ ,  $P = 0.858$ ,  $n = 35$  species). Second, sex-specific dispersal can bias the ASR owing to the higher mortality in the sex with longer dispersal distances. However, we found no evidence of a relationship of sex bias in dispersal either with the GSD in reptiles or with the ASR in birds (Supplementary Information 1). For these reasons, and because data on lifespan and/or sex-specific dispersal are not available for most species in our ASR data set, we did not include these variables in the main multi-predictor models.

Our final data set comprises data on 39 amphibian species and 67 reptile species (in total,  $n = 229$  ASR records from different populations), 187 bird species and 51 mammalian species (a total of 344 species). We could not find body size and latitude data for some species, thus sample sizes were reduced in multi-predictor models. All species-level data and their sources are given in Supplementary Data. **Data analysis.** To assess the reliability of the amphibian and reptile ASR estimates, we calculated the repeatability of ASR as the intraclass correlation coefficient (ICC) following ref. 44, using only those species for which we had at least two ASR estimates from different populations. These analyses show a moderate repeatability of ASR, and that a significant part of ASR variation is interspecific (amphibians: ICC = 0.559,  $F_{(22,96)} = 7.27$ ,  $P < 0.001$ ,  $n = 23$  species,  $n = 120$  records; reptiles: ICC = 0.524,  $F_{(13,26)} = 4.11$ ,  $P = 0.001$ ,  $n = 14$  species,  $n = 40$  records). For birds, our earlier analyses showed that 44% of the ASR variation was interspecific, and that the direction of ASR (that is, male- or female-biased) was highly conserved: in 44 out of 55 species (80%), the direction of the ASR bias was the same for all repeated estimates<sup>4</sup>. For mammals, we did not find enough multiple ASR data within species to estimate repeatability.

In the comparative analyses we used the topology of ref. 45 for amphibians, a composite phylogeny for reptiles<sup>46–48</sup>, ref. 49 for birds<sup>10</sup>, the family-level relationships of ref. 50 and the genus/species level relationships of ref. 51 for mammals. For analyses across tetrapods, the branching topology between these four major clades was based on recent tetrapod phylogenies<sup>52,53</sup> (Fig. 1). Because we did not have branch length information for these composite phylogenies, we ran the analyses using arbitrary gradual branch lengths according to Nee's method<sup>54</sup>. However, our results remained consistent when we repeated the analyses with other branch length assumptions (Pagel's method and unit branch lengths<sup>54</sup>; Extended Data Table 2).

To test the association between ASR bias (male- versus female-biased) and GSD (XY versus ZW) in phylogenetically corrected analyses, we used PDM<sup>19</sup> as implemented in BayesTrait<sup>55</sup>. We used maximum likelihood methods to fit independent and dependent models for transitions in ASR bias and GSD states, and compared the fit of these two models by a likelihood ratio test<sup>19</sup>. To test the ASR difference between XY and ZW species, we used PGLS models with maximum likelihood estimates of Pagel's  $\lambda$  values<sup>18</sup> using the R<sup>66</sup> package 'caper'<sup>38,57</sup>. ASR was the response variable in all models, and the genetic sex-determination system was fitted as the predictor (Table 1 and Extended Data Table 1). The parameter estimate  $b$  shows the difference in ASR (proportion of males in the population) between ZW and XY species. To test the robustness of the bivariate results, we added body size, breeding latitude and sexual size dimorphism as predictors in multi-predictor models to control for their potential confounding effects (Table 2). As in earlier ASR studies<sup>4,5</sup>, the distribution of ASR values did not deviate significantly from normal in the four clades separately as well as in tetrapods as a whole; our results remain qualitatively identical when ASR is arc-sine-transformed before PGLS analyses (amphibians:  $b \pm \text{s.e.m.} = 0.10 \pm 0.03$ ,  $t_{37} = 3.44$ ,  $P = 0.001$ ,  $n = 39$ ; reptiles:  $b \pm \text{s.e.m.} = 0.12 \pm 0.02$ ,  $t_{65} = 5.95$ ,  $P < 0.001$ ,  $n = 67$ ; tetrapods:  $b \pm \text{s.e.m.} = 0.11 \pm 0.02$ ,  $t_{342} = 5.24$ ,  $P < 0.001$ ,  $n = 344$ ).

The difference between XY and ZW systems for tetrapods is not sensitive to the inclusion of large clades with uniform sex-determination systems (snakes and birds are all ZW, mammals are all XY) because it remains unchanged when each of these clades is reduced to a single datum of its mean ASR (PGLS:  $b \pm \text{s.e.m.} = 0.10 \pm 0.02$ ,  $t = 5.07$ ,  $P < 0.001$ ,  $R^2 = 0.232$ ,  $n = 87$ ). Furthermore, our result is also robust to between-species differences in sample size: when we added  $\log(\text{number of individuals})$  to the previous model, the effect of sex determination

remained significant ( $b \pm \text{s.e.m.} = 0.15 \pm 0.07$ ,  $t = 2.08$ ,  $P = 0.041$ ), while sample size had no significant effect on ASR ( $b \pm \text{s.e.m.} = 0 \pm 0.01$ ,  $t = 0.35$ ,  $P = 0.72$ ,  $n = 78$ ). Furthermore, sample size was not a significant predictor of ASR when we added it as a fourth confounding variable in the full PGLS model ( $b \pm \text{s.e.m.} = 0 \pm 0.01$ ,  $t = 1.16$ ,  $P = 0.250$ ,  $n = 78$ ), and the effect of other predictors remained qualitatively the same as in Table 2. Finally, the results do not change when we only used the most reliable ASR data (based on mark-recapture or culling methods): sex-determination system is significantly related to ASR in amphibians, reptiles tetrapods (PGLS results, amphibians:  $b \pm \text{s.e.m.} = 0.09 \pm 0.03$ ,  $t = 3.07$ ,  $P = 0.004$ ,  $n = 35$  species; reptiles:  $b \pm \text{s.e.m.} = 0.11 \pm 0.03$ ,  $t = 3.974$ ,  $P < 0.001$ ,  $n = 22$ ; tetrapods with snakes, birds and mammals included as single data points:  $b \pm \text{s.e.m.} = 0.10 \pm 0.02$ ,  $t = 4.23$ ,  $P < 0.001$ ,  $n = 55$ ).

**Population genetic models.** We developed population genetic models of the effects that deleterious mutation and sex-antagonistic selection might have on the ASR (Supplementary Information 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 Information 2. Here we summarize the key results.

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

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

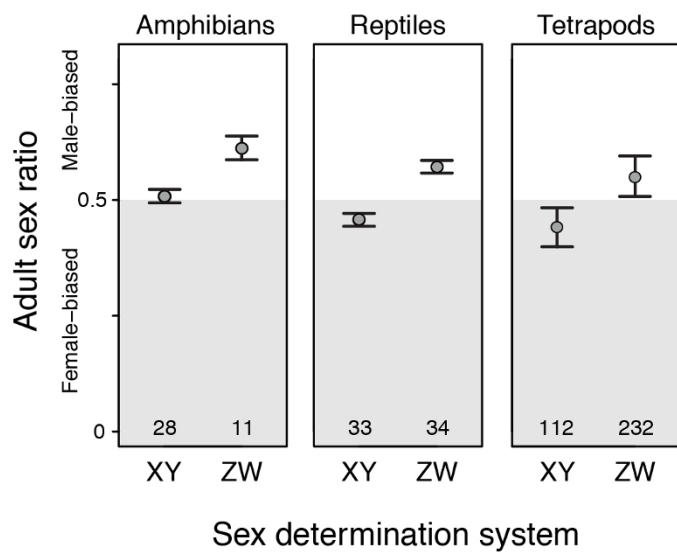
where  $U_X$  and  $U_Y$  are the total rates of mutation to deleterious alleles across all loci on the X and Y chromosomes. With ZW sex determination, the mean viability of females to males is

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

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 per cent. This degree of bias is substantially less than that seen in our data. We emphasize that the conclusion could be quite different using other parameter values, or if the model was extended to include stochastic effects.

The second hypothesis to explain biased ASRs that we explored with models is sex-antagonistic selection, the situation in which alleles are selected differently in females and males. In Supplementary Information 2, we use numerical examples to show that under both XY and ZW sex determination, either a female-biased or male-biased ASR can result. Thus there does not seem to be a robust generalization about how sex-antagonistic selection will bias the ASR.

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**Extended Data Figure 1 | Phylogenetically corrected mean and s.e.m. of ASR in clades with different sex-determination systems.** Parameter estimates for the mean and associated s.e.m. were calculated by PGLS models<sup>18</sup> presented in Extended Data Table 2 (with branch lengths estimated by Nee's method<sup>54</sup>).

Extended Data Table 1 | Detailed analyses of the effect of sex-determination system on the ASR.

	Species level		Phylogenetically corrected			
	t-test		LR	PDM	PGLS	
	t-value	p-value (n)		p-value (n)	t-value	p-value (n)
Amphibians (XY vs. ZW)	3.039	0.008 (39)	10.5	0.033 (39)	3.418	0.002 (39)
Reptiles (XY vs. ZW)	6.018	< 0.001 (67)	11.3	0.023 (67)	5.996	< 0.001 (67)
Mammals (XY) vs. birds (ZW)	8.982	< 0.001 (238)	not tested		not tested	
Tetrapods, all species (XY vs. ZW)	9.790	< 0.001 (344)	53.6	< 0.001 (344)	5.313	< 0.001 (344)
Tetrapods, reduced † (XY vs. ZW)	4.801	< 0.001 (87)	17.9	0.001 (87)	5.072	< 0.001 (87)

These are extensions of Table 1 showing details of the phylogenetically uncorrected (*t*-tests) and phylogenetically corrected (PGLS<sup>18</sup> and PDM<sup>19</sup>) analyses. 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. In the reduced analysis (marked by †), snakes, birds and mammals were each included as a single datum with mean species values.



**Extended Data Table 2 | Phylogenetically controlled analyses of the relationship between ASR and genetic sex-determination system using different branch length assumptions.**

Taxa	Branch lengths	$b \pm SE$	t	p	$R^2$	$\lambda$
Amphibians (n = 39)	Nee's	$0.101 \pm 0.030$	3.418	0.002	0.240	0.000
	Pagel's	$0.101 \pm 0.030$	3.418	0.002	0.240	0.000
	Unit branch lengths	$0.076 \pm 0.027$	2.821	0.008	0.177	0.000
Reptiles (n = 67)	Nee's	$0.114 \pm 0.019$	5.996	< 0.001	0.356	0.000
	Pagel's	$0.114 \pm 0.019$	5.968	< 0.001	0.354	0.000
	Unit branch lengths	$0.114 \pm 0.020$	5.702	< 0.001	0.333	0.000
Tetrapods (n = 344)	Nee's	$0.109 \pm 0.020$	5.313	< 0.001	0.076	0.409
	Pagel's	$0.106 \pm 0.021$	4.998	< 0.001	0.068	0.332
	Unit branch lengths	$0.093 \pm 0.020$	4.581	< 0.001	0.058	0.469

These are the results of PGLS models<sup>18</sup> as implemented in the R package 'caper'<sup>57</sup>, showing parameter estimates ( $b$ ) as the difference in ASR ( $ZW - XY$ ), the proportion of interspecific variance ( $R^2$ ) in ASR explained by the sex-determination system (female-heterogametic,  $ZW$ ; or male-heterogametic,  $XY$ ), calculated by PGLS; and the degree of phylogenetic dependence ( $\lambda$ ). The models assume gradual branch lengths calculated either by Nee's or by Pagel's method, or unit branch lengths<sup>54</sup>.