

•**REVIEW**• December 2018 Vol.61 No.12: 1503–1514 <https://doi.org/10.1007/s11427-018-9415-7>

# **Diverse and variable sex determination mechanisms in vertebrates**

Xi-Yin Li & Jian-Fang Gui[\\*](#page-0-0)

*State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, College of Modern Agriculture Sciences, University of Chinese Academy of Sciences, The Innovative Academy of Seed Design, Chinese Academy of Sciences, Wuhan 430072, China*

Received August 30, 2018; accepted September 27, 2018; published online November 13, 2018

Sex is prevalent in nature and sex determination is one of the most fundamental biological processes, while the way of initiating female and male development exhibits remarkable diversity and variability across vertebrates. The knowledge on why and how sex determination mechanisms evolve unusual plasticity remains limited. Here, we summarize sex determination systems, master sex-determining genes and gene-regulatory networks among vertebrates. Recent research advancements on sex determination system transition are also introduced and discussed in some non-model animals with multiple sex determination mechanisms. This review will provide insights into the origin, transition and evolutionary adaption of different sex determination strategies in vertebrates, as well as clues for future perspectives in this field.

**sex determination, sex-determining gene, sex chromosome, sex transition, sex differentiation, sex control breeding**

**Citation:** Li, X.Y., and Gui, J.F. (2018). Diverse and variable sex determination mechanisms in vertebrates. Sci China Life Sci 61, 1503–1514. [https://doi.org/](https://doi.org/10.1007/s11427-018-9415-7) [10.1007/s11427-018-9415-7](https://doi.org/10.1007/s11427-018-9415-7)

Most vertebrates are gonochoristic (two sexes present in different individuals) [\(Herpin and Schartl, 2015](#page-9-0); [Mei and](#page-10-0) [Gui, 2015](#page-10-0)), and females and males are determined via two broad strategies including genotypic sex determination (GSD) and environmental sex determination (ESD) ([Bach](#page-8-0)[trog et al., 2014](#page-8-0); [Capel, 2017\)](#page-8-1). GSD refers to sex determination that is driven by genotypic elements with sex difference, and the primary sex of an individual with GSD is usually determined at the moment of fertilization. Diverse mechanisms of GSD can be generally divided into male heterogametic system of XY sex chromosomes and female heterogametic system of ZW sex chromosomes, which have been identified in mammals ([Koopman et al., 1991\)](#page-9-1), birds ([Smith et al., 2009\)](#page-10-1) and most reptiles ([Gamble et al., 2015\)](#page-8-2), amphibians [\(Yoshimoto et al., 2008](#page-11-0)), and fishes [\(Matsuda et](#page-9-2) [al., 2002\)](#page-9-2). ESD refers to sex determination that is triggered by the effects of environmental factors during development. Diverse stimuli for ESD have been revealed to include temperature [\(Holleley et al., 2015\)](#page-9-3), photoperiod [\(Brown et](#page-8-3) [al., 2014](#page-8-3)), social factors ([Warner et al., 1996](#page-10-2)), and so on. GSD and ESD actually are not mutually exclusive, and transitions between these two seemingly distinct sex determination strategies have been unveiled in many species [\(Holleley et al., 2015](#page-9-3); [Li et al., 2018](#page-9-4); [Pennell et al., 2018](#page-10-3)).

Here, we summarize diverse sex determination systems, variable master sex-determining genes and plastic generegulatory networks across vertebrates. We also introduce the recent advancements on transitions between different sex determination systems in some ectotherms, which are at special evolutionary stages and have multiple sex determination mechanisms co-existed. Thus the present review will help us in further understanding the origin, transition and evolutionary adaption of different sex determination mechanisms.

# **DIVERSE SEX DETERMINATION SYSTEMS AMONG VERTEBRATES**

### **XX/XY system and XX/XY variants**

Male heterogametic XX/XY sex determination system is

<span id="page-0-0"></span>\*Corresponding author (email: jfgui@ihb.ac.cn)

prevalent in mammals, and sex-determining region Y (*Sry*) located in mammalian Y chromosome is the first sex-determining gene identified in vertebrates [\(Koopman et al.,](#page-9-1) [1991](#page-9-1)). *Sry* encodes a transcription factor with a high mobility group (HMG) box, which is transiently expressed and initiates testis differentiation and male development via triggering differentiation of Sertoli cells ([Koopman et al., 1991\)](#page-9-1). XX/XY sex determination system also have been observed in reptiles, amphibians and fishes ([Figure 1](#page-2-0)), but sex chromosomes with limited Y chromosome degeneration are morphologically indistinguishable in many species of these classes ([Gamble et al., 2015](#page-8-2)). Till now, no sex-determining gene(s) have been identified on the XY sex chromosomes without *Sry* gene in reptiles and amphibians. By contrast, numerous sex-determining genes have been revealed in many fish species with XX/XY systems, such as *dmy* in medaka (*Oryzias latipes*) ([Matsuda et al., 2002\)](#page-9-2), *sox3y* in Indian ricefish (*Oryzias dancena*) ([Takehana et al., 2014\)](#page-10-4), *amhy* in perjerry (*Odontesthes hatcheri*) and Nile tilapia (*Oreochromis niloticus*) ([Hattori et al., 2012](#page-9-5); [Li et al., 2015\)](#page-9-6), and *gsdfy* in Luzon ricefish (*Oryzias luzonensis*) ([Myosho et](#page-10-5) [al., 2012\)](#page-10-5).

Although most mammals depend on XY system with *Sry* at the top of the sex-determining cascade, variants of XX/XY system have evolved in some mammalian species. In the spiny rats (*Tokudaia osimensis osimensis* and *Tokudaia osimensis* spp.) ([Sutou et al., 2001\)](#page-10-6), Y chromosomes and *Sry* gene have been lost, and both females and males have an identical XO karyotype. Two vole species (*Ellobius lutescens* and *Ellobius tancrei*) have no Y chromosome and no *Sry* gene either [\(Just et al., 1995\)](#page-9-7). Although male differentiation pathway is conserved in the XO mammalian species ([Otake and Kuroiwa, 2016\)](#page-10-7), it is still unknown that which gene(s) determine sex in these mammals without *Sry*. Sex determination systems in monotremes are different to XX/XY systems in marsupials and placentals. Female platypuses (*Ornithorhynchus anatinus*) have five pairs of X chromosomes  $(X_1X_2X_3X_4X_5)$ , and males have the five X chromosomes  $(X_1X_2X_3X_4X_5)$  and five Y chromosomes  $(Y_1Y_2Y_3Y_4Y_5)$  [\(Rens et al., 2004](#page-10-8)). The short-beaked echidna (*Tachyglossus aculeatus*) also has similar sex chromosome system with five X chromosomes  $(X_1X_2X_3X_4X_5)$  and four Y chromosomes  $(Y_1Y_2Y_3Y_4)$  that are not completely homologous to those of platypus ([Rens et al., 2007\)](#page-10-9). However, these two monotreme mammals have no *Sry* gene [\(Wallis et](#page-10-10) [al., 2008\)](#page-10-10), and the most probable sex-determining gene is *Amh* gene on  $Y_5$  chromosome [\(Cortez et al., 2014](#page-8-4)). Moreover, variants of XX/XY system have also been identified in non-mammalian vertebrates such as  $X_1Y_1Y_2$  system in neotropical fish (*Hoplias malabaricus*) [\(Cioffi and Bertollo,](#page-8-5) [2010](#page-8-5)) and X1X2Y system in leaf litter frog (*Eleutherodactylus maussi*) [\(Schmid et al., 2002](#page-10-11)).

#### **ZZ/ZW system and ZZ/ZW variants**

Unlike mammals, all studied birds have female heterogametic ZZ/ZW sex chromosomal system, and their sex is determined via the dosage of doublesex and mab-3 related transcription factor 1 (*Dmrt1*) on Z chromosome or an unknown female-determining gene on the W chromosome [\(Smith et al., 2009\)](#page-10-1). *Dmrt1* gene encodes a transcription factor with a conserved DNA-binding domain, which is highly expressed in male gonads in fishes, reptiles, birds and mammals [\(Ge et al., 2017](#page-8-6); [Li et al., 2014a;](#page-9-8) [Smith et al.,](#page-10-12) [1999\)](#page-10-12). In birds, knockdown of *Dmrt1* expression via RNA interference (RNAi) in the early chicken embryos leads to feminization of the gonads in genotypic males (ZZ) ([Smith et](#page-10-1) [al., 2009](#page-10-1)), while overexpression of *Dmrt1* induces male pathway and antagonizes female pathway embryonic gonads [\(Lambeth et al., 2014\)](#page-9-9). Snakes also have ZZ/ZW sex determination system, and sex chromosomes in advanced snakes have been demonstrated to exhibit significant evolutionary stability (Rovatsos et al., 2015). Snake Z chromosome is homologous to the chicken autosome rather than to the chicken Z chromosomes, which indicates that sex chromosomes in snakes and birds were derived from different autosomal pairs of the common ancestor [\(Matsubara et al.,](#page-9-10) [2006\)](#page-9-10). ZZ/ZW system also have been identified in some species of amphibians and fishes [\(Figure 1](#page-2-0)), and the corresponding sex-determining genes have also been illustrated, including *Dm-w* on the W chromosome of the clawed frog (*Xenopus laevis*) [\(Yoshimoto et al., 2008](#page-11-0)) and *dmrt1* on Z chromosome of the half-smooth tongue sole (*Cynoglossus semilaevis*) [\(Chen et al., 2014;](#page-8-7) [Cui et al., 2017](#page-8-8)).

Variants of ZZ/ZW system have evolved in some amphibian and fish species. In the New Zealand frog (*Leiopelma hochstetteri*), Z chromosome has been lost and sex is determined via univalent W chromosome in female ([Green,](#page-9-11) [1988\)](#page-9-11), showing a unique OW female and OO male sex determination system [\(Ferro et al., 2018](#page-8-9)). Besides, multiple sex chromosome systems also have been identified in the catfish (*Ancistrus sp.2*) with Z1Z2W1W2 female and Z1Z1Z2Z2 male sex determination system ([de Oliveira et al., 2007](#page-8-10)). ZW1W2 female and ZZ male system have been uncovered in the lizardfish (*Trachinocephalus myops*) [\(Kitano and Pei](#page-9-12)[chel, 2012](#page-9-12)).

#### **Extra chromosomes for GSD**

Extra chromosomes, also known as B chromosomes or supernumerary chromosomes, are dispensable for the normal life cycle of host individuals ([Houben et al., 2014](#page-9-13)). Compared with standard A chromosomes including autosomes and sex chromosomes, extra chromosomes do not follow the rules of Mendelian inheritance, as they do not pair with A chromosomes ([Martis et al., 2012](#page-9-14)). Recently, active genes



<span id="page-2-0"></span>[Figure 1](#page-2-0) Diverse sex determination systems among vertebrate clades. "Variant" indicates absence of a sex chromosome or presence of multiple sex chromosomes. ESD, environmental sex determination.

have been identified on the extra chromosomes, which have functional effect on the host phenotypes especially the sex ([Camacho et al., 2011](#page-8-11); [Ma et al., 2017\)](#page-9-15). In the Lake Victoria cichlid fish (*Lithochromis rubripinnis*), B chromosomes restricted to females have been found to have functional effect on female sex determination [\(Yoshida et al., 2010](#page-11-1)). In polyploid gibel carp (*Carassius gibelio*), 3–4 extra microchromosomes with repetitive sequences and transposable elements have been identified in male individuals. Moreover, sex-reversed females (genotypic males) induced by estradiol hormone treatment have been used to establish gynogenetic families, and the proportions of males in these gynogenetic families have been revealed to be closely with the extra microchromosome number of the sex-reversed females. Thus, these findings suggest that the extra microchromosomes in males resembling common feature of sex chromosomes play male determination role in gibel carp ([Li et](#page-9-16) [al., 2016](#page-9-16)). Although extra chromosomes have been revealed to be associated with sex determination in many vertebrates ([Camacho et al., 2011](#page-8-11)) and contain functional gene related with testis development and spermatogenesis ([Li et al.,](#page-9-17) [2017](#page-9-17)), the master sex-determining gene(s) on the extra chromosomes and the corresponding mechanism remain unknown.

### **ESD in ectotherms**

ESD widely exists in ectotherms including reptiles and fishes, but have not been identified in amphibians although sex reversal induced by environmental factors has been revealed both in the wild populations and laboratory strains of common frog *Rana temporaria* ([Alho et al., 2010;](#page-8-12) [Flament,](#page-8-13) [2016\)](#page-8-13). The most common form of ESD is temperature-dependent sex determination (TSD). TSD in reptiles has been studied most extensively, and sex ratios of reptiles with TSD exhibit three main patterns. The first pattern is that females develop at high incubation temperature and males develop at low temperature, such as the red-eared slider turtle (*Trachemys scripta*) [\(Ge et al., 2018](#page-8-14)). The second pattern is that high incubation temperature leads to male occurrence and low incubation temperature leads to female occurrence, such as the tuatara (*Sphenodon guntheri*) ([Mitchell et al., 2006](#page-10-13)). The third pattern is that almost all females are produced at high and low temperature, while males (or both sexes) are produced at intermediate temperature, such as the common snapping turtle (*Chelydra serpentina*) [\(Schroeder et al.,](#page-10-14) [2016\)](#page-10-14). Some species in fish also have TSD, whereby the ambient temperature during development determines the sex of offspring, including gynogenetic gibel carp (*C. gibelio*) [\(Li et al., 2018](#page-9-4)) and topminnow (*Poeciliopsis lucida*) [\(Os](#page-10-15)[pina-Alvarez and Piferrer, 2008](#page-10-15)).

Although TSD has been identified in rainbow agama (*Agama agama*) for half a century, the molecular mechanism for how temperature determines sex has only been unveiled recently in red-eared slider turtle (*T. scripta*). The epigenetic regulatory switch *Kdm6b* is revealed to play a causal maledetermining role via eliminating H3K27 trimethylation at the promoter of *Dmrt1* ([Ge et al., 2018](#page-8-14)), which was demonstrated to be a strong candidate gene for male sex determination ([Ge et al., 2017](#page-8-6)). Therefore, these studies provide insights into the evolutionary trajectories and consequences of plastic sex determination strategies in vertebrates ([Li and](#page-9-18)

#### [Gui, 2018\)](#page-9-18).

Moreover, photoperiod, social factors, dissolved oxygen, external hormones, and nutrients also can be the environmental factors for regulating sex determination ([Baroiller et](#page-8-15) [al., 2009;](#page-8-15) [Capel, 2017](#page-8-1)). In the California grunion (*Leuresthes tenuis*) with photoperiod-dependent sex determination, longer day lengths lead to more females in the offspring, while more males are produced at shorter day lengths ([Brown et al., 2014](#page-8-3)). Some fishes can change sex via social interaction with conspecifics. In the gobiid fish (*Trimma okinawae*), the largest female sex reversal to male upon the removal of the dominant male from a breeding group, but the resultant males retaining both ovarian and testis can change sex to females again in the presence of larger male in the group (Sunobe and Nakazono, 1993).

# **VARIABLE MASTER SEX-DETERMINING GENES**

#### *Sox* **family genes**

Sry-related HMG box (*Sox*) genes have been vastly involved in vertebrate sex determination and differentiation ([Table 1\)](#page-4-0). *Sry* gene is almost the universal master male sex-determining gene in therian mammals, and gain- and loss-of-function studies have shown that *Sry* is sufficient and necessary for triggering male development. The transcription factor *Sry* is expressed transiently and initiates its target gene *Sox9*, which is critical for differentiation of Sertoli cells and testicle development [\(Barrionuevo et al., 2006;](#page-8-16) [Chaboissier et al.,](#page-8-17) [2004](#page-8-17); [Vidal et al., 2001](#page-10-16)). *Sry* gene is proposed to be the allelic diversification of *Sox3* gene, as the HMG box of Sry and Sox3 share high level of homology [\(Sato et al., 2010\)](#page-10-17). Although *Sox3* gene has no primary sex-determining function in mammals *per se* [\(Rizzoti et al., 2004](#page-10-18)), ectopic expression of *Sox3* during gonadal development in the XX mice leads to complete sex reversal from XX females to males ([Sutton et al., 2011](#page-10-19)).

Ortholog of *sox3* gene on the Y chromosome has been recruited for male determination in the Indian ricefish (*Oryzias dancena*) [\(Takehana et al., 2014](#page-10-4)). It has been found that the male-specific *cis*-regulatory element on the Y chromosome upregulates neighbouring *sox3y* expression during gonad development. *Sox3y* transgenic fish induces sex reversal of XX female, and *sox3y* loss-of-function in XY male leads to female development, which confirms the master male sex-determining role of *sox3y*. Recently, *Sox5* gene has been revealed to be involved in sex determination in medaka (*O. latipes*), which has the master sex-determining gene *dmy* ([Schartl et al., 2018](#page-10-20)). *Sox5* downregulates the activity of *dmy* via binding to the *dmy* promoter, and *sox5* mutants have complete female-to-male sex reversal [\(Schartl et al., 2018](#page-10-20)).

#### *Dmrt1* **and its paralog genes**

Doublesex and Mab-3 (DM) domain containing genes are involved in sex determination and sexual development among vast phylogenetic taxa including mammals, birds, reptiles, amphibians, fishes, flies, worms and corals [\(Bach](#page-8-0)[trog et al., 2014;](#page-8-0) [Matson and Zarkower, 2012](#page-9-19)). *Dmrt1* gene has been identified to play an essential role for male pathway among vertebrates [\(Ge et al., 2017;](#page-8-6) [Herpin and Schartl,](#page-9-0) [2015;](#page-9-0) [Webster et al., 2017](#page-11-2)), and *Dmrt1* or its paralogs has held a conserved position as the master sex-determining gene triggering the gonadal sex differentiation in many species [\(Table 1](#page-4-0)). In birds ([Smith et al., 2009\)](#page-10-1) and half-smooth tongue sole (*C. semilaevis*) [\(Chen et al., 2014](#page-8-7); [Cui et al.,](#page-8-8) [2017\)](#page-8-8), *Dmrt1* gene on the Z chromosome has been illustrated as sex-determining gene *per se*. In medaka (*O. latipes*), the sex-determining switch *dmy* has been confirmed as a duplicated copy of *dmrt1* on the Y chromosome ([Matsuda, 2005](#page-9-20)). In African clawed frog (*X. laevis*), the female sex-determining gene *Dm-w* is proposed to be a duplicate of *Dmrt1* on the W chromosome [\(Yoshimoto et al., 2008\)](#page-11-0).

In the red-eared slider turtle (*T. scripta*) with TSD, *Dmrt1* exhibits a temperature-dependent sexually dimorphic expression prior to sexual differentiation. Loss- and gain-offunction analyses revealed that *Dmrt1* is necessary and sufficient for testicular differentiation, and DNA methylation of the *Dmrt1* promoter is tightly linked to temperature shifts. These findings demonstrate that *Dmrt1* is a strong candidate for master male sex determination in this TSD turtle ([Ge et](#page-8-6) [al., 2017](#page-8-6)).

#### **TGF-β signaling pathway**

Members of the transforming growth factor beta (TGF-β) signaling pathway also have been recruited to be sex-determining genes in vertebrates especially in fishes [\(Table 1](#page-4-0)). The anti-Müllerian hormone (*amh*), a growth factor from TGF-β family, controls the degeneration of the female primordial duct in mammals, which plays an essential role in male development among vertebrates. In platypus (*Ornithorhynchus anatinus*), *Amhy* on the  $Y_5$  chromosomes has been proposed to be the prime candidate for sex-determining gene ([Cortez et al., 2014](#page-8-4)). In the perjerrey (*Odontesthes hatcheri*), *amhy*, the duplicated copy of *amh* on Y chromosome, has become the male sex-determining gene ([Hattori et](#page-9-5) [al., 2012](#page-9-5)). In Nile tilapia (*Oreochromis niloticus*), a Y-specific duplicate of *amh* also plays an essential role for male sex determination ([Li et al., 2015](#page-9-6)). A SNP that changes an amino acid (His/Asp384) in *amhr2* is associated with sex determination in the fugu (*Takifugu rubripes*) [\(Kamiya et al.,](#page-9-21) [2012\)](#page-9-21).

Gonadal soma derived factor (*gsdf*), a growth factor from TGF-β family, has been identified only in fish and assumed

<span id="page-4-0"></span>**[Table 1](#page-4-0)** Master sex-determining genes or candidate genes in vertebrates

Master sex-determining genes	Species	Sex-determining systems	Gene ancestors	References
Sry	Therian mammals	XY	Sox3	(Koopman et al., 1991)
$s\alpha x3y$	Indian ricefish (Oryzias dancena)	XY	sox3	(Takehana et al., 2014)
Dmrt1	<b>Birds</b>	ZW	-	(Smith et al., 2009)
dmrt1	Half-smooth tongue sole (Cynoglossus semilaevis)	ZW	-	(Chen et al., 2014; Cui et al., 2017)
Dmrt1	Red-eared slider turtle ( <i>Trachemys scripta</i> )	<b>TSD</b>		(Ge et al., 2017)
dmy	Medaka (Oryzias latipes)	XY	dmrt1	(Matsuda et al., 2002)
$Dm-w$	African clawed frog (Xenopus laevis)	ZW	Dmrt1	(Yoshimoto et al., 2008)
Amhy	Platypus ( <i>Ornithorhynchus anatinus</i> )	$X_1X_2X_3X_4X_5Y_1Y_2Y_3Y_4Y_5$	Amh	(Cortez et al., $2014$ )
amhy	Perjerrey (Odontesthes hatcheri)	XY	amh	(Hattori et al., 2012)
amhy	Nile tilapia (Oreochromis <i>niloticus</i> )	XY	amh	(Li et al., 2015)
amhr2	Fugu (Takifugu rubripes)	XY	amhr	(Kamiya et al., 2012)
gsdfy	Luzon ricefish (Oryzias luzonensis)	XY	gsdf	(Myosho et al., $2012$ )
gdf6y	Turquoise killifish (Nothobranchius furzeri)	XY	gdf6	(Reichwald et al., 2015)
sdy	Rainbow trout (Oncorhynchus mykiss)	XY	irf9	(Yano et al., 2012)

to play an important role in testis development. In Luzon ricefish (*Oryzias luzonensis*), a sister species of medaka (*O. latipes*), *gsdfy* has replaced *dmy* as the master sex-determining gene ([Myosho et al., 2012\)](#page-10-5). In the sablefish (*Anoplopoma fimbria*), sex-specific insertions immediately upstream the sex-determining related gene *gsdf* implicates *gsdf* as an excellent candidate for master sex determination ([Rondeau et al., 2013\)](#page-10-21).

Growth differentiation factor 6 on Y chromosome (*gdf6y*), a member of the TGF-β family, is transiently expressed shortly after hatching and proposed to be the master sexdetermining gene in the short-lived killifish (*Nothobranchius furzeri*) ([Reichwald et al., 2015\)](#page-10-22).

#### **Other gene recruited for master sex determination**

In rainbow trout (*Oncorhynchus mykiss*), *sdy* gene, the duplicate of the autosomal interferon regulatory factor 9 (*irf9*), encodes a protein that has lost the DNA-binding domain but preserved its protein interaction domain. Overexpression of *sdy* induces testicular differentiation, and targeted inactivation of *sdy* leads to ovarian differentiation. These results demonstrate that *sdy* is the sex-determining gene in *O. mykiss*; however, how *sdy* triggers male gonad development remains unclear ([Yano et al., 2012\)](#page-11-3).

Extraordinary diversity of sex-determining switches among vertebrates indicates that master sex-determining genes arise repeatedly and independently not only from the members of sexual regulatory network, but also from the *de novo* evolution of other genes.

# **GENE REGULATING NETWORK OF SEX DETERMINATION**

In mice, expression of *Sry* in the somatic supporting cells of males with Y chromosome activates its direct downstream target *Sox9*, which is critical for testis determination [\(Bar](#page-8-16)[rionuevo et al., 2006](#page-8-16); [Chaboissier et al., 2004](#page-8-17); [Gonen et al.,](#page-8-18) [2018;](#page-8-18) [Vidal et al., 2001\)](#page-10-16). Activation of *Sox9* leads to upregulation of *Fgf9* and other male differentiation related genes, which triggers male development of individuals with a Y chromosome. *Fgf9* plays repression role of *Wnt4* and the female pathway, and loss of *Fgf9* causes XY sex reversal to female [\(Kim et al., 2006\)](#page-9-22). In individuals without Y chromosome, female development is induced by activation of *Wnt4* and other female differentiation related genes such as *β-catenin*, *Foxl2*, *Fst*, *Rspo1*, *Ctnnb1* and so on [\(Capel,](#page-8-1) [2017\)](#page-8-1). Moreover, relationship between epigenetic regulation and mammalian sex determination also has been gradually illustrated. Mice lacking the H3K9 demethylase Jmjd1a (also called Tsga/Jhdm2a/Kdm3a) show male-to-female sex reversal, and Jmjd1a has been demonstrated to directly and positively control the *Sry* expression by regulating H3K9me2 levels [\(Kuroki et al., 2013](#page-9-23)). Most recently, histone acetyltransferases p300/CBP has been reported to be crucial for mammalian sex determination via regulating histone acetylation at the *Sry* locus, and loss of p300/CBP causes XY gonadal sex reversal ([Carré et al., 2018](#page-8-19)) [\(Figure 2](#page-5-0)A).

In the chicken with ZZ chromosomes, *Dmrt1* is sufficient to activate *Hemgn*, *Sox9* and *Amh* [\(Lambeth et al., 2014\)](#page-9-9), and *Hemgen* and *Sox9* also participate in the upregulation of *Dmrt1* [\(Nakata et al., 2013\)](#page-10-23). As *Hemgen* expression starts to disappear after day 8.5, it is assumed that *Sox9* expression represses *Hemgen* and maintains *Dmrt1* expression at a high functional level which blocks the expression of *Foxl2* [\(Na](#page-10-23)[kata et al., 2013](#page-10-23); [Sánchez and Chaouiya, 2018](#page-10-24)). Thus permanent activation of *Dmrt1* during gonadal development leads to male development. In the chicken ZW gonad, *Dmrt1* expression is too low to activate *Hemgn* and *Sox9*, then the expression of *Foxl2* reaches its functional level. *Foxl2* can activate the Aromatase, which is the terminal enzyme for Oestrogen [\(Govoroun et al., 2004](#page-8-20)). Thus repression of *Dmrt1* and *Sox9* ([Lambeth et al., 2013](#page-9-24)) and activation of *Foxl2*, Aromatase and Oestrogen lead to female development [\(Sánchez and Chaouiya, 2018\)](#page-10-24) [\(Figure 2B](#page-5-0)).

In the red-eared slider turtle (*T. scripta*) with TSD, *Dmrt1* exhibits a temperature-dependent sexually dimorphic expression and is a strong candidate sex-determining gene [\(Ge](#page-8-6) [et al., 2017](#page-8-6)). Recently, the histone H3 lysine 27 demethylase Kdm6b has been revealed to promote the transcription of *Dmrt1* via eliminating the trimethylation of H3K27 near its



<span id="page-5-0"></span>**[Figure 2](#page-5-0)** Gene-regulatory network of sex determination and gonadal differentiation. A, In mice, *Sry*, whose expression is modulated by *Jmjd1a* and *p300/ CBP*, upregulates *Sox9* to initiate activation of the male pathway. B, In chickens, high amount of *Dmrt1* expression in the individual with ZZ chromosomes activates *Hemgn*, *Sox9* and *Amh*, and leads to testicle development. Low amount of *Dmrt1* expression in the individual with ZW chromosomes is unable to activate *Hemgn* and *Sox9*, meanwhile upregulation of *Foxl2*, Aromatase and Oestrogen leads to ovarian development. C, In the red-eared slider turtle (*T. scripta*), the epigenetic switch Kdm6b regulates the expression of sex-determining gene *Dmrt1* via eliminating H3K27 trimethylation at the promoter of *Dmrt1*. D, In the African clawed frog (*X. laevis*), *Dmrt1* activates testicle developmental pathway in males with ZZ chromosomes via stimulating target genes, while *Dm-w* induces ovarian differentiation via antagonizing *Dmrt1* in females with ZW chromosomes. E, In fishes with XY sex chromosomes, master sex-determining genes on Y chromosomes initiate male pathway, while in the individual with XX sex chromosomes, absence of master male sex-determining gene leads to activation of female pathway. Male pathway is indicated in blue and female pathway is showed in red.

promoter ([Ge et al., 2018](#page-8-14)). At male-producing temperature (MPF 26°C), expression of *Kdm6b* reaches its functional level, and high amounts of Kdm6b activate *Dmrt1* expression and determine the male sex. At female-producing temperature (FPM 32°C), *Kdm6b* expression is down-regulated and the trimethylation of H3K27 on the *Dmrt1* promoter suppresses its expression, which leads to female development ([Figure 2C](#page-5-0)).

*Dm-w*, the paralogue of *Dmrt1* on the W chromosome, is the female sex-determining gene in African clawed frog (*X. laevis*) ([Yoshimoto et al., 2008](#page-11-0)). *Dm-w* is expressed transiently in the primordial gonads during the sex determination period, while expression of *Dmrt1* is still detected after the sex determination period. The DNA-binding domain of Dmw shows high level of sequence identity with the corresponding region of Dmrt1; however, Dm-w has no significant sequence similarity with the Dmrt1's transactivation domain [\(Yoshimoto et al., 2010\)](#page-11-4). Moreover, *Dm-w* is able to dose-dependently antagonize the transcriptional activity of *Dmrt1 in vitro*. Thus, these findings suggest *Dm-w* directs female sex determination via antagonizing *Dmrt1* [\(Yoshi](#page-11-5)[moto and Ito, 2011\)](#page-11-5) [\(Figure 2](#page-5-0)D).

In fishes with XY sex chromosomes, master sex-determining genes on Y chromosomes, including *dmy*, *amhy*, *amhr2*, *gsdfy*, *gdf6y*, *sox3y* and *sdy*, are expressed highly during sex determination period. High expression level of sex-determining switch is able to initiate downstream genetic network of male differentiation, which contains the essential genes for testicle development, such as *dmrt1*, *sox9*, *sf1* and *wt1*. While in the individual with XX sex chromosomes, absence of master male sex-determining gene leads to activation of the genetic network of female differentiation, which contains the essential genes for ovary development, such as *foxl2*, *cyp19a1a*, *wnt4* and *rspo1* ([Figure 2E](#page-5-0)). For instance, divergent *foxl2a* and *foxl2b* cooperate to regulate ovarian development and prevent the ovary from differentiating as testis in the model organism zebrafish (*Danio rerio*) ([Yang et al., 2017\)](#page-11-6), and *dmrt1* and *amh* have been identified to play important roles in differentiation of male germ cells and testicle development [\(Lin et al., 2017](#page-9-25); [Web](#page-11-2)[ster et al., 2017\)](#page-11-2). In Nile tilapia (*O. niloticus*) with the sex determiner *amhy* [\(Li et al., 2015\)](#page-9-6), knockout of *gsdf* and *amhrII* induce in male-to-female sex reversal [\(Jiang et al.,](#page-9-26) [2016](#page-9-26); [Li et al., 2015\)](#page-9-6), while disruption of *foxl2* and *cyp19a1a* result in complete female-to-male sex reversal [\(Zhang et al.,](#page-11-7) [2017](#page-11-7)). In yellow catfish (*Pelteobagrus fulvidraco*) with XY sex determination system ([Dan et al., 2013;](#page-8-21) [Wang et al.,](#page-10-25) [2009](#page-10-25)), the Y chromosome linked gene *pfpdzl* has been revealed to be essential for male sex differentiation and maintenance through upregulating expression of *amh*, *dmrt1* and *sox9a1*, and downregulating expression of *cyp19a1*, *foxl2* and *wnt4* ([Dan et al., 2018\)](#page-8-22).

Although master sex-determining genes are variable

among species and evolve independently ([Table 1\)](#page-4-0), the genes involved in the pathway of sex differentiation are relatively conserved [\(Figure 2](#page-5-0)) and the morphology of adult gonad is also similar across different vertebrate taxa [\(DeFalco and](#page-8-23) [Capel, 2009](#page-8-23); [Herpin and Schartl, 2015](#page-9-0)). *Sox9*, *dmrt1* and *amh* are commonly involved in the pathway of testicle development and spermatogenesis, while *foxl2* and *cyp19a1a* are essential for ovarian development and oogenesis ([Figure](#page-5-0) [2\)](#page-5-0). *Sox9* is critical for testis determination, which was demonstrated by gain- and loss-of-function studies [\(Barrio](#page-8-16)[nuevo et al., 2006](#page-8-16); [Chaboissier et al., 2004;](#page-8-17) [Vidal et al.,](#page-10-16) [2001\)](#page-10-16). Recent findings reveal that the deletion of a single distal enhancer of *Sox9* is able to induce XY sex reversal in mice [\(Gonen et al., 2018](#page-8-18)). *Dmrt1* has been identified as sexdetermining switch in birds, half-smooth tongue sole (*C. semilaevis*) and red-eared slider turtle (*T. scripta*), and in the other vertebrates *dmrt1* also plays essential role for male development [\(Li et al., 2014a;](#page-9-8) [Matson and Zarkower, 2012](#page-9-19)). Meanwhile, *amh* has been illustrated to be a key component of male sex determination and testicle differentiation across vertebrates [\(Herpin and Schartl, 2015](#page-9-0); [Lin et al., 2017\)](#page-9-25). On the other hand, *foxl2* is a highly conserved gene for ovarian development and maintenance [\(Loffler et al., 2003\)](#page-9-27), and *cyp19a1a* is a critical gene of steroidogenesis, which converts androgens to estrogens ([Simpson et al., 1994;](#page-10-26) [Xiong et](#page-11-8) [al., 2015](#page-11-8)). Inhibition or deletion of *foxl2* or *cyp19a1a* induces female-to-male sex reversal in many species, and *foxl2* and *cyp19a1a* are believed to be involved in the process of ovarian differentiation in nearly all species studied [\(Kitano et](#page-9-28) [al., 2000;](#page-9-28) [Lau et al., 2016](#page-9-29); [Yang et al., 2017;](#page-11-6) [Zhang et al.,](#page-11-7) [2017\)](#page-11-7).

# **TRANSITIONS BETWEEN SEX DETERMINATION SYSTEMS**

Compared with relatively stable GSD systems in mammals and birds, sex determination systems exhibit contrasting diversity in ectotherms, including male heterogametic GSD, female heterogametic GSD, and ESD. Transitions between different sex determination strategies occur frequently in reptiles, amphibians and fishes [\(Capel, 2017](#page-8-1); [Pennell et al.,](#page-10-3) [2018\)](#page-10-3).

Comparative genomic mapping in reptiles has revealed the homology in sex chromosomes across reptile groups, meanwhile wide distribution of diverse sex determination systems has also been uncovered among reptiles. Thus, it is apparent that transitions between sex-determining systems occurred many times in reptiles, especially in geckos [\(Gamble et al., 2015;](#page-8-2) [Sarre et al., 2011](#page-10-27)). Moreover, different sex-determining systems have been demonstrated to coexist in one species such as the Australian bearded dragon (*Pogona vitticeps*) [\(Quinn et al., 2007\)](#page-10-28), in which sex reversal can

induce the rapid transition from GSD to TSD [\(Holleley et al.,](#page-9-3) [2015](#page-9-3)). The lizards (*P. vitticeps*) have female heterogametic sex chromosomes that females have a Z and a W chromosome while males have two Z chromosomes. However, laboratory experiments revealed that high incubation temperature induces ZZ offspring sex-reversed to females, and also nearly 20% of ZZ female individuals have been detected in wild populations ([Holleley et al., 2015](#page-9-3)). The ZZ sex-reversed females mating with ZZ normal males produces fertile offspring without W chromosome, whose phenotypic sex is determined by incubation temperature solely. The novel transition pathway from GSD to TSD demonstrates that TSD can evolve rapidly in response to extreme ambient conditions such as high temperature, without sex-specific selective advantages [\(Holleley et al., 2015](#page-9-3)).

In amphibians, species studied till now all display GSD including XX/XY and ZZ/ZW systems, although temperature effect has been identified previously ([Alho et al., 2010;](#page-8-12) [Flament, 2016\)](#page-8-13). The Japanese wrinkled frog (*Rana rugosa*) exhibits both male and female heterogamety, that the northern populations have ZZ/ZW system and the southern populations have XX/XY system [\(Miura, 2007;](#page-10-29) [Ogata et al.,](#page-10-30) [2003](#page-10-30)). Transition of sex-determining system from XY to ZW has been proposed, as part of ZW population belongs to the XY group but not to the main ZW group via phylogenetic analysis ([Ogata et al., 2007](#page-10-31)). Recently, the simultaneous presence of three different sex chromosomes, W, Z, and Y, has been identified in the clawed frog (*Xenopus tropicalis*), containing three kinds of males (YZ, YW and ZZ) and two kinds of females (ZW and WW) [\(Roco et al., 2015\)](#page-10-32). The existence of both male and female heterogametic individuals in one species provides the opportunity to seek emergence of neo sex-determining genes and transitions between sex-determining systems ([Schartl, 2015\)](#page-10-33).

Fishes exhibit the most diverse sex-determination mechanisms ([Baroiller and D'Cotta, 2016](#page-8-24); [Mei and Gui, 2015](#page-10-0)), and coexistence of different sex-determining systems has also been found in the same species, such as zebrafish (*Danio rerio*) [\(Anderson et al., 2012](#page-8-25); [Wilson et al., 2014;](#page-11-9) [Yang et al.,](#page-11-6) [2017\)](#page-11-6), pejerrey (*Odontesthes bonariensis*) [\(Yamamoto et al.,](#page-11-10) [2014\)](#page-11-10) and gibel carp (*C. gibelio*) [\(Li et al., 2018;](#page-9-4) [Li et al.,](#page-9-16) [2016\)](#page-9-16). Gibel carp (*C. gibelio*) with two rounds of polyploidy origins is a hexaploid form of *Carassius* species complex [\(Li](#page-9-30) [et al., 2014b](#page-9-30); [Zhou and Gui, 2017;](#page-11-11) [Zhou et al., 2018](#page-11-12)), and has a wide geographic distribution among Eurasian continent and neighboring islands ([Gui and Zhou, 2010;](#page-9-31) [Liu et al.,](#page-9-32) [2017a](#page-9-32); [Liu et al., 2017b\)](#page-9-33). Compared with other unisexual vertebrates, rare but significant male incidences have been observed in natural habitats, and dual reproduction modes including unisexual gynogenesis and sexual reproduction have been illustrated [\(Gui and Zhou, 2010;](#page-9-31) [Zhang et al.,](#page-11-13) [2015\)](#page-11-13). The maternal individual of *C. gibelio* mating with the male individual of another species *C. carpio* leads to gynogenesis, which produces offspring with nearly identical genetic background as mother's ([Gui and Zhou, 2010](#page-9-31)), and the offspring's phenotypic sex is determined via ambient temperature during development ([Li et al., 2018;](#page-9-4) [Zhu et al.,](#page-11-14) [2018\)](#page-11-14). The maternal individual of *C. gibelio* mating with genotypic male of *C. gibelio* induces sexual reproduction, and the genetic male-specific marker is consistently linked to males, whose sex is determined via extra microchromosomes [\(Li et al., 2018](#page-9-4); [Li et al., 2016;](#page-9-16) [Zhu et al., 2018\)](#page-11-14) [\(Figure 3](#page-7-0)).



<span id="page-7-0"></span>**[Figure 3](#page-7-0)** Sex determination system transition between GSD and TSD in *Carassius gibelio*. Offspring without genetic difference are produced via gynogenesis, and males of TSD are determined by high ambient temperature during development. Offspring with genetic difference are produced via sexual reproduction, and males of GSD are determined by extra microchromosomes. ♀, female; ♂, male; -, without the genetic male-specific marker; +, with the genetic male-specific marker; TSD, temperature-dependent sex determination; GSD, genotypic sex determination.

These findings have revealed a close association of sex-determining system transition between TSD and GSD and reproductive mode transition between unisexual gynogenesis and sexual reproduction ([Li et al., 2018](#page-9-4); [Zhu et al., 2018](#page-11-14)).

## **CONCLUSION AND PERSPECTIVES**

Along with whole genome sequencing ([Reichwald et al.,](#page-10-22) [2015](#page-10-22)), restriction site-associated DNA sequencing ([Gamble](#page-8-2) [et al., 2015\)](#page-8-2), transcriptome sequencing [\(Rondeau et al.,](#page-10-21) [2013](#page-10-21)), epigenetic modification [\(Shao et al., 2014;](#page-10-34) [Shao et al.,](#page-10-35) [2018](#page-10-35)) and molecular cytogenetic analysis ([Li et al., 2016\)](#page-9-16), diverse and variable sex-determining mechanisms have been revealed in vertebrates. However, knowledge on evolutionary trajectories and consequences of different sex determination systems remains limited. These ectothermic organisms with multiple sex determination strategies are supposed to be under the evolutionary process of sex determination mechanism transitions, such as the bearded dragon (*P. vitticeps*), wrinkled frog (*R. rugosa*) and gibel carp (*C. gibelio*). Thus, illustration of detailed knowledge on these species will accelerate to solve these enigmas, such as genomic and epigenetic modification, molecular regulatory cascades and networks of plastic sex determination systems, as well as environmental adaptation and ecological novelty during the evolutionary process.

**Compliance and ethics** *The author(s) declare that they have no conflict of interest.*

**Acknowledgements** *This work was supported by the Key Program of Frontier Sciences of the Chinese Academy of Sciences (QYZDY-SSW-SMC025), the National Natural Science Foundation of China (31502148 and 31873036), the Earmarked Fund for Modern Agro-industry Technology Research System (NYCYTX-49), the Autonomous Project of the State Key Laboratory of Freshwater Ecology and Biotechnology (2016FBZ01), the Autonomous Project of the Institute of Hydrobiology, Chinese Academy of Sciences (Y25A171) and the Knowledge Innovation Program of the Chinese Academy of Science.*

- <span id="page-8-12"></span>Alho, J.S., Matsuba, C., and Merilä, J. (2010). Sex reversal and primary sex ratios in the common frog (*Rana temporaria*). [Mol Ecol](https://doi.org/10.1111/j.1365-294X.2010.04607.x) 19, 1763–1773.
- <span id="page-8-25"></span>Anderson, J.L., Rodríguez Marí, A., Braasch, I., Amores, A., Hohenlohe, P., Batzel, P., and Postlethwait, J.H. (2012). Multiple sex-associated regions and a putative sex chromosome in zebrafish revealed by RAD mapping and population genomics. [PLoS ONE](https://doi.org/10.1371/journal.pone.0040701) 7, e40701.
- <span id="page-8-0"></span>Bachtrog, D., Mank, J.E., Peichel, C.L., Kirkpatrick, M., Otto, S.P., Ashman, T.L., Hahn, M.W., Kitano, J., Mayrose, I., Ming, R., et al. (2014). Sex determination: why so many ways of doing it? [PLoS Biol](https://doi.org/10.1371/journal.pbio.1001899) 12, e1001899.
- <span id="page-8-24"></span>Baroiller, J.F., and D'Cotta, H. (2016). The reversible sex of gonochoristic fish: insights and consequences. [Sex Dev](https://doi.org/10.1159/000452362) 10, 242–266.
- <span id="page-8-15"></span>Baroiller, J.F., D'Cotta, H., and Saillant, E. (2009). Environmental effects on fish sex determination and differentiation. [Sex Dev](https://doi.org/10.1159/000223077) 3, 118–135.
- <span id="page-8-16"></span>Barrionuevo, F., Bagheri-Fam, S., Klattig, J., Kist, R., Taketo, M.M., Englert, C., and Scherer, G. (2006). Homozygous inactivation of Sox9 causes complete XY sex reversal in mice. [Biol Reproduction](https://doi.org/10.1095/biolreprod.105.045930) 74, 195– 201.
- <span id="page-8-3"></span>Brown, E.E., Baumann, H., and Conover, D.O. (2014). Temperature and photoperiod effects on sex determination in a fish. [J Exp Mar Biol Ecol](https://doi.org/10.1016/j.jembe.2014.07.009) 461, 39–43.
- <span id="page-8-11"></span>Camacho, J.P.M., Schmid, M., and Cabrero, J. (2011). B chromosomes and sex in animals. [Sex Dev](https://doi.org/10.1159/000324930) 5, 155–166.
- <span id="page-8-1"></span>Capel, B. (2017). Vertebrate sex determination: evolutionary plasticity of a fundamental switch. [Nat Rev Genet](https://doi.org/10.1038/nrg.2017.60) 18, 675–689.
- <span id="page-8-19"></span>Carré, G.A., Siggers, P., Xipolita, M., Brindle, P., Lutz, B., Wells, S., and Greenfield, A. (2018). Loss of p300 and CBP disrupts histone acetylation at the mouse *Sry* promoter and causes XY gonadal sex reversal. [Human Mol Genets](https://doi.org/10.1093/hmg/ddx398) 27, 190–198.
- <span id="page-8-17"></span>Chaboissier, M.C., Kobayashi, A., Vidal, V.I.P., Lützkendorf, S., van de Kant, H.J.G., Wegner, M., de Rooij, D.G., Behringer, R.R., and Schedl, A. (2004). Functional analysis of *Sox8* and *Sox9* during sex determination in the mouse. [Development](https://doi.org/10.1242/dev.01087) 131, 1891–1901.
- <span id="page-8-7"></span>Chen, S., Zhang, G., Shao, C., Huang, Q., Liu, G., Zhang, P., Song, W., An, N., Chalopin, D., Volff, J.N., et al. (2014). Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. [Nat Genet](https://doi.org/10.1038/ng.2890) 46, 253–260.
- <span id="page-8-5"></span>Cioffi, M.B., and Bertollo, L.A.C. (2010). Initial steps in XY chromosome differentiation in *Hoplias malabaricus* and the origin of an X1X2Y sex chromosome system in this fish group. [Heredity](https://doi.org/10.1038/hdy.2010.18) 105, 554–561.
- <span id="page-8-4"></span>Cortez, D., Marin, R., Toledo-Flores, D., Froidevaux, L., Liechti, A., Waters, P.D., Grützner, F., and Kaessmann, H. (2014). Origins and functional evolution of Y chromosomes across mammals. [Nature](https://doi.org/10.1038/nature13151) 508, 488–493.
- <span id="page-8-8"></span>Cui, Z., Liu, Y., Wang, W., Wang, Q., Zhang, N., Lin, F., Wang, N., Shao, C., Dong, Z., Li, Y., et al. (2017). Genome editing reveals *dmrt1* as an essential male sex-determining gene in Chinese tongue sole (*Cynoglossus semilaevis*). [Sci Rep](https://doi.org/10.1038/srep42213) 7, 42213.
- <span id="page-8-21"></span>Dan, C., Mei, J., Wang, D., and Gui, J.F. (2013). Genetic differentiation and efficient sex-specific marker development of a pair of Y- and X-linked markers in yellow catfish. [Int J Biol Sci](https://doi.org/10.7150/ijbs.7203) 9, 1043–1049.
- <span id="page-8-22"></span>Dan, C., Lin, Q., Gong, G., Yang, T., Xiong, S., Xiong, Y., Huang, P., Gui, J.F., and Mei, J. (2018). A novel PDZ domain-containing gene is essential for male sex differentiation and maintenance in yellow catfish (*Pelteobagrus fulvidraco*). [Sci Bull](https://doi.org/10.1016/j.scib.2018.08.012), doi: 10.1016/j.scib.2018.08.012.
- <span id="page-8-10"></span>de Oliveira, R.R., Feldberg, E., dos Anjos, M.B., and Zuanon, J. (2007). Occurrence of multiple sexual chromosomes (XX/XY1Y2 and Z1Z1Z2Z2/Z1Z2W1W2) in catfishes of the genus *Ancistrus* (Siluriformes: Loricariidae) from the Amazon basin. [Genetica](https://doi.org/10.1007/s10709-007-9231-9) 134, 243–249.
- <span id="page-8-23"></span>DeFalco, T., and Capel, B. (2009). Gonad morphogenesis in vertebrates: divergent means to a convergent end. [Annu Rev Cell Dev Biol](https://doi.org/10.1146/annurev.cellbio.042308.13350) 25, 457– 482.
- <span id="page-8-9"></span>Ferro, J.M., Cardozo, D.E., Suárez, P., Boeris, J.M., Blasco-Zúñiga, A., Barbero, G., Gomes, A., Gazoni, T., Costa, W., Nagamachi, C.Y., et al. (2018). Chromosome evolution in Cophomantini (Amphibia, Anura, Hylinae). [PLoS ONE](https://doi.org/10.1371/journal.pone.0192861) 13, e0192861.
- <span id="page-8-13"></span>Flament, S. (2016). Sex reversal in amphibians. [Sex Dev](https://doi.org/10.1159/000448797) 10, 267–278.
- <span id="page-8-2"></span>Gamble, T., Coryell, J., Ezaz, T., Lynch, J., Scantlebury, D.P., and Zarkower, D. (2015). Restriction site-associated DNA sequencing (RAD-seq) reveals an extraordinary number of transitions among gecko sex-determining systems. [Mol Biol Evol](https://doi.org/10.1093/molbev/msv023) 32, 1296–1309.
- <span id="page-8-14"></span>Ge, C., Ye, J., Weber, C., Sun, W., Zhang, H., Zhou, Y., Cai, C., Qian, G., and Capel, B. (2018). The histone demethylase KDM6B regulates temperature-dependent sex determination in a turtle species. [Science](https://doi.org/10.1126/science.aap8328) 360, 645–648.
- <span id="page-8-6"></span>Ge, C., Ye, J., Zhang, H., Zhang, Y., Sun, W., Sang, Y., Capel, B., and Qian, G. (2017). *Dmrt1* induces the male pathway in a turtle species with temperature-dependent sex determination. [Development](https://doi.org/10.1242/dev.152033) 144, 2222– 2233.
- <span id="page-8-18"></span>Gonen, N., Futtner, C.R., Wood, S., Garcia-Moreno, S.A., Salamone, I.M., Samson, S.C., Sekido, R., Poulat, F., Maatouk, D.M., and Lovell-Badge, R. (2018). Sex reversal following deletion of a single distal enhancer of *Sox9*. [Science](https://doi.org/10.1126/science.aas9408) 360, 1469–1473.
- <span id="page-8-20"></span>Govoroun, M.S., Pannetier, M., Pailhoux, E., Cocquet, J., Brillard, J.P.,

Couty, I., Batellier, F., and Cotinot, C. (2004). Isolation of chicken homolog of the *FOXL2* gene and comparison of its expression patterns with those of aromatase during ovarian development. [Dev Dyn](https://doi.org/10.1002/dvdy.20189) 231, 859–870.

- <span id="page-9-11"></span>Green, D.M. (1988). Cytogenetics of the endemic New Zealand frog, *Leiopelma hochstetteri*: extraordinary supernumerary chromosome variation and a unique sex-chromosome system. [Chromosoma](https://doi.org/10.1007/BF00331795) 97, 55– 70.
- <span id="page-9-31"></span>Gui, J.F., and Zhou, L. (2010). Genetic basis and breeding application of clonal diversity and dual reproduction modes in polyploid *Carassius auratus gibelio*. [Sci China Life Sci](https://doi.org/10.1007/s11427-010-0092-6) 53, 409–415.
- <span id="page-9-5"></span>Hattori, R.S., Murai, Y., Oura, M., Masuda, S., Majhi, S.K., Sakamoto, T., Fernandino, J.I., Somoza, G.M., Yokota, M., and Strüssmann, C.A. (2012). A Y-linked anti-Mullerian hormone duplication takes over a critical role in sex determination. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.1018392109) 109, 2955– 2959.
- <span id="page-9-0"></span>Herpin, A., and Schartl, M. (2015). Plasticity of gene-regulatory networks controlling sex determination: of masters, slaves, usual suspects, newcomers, and usurpators. [EMBO Rep](https://doi.org/10.15252/embr.201540667) 16, 1260–1274.
- <span id="page-9-3"></span>Holleley, C.E., O'Meally, D., Sarre, S.D., Marshall Graves, J.A., Ezaz, T., Matsubara, K., Azad, B., Zhang, X., and Georges, A. (2015). Sex reversal triggers the rapid transition from genetic to temperaturedependent sex. [Nature](https://doi.org/10.1038/nature14574) 523, 79–82.
- <span id="page-9-13"></span>Houben, A., Banaei-Moghaddam, A.M., Klemme, S., and Timmis, J.N. (2014). Evolution and biology of supernumerary B chromosomes. [Cell](https://doi.org/10.1007/s00018-013-1437-7) [Mol Life Sci](https://doi.org/10.1007/s00018-013-1437-7) 71, 467–478.
- <span id="page-9-26"></span>Jiang, D.N., Yang, H.H., Li, M.H., Shi, H.J., Zhang, X.B., and Wang, D.S. (2016). *gsdf* is a downstream gene of *dmrt1* that functions in the male sex determination pathway of the Nile tilapia. [Mol Reprod Dev](https://doi.org/10.1002/mrd.22642) 83, 497–508.
- <span id="page-9-7"></span>Just, W., Rau, W., Vogel, W., Akhverdian, M., Fredga, K., Marshall Graves, J.A., and Lyapunova, E. (1995). Absence of *Sry* in species of the vole *Ellobius*. [Nat Genet](https://doi.org/10.1038/ng1095-117) 11, 117–118.
- <span id="page-9-21"></span>Kamiya, T., Kai, W., Tasumi, S., Oka, A., Matsunaga, T., Mizuno, N., Fujita, M., Suetake, H., Suzuki, S., Hosoya, S., et al. (2012). A transspecies missense SNP in *amhr2* is associated with sex determination in the tiger pufferfish, *Takifugu rubripes* (fugu). [PLoS Genet](https://doi.org/10.1371/journal.pgen.1002798) 8, e1002798.
- <span id="page-9-22"></span>Kim, Y., Kobayashi, A., Sekido, R., DiNapoli, L., Brennan, J., Chaboissier, M.C., Poulat, F., Behringer, R.R., Lovell-Badge, R., and Capel, B. (2006). *Fgf9* and *Wnt4* act as antagonistic signals to regulate mammalian sex determination. [PLoS Biol](https://doi.org/10.1371/journal.pbio.0040187) 4, e187.
- <span id="page-9-12"></span>Kitano, J., and Peichel, C.L. (2012). Turnover of sex chromosomes and speciation in fishes. [Environ Biol Fish](https://doi.org/10.1007/s10641-011-9853-8) 94, 549–558.
- <span id="page-9-28"></span>Kitano, T., Takamune, K., Nagahama, Y., and Abe, S.I. (2000). Aromatase inhibitor and 17?-methyltestosterone cause sex-reversal from genetical females to phenotypic males and suppression of P450 aromatase gene expression in Japanese flounder (*Paralichthys olivaceus*). [Mol Reprod](https://doi.org/10.1002/(SICI)1098-2795(200005)56:1<1::AID-MRD1>3.0.CO;2-3) [Dev](https://doi.org/10.1002/(SICI)1098-2795(200005)56:1<1::AID-MRD1>3.0.CO;2-3) 56, 1-5.
- <span id="page-9-1"></span>Koopman, P., Gubbay, J., Vivian, N., Goodfellow, P., and Lovell-Badge, R. (1991). Male development of chromosomally female mice transgenic for *Sry*. [Nature](https://doi.org/10.1038/351117a0) 351, 117–121.
- <span id="page-9-23"></span>Kuroki, S., Matoba, S., Akiyoshi, M., Matsumura, Y., Miyachi, H., Mise, N., Abe, K., Ogura, A., Wilhelm, D., Koopman, P., et al. (2013). Epigenetic regulation of mouse sex determination by the histone demethylase Jmjd1a. [Science](https://doi.org/10.1126/science.1239864) 341, 1106–1109.
- <span id="page-9-24"></span>Lambeth, L.S., Cummins, D.M., Doran, T.J., Sinclair, A.H., and Smith, C. A. (2013). Overexpression of aromatase alone is sufficient for ovarian development in genetically male chicken embryos. [PLoS ONE](https://doi.org/10.1371/journal.pone.0068362) 8, e68362.
- <span id="page-9-9"></span>Lambeth, L.S., Raymond, C.S., Roeszler, K.N., Kuroiwa, A., Nakata, T., Zarkower, D., and Smith, C.A. (2014). Over-expression of *DMRT1* induces the male pathway in embryonic chicken gonads. [Dev Biol](https://doi.org/10.1016/j.ydbio.2014.02.012) 389, 160–172.
- <span id="page-9-29"></span>Lau, E.S.W., Zhang, Z., Qin, M., and Ge, W. (2016). Knockout of zebrafish ovarian aromatase gene (*cyp19a1a*) by TALEN and CRISPR/Cas9 Leads to all-male offspring due to failed ovarian differentiation. [Sci Rep](https://doi.org/10.1038/srep37357) 6, 37357.
- <span id="page-9-6"></span>Li, M., Sun, Y., Zhao, J., Shi, H., Zeng, S., Ye, K., Jiang, D., Zhou, L., Sun, L., Tao, W., et al. (2015). A tandem duplicate of anti-Müllerian hormone with a missense SNP on the Y chromosome is essential for male sex determination in Nile tilapia, *Oreochromis niloticus*. [PLoS](https://doi.org/10.1371/journal.pgen.1005678) [Genet](https://doi.org/10.1371/journal.pgen.1005678) 11, e1005678.
- <span id="page-9-18"></span>Li, X.Y., and Gui, J.F. (2018). An epigenetic regulatory switch controlling temperature-dependent sex determination in vertebrates. [Sci China Life](https://doi.org/10.1007/s11427-018-9314-3) [Sci](https://doi.org/10.1007/s11427-018-9314-3) 61, 996–998.
- <span id="page-9-17"></span>Li, X.Y., Liu, X.L., Ding, M., Li, Z., Zhou, L., Zhang, X.J., and Gui, J.F. (2017). A novel male-specific SET domain-containing gene *setdm* identified from extra microchromosomes of gibel carp males. [Sci Bull](https://doi.org/10.1016/j.scib.2017.04.002) 62, 528–536.
- <span id="page-9-4"></span>Li, X.Y., Liu, X.L., Zhu, Y.J., Zhang, J., Ding, M., Wang, M.T., Wang, Z. W., Li, Z., Zhang, X.J., Zhou, L., et al. (2018). Origin and transition of sex determination mechanisms in a gynogenetic hexaploid fish. [Heredity](https://doi.org/10.1038/s41437-017-0049-7) 121, 64–74.
- <span id="page-9-8"></span>Li, X.Y., Li, Z., Zhang, X.J., Zhou, L., and Gui, J.F. (2014a). Expression characterization of testicular *DMRT1* in both Sertoli cells and spermatogenic cells of polyploid gibel carp. [Gene](https://doi.org/10.1016/j.gene.2014.07.031) 548, 119–125.
- <span id="page-9-16"></span>Li, X.Y., Zhang, Q.Y., Zhang, J., Zhou, L., Li, Z., Zhang, X.J., Wang, D., and Gui, J.F. (2016). Extra microchromosomes play male determination role in polyploid gibel carp. [Genetics](https://doi.org/10.1534/genetics.115.185843) 203, 1415–1424.
- <span id="page-9-30"></span>Li, X.Y., Zhang, X.J., Li, Z., Hong, W., Liu, W., Zhang, J., and Gui, J.F. (2014b). Evolutionary history of two divergent *Dmrt1* genes reveals two rounds of polyploidy origins in gibel carp. [Mol Phylogenets Evol](https://doi.org/10.1016/j.ympev.2014.05.005) 78, 96–104.
- <span id="page-9-25"></span>Lin, Q., Mei, J., Li, Z., Zhang, X., Zhou, L., and Gui, J.F. (2017). Distinct and cooperative roles of *amh* and *dmrt1* in self-renewal and differentiation of male germ cells in zebrafish. [Genetics](https://doi.org/10.1534/genetics.117.300274) 207, 1007– 1022.
- <span id="page-9-32"></span>Liu, X.L., Jiang, F.F., Wang, Z.W., Li, X.Y., Li, Z., Zhang, X.J., Chen, F., Mao, J.F., Zhou, L., and Gui, J.F. (2017a). Wider geographic distribution and higher diversity of hexaploids than tetraploids in *Carassius* species complex reveal recurrent polyploidy effects on adaptive evolution. [Sci Rep](https://doi.org/10.1038/s41598-017-05731-0) 7, 5395.
- <span id="page-9-33"></span>Liu, X.L., Li, X.Y., Jiang, F.F., Wang, Z.W., Li, Z., Zhang, X.J., Zhou, L., and Gui, J.F. (2017b). Numerous mitochondrial DNA haplotypes reveal multiple independent polyploidy origins of hexaploids in *Carassius* species complex. [Ecol Evol](https://doi.org/10.1002/ece3.3462) 7, 10604-10615.
- <span id="page-9-27"></span>Loffler, K.A., Zarkower, D., and Koopman, P. (2003). Etiology of ovarian failure in blepharophimosis ptosis epicanthus inversus syndrome: *FOXL2* is a conserved, early-acting gene in vertebrate ovarian development. [Endocrinology](https://doi.org/10.1210/en.2002-0095) 144, 3237–3243.
- <span id="page-9-15"></span>Ma, W., Gabriel, T.S., Martis, M.M., Gursinsky, T., Schubert, V., Vrána, J., Doležel, J., Grundlach, H., Altschmied, L., Scholz, U., et al. (2017). Rye B chromosomes encode a functional Argonaute-like protein with *in vitro* slicer activities similar to its A chromosome paralog. [New Phytol](https://doi.org/10.1111/nph.14110) 213, 916–928.
- <span id="page-9-14"></span>Martis, M.M., Klemme, S., Banaei-Moghaddam, A.M., Blattner, F.R., Macas, J., Schmutzer, T., Scholz, U., Gundlach, H., Wicker, T., Šimková, H., et al. (2012). Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. [Proc](https://doi.org/10.1073/pnas.1204237109) [Natl Acad Sci USA](https://doi.org/10.1073/pnas.1204237109) 109, 13343–13346.
- <span id="page-9-19"></span>Matson, C.K., and Zarkower, D. (2012). Sex and the singular DM domain: insights into sexual regulation, evolution and plasticity. [Nat Rev Genet](https://doi.org/10.1038/nrg3161) 13, 163–174.
- <span id="page-9-10"></span>Matsubara, K., Tarui, H., Toriba, M., Yamada, K., Nishida-Umehara, C., Agata, K., and Matsuda, Y. (2006). Evidence for different origin of sex chromosomes in snakes, birds, and mammals and step-wise differentiation of snake sex chromosomes. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.0605274103) 103, 18190–18195.
- <span id="page-9-20"></span>Matsuda, M. (2005). Sex Determination in the Teleost Medaka, *Oryzias latipes*. [Annu Rev Genet](https://doi.org/10.1146/annurev.genet.39.110304.095800) 39, 293–307.
- <span id="page-9-2"></span>Matsuda, M., Nagahama, Y., Shinomiya, A., Sato, T., Matsuda, C., Kobayashi, T., Morrey, C.E., Shibata, N., Asakawa, S., Shimizu, N., et al. (2002). *DMY* is a Y-specific DM-domain gene required for male development in the medaka fish. [Nature](https://doi.org/10.1038/nature751) 417, 559–563.
- <span id="page-10-0"></span>Mei, J., and Gui, J.F. (2015). Genetic basis and biotechnological manipulation of sexual dimorphism and sex determination in fish. [Sci](https://doi.org/10.1007/s11427-014-4797-9) [China Life Sci](https://doi.org/10.1007/s11427-014-4797-9) 58, 124–136.
- <span id="page-10-13"></span>Mitchell, N.J., Nelson, N.J., Cree, A., Pledger, S., Keall, S.N., and Daugherty, C.H. (2006). Support for a rare pattern of temperaturedependent sex determination in archaic reptiles: evidence from two species of tuatara (*Sphenodon*). [Front Zool](https://doi.org/10.1186/1742-9994-3-9) 3, 9–12.
- <span id="page-10-29"></span>Miura, I. (2007). An evolutionary witness: the frog *Rana rugosa* underwent change of heterogametic sex from XY male to ZW female. [Sex Dev](https://doi.org/10.1159/000111764) 1, 323–331.
- <span id="page-10-5"></span>Myosho, T., Otake, H., Masuyama, H., Matsuda, M., Kuroki, Y., Fujiyama, A., Naruse, K., Hamaguchi, S., and Sakaizumi, M. (2012). Tracing the emergence of a novel sex-determining gene in medaka, *Oryzias luzonensis*. [Genetics](https://doi.org/10.1534/genetics.111.137497) 191, 163–170.
- <span id="page-10-23"></span>Nakata, T., Ishiguro, M., Aduma, N., Izumi, H., and Kuroiwa, A. (2013). Chicken hemogen homolog is involved in the chicken-specific sexdetermining mechanism. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.1218714110) 110, 3417–3422.
- <span id="page-10-31"></span>Ogata, M., Hasegawa, Y., Ohtani, H., Mineyama, M., and Miura, I. (2007). The ZZ/ZW sex-determining mechanism originated twice and independently during evolution of the frog, *Rana rugosa*. [Heredity](https://doi.org/10.1038/sj.hdy.6801068) 100, 92–99.
- <span id="page-10-30"></span>Ogata, M., Ohtani, H., Igarashi, T., Hasegawa, Y., Ichikawa, Y., Miura, I. (2003). Change of the heterogametic sex from male to female in the frog. Genetics 164, 613-620.
- <span id="page-10-15"></span>Ospina-Alvarez, N., and Piferrer, F. (2008). Temperature-dependent sex determination in fish revisited: prevalence, a single sex ratio response pattern, and possible effects of climate change. [PLoS ONE](https://doi.org/10.1371/journal.pone.0002837) 3, e2837.
- <span id="page-10-7"></span>Otake, T., and Kuroiwa, A. (2016). Molecular mechanism of male differentiation is conserved in the SRY-absent mammal, *Tokudaia osimensis*. [Sci Rep](https://doi.org/10.1038/srep32874) 6, 32874.
- <span id="page-10-3"></span>Pennell, M.W., Mank, J.E., and Peichel, C.L. (2018). Transitions in sex determination and sex chromosomes across vertebrate species. [Mol](https://doi.org/10.1111/mec.14540) [Ecol](https://doi.org/10.1111/mec.14540) 27, 3950–3963.
- <span id="page-10-28"></span>Quinn, A.E., Georges, A., Sarre, S.D., Guarino, F., Ezaz, T., and Graves, J. A.M. (2007). Temperature sex reversal implies sex gene dosage in a reptile. [Science](https://doi.org/10.1126/science.1135925) 316, 411.
- <span id="page-10-22"></span>Reichwald, K., Petzold, A., Koch, P., Downie, B.R., Hartmann, N., Pietsch, S., Baumgart, M., Chalopin, D., Felder, M., Bens, M., et al. (2015). Insights into sex chromosome evolution and aging from the genome of a short-lived fish. [Cell](https://doi.org/10.1016/j.cell.2015.10.071) 163, 1527–1538.
- <span id="page-10-8"></span>Rens, W., Grützner, F., O'brien, P.C.M., Fairclough, H., Graves, J.A.M., and Ferguson-Smith, M.A. (2004). From The Cover: Resolution and evolution of the duck-billed platypus karyotype with an X1Y1X2Y2X3Y3X4Y4X5Y5 male sex chromosome constitution. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.0405702101) 101, 16257–16261.
- <span id="page-10-9"></span>Rens, W., O'Brien, P.C.M., Grützner, F., Clarke, O., Graphodatskaya, D., Tsend-Ayush, E., Trifonov, V.A., Skelton, H., Wallis, M.C., Johnston, S., et al. (2007). The multiple sex chromosomes of platypus and echidna are not completely identical and several share homology with the avian Z. [Genome Biol](https://doi.org/10.1186/gb-2007-8-11-r243) 8, R243.
- <span id="page-10-18"></span>Rizzoti, K., Brunelli, S., Carmignac, D., Thomas, P.Q., Robinson, I.C., and Lovell-Badge, R. (2004). *SOX3* is required during the formation of the hypothalamo-pituitary axis. [Nat Genet](https://doi.org/10.1038/ng1309) 36, 247–255.
- <span id="page-10-32"></span>Roco, Á.S., Olmstead, A.W., Degitz, S.J., Amano, T., Zimmerman, L.B., and Bullejos, M. (2015). Coexistence of Y, W, and Z sex chromosomes in *Xenopus tropicalis*. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.1505291112) 112, E4752–E4761.
- <span id="page-10-21"></span>Rondeau, E.B., Messmer, A.M., Sanderson, D.S., Jantzen, S.G., von Schalburg, K.R., Minkley, D.R., Leong, J.S., Macdonald, G.M., Davidsen, A.E., Parker, W.A., et al. (2013). Genomics of sablefish (*Anoplopoma fimbria*): expressed genes, mitochondrial phylogeny, linkage map and identification of a putative sex gene. [BMC](https://doi.org/10.1186/1471-2164-14-452) [Genomics](https://doi.org/10.1186/1471-2164-14-452) 14, 452.
- Rovatsos, M., Vukić, J., Lymberakis, P., and Kratochvíl, L. (2015). Evolutionary stability of sex chromosomes in snakes. [Proc R Soc B](https://doi.org/10.1098/rspb.2015.1992) 282, 20151992.
- <span id="page-10-24"></span>Sánchez, L., and Chaouiya, C. (2018). Logical modelling uncovers developmental constraints for primary sex determination of chicken

<span id="page-10-27"></span>gonads. [J R Soc Interface](https://doi.org/10.1098/rsif.2018.0165) 15, 20180165.

- Sarre, S.D., Ezaz, T., and Georges, A. (2011). Transitions between sexdetermining systems in reptiles and amphibians. [Annu Rev Genom](https://doi.org/10.1146/annurev-genom-082410-101518) [Hum Genet](https://doi.org/10.1146/annurev-genom-082410-101518) 12, 391–406.
- <span id="page-10-17"></span>Sato, Y., Shinka, T., Sakamoto, K., Ewis, A.A., and Nakahori, Y. (2010). The male-determining gene *SRY* is a hybrid of *DGCR8* and *SOX3*, and is regulated by the transcription factor *CP2*. [Mol Cell Biochem](https://doi.org/10.1007/s11010-009-0308-x) 337, 267–275.
- <span id="page-10-33"></span>Schartl, M. (2015). Sex determination by multiple sex chromosomes in *Xenopus tropicalis*. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.1513518112) 112, 10575–10576.
- <span id="page-10-20"></span>Schartl, M., Schories, S., Wakamatsu, Y., Nagao, Y., Hashimoto, H., Bertin, C., Mourot, B., Schmidt, C., Wilhelm, D., Centanin, L., et al. (2018). *Sox5* is involved in germ-cell regulation and sex determination in medaka following co-option of nested transposable elements. [BMC Biol](https://doi.org/10.1186/s12915-018-0485-8) 16, 16.
- <span id="page-10-11"></span>Schmid, M., Feichtinger, W., Steinlein, C., Haaf, T., Schartl, M., Visbal García, R., Manzanilla Pupo, J., and Fernández Badillo, A. (2002). Chromosome banding in amphibia. [Cytogenet Genome Res](https://doi.org/10.1159/000071612) 99, 330– 343.
- <span id="page-10-14"></span>Schroeder, A.L., Metzger, K.J., Miller, A., and Rhen, T. (2016). A novel candidate gene for temperature-dependent sex determination in the common snapping turtle. [Genetics](https://doi.org/10.1534/genetics.115.182840) 203, 557–571.
- <span id="page-10-34"></span>Shao, C., Li, Q., Chen, S., Zhang, P., Lian, J., Hu, Q., Sun, B., Jin, L., Liu, S., Wang, Z., et al. (2014). Epigenetic modification and inheritance in sexual reversal of fish. [Genome Res](https://doi.org/10.1101/gr.162172.113) 24, 604–615.
- <span id="page-10-35"></span>Shao, G.M., Li, X.Y., Wang, Y., Wang, Z.W., Li, Z., Zhang, X.J., Zhou, L., and Gui, J.F. (2018). Whole genome incorporation and epigenetic stability in a newly synthetic allopolyploid of gynogenetic gibel carp. [Genome Biol Evol](https://doi.org/10.1093/gbe/evy165) 10, 2394–2407.
- <span id="page-10-26"></span>Simpson, E.R., Mahendroo, M.S., Means, G.D., Kilgore, M.W., Hinshelwood, M.M., Graham-lorence, S., Amarneh, B., Ito, Y., Fisher, C.R., Michael, M.D., et al. (1994). Aromatase cytochrome P450, the enzyme responsible for estrogen biosynthesis. [Endocr Rev](https://doi.org/10.1210/edrv-15-3-342) 15, 342–355.
- <span id="page-10-12"></span>Smith, C.A., McClive, P.J., Western, P.S., Reed, K.J., and Sinclair, A.H. (1999). Conservation of a sex-determining gene. [Nature](https://doi.org/10.1038/45130) 402, 601–602.
- <span id="page-10-1"></span>Smith, C.A., Roeszler, K.N., Ohnesorg, T., Cummins, D.M., Farlie, P.G., Doran, T.J., and Sinclair, A.H. (2009). The avian Z-linked gene *DMRT1* is required for male sex determination in the chicken. [Nature](https://doi.org/10.1038/nature08298) 461, 267– 271.
- Sunobe, T., and Nakazono, A. (1993). Sex change in both directions by alteration of social dominance in *Trimma okinawae* (Pisces: Gobiidae). [Ethology](https://doi.org/10.1111/j.1439-0310.1993.tb00450.x) 94, 339–345.
- <span id="page-10-6"></span>Sutou, S., Mitsui, Y., and Tsuchiya, K. (2001). Sex determination without the Y Chromosome in two Japanese rodents *Tokudaia osimensis osimensis* and *Tokudaia osimensis spp*.. [Mammalian Genome](https://doi.org/10.1007/s003350010228) 12, 17– 21.
- <span id="page-10-19"></span>Sutton, E., Hughes, J., White, S., Sekido, R., Tan, J., Arboleda, V., Rogers, N., Knower, K., Rowley, L., Eyre, H., et al. (2011). Identification of *SOX3* as an XX male sex reversal gene in mice and humans. [J Clin](https://doi.org/10.1172/JCI42580) [Invest](https://doi.org/10.1172/JCI42580) 121, 328–341.
- <span id="page-10-4"></span>Takehana, Y., Matsuda, M., Myosho, T., Suster, M.L., Kawakami, K., Shin-I, T., Kohara, Y., Kuroki, Y., Toyoda, A., Fujiyama, A., et al. (2014). Co-option of *Sox3* as the male-determining factor on the Y chromosome in the fish *Oryzias dancena*. [Nat Commun](https://doi.org/10.1038/ncomms5157) 5, 4157.
- <span id="page-10-16"></span>Vidal, V.P.I., Chaboissier, M.C., de Rooij, D.G., and Schedl, A. (2001). *Sox9* induces testis development in XX transgenic mice. [Nat Genet](https://doi.org/10.1038/90046) 28, 216–217.
- <span id="page-10-10"></span>Wallis, M.C., Waters, P.D., Delbridge, M.L., Kirby, P.J., Pask, A.J., Grützner, F., Rens, W., Ferguson-Smith, M.A., and Graves, J.A.M. (2008). Sex determination in platypus and echidna: autosomal location of *SOX3* confirms the absence of *SRY* from monotremes. [Chromosome](https://doi.org/10.1007/s10577-007-1185-3) [Res](https://doi.org/10.1007/s10577-007-1185-3) 15, 949–959.
- <span id="page-10-25"></span>Wang, D., Mao, H.L., Chen, H.X., Liu, H.Q., and Gui, J.F. (2009). Isolation of Y- and X-linked SCAR markers in yellow catfish and application in the production of all-male populations. [Animal Genets](https://doi.org/10.1111/j.1365-2052.2009.01941.x) 40, 978–981.
- <span id="page-10-2"></span>Warner, R.R., Fitch, D.L., and Standish, J.D. (1996). Social control of sex

change in the shelf limpet, *Crepidula norrisiarum*: size-specific responses to local group composition. [J Exp Mar Biol Ecol](https://doi.org/10.1016/0022-0981(96)02582-8) 204, 155– 167.

- <span id="page-11-2"></span>Webster, K.A., Schach, U., Ordaz, A., Steinfeld, J.S., Draper, B.W., and Siegfried, K.R. (2017). *Dmrt1* is necessary for male sexual development in zebrafish. [Dev Biol](https://doi.org/10.1016/j.ydbio.2016.12.008) 422, 33–46.
- <span id="page-11-9"></span>Wilson, C.A., High, S.K., McCluskey, B.M., Amores, A., Yan, Y., Titus, T. A., Anderson, J.L., Batzel, P., Carvan, M.J., Schartl, M., et al. (2014). Wild sex in zebrafish: loss of the natural sex determinant in domesticated strains. [Genetics](https://doi.org/10.1534/genetics.114.169284) 198, 1291–1308.
- <span id="page-11-8"></span>Xiong, S., Jing, J., Wu, J., Ma, W., Dawar, F.U., Mei, J., and Gui, J.F. (2015). Characterization and sexual dimorphic expression of Cytochrome P450 genes in the hypothalamic–pituitary–gonad axis of yellow catfish. [Gen Comp Endocrinol](https://doi.org/10.1016/j.ygcen.2015.04.015) 216, 90–97.
- <span id="page-11-10"></span>Yamamoto, Y., Zhang, Y., Sarida, M., Hattori, R.S., and Strüssmann, C.A. (2014). Coexistence of genotypic and temperature-dependent sex determination in pejerrey *Odontesthes bonariensis*. [PLoS ONE](https://doi.org/10.1371/journal.pone.0102574) 9, e102574.
- <span id="page-11-6"></span>Yang, Y.J., Wang, Y., Li, Z., Zhou, L., and Gui, J.F. (2017). Sequential, divergent, and cooperative requirements of *Foxl2a* and *Foxl2b* in ovary development and maintenance of zebrafish. [Genetics](https://doi.org/10.1534/genetics.116.199133) 205, 1551–1572.
- <span id="page-11-3"></span>Yano, A., Guyomard, R., Nicol, B., Jouanno, E., Quillet, E., Klopp, C., Cabau, C., Bouchez, O., Fostier, A., and Guiguen, Y. (2012). An immune-related gene evolved into the master sex-determining gene in rainbow trout, *Oncorhynchus mykiss*. [Curr Biol](https://doi.org/10.1016/j.cub.2012.05.045) 22, 1423–1428.
- <span id="page-11-1"></span>Yoshida, K., Terai, Y., Mizoiri, S., Aibara, M., Nishihara, H., Watanabe, M., Kuroiwa, A., Hirai, H., Hirai, Y., Matsuda, Y., et al. (2010). B chromosomes have a functional effect on female sex determination in Lake Victoria cichlid fishes. [PLoS Genet](https://doi.org/10.1371/journal.pgen.1002203) 7, e1002203.
- <span id="page-11-4"></span>Yoshimoto, S., Ikeda, N., Izutsu, Y., Shiba, T., Takamatsu, N., and Ito, M. (2010). Opposite roles of *DMRT1* and its W-linked paralogue, DM-W, in sexual dimorphism of *Xenopus laevis*: implications of a ZZ/ZW-type sex-determining system. [Development](https://doi.org/10.1242/dev.048751) 137, 2519–2526.
- <span id="page-11-5"></span>Yoshimoto, S., and Ito, M. (2011). A ZZ/ZW-type sex determination in *Xenopuslaevis*. [FEBS J](https://doi.org/10.1111/j.1742-4658.2011.08031.x) 278, 1020–1026.
- <span id="page-11-0"></span>Yoshimoto, S., Okada, E., Umemoto, H., Tamura, K., Uno, Y., Nishida-Umehara, C., Matsuda, Y., Takamatsu, N., Shiba, T., and Ito, M. (2008). A W-linked DM-domain gene, DM-W, participates in primary ovary development in *Xenopus laevis*. [Proc Natl Acad Sci USA](https://doi.org/10.1073/pnas.0712244105) 105, 2469– 2474.
- <span id="page-11-13"></span>Zhang, J., Sun, M., Zhou, L., Li, Z., Liu, Z., Li, X.Y., Liu, X.L., Liu, W., and Gui, J.F. (2015). Meiosis completion and various sperm responses lead to unisexual and sexual reproduction modes in one clone of polyploid *Carassius gibelio*. [Sci Rep](https://doi.org/10.1038/srep10898) 5, 10898.
- <span id="page-11-7"></span>Zhang, X., Li, M., Ma, H., Liu, X., Shi, H., Li, M., and Wang, D. (2017). Mutation of *foxl2* or *cyp19a1a* results in female to male sex reversal in XX Nile tilapia. [Endocrinology](https://doi.org/10.1210/en.2017-00127) 158, 2634–2647.
- <span id="page-11-11"></span>Zhou, L., and Gui, J. (2017). Natural and artificial polyploids in aquaculture. [Aquac Fish](https://doi.org/10.1016/j.aaf.2017.04.003) 2, 103–111.
- <span id="page-11-12"></span>Zhou, L., Wang, Z.W., Wang, Y., and Gui, J.F. (2018). Crucian carp and gibel carp culture. In: Aquaculture in China: Success Stories and Modern Trends, J.F. Gui, Q.S. Tang, Z.J. Li, J.S. Liu, S.S. De Silva, eds. (Oxford: John Wiley & Sons Ltd.), pp. 149–157.
- <span id="page-11-14"></span>Zhu, Y.J., Li, X.Y., Zhang, J., Li, Z., Ding, M., Zhang, X.J., Zhou, L., and Gui, J.F. (2018). Distinct sperm nucleus behaviors between genotypic and temperature-dependent sex determination males are associated with replication and expression-related pathways in a gynogenetic fish. [BMC](https://doi.org/10.1186/s12864-018-4823-6) [Genomics](https://doi.org/10.1186/s12864-018-4823-6) 19, 437.