ANNUAL REVIEWS

Annual Review of Animal Biosciences

Diversity and Convergence of Sex-Determination Mechanisms in Teleost Fish

Jun Kitano,[1] Satoshi Ansai,[2,3] Yusuke Takehana,[4] and Yoji Yamamoto[5]

[1]Ecological Genetics Laboratory, National Institute of Genetics, Mishima, Shizuoka, Japan; email: jkitano@nig.ac.jp

[2]Graduate School of Life Sciences, Tohoku University, Sendai, Miyagi, Japan

[3]Graduate School of Agriculture, Kyoto University, Kyoto, Japan; email: ansai.satoshi.7h@kyoto-u.ac.jp

[4]Faculty of Bio-Science, Nagahama Institute of Bio-Science and Technology, Nagahama, Shiga, Japan; email: y_takehana@nagahama-i-bio.ac.jp

[5]Department of Marine Biosciences, Tokyo University of Marine Science and Technology, Tokyo, Japan; email: yyamam0@kaiyodai.ac.jp

Annu. Rev. Anim. Biosci. 2024. 12:233–59

First published as a Review in Advance on October 20, 2023

The *Annual Review of Animal Biosciences* is online at animal.annualreviews.org

https://doi.org/10.1146/annurev-animal-021122-113935

Keywords

hotspot genes, convergent evolution, sex chromosome turnover, neo-sex chromosome, global warming, environmental sex determination, ESD

Abstract

Sexual reproduction is prevalent across diverse taxa. However, sex-determination mechanisms are so diverse that even closely related species often differ in sex-determination systems. Teleost fish is a taxonomic group with frequent turnovers of sex-determining mechanisms and thus provides us with great opportunities to investigate the molecular and evolutionary mechanisms underlying the turnover of sex-determining systems. Here, we compile recent studies on the diversity of sex-determination mechanisms in fish. We demonstrate that genes in the TGF-β signaling pathway are frequently used for master sex-determining (MSD) genes. MSD genes arise via two main mechanisms, duplication-and-transposition and allelic mutations, with a few exceptions. We also demonstrate that temperature influences sex determination in many fish species, even those with sex chromosomes, with higher temperatures inducing differentiation into males in most cases. Finally, we review theoretical models for the turnover of sex-determining mechanisms and discuss what questions remain elusive.

1. INTRODUCTION

Sexual reproduction is prevalent across diverse taxa, suggesting that sexual reproduction can confer fitness advantages to many organisms (1, 2). For example, in diploid organisms, segregation enables an advantageous mutation that appeared in only one chromosome to be brought together and produces a homozygous state in the descendant generations (3). This contrasts with a parthenogenetic population, where the population must wait for two independent advantageous mutations to arise in the same individual (3). Sexual reproduction also accompanies recombination, which removes deleterious mutations efficiently. Without recombination, deleterious mutations tend to accumulate continuously and reduce organismic fitness (4). Recombination also produces new combinations of alleles every generation, which is advantageous in the arms race against rapidly evolving pathogens (5, 6). In animals, sexual reproduction generally occurs between males that produce smaller sperm with high motility and females that produce larger eggs with deposited nutrients. Such anisogamy, i.e., different gametic sizes between sexes, is thought to result from disruptive selection (7–9).

Despite the prevalence of sexual reproduction between males and females in animals, sex-determination mechanisms are so diverse that even closely related species often differ in sex-determination systems (1, 2). What molecular mechanisms underlie the transitions of sex-determining mechanisms? What evolutionary and ecological factors drive such turnovers? Taxa with frequent turnovers of sex-determining mechanisms provide us with great opportunities to answer these questions. Teleostei is a taxonomic group containing species with a variety of sex-determining mechanisms (10–12). In addition, as we review below, sex-determining genes and sex chromosomes have been identified in many teleost fishes.

Here, we review current knowledge on sex-determination mechanisms and the turnover of sex chromosomes in teleost fish. We focus on genetic sex determination (GSD) and temperature-dependent sex determination (TSD). For other types of environment-dependent sex determination, such as social determination, please see other reviews (13–15). We also review theoretical models for the turnover of sex-determination mechanisms and discuss future studies needed to explore unsolved questions.

2. DIVERSITY AND CONVERGENCE OF MSD GENES

2.1. Comprehensive List of Teleost MSD Genes

Recent advances in genome sequencing technologies have identified master sex-determining (MSD) genes in an increasing number of teleost fishes (**Table 1**, **Figure 1**). To date, MSD genes have been identified in 114 species (**Table 1**, **Figure 1**). Genes related to transforming growth factor-β (TGF-β) signaling, which are known to induce gonadal masculinization, are widely used as MSD genes across teleost fishes. The *anti-Müllerian hormone* (*amh*) gene has been identified as an MSD gene of 33 species across 12 genera, including the Patagonian pejerrey (16), threespine stickleback (17), Nile tilapia (18), northern pike (19), and Japanese flounder (20). The gene encoding its receptor, *amh receptor 2* (*amhr2*), is also used in 30 species across 9 genera, such as the tiger pufferfish (21), Midas cichlids (22), and Pangasiidae catfishes (23). Other genes encoding TGF-β ligands, *gonadal soma-derived factor* (*gsdf*) and *growth differentiation factor 6* (*gdf6*), are also used in 6 species of 4 genera and 3 species of 2 genera, respectively. More recently, a TGF-β receptor gene, *bone morphogenetic protein receptor type 1b* (*bmpr1b*), and a downstream factor of TGF-β signaling, *inhibitor of DNA binding 2b* (*id2b*), have been identified as MSD genes. Interestingly, most fish species (73 of 75) using the TGF-β-related genes as the MSD genes have an XX/XY sex chromosome system; exceptions are the Pacific halibut, which uses *bmpr1ba* for the MSD gene in a

Table 1 Master sex-determining genes identified in teleost fishes

Order	Genus	Species	Gene	Function	Chr	Mutation	Reference
Anabantiformes	*Betta*	*splendens*	*dmrt1*	TF	Y	Allelic	27
Atheriniformes	*Odontesthes*	*hatcheri*	*amhy*	TGF-β	Y	D&T	16
		bonariensis	*amhy*	TGF-β	Y	D&T	54
		argentinensis	*amhy*	TGF-β	Y	D&T	149
		incisa	*amhy*	TGF-β	Y	D&T	
		mauleanum	*amhy*	TGF-β	Y	D&T	
		perugiae	*amhy*	TGF-β	Y	D&T	
		piquava	*amhy*	TGF-β	Y	D&T	
		regia	*amhy*	TGF-β	Y	D&T	
		smitti	*amhy*	TGF-β	Y	D&T	
		humensis	*amhy*	TGF-β	Y	D&T	
		mirinensis	*amhy*	TGF-β	Y	D&T	
		nigricans	*amhy*	TGF-β	Y	D&T	
	Hypoatherina	*tsurugae*	*amhy*	TGF-β	Y	D&T	150
Beloniformes	*Oryzias*	*latipes*	*dmy*	TF	Y	D&T	26
		sakaizumii	*dmy*	TF	Y	D&T	
		sinensis	*dmy*	TF	Y	D&T	112
		curvinotus	*dmy*	TF	Y	D&T	151
		luzonensis	*gsdf*^{Y}	TGF-β	Y	Allelic	92
		dancena	*sox3*^{Y}	TF	Y	Allelic	29
		eversi	*amh*	TGF-β	Y	Allelic	152
		marmoratus	*sox3*^{Y}	TF	Y	Allelic	30
		profundicola	*sox3*^{Y}	TF	Y	Allelic	
Carangiformes	*Seriola*	*quinqueradiata*	*hsd17b1*	Steroid	W	Allelic	32
		dumerili	*hsd17b1*	Steroid	W	Allelic	
		lalandi	*hsd17b1*	Steroid	W	Allelic	
		dorsalis	*hsd17b1*	Steroid	W	Allelic	153
		aureovittata	*hsd17b1*	Steroid	W	Allelic	154
	Pseudocaranx	*georgianus*	*cyp19a1a*-like	Steroid	Y	D&T	33
Characiformes	*Astyanax*	*mexicanus*	*gdf6b*	TGF-β	B	D&T	25
Cichliformes	*Oreochromis*	*aureus*	*paics*	Other	W	Tandem	42
		niloticus	*amhy*	TGF-β	Y	Tandem	18
	Amphilophus	*amarillo*	*amhr2Y*	TGF-β	Y	D&T	22
		astorquii	*amhr2Y*	TGF-β	Y	D&T	
		chancho	*amhr2Y*	TGF-β	Y	D&T	
		citrinellus	*amhr2Y*	TGF-β	Y	D&T	
		flaveolus	*amhr2Y*	TGF-β	Y	D&T	
		globosus	*amhr2Y*	TGF-β	Y	D&T	
		labiatus	*amhr2Y*	TGF-β	Y	D&T	
		sagittae	*amhr2Y*	TGF-β	Y	D&T	
		tolteca	*amhr2Y*	TGF-β	Y	D&T	
		viridis	*amhr2Y*	TGF-β	Y	D&T	
		xiloaensis	*amhr2Y*	TGF-β	Y	D&T	
		zaliosus	*amhr2Y*	TGF-β	Y	D&T	

(*Continued*)

Table 1 (*Continued*)

Order	Genus	Species	Gene	Function	Chr	Mutation	Reference
Clupeiformes	*Clupea*	*harengus*	*bmpr1bbY*	TGF-β	Y	D&T	155
Cyprinodontiformes	*Nothobranchius*	*furzeri*	*gdf6Y*	TGF-β	Y	Allelic	156
		kadleci	*gdf6Y*	TGF-β	Y	Allelic	157
Esociformes	*Esox*	*lucius*	*amhby*	TGF-β	Y	D&T	19
		aquitanicus	*amhby*	TGF-β	Y	D&T	158
		cisalpinus	*amhby*	TGF-β	Y	D&T	
		reichertii	*amhby*	TGF-β	Y	D&T	
		masquinongy	*amhby*	TGF-β	Y	D&T	
		americanus	*amhby*	TGF-β	Y	D&T	
		niger	*amhby*	TGF-β	Y	D&T	
	Novumbra	*hubbsi*	*amhby*	TGF-β	Y	D&T	
Gadiformes	*Gadus*	*morhua*	*zkY*	Other	Y	D&T	39
		macrocephalus ogac	*zkY*	Other	Y	D&T	
	Arctogadus	*glacialis*	*zkY*	Other	Y	D&T	
Osmeriformes	*Plecoglossus*	*altivelis*	*amhr2bY*	TGF-β	Y	D&T	159
Osteoglossiformes	*Arapaima*	*gigas*	*id2bbY*	TGF-β	Y	D&T	160
Perciformes	*Perca*	*flavescens*	*amhr2bY*	TGF-β	Y	D&T	161
	Gasterosteus	*aculeatus*	*amhy*	TGF-β	Y	D&T	17
		nipponicus	*amhy*	TGF-β	Y	D&T	162
		wheatlandi	*amhy*	TGF-β	Y	D&T	
	Culaea	*inconstans*	*amhy*	TGF-β	Y	D&T	163
	Ophiodon	*elongatus*	*amhy*	TGF-β	Y	D&T	164
	Anoplopoma	*fimbria*	*gsdfY*	TGF-β	Y	Allelic	165
	Sebastes	*schlegelii*	*amhy*	TGF-β	Y	D&T	166
		koreanus	*amhy*	TGF-β	Y	D&T	
		pachycephalus	*amhy*	TGF-β	Y	D&T	
	Cyclopterus	*lumpus*	*amhy*	TGF-β	Y	Tandem	167
Perciformes?	*Selenotoca*	*multifasciata*	*dmrt1Y*	TF	Y	Allelic	168
Pleuronectiformes	*Cynoglossus*	*semilaevis*	*dmrt1*	TF	W	Allelic	28
	Hippoglossus	*stenolepis*	*bmpr1ba*	TGF-β	W	Allelic	24
	Scophthalmus	*maximus*	*sox2*	TF	W	Allelic	31
	Solea	*senegalensis*	*fshr*	Other	Y	Allelic	41
	Hippoglossus	*hippoglossus*	*gsdf*	TGF-β	Y	Allelic	169
	Paralichthys	*olivaceus*	*amhy*	TGF-β	Y	Allelic	20
Salmoniformes	*Oncorhynchus*	*mykiss*	*sdY*	Other	Y	D&T	36
		masou	*sdY*	Other	Y	D&T	37
		tshawytscha	*sdY*	Other	Y	D&T	
	Stenodus	*leucichthys*	*sdY*	Other	Y	D&T	
	Thymallus	*thymallus*	*sdY*	Other	Y	D&T	
	Salvelinus	*malma malma*	*sdY*	Other	Y	D&T	
		alpinus	*sdY*	Other	Y	D&T	
		fontinalis	*sdY*	Other	Y	D&T	
		namaycush	*sdY*	Other	Y	D&T	
	Salmo	*trutta*	*sdY*	Other	Y	D&T	
		salar	*sdY*	Other	Y	D&T	

(*Continued*)

Table 1 (*Continued*)

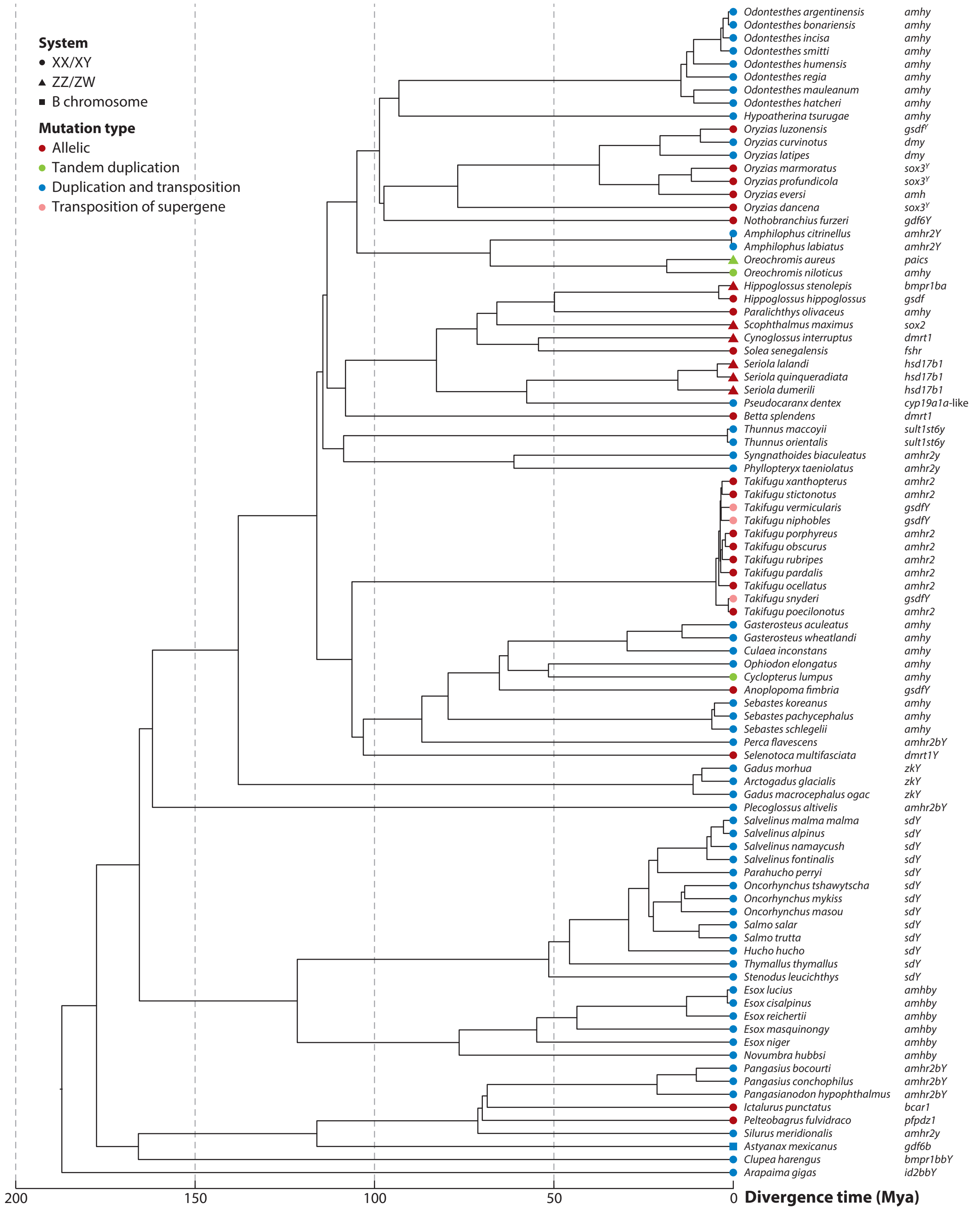
Order	Genus	Species	Gene	Function	Chr	Mutation	Reference
	Hucho	*hucho*	*sdY*	Other	Y	D&T	
	Parahucho	*perryi*	*sdY*	Other	Y	D&T	
Scombriformes	*Thunnus*	*orientalis*	*sult1st6y*	Steroid	Y	D&T	34
		maccoyii	*sult1st6y*	Steroid	Y	D&T	
Siluriformes	*Silurus*	*meridionalis*	*amhr2y*	TGF-β	Y	D&T	170
	Ictalurus	*punctatus*	*bcar1*	Steroid	Y	Allelic	35
	Pangasianodon	*hypophthalmus*	*amhr2by*	TGF-β	Y	D&T	23
	Pangasius	*bocourti*	*amhr2by*	TGF-β	Y	D&T	
		conchophilus	*amhr2by*	TGF-β	Y	D&T	
		djambal	*amhr2by*	TGF-β	Y	D&T	
	Pelteobagrus	*fulvidraco*	*pfpdz1*	Other	Y	Allelic	40
Syngnathiformes	*Phyllopteryx*	*taeniolatus*	*amhr2y*	TGF-β	Y	D&T	171
	Syngnathoides	*biaculeatus*	*amhr2y*	TGF-β	Y	D&T	
Tetraodontiformes	*Takifugu*	*rubripes*	*amhr2*	TGF-β	Y	Allelic	21
		obscurus	*amhr2*	TGF-β	Y	Allelic	93
		ocellatus	*amhr2*	TGF-β	Y	Allelic	
		xanthopterus	*amhr2*	TGF-β	Y	Allelic	
		stictonotus	*amhr2*	TGF-β	Y	Allelic	
		porphyreus	*amhr2*	TGF-β	Y	Allelic	
		poecilonotus	*amhr2*	TGF-β	Y	Allelic	172
		chrysops	*amhr2*	TGF-β	Y	Allelic	93
		pardalis	*amhr2*	TGF-β	Y	Allelic	172
		niphobles	*gsdfY*	TGF-β	Y	Super	93
		snyderi	*gsdfY*	TGF-β	Y	Super	
		vermicularis	*gsdfY*	TGF-β	Y	Super	

Abbreviations: allelic, allelic mutation; Chr, chromosome; D&T, duplication and transposition; steroid, steroidogenesis; super, supergene; tandem, tandem duplication; TF, transcription factor; TGF-β, TGF-β signaling.

ZZ/ZW system (24), and the Pachón cavefish, which uses *gdf6b* for a B chromosome–mediated sex-determination system (25).

Similar to in mammalian species, transcription factor genes have been identified as MSD genes in several teleost fishes. The *doublesex and mab-3 related transcription factor 1* (*dmrt1*) gene, which has a DNA-binding domain conserved among the genes controlling sexual dimorphism in insects (*doublesex*) and nematodes (*mab-3*), is used in 7 species of 4 genera of teleosts, including the Japanese medaka (26) and Siamese fighting fish (27). The *dmrt1* gene contributes to the XX/XY system in most species (6 of 7) but also contributes to the ZZ/ZW system in the Chinese tongue sole (28). Furthermore, two *sex-determining region Y* (*SRY*)-related HMG box (Sox) genes, *sox3* and *sox2*, are used in the XX/XY system of *Oryzias* fishes (29, 30) and the ZZ/ZW system of turbot (31), which share a DNA-binding domain with a mammalian MSD gene, *SRY*.

Recent studies also demonstrated that genes encoding enzymes for steroidogenesis can become MSD genes in teleost fishes. The MSD gene in the W chromosome of four *Seriola* fishes is *17β-hydroxysteroid dehydrogenase 1 (hsd17b1)* (32). This gene encodes hydroxysteroid 17-β dehydrogenase 1, which is responsible for the interconversion of estrone/estradiol or androstenedione/testosterone (32). A duplicated copy of the *cytochrome P450 family 19 subfamily A member 1a* (*cyp19a1a*) gene, encoding an aromatase transforming testosterone to estradiol, is used in the XX/XY system of the New Zealand silver trevally (33). Furthermore, several novel genes



(Caption appears on following page)

Figure 1 (*Figure appears on preceding page*)

Master sex-determining (MSD) genes mapped to a time-calibrated phylogenetic tree of teleost fishes. The MSD genes and their chromosomal systems and mutation types compiled in **Table 1** were mapped on a timetree of The Fish Tree of Life (**https://fishtreeoflife.org/downloads/**) (193). Of 114 species, 90 could be mapped to the timetree. The x-axis indicates the time scale in millions of years ago (Mya).

potentially involved in steroidogenesis have been identified as MSD genes. For example, the MSD gene of tunas is *sulfotransferase family 1, cytosolic sulfotransferase 6* (*sult1st6*), which encodes an enzyme potentially involved in the inactivation of estrogen by sulfation (34). *Breast cancer antiresistance 1* (*bcar1*), the MSD gene on the Y chromosome of the channel catfish, is also suggested to inhibit estrogen signal transduction (35).

Other types of genes have also been identified as MSD genes. *Sexually dimorphic on the Y chromosome* (*sdY*) is used as the MSD gene on the Y chromosome of rainbow trout (36) and other salmonid fishes (37). This gene is homologous with the C-terminal domain of interferon regulatory factor 9 (36) and may prevent the activation of the feminizing pathway by interacting with the *foxl2* gene (38). *Zinc knuckle on the Y chromosome* (*zkY*) is the Y chromosome–specific copy encoding the zinc knuckle protein in cod fishes (39). A novel PDZ domain–containing gene (*pfpdz1*) and *follicle-stimulating hormone receptor* (*fshr*) have been identified as the MSD genes of the yellow catfish (40) and Senegal sole (41), respectively. Furthermore, a tandemly duplicated copy of *phosphoribosylaminoimidazole carboxylase* (*paics*) becomes the MSD gene on the W chromosome of the blue tilapia (42). However, how these novel MSD genes regulate sex-determination processes remains largely elusive.

2.2. How MSD Genes Determine the Sex

In several fishes, detailed molecular mechanisms by which MSD genes activate sex differentiation pathways have been elucidated (**Figure 2**). In the Japanese medaka fish (*Oryzias latipes*), *dmy*, the Y-specific paralog of autosomal *dmrt1*, is isolated as the MSD gene (26). The expression of *dmy* in gonadal somatic cells triggers the male pathway and represses the female pathway (26). DMY upregulates *gsdf* and *dmrt1* expression in Sertoli cell precursors (43–47), which may activate other genes involved in testis differentiation. Loss of *amhr2* function leads to male-to-female sex reversal (48), suggesting its involvement in the male pathway. Differentiating Sertoli cells assemble into seminiferous tubule structures with germ cells and androgen-producing Leydig cells, followed by spermatogenesis. *cyp11b* and *11β-hydroxysteroid dehydrogenase* (*hsd11b*) encode two enzymes downstream in the male pathway, and their expression in Leydig cells promotes the conversion of testosterone to the active androgen, 11-ketotestosterone (11-KT), which induces the male phenotypes but is not involved in spermatogenesis (49–51).

Absent *dmy*, *forkhead box L2* (*foxl2*) is expressed in gonadal somatic cells, and it is considered to upregulate other downstream genes involved in granulosa and theca cell differentiation (52). In addition, *foxl3* is necessary for female fate decision in germ cells through repressing the initiation of spermatogenesis (51). Such a female pathway leads to oocyte production and ovarian follicle formation. Next, the expression of *cyp19a1a*, encoding aromatase in theca cells, converts testosterone to 17β-estradiol, which induces the female phenotype and maintains the ovarian structure but is not involved in early oogenesis (50, 53).

Similar sex-differentiation pathways are also observed in the pejerrey (*Odontesthes bonariensis*), which has another MSD gene, *amhy*, the Y-specific paralog of autosomal *amh* (*amha*) (54). Expression of *amhy* and *amha* can initiate the male pathway (54). However, their downstream components look similar between the medaka and the pejerrey. For example, *dmrt1*, *cyp11b*, and *hsd11b* are expressed in a male-specific manner, whereas *foxl2* and *cyp19a1* are expressed in a

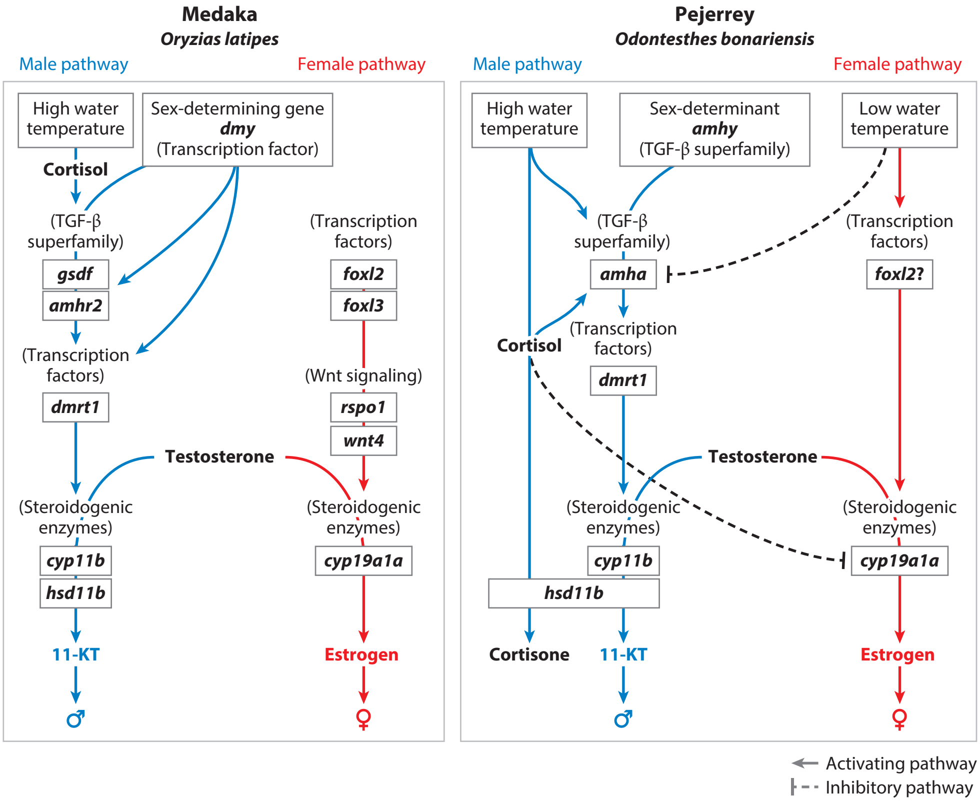


Figure 2

Sex-determining genes mapped to the sex-determining pathways in the Japanese medaka (*Oryzias latipes*) and the pejerrey (*Odontesthes bonariensis*). Blue lines indicate the male pathway, red lines indicate the female pathway, and dotted lines indicate the inhibitory pathways.

female-specific manner (55, 56), suggesting their conserved roles in sex differentiation among different fish species. Compared to XY systems, how MSD genes in ZW systems are involved in female determination remains unknown.

3. DIVERSITY AND CONVERGENCE IN TSD AND TEMPERATURE EFFECTS

3.1. Comprehensive List of Teleost TSD

Environmental temperature during early development can influence sexual differentiation and determine sex in several species, a process called temperature-dependent sex determination (TSD) (57, 58). Depending on the relationship between temperature and frequency of the production of one or another sex, TSD can be classified into several types (57). Here, we follow a previous classification used for reptiles, with a few modifications (**Figure 3**). In Type Ia, exposure to high temperatures during development induces differentiation into females. Type Ib is the converse case, where high temperatures induce differentiation into males. Type II refers to the case where extreme temperatures (high or low) induce differentiation into a particular sex. In several reptilian species, extreme temperatures induce differentiation into females (57), which we call Type IIa.

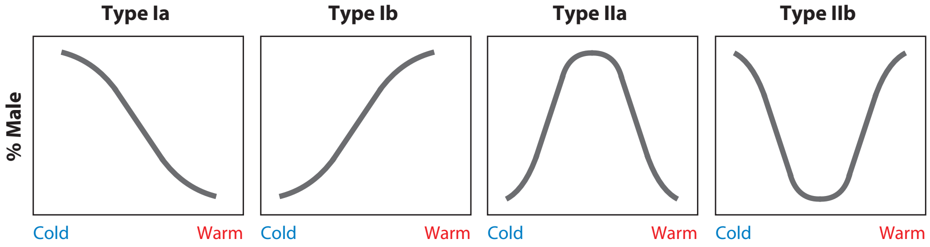


Figure 3

Schematic illustrations of distinct types of temperature-dependent sex determination. The x-axis indicates the temperature experienced during the early embryo stage; the y-axis indicates the percentage of individuals differentiated into phenotypic males (% Male). Here, we assume that the relationship between environmental temperature and % Male is composed of sigmoidal curves, but the shape of the function would depend on the species.

In contrast, when extreme temperatures induce differentiation into males, we call it Type IIb. It should be noted that Type Ia and Type Ib may be one side of Type IIa and Type IIb, but fish cannot survive at one side of the extreme temperatures.

Although TSD and GSD were once thought to be mutually exclusive, they are now considered to be opposite ends of a continuum, with many species having a mixture of TSD and GSD (59–61) (**Figure 4**). Therefore, we cannot draw a clear line between GSD and TSD. In this review, we include cases with any thermal effects on sex determination in the category of TSD, following a previous study (62).

In fish, TSD was first reported in the Atlantic silverside (63). Since then, temperature effects on sex determination have been observed in many fish species across diverse taxa (62). Here, we have compiled the data reported to date on how temperature affects sex determination in fish (**Table 2**). We have found that TSD has been reported in 77 species (**Table 2**). The existence of sex chromosomes has not been confirmed in 43 species, whereas 34 species show evidence for the presence of sex chromosomes (XX/XY in 28 species, ZZ/ZW in 6 species). Even MSD genes have been identified in 19 species. Thus, GSD and TSD coexist in many teleost species.

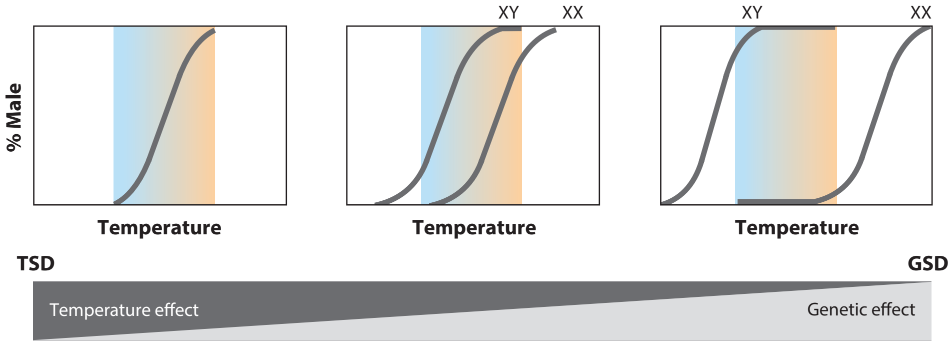


Figure 4

Spectrum between temperature-dependent sex determination (TSD; Type Ib in this figure) and genetic sex determination (GSD; XX/XY system in this figure). TSD and GSD represent opposite ends of the continuum. Here, we assume that the relationship between the temperature and the percentage of individuals differentiated into phenotypic males (% Male) is a sigmoidal curve, but the shape of the function depends on the species. The temperature range that organisms experience is shown in color gradients.

Table 2 Compilation of the data on the temperature effects on sex determination in fish

Order	Genus	Species	SC type	MSD gene	TE type	Reference
Anabantiformes	*Trichogaster*	*lalius*	XX/XY	ND	Ia	173
Atheriniformes	*Chirostoma*	*estor*	ND	ND	Ib	174
	Hypoatherina	*tsurugae*	XX/XY	*amhy*	Ib	65
	Leuresthes	*tenuis*	ND	ND	Ib	175
	Menidia	*menidia*	ND	ND	Ib	62
		peninsulae	ND	ND	Ib	
	Odontesthes	*argentinensis*	XX/XY	*amhy*	Ib	
		bonariensis	XX/XY	*amhy*	Ib	
		hatcheri	XX/XY	*amhy*	Ib	
Beloniformes	*Oryzias*	*latipes*	XX/XY	*dmy*	Ib	
		sakaizumii	XX/XY	*dmy*	Ib	67
Centrarchiformes	*Lepomis*	*macrochirus*	ZZ/ZW	ND	Ia/Ib	176
Cichliformes	*Apistogramma*	spp. (33 spp.)	ND	ND	Ib	62
	Oreochromis	*aureus*	ZZ/ZW	*paics*	Ib	
		niloticus	XX/XY	*amhy*	Ia/Ib	
		mossambicus	XX/XY	ND	Ib	
Cypriniformes	*Carassius*	*auratus*	XX/XY	ND	Ib	
		gibelio	Microchromosomes	ND	Ib	177
		carassius grandoculis	XX/XY	ND	Ib	178
	Cyprinus	*carpio*	XX/XY	ND	Ib	179
	Danio	*rerio*	(ZZ/ZW in wild)	ND	Ia/Ib	62, 180
	Gnathopogon	*caerulescens*	XX/XY	ND	Ib	181
	Misgurnus	*anguillicaudatus*	XX/XY	ND	Ib	62
Cyprinodontiformes	*Limia*	*melanogaster*	ND	ND	Ib	
	Poecilia	*sphenops*	ZZ/ZW	ND	Ib	
	Poeciliopsis	*lucida*	ND	ND	Ib	
Gadiformes	*Gadus*	*chalcogrammus*	ND	ND	Ib	182
Perciformes	*Anoplopoma*	*fimbria*	XX/XY	*gsdfY*	Ib	183
	Dicentrarchus	*labrax*	ND	ND	Ia/Ib	62
Pleuronectiformes	*Cynoglossus*	*semilaevis*	ZZ/ZW	*dmrt1*	Ib	28
	Paralichthys	*olivaceus*	XX/XY	*amhy*	IIb	62
		lethostigma	XX/XY	ND	IIb/Ib	62, 184
		dentatus	XX/XY	ND	Ib	185
	Pseudopleuronectes (Limanda)	*yokohamae*	XX/XY	ND	Ib	62
	Scophthalmus	*maximus*	ZZ/ZW	*sox2*	Ia/Ib	186
	Solea	*senegalensis*	XX/XY	*fshr*	Ib[a]	187
	Verasper	*moseri*	XX/XY	ND	Ib	62
Salmoniformes	*Oncorhynchus*	*nerka*	XX/XY	*sdy*	Ia/Ib	
		mykiss	XX/XY	*sdy*	Ia/Ib	188
Scorpaeniformes	*Sebastes*	*schlegelii*	XX/XY	*amhy*	Ia/Ib	62, 189
Siluriformes	*Clarias*	*gariepinus*	XX/XY (ZZ/ZW)	ND	Ib	190
	Hoplosternum	*littorale*	ND	ND	Ib	62
	Ictalurus	*punctatus*	XX/XY	*bcar1*	Ia	
	Tachysurus	*fulvidraco*	XX/XY	*pfpdz1*	Ib	191
Tetraodontiformes	*Takifugu*	*rubripes*	XX/XY	*amhr2*	Ia	192

[a] Based on an unpublished observation.

Abbreviations: MSD, master sex-determining; ND, not determined; SC, sex chromosome; TE, temperature effect.

Among fish showing TSD, Type Ib is the most common (64 out of 77 species) (**Table 2**). In contrast, few species showed Type Ia (3 species: dwarf gourami, channel catfish, and tiger pufferfish) or Type IIb (1 species: olive flounder). Type IIa has never been found in fish. In addition, some species exhibit different types of TSD even within the same species. Such phenomena are commonly observed in popular aquaculture species, such as the Nile tilapia (Type Ia or Ib), the European sea bass (Type Ia or Ib), and the southern flounder (Type Ib or IIb). Therefore, the mixture of different types may result from intentional or unintentional multigenerational selective breeding or phenotypic plasticity induced by a specific aquaculture environment. Whether variations in TSD types within species are common in natural populations remains elusive. Because most cases listed in **Table 2** were identified based on laboratory experiments, how TSD acts in natural populations is not well understood, except for a few cases (64, 65).

Type Ib TSD postulates that exposure to high temperatures induces sex reversal from genotypic females (e.g., XX or ZW) to phenotypic males, and exposure to low temperatures induces sex reversal from genotypic males (e.g., XY or ZZ) to phenotypic females. Although the former has been observed in most fish species classified as Type Ib, the latter is rare and found in only a few species, such as fish belonging to the order Atheriniformes (66). Furthermore, Type Ib is more likely to coexist with an XX/XY system (19 of 22 species with sex chromosomes and/or MSD genes) than with a ZZ/ZW system. Taken together, there are many cases of XX individuals becoming males through exposure to high temperatures, whereas the other types of sex changes are rare. We discuss the possible reasons for this in Section 7.

3.2. How Does Temperature Modulate Sex Determination?

As described in the previous section, both the medaka and pejerrey show GSD, yet temperature can significantly affect their sex determination and differentiation. In the medaka, a high water temperature (32°C) during gonadal development produces XX males via an elevation of the glucocorticoid stress hormone cortisol (67, 68). This temperature-/cortisol-induced masculinization is correlated with *gsdf* expression (69) and is not observed in *gsdf*- or *amhr2*-deficient mutants (70), suggesting that high temperatures can drive the male pathway through activating *gsdf/amhr2* signaling.

Similarly to in the medaka, high temperatures (25°C or higher) produce XX males by increasing cortisol in the pejerrey (56). However, different genes are involved in this process between these two species (56). In the pejerrey, high temperatures induce elevated cortisol and 11-KT levels, concomitant with upregulation and downregulation of genes associated with testicular (e.g., *amha* and *dmrt1*) and ovarian (e.g., *cyp19a1a*) differentiation, respectively. A pivotal player in the crosstalk between the stress and reproductive axes is the steroidogenic enzyme HSD11B (71, 72). This enzyme converts 11-β-hydroxytestosterone to 11-KT as a by-product of its primary function of inactivating cortisol to cortisone. Thus, in the pejerrey, the androgen production induced by the cortisol-mediated stress response is thought to be the central mechanism of high-temperature-induced masculinization.

The pejerrey is one of the few species in which exposure to low temperatures (25°C or lower) induces XY females. Interestingly, *amhy* expression is significantly downregulated during the critical period of sex determination, independent of environmental temperature (56). At high water temperatures, *amha* is upregulated as *amhy* begins to be downregulated, whereas *amha* expression is maintained as low at low water temperatures. This unique spontaneous downregulation of *amhy* during the critical period of sex determination may be key to the sex reversal of XY males to phenotypic females by low temperatures. In contrast, expression of *cyp19a1a* is maintained at a relatively high level during the critical period of sex determination in the pejerrey, regardless of sex genotype or temperature (56). These observations suggest that ontogenetically programmed ovarian development is a default state that is self-sustained without any timely and potent masculinization signals (AMH and/or high water temperatures) (66).

In other teleost species, epigenetic regulation is another potential key mechanism underlying TSD (73). In European sea bass, high-temperature-induced masculinization was associated with hypermethylation of the *cyp19a1a* promoter and downregulation of its expression (74). In the half-smooth tongue sole, *dmrt1* hypermethylation and downregulation occur in ZW females without high-temperature stimuli (28). But this hypermethylation pattern can be eliminated via incubation at high temperatures during the sex-determination period, leading to the masculinization of ZW females (28). Notably, this epigenetic modification in the half-smooth tongue sole can be transmitted from parents to offspring: Sex reversal occurs at higher rates without high-temperature stimuli in the offspring of sex-reversed individuals (28, 75). These examples demonstrate that even in fish species with GSD, temperatures can alter sexual fate through the stress hormone–mediated pathway and/or epigenetic regulation.

4. HOTSPOT GENES IN THE CONVERGENT EVOLUTION OF GSD

Molecular mechanisms of the evolution of sex-determining genes can provide great insights into several fundamental questions in convergent evolution, namely, the repeated evolution of the same phenotype/system in phylogenetically independent lineages. One long-standing question in convergent evolution is whether the same genes cause repeated phenotypic changes (76–79). If this is the case, another fundamental question would be why particular hotspot genes are used repeatedly for convergent evolution (76, 80, 81).

A potential explanation for the repeated use of the same gene is limited options (82). If limited numbers of genes can change sex, the same genes would repeatedly become MSD genes (83). However, the most up-to-date compilation shows several options for MSD genes (**Figure 1** and **Table 1**). Another hypothesis is that genes located at a hub between upstream regulators and downstream effectors are likely to become hotspot genes, such as the case of *shavenbaby* in the evolution of cuticle in *Drosophila* and *MYB* in the evolution of plant pigmentation (80, 81). This hypothesis relies on the idea that mutations at genes in the upstream pathways will change so many traits that the effects are deleterious, but that mutations at genes in the downstream pathways would change only a few traits and have minor phenotypic effects. Therefore, genes located at a hub may have optimal pleiotropy.

As **Figure 1** and **Table 1** show, genes in the TGF-β signaling pathway, particularly *amh*, are used frequently for sex determination in fish (see also 84). Many MSD genes are duplicated copies of genes in the TGF-β signaling pathway, with the ancestral copy retaining the original function. Therefore, the MSD genes can regulate the TGF-β signaling pathway while maintaining the core male and female pathways (85). The TGF-β pathway may be located at a hub between input signals triggering sex determination and hormonal outputs. Changes in the upstream pathway, such as temperature-sensing systems, would alter many physiological functions and be detrimental to organisms. In contrast, changes in the downstream pathway, such as steroid-dependent expression of sexual dimorphism in peripheral tissues, would not change the gonadal sex itself. Therefore, the TGF-β signaling pathway may be an optimal place for changing the gonadal sex differentiation.

Although at first glance the core male and female pathways seem to be conserved between the medaka and pejerrey, a closer look shows that they differ at several points (**Figure 2**). Further comparative studies on the molecular pathways of sex determination in many fish species will improve our understanding of the evolution of gene regulatory networks and their association with convergent evolution.

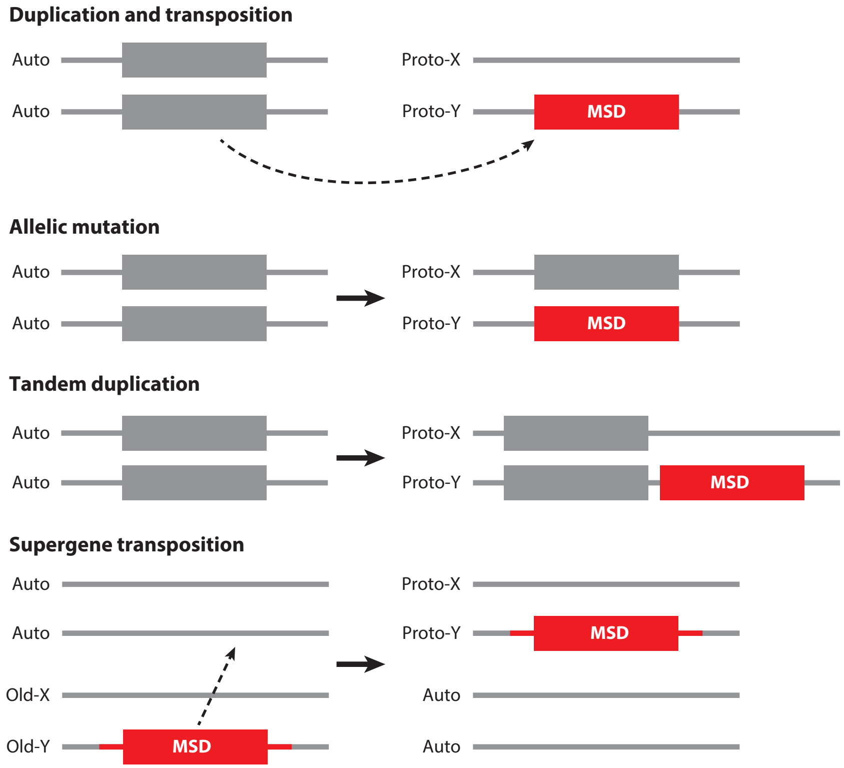


Figure 5

The origin of master sex-determining (MSD) loci. Several mechanisms by which a new male-determining locus appears. The examples here depict the XY system. Gray boxes indicate ancestral genes; red boxes indicate male-determining genes.

5. THE EVOLUTION OF GENES WITH NEW FUNCTIONS

Molecular studies of the evolution of MSD genes will also elucidate how genes with new functions originate. The evolution of new genes is a rich source of genetic variation that can fuel adaptation and speciation (86). Although new genes are proposed to arise by tinkering with old genes (86, 87), there are yet few empirical examples of functionally important young new genes. Therefore, studies on fish sex-determination genes provide a great opportunity to explore the evolution of new genes.

The compilation of sex-determining genes in fish shows four mechanisms by which a new sex-determining locus evolves (**Figure 5**). First, an MSD gene can arise via duplication and transposition. An autosomal gene encoding a protein in the pathway of sexual differentiation is duplicated and transposed to a different chromosome, where it acquires a dominant sex-determining effect. In the Japanese medaka, the MSD gene, *dmy*, is a duplicate copy of an autosomal *dmrt1* gene (26, 88). *dmy* is expressed earlier during embryogenesis in somatic cells of XY gonad than the ancestral *dmrt1*, indicating that *cis*-regulatory mutations occurred on *dmy* (26, 88). This *cis*-regulatory change may be caused by a transposon insertion (89). A recent study further showed that an amino acid change in DMY enhances its functional activity as a transcription factor (90). These results indicate that multiple mutations, both *cis*-regulatory and amino acid mutations, contribute to the acquisition of the male-determining function. *sdY* in salmonids is another example of MSD originating from the duplication-and-transposition mechanism (36, 37). Although the ancestral gene is involved in immunity and has nothing to do with sex determination, the duplicated copy comes to interact with the *foxl2* gene to function as an MSD (38, 91).

Second, allelic mutations can also create a new MSD gene. One allele becomes dominant over another located at the same locus and becomes an MSD gene. In the tiger pufferfish, a single SNP in *amhr2*, which changes an amino acid in the kinase domain, is responsible for the evolution of MSD (21). Similarly, in *Seriola* fishes, a nonsynonymous SNP in *hsd17b1* is likely accountable for the MSD function (32). *Cis*-regulatory mutations without amino acid changes can also lead to the evolution of MSD genes, such as *sox3* in *Oryzias dancena* (29) and *gsdf* in *Oryzias luzonensis* (92).

Third are cases in which tandem duplication occurred and one allele acquired a dominant sex-determining effect. Such cases are rare but found in the Nile tilapia, where one duplicated copy of *amh*, *amhy*, carries a missense SNP and acquires the male-determining function (18).

Finally, recycling of a supergene containing a sex-determining gene and a few other genes has been found in congeneric species of *Takifugu* (93). This supergene contains *gsdf*, which is likely to be an MSD gene. The functions of other genes in the supergene remain elusive. This supergene is flanked by transposons and can be transposed from one chromosome to another, creating a new sex-determining locus. This type of supergene is thus far reported only in Tetraodontiformes (93), and its prevalence is unknown.

Although more case studies are necessary to make solid conclusions, our compilation indicates that duplication-and-transposition and allelic mutations seem to be two prevalent modes of the evolution of new sex-determining genes in fish (**Figure 1**, **Table 1**). Further detailed molecular studies will reveal how many and what types of mutations are necessary for an ancestral gene to get a new function.

6. EVOLUTIONARY FORCES OF SEX CHROMOSOME TURNOVER

We have thus far reviewed the proximate mechanisms by which new mutations with sex-determining effects originate. How are such new mutations fixed in populations, and how might they take over the MSD functions? Here, we review the ultimate causes of the turnover of sex-determination genes and sex chromosomes.

We first consider a case in which sex chromosome turnover starts with a new sex-determining gene appearing in a population with a preexisting MSD gene (94). Another possible route for sex chromosome turnover would include the transition from GSD controlled by one locus to environmental sex determination (ESD), followed by the transition from ESD to GSD controlled by another locus. In this case, the population does not pass a polymorphic state. Evolutionary forces that can drive the transitions between GSD and ESD are discussed in the next section.

Following the polymorphic state with two sex chromosomes, the turnover is completed by the loss of the old MSD gene and the fixation of the new sex-determining gene. When a new sex-determining gene first appears in a population, the initial allele frequency of the new sex-determining gene is generally lower than that of the old MSD gene. Therefore, the new sex-determining gene has a lower probability of fixation than that of the old MSD gene and is likely to be lost by genetic drift unless the population size is very small.

What can drive the fixation of the new sex-determining gene? If the new sex-determining gene has any fitness advantage over the old MSD gene, the new sex-determining gene will spread and can be fixed (94, 95). Theoretical studies have proposed several possible scenarios (**Figure 6**). First, the presence of a sexually antagonistic allele near a new sex-determining gene can induce a sex chromosome turnover (96, 97). For example, if a new male-determining gene is linked to a male-beneficial allele, males that carry the new sex-determining gene will have higher fitness over males that carry the old MSD gene. Second, a new sex-determining gene linked to an allele with

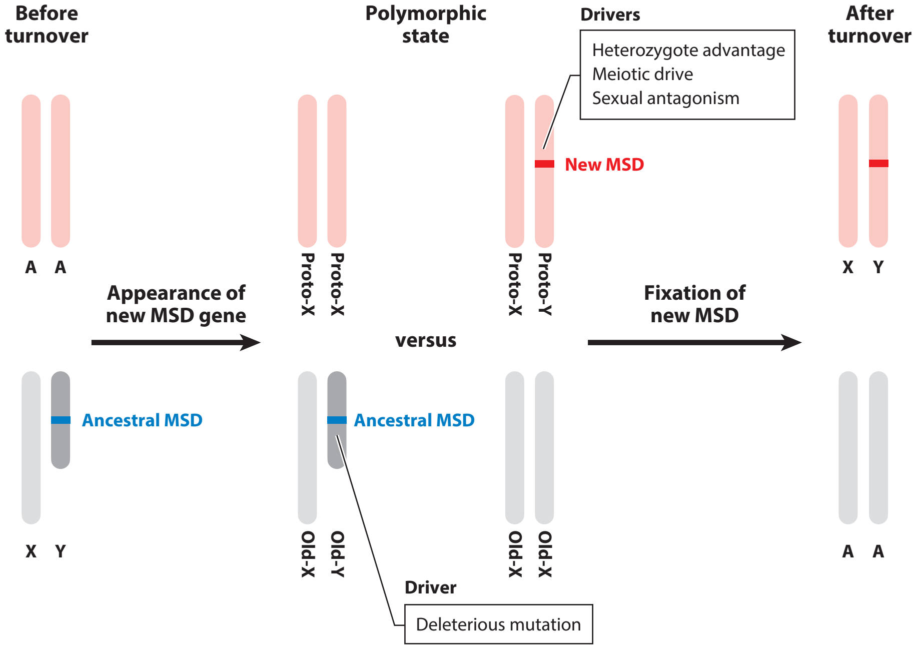


Figure 6

Model of sex chromosome turnover. Here, we show the case of the nonhomologous transition between XY systems: A nonhomologous turnover means that a new master sex-determining (MSD) gene appears on a chromosome different from that with the old MSD gene. Sex chromosome turnover starts with the appearance of a new MSD gene (*red*). Once the new MSD gene is fixed after the transition state with polymorphism of the ancestral and the new MSD genes, the sex chromosome turnover is complete. The presence of alleles with sexually antagonistic effects (male-beneficial and female-detrimental), heterozygote advantage, and meiotic drive near the new MSD gene can drive the fixation of the new MSD gene. Deleterious mutations near the ancestral MSD gene can drive the loss of the ancestral MSD gene, namely, the fixation of the new MSD gene.

heterozygote advantage will also increase its frequency because the sex-determining locus can be heterozygous in the heterogametic sex (98). Third, when a new sex-determining gene is linked to a meiotic driver, it will also increase its frequency because of the advantage of transmission to the next generation (99, 100). Because meiotic drive of sex chromosomes can skew the sex ratio, suppressors of drivers will soon evolve within populations to restore the sex ratio to 1:1 (101). However, the meiotic drive will increase the allele frequency at the initial stage, preventing a loss caused by genetic drift. Fourth, the presence of deleterious mutations near the old MSD gene would reduce the fitness of individuals carrying the old MSD and increase the relative fitness of individuals carrying the new sex-determining gene, leading to the sex chromosome turnover (102, 103). Accumulation of deleterious mutations on nonrecombining regions of sex chromosomes is observed widely in diverse taxa (104), although sex chromosomes show no apparent degeneration in several fishes (2). These mechanisms do not necessarily work alone. The combination of multiple mechanisms can induce repeated turnover cycles (105). For example, a combination of sexually antagonistic selection for a new sex chromosome and deleterious mutations on an old sex chromosome can induce endless cycles of sex chromosome turnovers (105).

In the case of the transition between an XY and a ZW system, selection for a 1:1 sex ratio can promote the fixation of a dominant sex chromosome even absent fitness difference between the old and new sex-determining loci (106, 107): If W is dominant over Y, W is likely to be fixed, and vice versa. Drift-induced stochastic fluctuation of the sex ratio produces selection for a 1:1 sex ratio, leading to increased frequency of a dominant sex chromosome (106). This evolutionary force is called drift-induced selection (106).

All of these studies were either theoretical or simulation based. Hence, we lack empirical studies testing these hypotheses. The prevalence of the polymorphic state, where two or more sex-determining genes segregate within a population, also remains elusive, as there are just a few examples in fish, such as the platyfish (108), Lake Malawi cichlids (109), and blue tilapia (110). A recent study with the Japanese medaka showed that artificial removal of an MSD gene from a wild-derived strain revealed a cryptic autosomal locus, a potential modifier of sex determination (111). This result suggests that sex-determining alleles with minor effects may be segregating in natural populations. Therefore, polygenic sex determination may be more common than thought previously. Furthermore, XY females with mutations in the MSD gene occasionally are found in natural populations of the Japanese medaka (26, 112). If a new sex-determining gene originates in such a population, the new sex-determining gene will take over the MSD function. Similarly, the zebrafish (*Danio rerio*), which has a ZW sex chromosome system in nature (113, 114), likely lost an MSD gene during domestication and shows polygenic sex determination in laboratory strains (115). Further empirical studies on natural fish populations will elucidate the evolutionary processes and mechanisms of sex chromosome turnover.

A sex chromosome turnover can also occur via sex chromosome–autosome fusion without the evolution of new MSD genes (116–118) (**Figure 7**). When an autosome is fused to a preexisting sex chromosome, the previously autosomal region becomes sex linked. This newly sex-linked chromosome is called a neo-sex chromosome. The fused neo-sex chromosome can replace the unfused ancestral sex chromosome via similar evolutionary forces, such as through the linkage of the neo-sex chromosome to alleles with sexually antagonistic effects (119–121), heterozygote advantage (98), and meiotic drive (122, 123). Previous meta-analyses showed that a Y-autosome fusion is

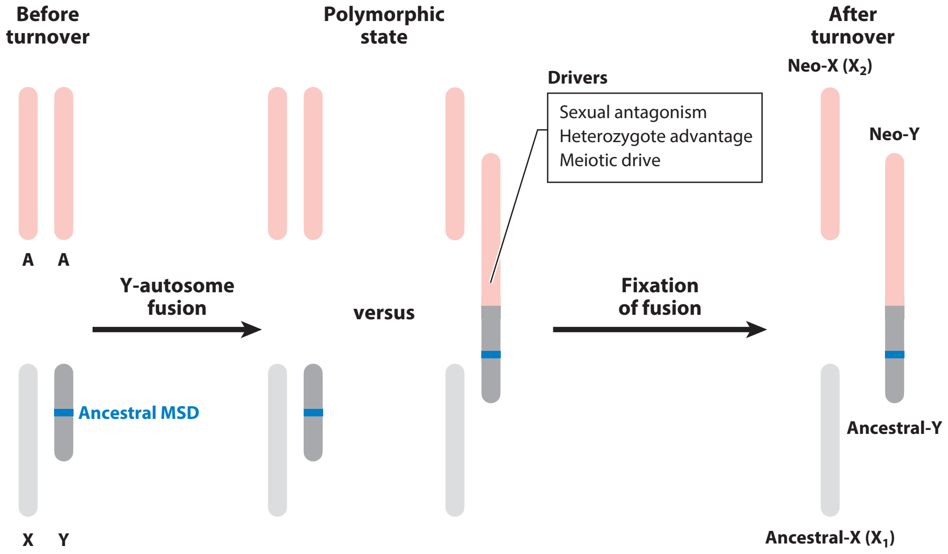


Figure 7

Model of sex chromosome–autosome fusion. Here, we show the case of Y-autosome fusion. Abbreviations: A, autosome; MSD, master sex-determining.

more common than other types of fusion in fish (116, 117, 124). The predominance of Y-autosome fusion is likely an outcome of the combination of slightly deleterious effects of chromosomal fusion and male-biased mutation rate or female-biased reproductive sex ratio (124). Alternatively, female meiotic drive for unfused chromosomes could explain the prevalence of Y-autosome fusions (124). Further empirical studies are necessary to test these hypotheses.

7. EVOLUTIONARY FORCES THAT DRIVE THE TRANSITION BETWEEN TSD AND GSD

As reviewed above, there is crosstalk between the GSD and TSD pathways (**Figure 2**). Therefore, it is not surprising that sex determination in fish with GSD is influenced by the environmental temperature. This supports the idea that GSD and TSD represent opposite ends of a continuum (**Figure 4**).

What evolutionary forces drive the transition from GSD to TSD, the move from the right to the left in the continuum of **Figure 4**? Charnov & Bull (125, pp. 828–29) proposed that ESD is advantageous "when an individual's fitness (as a male or female) is strongly influenced by environmental conditions and where the individual has little control over which environment it will experience." Conover (126) presented a nice empirical example consistent with this scenario in the Atlantic silverside, which has the Type Ib TSD. In this species, offspring produced early in the breeding season are exposed to low temperatures and tend to become females. In contrast, offspring born later in the breeding season are exposed to high temperatures and tend to become males. Individuals born earlier have more time to grow and reach a larger size in the breeding season than those born later. Because a larger body size benefits females more than males during reproduction in this species, this TSD is considered advantageous (126). When TSD is advantageous, it will invade organisms with GSD (127). However, further empirical studies are necessary to test these hypotheses.

As described in Section 3.1, Type Ib TSD is the most common in fish. Among species with Type Ib TSD, sex reversal from genotypic females with XX to phenotypic males is the most common. There are several possible explanations for this pattern, although none of them alone can explain it. First, it may be relatively easy to reverse an XX genotype that does not carry an MSD gene to a phenotypic male via temperature stimuli (see Section 3.2), whereas it may be difficult to override the genotypic effect of the dominant sex determinator on the Y chromosome by temperature stimuli alone. Second, the predominance of XX males compared with XY females in Type Ib may be attributable to an accumulation of deleterious mutations on the Y chromosome (see Section 6). When XY females mate with XY males, some progeny will show the YY genotype, which may be deleterious. Therefore, alleles that can change XY individuals into females may not spread within populations. However, as mentioned in Section 6, fish sometimes do not show any degeneration of Y chromosomes, so it is unclear how deleterious the YY genotype is in fish. Third, hot temperatures may be more stressful for fish than cold temperatures, and stressful conditions may favor a male-biased sex ratio (128). As seen in Section 3.2, sex reversal is mediated by the glucocorticoid stress hormone. Producing eggs requires more energy than producing sperm. Therefore, under stressful conditions with limited resources, the production of males may be adaptive (128). The combination of some of these may lead to the predominance of sex reversal of XX fish to males.

What evolutionary forces drive the transition from TSD to GSD? In TSD, spatial variation and temporal fluctuation of environmental temperatures can cause fluctuations in the sex ratio. A 1:1 sex ratio is generally optimal because of the frequency-dependent selection of the minority sex (129). If the sex ratio is strongly biased due to environmental fluctuations, monogenic GSD, which can ensure a stable 1:1 sex ratio, would become favored (95, 130). For example, suppose that a fish population with Type Ib TSD becomes exposed to warmer temperatures. Then, the sex ratio would be male biased, favoring the evolution of a female sex-determining gene (131).

8. FUTURE RESEARCH DIRECTIONS

8.1. Key Questions in Evolutionary Genetics of Sex Determination

What genes become hotspots? Why are there hotspot genes? Although particular genes in the TGF-β pathway seem to be hotspot genes for MSD, we cannot exclude the possibility of publication bias. When a sex-linked locus is identified, we would first search for previously known MSD genes at that locus. If we find known MSD genes at the locus, we can publish them quickly. Unless any known MSD genes are present, it would take more time to identify novel causative genes. However, recent technological advances in haplotype-resolved genome assembly and genome editing will help to identify more sex-determining genes across more diverse taxa (132–134), leading to a more unbiased list of MSD genes in the near future.

How many and what types of mutations are necessary for MSD function? To answer this question, a detailed analysis of causative mutations is essential. If multiple mutations are necessary, linkage among these mutations would be required for exerting the MSD function, favoring recombination suppression at the MSD gene locus (1). Once recombination suppression evolves around MSD, regions with recombination suppression would further expand without sexually antagonistic selection (135–137). Thus, identification of causative mutations of MSD can help to resolve the question of how recombination suppression evolves on sex chromosomes (138–140). Base editing and gene replacement technologies will help to provide answers.

What are the drivers and consequences of sex chromosome turnover? Although there are many theoretical studies on the evolutionary forces driving sex chromosome turnover, empirical support is lacking. Furthermore, sex chromosome turnover may promote the evolution of new sexually dimorphic traits and reproductive isolation (116), but this also requires solid empirical evidence. Several studies have identified loci involved in sexually dimorphic traits (141, 142) and signatures of sexually antagonistic selection (143) on neo-sex chromosomes. However, whether these loci drove or evolved after the turnover remains elusive. Further comparative studies of the functions of genes located on the newly evolved sex chromosomes, as well as on the ancestral chromosomes across diverse taxa, may help to answer these questions.

8.2. Applications to Aquaculture and Conservation Biology

A better understanding of the sex-determination mechanisms in teleost fishes also has benefits for aquaculture. Identifying MSD genes and/or their causal mutations enables us to determine the sex of farmed fish via molecular genetic techniques, even those in premature or nonbreeding conditions. Genotyping of the MSD gene/mutation allows for easy and precise identification of sex-reversed fish (e.g., XX males and XY females) in aquaculture stocks of tiger pufferfish (144) and Chinook salmon (145). Additionally, understanding the detailed mechanisms of GSD and TSD will facilitate the development of efficient and robust techniques for artificial sex reversal using temperature control, steroid hormone administration, and genetic/chromosome engineering. Both molecular sexing and sex-reversal techniques will be helpful for the sex control of aquaculture stocks (e.g., production of all-female stocks) and for the broodstock management of salmonids, flatfishes, and other cultured fish (146).

As we have seen, temperature influences the sex determination of many fish species. Therefore, global warming would affect the sex ratio of organisms with TSD. A strongly biased sex ratio may bring these species to the risk of extinction (147). However, if they could quickly evolve GSD or other counter-mechanisms, such as transgenerational plasticity for temperature-induced sex bias (147, 148), they could persist. Therefore, investigating the evolutionary mechanisms of GSD and TSD in fish can help us understand how fish diversity will change in response to future global warming and climate change.

9. CONCLUDING REMARKS

The diversity of sex-determining mechanisms remains a mystery. However, detailed molecular mechanisms of sex determination, including GSD and TSD, have now been revealed in several teleost species. The findings to date provide clues to the proximate mechanisms of the transition between different sex-determining systems. Furthermore, many theoretical studies have presented models for the ultimate causes of the transitions. However, we still lack empirical data testing the theoretical models. Further integrative studies of detailed molecular mechanisms of sex determination in diverse taxa, as well as evolutionary ecology research on sex-determining systems in natural populations, will elucidate the evolutionary mechanisms creating the diversity of sex-determining mechanisms, one of the mysteries of life.

DISCLOSURE STATEMENT

The authors are not aware of any affiliations, memberships, funding, or financial holdings that might be perceived as affecting the objectivity of this review.

ACKNOWLEDGMENTS

This research was supported by JSPS Kakenhi (22H04983 to J.K.; 21K15143 to S.A.; 19H03269 to Y.T. and S.A.; 19H03048 and 19H01162 to Y.Y.) and JST CREST (JPMJCR20S2 to J.K. and S.A.). Cynthia Kulongowski with Edanz edited the language of a draft of this manuscript.

LITERATURE CITED

1. Beukeboom LW, Perrin N. 2014. *The Evolution of Sex Determination*. Oxford, UK: Oxford Univ. Press
2. Bachtrog D, Mank JE, Peichel CL, Kirkpatrick M, Otto SP, et al. 2014. Sex determination: Why so many ways of doing it? *PLOS Biol.* 12(7):e1001899
3. Kirkpatrick M, Jenkins CD. 1989. Genetic segregation and the maintenance of sexual reproduction. *Nature* 339(6222):300–1
4. Kondrashov AS. 1988. Deleterious mutations and the evolution of sexual reproduction. *Nature* 336(6198):435–40
5. Hamilton WD. 1980. Sex versus non-sex versus parasite. *Oikos* 35(2):282–90
6. Hamilton WD, Axelrod R, Tanese R. 1990. Sexual reproduction as an adaptation to resist parasites (a review). *PNAS* 87(9):3566–73
7. Parker GA, Baker RR, Smith VG. 1972. The origin and evolution of gamete dimorphism and the male-female phenomenon. *J. Theor. Biol.* 36(3):529–53
8. Lehtonen J, Kokko H. 2011. Two roads to two sexes: unifying gamete competition and gamete limitation in a single model of anisogamy evolution. *Behav. Ecol. Sociobiol.* 65(3):445–59
9. Maynard Smith J. 1978. *The Evolution of Sex*. Cambridge, UK: Cambridge Univ. Press
10. Nagahama Y, Chakraborty T, Paul-Prasanth B, Ohta K, Nakamura M. 2021. Sex determination, gonadal sex differentiation, and plasticity in vertebrate species. *Physiol. Rev.* 101(3):1237–308
11. Kikuchi K, Hamaguchi S. 2013. Novel sex-determining genes in fish and sex chromosome evolution. *Dev. Dyn.* 242(4):339–53
12. Mank JE, Avise JC. 2009. Evolutionary diversity and turn-over of sex determination in teleost fishes. *Sex Dev.* 3(2–3):60–67
13. Godwin J. 2009. Social determination of sex in reef fishes. *Semin. Cell Dev. Biol.* 20(3):264–70

14. Gemmell NJ, Todd EV, Goikoetxea A, Ortega-Recalde O, Hore TA. 2019. Natural sex change in fish. *Curr. Top. Dev. Biol.* 134:71–117
15. Ortega-Recalde O, Goikoetxea A, Hore TA, Todd EV, Gemmell NJ. 2020. The genetics and epigenetics of sex change in fish. *Annu. Rev. Anim. Biosci.* 8:47–69
16. Hattori RS, Murai Y, Oura M, Masuda S, Majhi SK, Sakamoto T, et al. 2012. A Y-linked anti-Müllerian hormone duplication takes over a critical role in sex determination. *PNAS* 109(8):2955–59
17. Peichel CL, McCann SR, Ross JA, Naftaly AFS, Urton JR, et al. 2020. Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution. *Genome Biol.* 21:177
18. Li M, Sun Y, Zhao J, Shi H, Zeng S, 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 Genet.* 11(11):e1005678
19. Pan Q, Feron R, Yano A, Guyomard R, Jouanno E, et al. 2019. Identification of the master sex determining gene in Northern pike (*Esox lucius*) reveals restricted sex chromosome differentiation. *PLOS Genet.* 15(8):e1008013
20. Hattori RS, Kumazawa K, Nakamoto M, Nakano Y, Yamaguchi T, et al. 2022. Y-specific *amh* allele, *amhy*, is the master sex-determining gene in Japanese flounder *Paralichthys olivaceus*. *Front. Genet.* 13:1007548
21. Kamiya T, Kai W, Tasumi S, Oka A, Matsunaga T, et al. 2012. A trans-species missense SNP in *Amhr2* is associated with sex determination in the tiger pufferfish, *Takifugu rubripes* (fugu). *PLOS Genet.* 8(7):e1002798
22. Nacif CL, Kratochwil CF, Kautt AF, Nater A, Machado-Schiaffino G, et al. 2023. Molecular parallelism in the evolution of a master sex-determining role for the anti-Mullerian hormone receptor 2 gene (*amhr2*) in Midas cichlids. *Mol. Ecol.* 32(6):1398–410
23. Wen M, Pan Q, Jouanno E, Montfort J, Zahm M, et al. 2022. An ancient truncated duplication of the anti-Müllerian hormone receptor type 2 gene is a potential conserved master sex determinant in the Pangasiidae catfish family. *Mol. Ecol. Resour.* 22(6):2411–28
24. Jasonowicz AJ, Simeon A, Zahm M, Cabau C, Klopp C, et al. 2022. Generation of a chromosome-level genome assembly for Pacific halibut (*Hippoglossus stenolepis*) and characterization of its sex-determining genomic region. *Mol. Ecol. Resour.* 22(7):2685–700
25. Imarazene B, Du K, Beille S, Jouanno E, Feron R, et al. 2021. A supernumerary "B-sex" chromosome drives male sex determination in the Pachón cavefish, *Astyanax mexicanus*. *Curr. Biol.* 31(21):4800–9.e9
26. Matsuda M, Nagahama Y, Shinomiya A, Sato T, Matsuda C, et al. 2002. *DMY* is a Y-specific DM-domain gene required for male development in the medaka fish. *Nature* 417(6888):559–63
27. Zhang W, Wang H, Brandt DYC, Hu B, Sheng J, et al. 2022. The genetic architecture of phenotypic diversity in the Betta fish (*Betta splendens*). *Sci. Adv.* 8(38):eabm4955
28. Chen S, Zhang G, Shao C, Huang Q, Liu G, et al. 2014. Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. *Nat. Genet.* 46(3):253–60
29. Takehana Y, Matsuda M, Myosho T, Suster ML, Kawakami K, et al. 2014. Co-option of *Sox3* as the male-determining factor on the Y chromosome in the fish *Oryzias dancena*. *Nat. Commun.* 5:4157
30. Myosho T, Takehana Y, Hamaguchi S, Sakaizumi M. 2015. Turnover of sex chromosomes in *celebensis* group medaka fishes. *G3* 5(12):2685–91
31. Martínez P, Robledo D, Taboada X, Blanco A, Moser M, et al. 2021. A genome-wide association study, supported by a new chromosome-level genome assembly, suggests *sox2* as a main driver of the undifferentiatiated ZZ/ZW sex determination of turbot (*Scophthalmus maximus*). *Genomics* 113(4):1705–18
32. Koyama T, Nakamoto M, Morishima K, Yamashita R, Yamashita T, et al. 2019. A SNP in a steroidogenic enzyme is associated with phenotypic sex in *Seriola* fishes. *Curr. Biol.* 29(11):1901–9.e8
33. Catanach A, Ruigrok M, Bowatte D, Davy M, Storey R, et al. 2021. The genome of New Zealand trevally (Carangidae: *Pseudocaranx georgianus*) uncovers a XY sex determination locus. *BMC Genom.* 22:785
34. Nakamura Y, Higuchi K, Kumon K, Yasuike M, Takashi T, et al. 2021. Prediction of the sex-associated genomic region in tunas (*Thunnus* fishes). *Int. J. Genom.* 2021:7226353

35. Bao L, Tian C, Liu S, Zhang Y, Elaswad A, et al. 2019. The Y chromosome sequence of the channel catfish suggests novel sex determination mechanisms in teleost fish. *BMC Biol.* 17:6
36. Yano A, Guyomard R, Nicol B, Jouanno E, Quillet E, et al. 2012. An immune-related gene evolved into the master sex-determining gene in rainbow trout, *Oncorhynchus mykiss*. *Curr. Biol.* 22(15):1423–28
37. Yano A, Nicol B, Jouanno E, Quillet E, Fostier A, et al. 2013. The sexually dimorphic on the Y-chromosome gene (*sdY*) is a conserved male-specific Y-chromosome sequence in many salmonids. *Evol. Appl.* 6(3):486–96
38. Bertho S, Herpin A, Branthonne A, Jouanno E, Yano A, et al. 2018. The unusual rainbow trout sex determination gene hijacked the canonical vertebrate gonadal differentiation pathway. *PNAS* 115(50):12781–86
39. Kirubakaran TG, Andersen Ø, De Rosa MC, Andersstuen T, Hallan K, et al. 2019. Characterization of a male specific region containing a candidate sex determining gene in Atlantic cod. *Sci. Rep.* 9:116
40. Dan C, Lin Q, Gong G, Yang T, Xiong S, et al. 2018. A novel PDZ domain-containing gene is essential for male sex differentiation and maintenance in yellow catfish (*Pelteobagrus fulvidraco*). *Sci. Bull.* 63(21):1420–30
41. de la Herrán R, Hermida M, Rubiolo JA, Gómez-Garrido J, Cruz F, et al. 2023. A chromosome-level genome assembly enables the identification of the follicule stimulating hormone receptor as the master sex-determining gene in the flatfish *Solea senegalensis*. *Mol. Ecol. Resour.* 23(4):886–904
42. Tao W, Xu L, Zhao L, Zhu Z, Wu X, et al. 2021. High-quality chromosome-level genomes of two tilapia species reveal their evolution of repeat sequences and sex chromosomes. *Mol. Ecol. Resour.* 21(2):543–60
43. Kobayashi T, Matsuda M, Kajiura-Kobayashi H, Suzuki A, Saito N, et al. 2004. Two DM domain genes, *DMY* and *DMRT1*, involved in testicular differentiation and development in the medaka, *Oryzias latipes*. *Dev. Dyn.* 231(3):518–26
44. Shibata Y, Paul-Prasanth B, Suzuki A, Usami T, Nakamoto M, et al. 2010. Expression of gonadal soma derived factor (GSDF) is spatially and temporally correlated with early testicular differentiation in medaka. *Gene Expr. Patterns* 10(6):283–89
45. Masuyama H, Yamada M, Kamei Y, Fujiwara-Ishikawa T, Todo T, et al. 2012. *Dmrt1* mutation causes a male-to-female sex reversal after the sex determination by *Dmy* in the medaka. *Chromosome Res.* 20:163–76
46. Imai T, Saino K, Matsuda M, Matsuda M. 2015. Mutation of gonadal soma-derived factor induces medaka XY gonads to undergo ovarian development. *Biochem. Biophys. Res. Commun.* 467(1):109–14
47. Horie Y, Myosho T, Sato T, Sakaizumi M, Hamaguchi S, Kobayashi T. 2016. Androgen induces gonadal soma-derived factor, *Gsdf*, in XX gonads correlated to sex-reversal but not *Dmrt1* directly, in the teleost fish, northern medaka (*Oryzias sakaizumii*). *Mol. Cell. Endocrinol.* 436:141–49
48. Morinaga C, Saito D, Nakamura S, Sasaki T, Asakawa S, et al. 2007. The *hotei* mutation of medaka in the anti-Müllerian hormone receptor causes the dysregulation of germ cell and sexual development. *PNAS* 104(23):9691–96
49. Kurokawa H, Saito D, Nakamura S, Katoh-Fukui Y, Ohta K, et al. 2007. Germ cells are essential for sexual dimorphism in the medaka gonad. *PNAS* 104(43):16958–63
50. Sato T, Suzuki A, Shibata N, Sakaizumi M, Hamaguchi S. 2008. The novel mutant *scl* of the medaka fish, *Oryzias latipes*, shows no secondary sex characters. *Zool. Sci.* 25(3):299–306
51. Nishimura T, Sato T, Yamamoto Y, Watakabe I, Ohkawa Y, et al. 2015. *foxl3* is a germ cell-intrinsic factor involved in sperm-egg fate decision in medaka. *Science* 349(6245):328–31
52. Nakamoto M, Matsuda M, Wang D-S, Nagahama Y, Shibata N. 2006. Molecular cloning and analysis of gonadal expression of *Foxl2* in the medaka, *Oryzias latipes*. *Biochem. Biophys. Res. Commun.* 344(1):353–61
53. Suzuki A, Tanaka M, Shibata N, Nagahama Y. 2004. Expression of aromatase mRNA and effects of aromatase inhibitor during ovarian development in the medaka, *Oryzias latipes*. *J. Exp. Zool. A* 301(3):266–73
54. Yamamoto Y, Zhang Y, Sarida M, Hattori RS, Strüssmann CA. 2014. Coexistence of genotypic and temperature-dependent sex determination in pejerrey *Odontesthes bonariensis*. *PLOS ONE* 9(7):e102574
55. Fernandino JI, Hattori RS, Shinoda T, Kumura H, Strobl-Mazzulla PH, et al. 2008. Dimorphic expression of *dmrt1* and *cyp19a1* (ovarian aromatase) during early gonadal development in pejerrey, *Odontesthes bonariensis*. *Sex Dev.* 2(6):316–24

56. Zhang Y, Hattori RS, Sarida M, García EL, Strüssmann CA, Yamamoto Y. 2018. Expression profiles of *amhy* and major sex-related genes during gonadal sex differentiation and their relation with genotypic and temperature-dependent sex determination in pejerrey *Odontesthes bonariensis*. *Gen. Comp. Endocrinol.* 265:196–201
57. Valenzuela N, Lance VA, eds. 2005. *Temperature-Dependent Sex Determination in Vertebrates*. Washington, DC: Smithsonian Books
58. Bull JJ. 1980. Sex determination in reptiles. *Q. Rev. Biol.* 55(1):3–21
59. Sarre SD, Georges A, Quinn A. 2004. The ends of a continuum: genetic and temperature-dependent sex determination in reptiles. *BioEssays* 26(6):639–45
60. Valenzuela N, Adams DC, Janzen FJ. 2003. Pattern does not equal process: Exactly when is sex environmentally determined? *Am. Nat.* 161(4):676–83
61. Baroiller J-F, D'Cotta H. 2016. The reversible sex of gonochoristic fish: insights and consequences. *Sex Dev*. 10(5–6):242–66
62. Ospina-Álvarez N, 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* 3(7):e2837
63. Conover DO, Kynard BE. 1981. Environmental sex determination: interaction of temperature and genotype in a fish. *Science* 213(4507):577–79
64. Honeycutt JL, Deck CA, Miller SC, Severance ME, Atkins EB, et al. 2019. Warmer waters masculinize wild populations of a fish with temperature-dependent sex determination. *Sci. Rep.* 9:6527
65. Miyoshi K, Hattori RS, Strüssmann CA, Yokota M, Yamamoto Y. 2020. Phenotypic/genotypic sex mismatches and temperature-dependent sex determination in a wild population of an Old World atherinid, the cobaltcap silverside *Hypoatherina tsurugae*. *Mol. Ecol.* 29(13):2349–58
66. Yamamoto Y, Hattori RS, Patiño R, Strüssmann CA. 2019. Environmental regulation of sex determination in fishes: insights from Atheriniformes. *Curr. Top. Dev. Biol.* 134:49–69
67. Sato T, Endo T, Yamahira K, Hamaguchi S, Sakaizumi M. 2005. Induction of female-to-male sex reversal by high temperature treatment in Medaka, *Oryzias latipes*. *Zool. Sci.* 22(9):985–88
68. Hayashi Y, Kobira H, Yamaguchi T, Shiraishi E, Yazawa T, et al. 2010. High temperature causes masculinization of genetically female medaka by elevation of cortisol. *Mol. Reprod. Dev.* 77(8):679–86
69. Kitano T, Hayashi Y, Shiraishi E, Kamei Y. 2012. Estrogen rescues masculinization of genetically female medaka by exposure to cortisol or high temperature. *Mol. Reprod. Dev.* 79(10):719–26
70. Hara S, Sawamura R, Kitano T. 2021. Cortisol induces masculinization of XX medaka through gonadal soma-derived growth factor (GSDF) and anti-Müllerian hormone receptor type 2 (AMHR2). *Fish. Sci.* 87(1):85–91
71. Fernandino JI, Hattori RS, Kishii A, Strüssmann CA, Somoza GM. 2012. The cortisol and androgen pathways cross talk in high temperature-induced masculinization: the 11β-hydroxysteroid dehydrogenase as a key enzyme. *Endocrinology* 153(12):6003–11
72. Hattori RS, Castañeda-Cortés DC, Arias Padilla LF, Strobl-Mazzulla PH, Fernandino JI. 2020. Activation of stress response axis as a key process in environment-induced sex plasticity in fish. *Cell. Mol. Life Sci.* 77(21):4223–36
73. Piferrer F. 2021. Epigenetic mechanisms in sex determination and in the evolutionary transitions between sexual systems. *Philos. Trans. R. Soc. Lond. B* 376(1832):20200110
74. Navarro-Martín L, Viñas J, Ribas L, Díaz N, Gutiérrez A, et al. 2011. DNA methylation of the gonadal aromatase (*cyp19a*) promoter is involved in temperature-dependent sex ratio shifts in the European sea bass. *PLOS Genet*. 7(12):e1002447
75. Shao C, Li Q, Chen S, Zhang P, Lian J, et al. 2014. Epigenetic modification and inheritance in sexual reversal of fish. *Genome Res*. 24(4):604–15
76. Stern DL. 2013. The genetic causes of convergent evolution. *Nat. Rev. Genet.* 14(11):751–64
77. Gompel N, Prud'homme B. 2009. The causes of repeated genetic evolution. *Dev. Biol.* 332(1):36–47
78. Christin P-A, Weinreich DM, Besnard G. 2010. Causes and evolutionary significance of genetic convergence. *Trends Genet*. 26(9):400–5
79. Arendt J, Reznick D. 2008. Convergence and parallelism reconsidered: What have we learned about the genetics of adaptation? *Trends Ecol. Evol.* 23(1):26–32

80. Martin A, Orgogozo V. 2013. The loci of repeated evolution: a catalog of genetic hotspots of phenotypic variation. *Evolution* 67(5):1235–50
81. Kopp A. 2009. Metamodels and phylogenetic replication: a systematic approach to the evolution of developmental pathways. *Evolution* 63(11):2771–89
82. Orr HA. 2005. The probability of parallel evolution. *Evolution* 59(1):216–20
83. Marshall Graves JA, Peichel CL. 2010. Are homologies in vertebrate sex determination due to shared ancestry or to limited options? *Genome Biol.* 11(4):205
84. Pan Q, Kay T, Depincé A, Adolfi M, Schartl M, et al. 2021. Evolution of master sex determiners: TGF-β signalling pathways at regulatory crossroads. *Philos. Trans. R. Soc. Lond. B* 376(1832):20200091
85. Adolfi MC, Herpin A, Schartl M. 2021. The replaceable master of sex determination: bottom-up hypothesis revisited. *Philos. Trans. R. Soc. Lond. B* 376(1832):20200090
86. Long M, VanKuren NW, Chen S, Vibranovski MD. 2013. New gene evolution: little did we know. *Annu. Rev. Genet.* 47:307–33
87. Ohno S. 1970. *Evolution by Gene Duplication*. Berlin: Springer
88. Nanda I, Kondo M, Hornung U, Asakawa S, Winkler C, et al. 2002. A duplicated copy of *DMRT1* in the sex-determining region of the Y chromosome of the medaka, *Oryzias latipes*. *PNAS* 99(18):11778–83
89. Herpin A, Braasch I, Kraeussling M, Schmidt C, Thoma EC, et al. 2010. Transcriptional rewiring of the sex determining *dmrt1* gene duplicate by transposable elements. *PLOS Genet*. 6(2):e1000844
90. Ogita Y, Mawaribuchi S, Nakasako K, Tamura K, Matsuda M, et al. 2020. Parallel evolution of two *dmrt1*-derived genes, *dmy* and *dm-w*, for vertebrate sex determination. *iScience* 23(1):100757
91. Bertho S, Herpin A, Schartl M, Guiguen Y. 2021. Lessons from an unusual vertebrate sex-determining gene. *Philos. Trans. R. Soc. Lond. B* 376(1832):20200092
92. Myosho T, Otake H, Masuyama H, Matsuda M, Kuroki Y, et al. 2012. Tracing the emergence of a novel sex-determining gene in medaka, *Oryzias luzonensis. Genetics* 191(1):163–70
93. Kabir A, Ieda R, Hosoya S, Fujikawa D, Atsumi K, et al. 2022. Repeated translocation of a supergene underlying rapid sex chromosome turnover in *Takifugu* pufferfish. *PNAS* 119(23):e2121469119
94. Bull JJ, Charnov EL. 1977. Changes in the heterogametic mechanism of sex determination. *Heredity* 39:1–14
95. van Doorn GS. 2014. Evolutionary transitions between sex-determining mechanisms: a review of theory. *Sex Dev*. 8(1–3):7–19
96. van Doorn GS, Kirkpatrick M. 2007. Turnover of sex chromosomes induced by sexual conflict. *Nature* 449(7164):909–12
97. van Doorn GS, Kirkpatrick M. 2010. Transitions between male and female heterogamety caused by sex-antagonistic selection. *Genetics* 186(2):629–45
98. Charlesworth B, Wall JD. 1999. Inbreeding, heterozygote advantage and the evolution of neo-X and neo-Y sex chromosomes. *Proc. R. Soc. Lond. B* 266(1414):51–56
99. Úbeda F, Patten MM, Wild G. 2015. On the origin of sex chromosomes from meiotic drive. *Proc. Biol. Sci.* 282(1798):20141932
100. Jayakar SD. 1987. Some two locus models for the evolution of sex-determining mechanisms. *Theor. Popul. Biol.* 32(2):188–215
101. Burt A, Trivers R. 2006. *Genes in Conflict: The Biology of Selfish Genetic Elements*. Cambridge, MA: Harvard Univ. Press
102. Blaser O, Grossen C, Neuenschwander S, Perrin N. 2013. Sex-chromosome turnovers induced by deleterious mutation load. *Evolution* 67(3):635–45
103. Saunders PA, Neuenschwander S, Perrin N. 2019. Impact of deleterious mutations, sexually antagonistic selection, and mode of recombination suppression on transitions between male and female heterogamety. *Heredity* 123(3):419–28
104. Charlesworth B, Charlesworth D. 2000. The degeneration of Y chromosomes. *Philos. Trans. R. Soc. Lond. B* 355(1403):1563–72
105. Blaser O, Neuenschwander S, Perrin N. 2014. Sex-chromosome turnovers: the hot-potato model. *Am. Nat.* 183(1):140–46
106. Veller C, Muralidhar P, Constable GWA, Nowak MA. 2017. Drift-induced selection between male and female heterogamety. *Genetics* 207(2):711–27

107. Saunders PA, Neuenschwander S, Perrin N. 2018. Sex chromosome turnovers and genetic drift: a simulation study. *J. Evol. Biol.* 31(9):1413–19

108. Kallman KD. 1984. A new look at sex determination in poeciliid fishes. In *Evolutionary Genetics of Fishes*, ed. BJ Turner, pp. 95–171. New York: Springer

109. Ser JR, Roberts RB, Kocher TD. 2010. Multiple interacting loci control sex determination in Lake Malawi cichlid fish. *Evolution* 64(2):486–501

110. Lee B-Y, Hulata G, Kocher TD. 2004. Two unlinked loci controlling the sex of blue tilapia (*Oreochromis aureus*). *Heredity* 92(6):543–49

111. Kitano J, Ansai S, Fujimoto S, Kakioka R, Sato M, et al. 2023. A cryptic sex-linked locus revealed by the elimination of a master sex-determining locus in medaka fish. *Am. Nat.* 202(2):231–40

112. Shinomiya A, Otake H, Togashi K-I, Hamaguchi S, Sakaizumi M. 2004. Field survey of sex-reversals in the medaka, *Oryzias latipes*: genotypic sexing of wild populations. *Zool. Sci.* 21(6):613–19

113. Sharma KK, Sharma OP, Tripathi NK. 1998. Female heterogamety in *Danio rerio* (Cypriniformes: Cyprinidae). *Proc. Natl. Acad. Sci. India B* 68:123–26

114. Wilson CA, High SK, McCluskey BM, Amores A, Yan T-l, et al. 2014. Wild sex in zebrafish: loss of the natural sex determinant in domesticated strains. *Genetics* 198(3):1291–308

115. Liew WC, Bartfai R, Lim Z, Sreenivasan R, Siegfried KR, Orban L. 2012. Polygenic sex determination system in zebrafish. *PLOS ONE* 7(4):e34397

116. Kitano J, Peichel CL. 2012. Turnover of sex chromosomes and speciation in fishes. *Environ. Biol. Fish.* 94(3):549–58

117. Sember A, Nguyen P, Perez MF, Altmanová, Ráb P, de Bello Cioffi M. 2021. Multiple sex chromosomes in teleost fishes from a cytogenetic perspective: state of the art and future challenges. *Philos. Trans. R. Soc. Lond. B* 376(1833):20200098

118. White MJD. 1973. *Animal Cytology and Evolution*. Cambridge, UK: Cambridge Univ. Press

119. Charlesworth D, Charlesworth B. 1980. Sex differences in fitness and selection for centric fusions between sex-chromosomes and autosomes. *Genet. Res.* 35(2):205–14

120. Matsumoto T, Kitano J. 2016. The intricate relationship between sexually antagonistic selection and the evolution of sex chromosome fusions. *J. Theor. Biol.* 404:97–108

121. Matsumoto T, Yoshida K, Kitano J. 2017. Contribution of gene flow to the evolution of recombination suppression in sex chromosomes. *J. Theor. Biol.* 431:25–31

122. Yoshida K, Kitano J. 2012. The contribution of female meiotic drive to the evolution of neo-sex chromosomes. *Evolution* 66(10):3198–208

123. Pokorná M, Altmanová M, Kratochvíl L. 2014. Multiple sex chromosomes in the light of female meiotic drive in amniote vertebrates. *Chromosome Res.* 22(1):35–44

124. Pennell MW, Kirkpatrick M, Otto SP, Vamosi JC, Peichel CL, et al. 2015. Y fuse? Sex chromosome fusions in fishes and reptiles. *PLOS Genet.* 11(5):e1005237

125. Charnov EL, Bull J. 1977. When is sex environmentally determined? *Nature* 266(5605):828–30

126. Conover DO. 1984. Adaptive significance of temperature-dependent sex determination in a fish. *Am. Nat.* 123(3):297–313

127. Bull JJ. 1981. Evolution of environmental sex determination from genotypic sex determination. *Heredity* 47(2):173–84

128. Geffroy B, Douhard M. 2019. The adaptive sex in stressful environments. *Trends Ecol. Evol.* 34(7):628–40

129. Fisher RA. 1930. *The Genetical Theory of Natural Selection*. Oxford, UK: Oxford Univ. Press

130. Bulmer MG, Bull JJ. 1982. Models of polygenic sex determination and sex ratio control. *Evolution* 36(1):13–26

131. Grossen C, Neuenschwander S, Perrin N. 2011. Temperature-dependent turnovers in sex-determination mechanisms: a quantitative model. *Evolution* 65(1):64–78

132. Ramos L, Antunes A. 2022. Decoding sex: elucidating sex determination and how high-quality genome assemblies are untangling the evolutionary dynamics of sex chromosomes. *Genomics* 114(2):110277

133. Rhie A, Nurk S, Cechova M, Hoyt SJ, Taylor DJ, et al. 2023. The complete sequence of a human Y chromosome. *Nature* 621:344–54

134. Ansai S, Kitano J. 2022. Speciation and adaptation research meets genome editing. *Philos. Trans. R. Soc. Lond. B* 377(1855):20200516

135. Jeffries DL, Gerchen JF, Scharmann M, Pannell JR. 2021. A neutral model for the loss of recombination on sex chromosomes. *Philos. Trans. R. Soc. Lond. B* 376(1832):20200096

136. Lenormand T, Roze D. 2022. Y recombination arrest and degeneration in the absence of sexual dimorphism. *Science* 375(6581):663–66

137. Jay P, Tezenas E, Véber A, Giraud T. 2022. Sheltering of deleterious mutations explains the stepwise extension of recombination suppression on sex chromosomes and other supergenes. *PLOS Biol.* 20(7):e3001698

138. Charlesworth D. 2017. Evolution of recombination rates between sex chromosomes. *Philos. Trans. R. Soc. Lond. B* 372(1736):20160456

139. Abbott JK, Nordén AK, Hansson B. 2017. Sex chromosome evolution: historical insights and future perspectives. *Proc. Biol. Sci.* 284(1854):20162806

140. Kratochvíl L, Stöck M, Rovatsos M, Bullejos M, Herpin A, et al. 2021. Expanding the classical paradigm: what we have learnt from vertebrates about sex chromosome evolution. *Philos. Trans. R. Soc. Lond. B* 376(1833):20200097

141. Kitano J, Ross JA, Mori S, Kume M, Jones FC, et al. 2009. A role for a neo-sex chromosome in stickleback speciation. *Nature* 461(7267):1079–83

142. Roberts RB, Ser JR, Kocher TD. 2009. Sexual conflict resolved by invasion of a novel sex determiner in Lake Malawi cichlid fishes. *Science* 326(5955):998–1001

143. Dagilis AJ, Sardell JM, Josephson MP, Su Y, Kirkpatrick M, Peichel CL. 2022. Searching for signatures of sexually antagonistic selection on stickleback sex chromosomes. *Philos. Trans. R. Soc. Lond. B* 377(1856):20210205

144. Matsunaga T, Ieda R, Hosoya S, Kuroyanagi M, Suzuki S, et al. 2014. An efficient molecular technique for sexing tiger pufferfish (fugu) and the occurrence of sex reversal in a hatchery population. *Fish. Sci.* 80(5):933–42

145. Bertho S, Herpin A, Jouanno E, Yano A, Bobe J, et al. 2022. A nonfunctional copy of the salmonid sex-determining gene (*sdY*) is responsible for the "apparent" XY females in Chinook salmon, *Oncorhynchus tshawytscha*. *G3* 12(2):jkab451

146. Wang H, Piferrer F, Chen S, Shen Z-G, eds. 2018. *Sex Control in Aquaculture*. Hoboken, NJ: John Wiley & Sons

147. Geffroy B, Wedekind C. 2020. Effects of global warming on sex ratios in fishes. *J. Fish Biol.* 97(3):596–606

148. McKenzie DJ, Geffroy B, Farrell AP. 2021. Effects of global warming on fishes and fisheries. *J. Fish Biol.* 98(6):1489–92

149. Hattori RS, Somoza GM, Fernandino JI, Colautti DC, Miyoshi K, et al. 2019. The duplicated Y-specific *amhy* gene is conserved and linked to maleness in silversides of the genus *Odontesthes*. *Genes* 10(9):679

150. Bej DK, Miyoshi K, Hattori RS, Strüssmann CA, Yamamoto Y. 2017. A duplicated, truncated *amh* gene is involved in male sex determination in an Old World silverside. *G3* 7(8):2489–95

151. Matsuda M, Sato T, Toyazaki Y, Nagahama Y, Hamaguchi S, Sakaizumi M. 2003. *Oryzias curvinotus* has *DMY*, a gene that is required for male development in the medaka, *O. latipes*. *Zool. Sci.* 20(2):159–61

152. Ansai S, Montenegro J, Masengi KWA, Nagano AJ, Yamahira K, Kitano J. 2022. Diversity of sex chromosomes in Sulawesian medaka fishes. *J. Evol. Biol.* 35(12):1751–64

153. Purcell CM, Seetharam AS, Snodgrass O, Ortega-García S, Hyde JR, Severin AJ. 2018. Insights into teleost sex determination from the *Seriola dorsalis* genome assembly. *BMC Genom.* 19:31

154. Li M, Xu X, Liu S, Fan G, Zhou Q, Chen S. 2022. The chromosome-level genome assembly of the Japanese yellowtail jack *Seriola aureovittata* provides insights into genome evolution and efficient oxygen transport. *Mol. Ecol. Resour.* 22(7):2701–12

155. Rafati N, Chen J, Herpin A, Pettersson ME, Han F, et al. 2020. Reconstruction of the birth of a male sex chromosome present in Atlantic herring. *PNAS* 117(39):24359–68

156. Reichwald K, Petzold A, Koch P, Downie BR, Hartmann N, et al. 2015. Insights into sex chromosome evolution and aging from the genome of a short-lived fish. *Cell* 163(6):1527–38

157. Štundlová J, Hospodářská M, Lukšíková K, Voleníková A, Pavlica T, et al. 2022. Sex chromosome differentiation via changes in the Y chromosome repeat landscape in African annual killifishes *Nothobranchius furzeri* and *N. kadleci*. *Chromosome Res.* 30(4):309–33

158. Pan Q, Feron R, Jouanno E, Darras H, Herpin A, et al. 2021. The rise and fall of the ancient northern pike master sex-determining gene. *eLife* 10:e62858

159. Nakamoto M, Uchino T, Koshimizu E, Kuchiishi Y, Sekiguchi R, et al. 2021. A Y-linked anti-Müllerian hormone type-II receptor is the sex-determining gene in ayu, *Plecoglossus altivelis*. *PLOS Genet*. 17(8):e1009705

160. Adolfi MC, Du K, Kneitz S, Cabau C, Zahm M, et al. 2021. A duplicated copy of *id2b* is an unusual sex-determining candidate gene on the Y chromosome of arapaima (*Arapaima gigas*). *Sci. Rep.* 11:21544

161. Feron R, Zahm M, Cabau C, Klopp C, Roques C, et al. 2020. Characterization of a Y-specific duplication/insertion of the anti-Mullerian hormone type II receptor gene based on a chromosome-scale genome assembly of yellow perch, *Perca flavescens*. *Mol. Ecol. Resour.* 20(2):531–43

162. Sardell JM, Josephson MP, Dalziel AC, Peichel CL, Kirkpatrick M. 2021. Heterogeneous histories of recombination suppression on stickleback sex chromosomes. *Mol. Biol. Evol.* 38(10):4403–18

163. Jeffries DL, Mee JA, Peichel CL. 2022. Identification of a candidate sex determination gene in *Culaea inconstans* suggests convergent recruitment of an *Amh* duplicate in two lineages of stickleback. *J. Evol. Biol.* 35(12):1683–95

164. Rondeau EB, Laurie CV, Johnson SC, Koop BF. 2016. A PCR assay detects a male-specific duplicated copy of anti-Müllerian hormone (*amh*) in the lingcod (*Ophiodon elongatus*). *BMC Res. Notes.* 9:230

165. Herpin A, Schartl M, Depincé A, Guiguen Y, Bobe J, et al. 2021. Allelic diversification after transposable element exaptation promoted *gsdf* as the master sex determining gene of sablefish. *Genome Res.* 31(8):1366–80

166. Song W, Xie Y, Sun M, Li X, Fitzpatrick CK, et al. 2021. A duplicated *amh* is the master sex-determining gene for *Sebastes* rockfish in the Northwest Pacific. *Open Biol.* 11(7):210063

167. Holborn MK, Einfeldt AL, Kess T, Duffy SJ, Messmer AM, et al. 2022. Reference genome of lumpfish *Cyclopterus lumpus* Linnaeus provides evidence of male heterogametic sex determination through the AMH pathway. *Mol. Ecol. Resour.* 22(4):1427–39

168. Jiang D-N, Huang Y-Q, Zhang J-M, Mustapha UF, Peng Y-X, et al. 2022. Establishment of the Y-linked *Dmrt1Y* as the candidate sex determination gene in spotbanded scat (*Selenotoca multifasciata*). *Aquacult. Rep.* 23:101085

169. Edvardsen RB, Wallerman O, Furmanek T, Kleppe L, Jern P, et al. 2022. Heterochiasmy and the establishment of *gsdf* as a novel sex determining gene in Atlantic halibut. *PLOS Genet*. 18(2):e1010011

170. Zheng S, Tao W, Yang H, Kocher TD, Wang Z, et al. 2022. Identification of sex chromosome and sex-determining gene of southern catfish (*Silurus meridionalis*) based on XX, XY and YY genome sequencing. *Proc. Biol. Sci.* 289(1971):20212645

171. Qu M, Liu Y, Zhang Y, Wan S, Ravi V, et al. 2021. Seadragon genome analysis provides insights into its phenotype and sex determination locus. *Sci. Adv.* 7(34):eabg5196

172. Ieda R, Hosoya S, Tajima S, Atsumi K, Kamiya T, et al. 2018. Identification of the sex-determining locus in grass puffer (*Takifugu niphobles*) provides evidence for sex-chromosome turnover in a subset of *Takifugu* species. *PLOS ONE* 13(1):e0190635

173. Ramee SW, Lipscomb TN, DiMaggio MA. 2020. Evaluation of the effect of larval stocking density, salinity, and temperature on stress response and sex differentiation in the Dwarf Gourami and Rosy Barb. *Aquacult. Rep.* 16:100287

174. Corona-Herrera GA, Tello-Ballinas JA, Hattori RS, Martínez-Palacios CA, Strüssmann CA, et al. 2016. Gonadal differentiation and temperature effects on sex determination in the freshwater pike silverside *Chirostoma estor* Jordan 1880. *Environ. Biol. Fish.* 99(5):463–71

175. Brown EE, Baumann H, Conover DO. 2014. Temperature and photoperiod effects on sex determination in a fish. *J. Exp. Mar. Biol. Ecol.* 461:39–43

176. Shen Z-G, Wang H-P, Yao H, O'Bryant P, Rapp D, Zhu K-Q. 2016. Sex determination in bluegill sunfish *Lepomis macrochirus*: effect of temperature on sex ratio of four geographic strains. *Biol. Bull.* 230(3):197–208

177. Li X-Y, Liu X-L, Zhu Y-J, Zhang J, Ding M, et al. 2018. Origin and transition of sex determination mechanisms in a gynogenetic hexaploid fish. *Heredity* 121(1):64–74

178. Fujioka Y. 2002. Effects of hormone treatments and temperature on sex-reversal of Nigorobuna *Carassius carassius grandoculis*. *Fish. Sci.* 68(4):889–93

179. Biswas C, Chakraborty S, Munilkumar S, Gireesh-Babu P, Sawant PB, et al. 2021. Effect of high temperature during larval and juvenile stages on masculinization of common carp (*Cyprinus carpio*, L). *Aquaculture* 530:735803

180. Sfakianakis DG, Leris I, Mylonas CC, Kentouri M. 2012. Temperature during early life determines sex in zebrafish, *Danio rerio* (Hamilton, 1822). *J. Biol. Res.* 17:68–73

181. Fujioka Y. 2006. Patterns of sex ratio response to water temperature during sex determination in honmoroko *Gnathopogon caerulescens*. *Fish. Sci.* 72(5):1034–41

182. Kim S-S, Kim DN-J, Lee C-J, Yoo H-K, Byun S-G, et al. 2020. The potential sex determination genes, Sox9a and Cyp19a, in walleye pollock (*Gadus Chalcogrammus*) are influenced by water temperature. *J. Mar. Sci. Eng.* 8(7):501

183. Huynh TB, Fairgrieve WT, Hayman ES, Lee JSF, Luckenbach JA. 2019. Inhibition of ovarian development and instances of sex reversal in genotypic female sablefish (*Anoplopoma fimbria*) exposed to elevated water temperature. *Gen. Comp. Endocrinol.* 279:88–98

184. Montalvo AJ, Faulk CK, Holt GJ. 2012. Sex determination in southern flounder, *Paralichthys lethostigma*, from the Texas Gulf Coast. *J. Exp. Mar. Biol. Ecol.* 432–33:186–90

185. Colburn HR, Nardi GC, Borski RJ, Berlinsky DL. 2009. Induced meiotic gynogenesis and sex differentiation in summer flounder (*Paralichthys dentatus*). *Aquaculture* 289(1):175–80

186. Haffray P, Lebègue E, Jeu S, Guennoc M, Guiguen Y, et al. 2009. Genetic determination and temperature effects on turbot *Scophthalmus maximus* sex differentiation: an investigation using steroid sex-inverted males and females. *Aquaculture* 294(1):30–36

187. Viñas J, Asensio E, Cañavate JP, Piferrer F. 2013. Gonadal sex differentiation in the Senegalese sole (*Solea senegalensis*) and first data on the experimental manipulation of its sex ratios. *Aquaculture* 384–87:74–81

188. Cole KS, Noakes DLG, Thompson N, Blouin M, Morrison B, Schreck CB. 2013. Exposure to elevated temperature during early development affects sexual development in *Oncorhynchus mykiss*. *North Pac. Anadromous Fish Comm. Tech. Rep.* 9:104–6

189. Omoto N, Koya Y, Chin B, Yamashita Y, Nakagawa M, Noda T. 2010. Gonadal sex differentiation and effect of rearing temperature on sex ratio in black rockfish (*Sebastes schlegeli*). *Ichthyol. Res.* 57(2):133–38

190. Santi S, Gennotte V, Toguyeni A, Mélard C, Antoine N, Rougeot C. 2016. Thermosensitivity of the sex differentiation process in the African catfish, *Clarias gariepinus*: determination of the thermosensitive period. *Aquaculture* 455:73–80

191. Yu Y, Chen M, Qi P-P, Chang L-Y, Wang T, et al. 2021. High temperature-induced masculinization in yellow catfish *Tachysurus fulvidraco*: a potential approach for environmental-friendly mono-sex production. *Aquaculture* 534:736263

192. Zhou H, Zhuang Z, Zhang R, Xu Q, Liang Y, et al. 2019. Temperature-control-induced masculinization in tiger puffer *Takifugu rubripes*. *J. Oceanol. Limnol.* 37(3):1125–35

193. Rabosky DL, Chang J, Title PO, Cowman PF, Sallan L, et al. 2018. An inverse latitudinal gradient in speciation rate for marine fishes. *Nature* 559(7714):392–95