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[REVIEW]

Gene Duplication of Androgen Receptor as an Evolutionary Driving Force Underlying the Diversity of Sexual Characteristics in Teleost Fishes

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Sexual dimorphism allows species to meet their fitness optima based on the physiological availability of each sex. Although intralocus sexual conflict appears to be a genetic constraint for the evolution of sex-specific traits, sex-linked genes and the regulation of sex steroid hormones contribute to resolving this conflict by allowing sex-specific developments. Androgens and their receptor, androgen receptor (Ar), regulate male-biased phenotypes. In teleost fish, *ar* ohnologs have emerged as a result of teleost-specific whole genome duplication (TSGD). Recent studies have highlighted the evolutionary differentiation of *ar* ohnologs responsible for the development of sexual characteristics, which sheds light on the need for comparative studies on androgen regulation among different species. In this review, we discuss the importance of *ar* signaling as a regulator of male-specific traits in teleost species because teleost species are suitable experimental models for comparative studies owing to their great diversity in male-biased morphological and physiological traits. To date, both in vivo and in vitro studies on teleost *ar* ohnologs have shown a substantial influence of *ars* as a regulator of male-specific reproductive traits such as fin elongation, courtship behavior, and nuptial coloration. In addition to these sexual characteristics, *ar* substantially influences immunity, inducing a sex-biased immune response. This review aims to provide a comprehensive understanding of the current state of teleost *ar* studies and emphasizes the potential of teleost fishes, given their availability, to find molecular evidence about what gives rise to the spectacular diversity among fish species.

Key words: sexual characteristics, teleost, androgen, androgen receptor, whole genome duplication, gene duplication, immunity

INTRODUCTION

The evolution of sexual dimorphism can be driven in

traits with different fitness optima between males and females (Darwin, 1871; Andersson, 1994; Arnegard et al., 2010). However, because males and females share much of their genome, the genetic correlation between the two sexes constrains the evolution of sexual dimorphism, which generates intra-locus sexual conflict (Cox and Calsbeek, 2009;

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Van Doorn, 2009). In addition to sex-linked genes, male-biased gene expression under the control of androgens is a possible mechanism to resolve such sexual conflicts by allowing the expression of certain traits specifically in mature male vertebrates (Williams and Carroll, 2009; Kitano et al., 2020). Previous studies have demonstrated that androgens contribute to the expression of a wide range of male-specific traits, including morphology and behavior, in vertebrates (Hau, 2007; Mank, 2007). Among vertebrates, teleost fishes exhibit a variety of sexual characteristics, such as fin elongation (Zauner et al., 2003), nuptial coloration (Ansai et al., 2021), copulatory organs (Ogino et al., 2004), and reproductive behaviors such as nest building (Hoar, 1962), courtship (Borg and Mayer, 1995), and aggressive behavior (Yamashita et al., 2020), in response to androgens. The effects of androgens on each tissue are mediated by the androgen receptor (Ar), which belongs to the nuclear receptor superfamily (Mangelsdorf et al., 1995; Baker, 1997; Laudet, 1997; Thornton and Kelley, 1998; Escriva et al., 2000). The Ar plays key roles in controlling the molecular processes involved in the development and evolution of sex characteristics. Most vertebrates have one Ar gene, but two distinct paralogs of the Ar genes (*ara* and *arb*) have been identified in several teleosts (Ikeuchi et al., 1999; Sperry and Thomas, 1999; Ogino et al., 2004). Recent studies have shown that teleost species have undergone teleost-specific whole genome duplication (TSGD), resulting in the production of two Ar ohnologs: *ara* and *arb* (Douard et al., 2008; Ogino et al., 2009). Because gene duplication can reduce the negative selection pressure on duplicated copies and drive the establishment of lineage-specific traits with novel biological functions (Ohno, 1970), *ar* ohnologs may have contributed to the diversification of sexual characteristics in the teleost lineage. Recent in vitro functional analyses and knockout (KO) studies of *ar* ohnologs indicate that the functional differentiation of *ara* and *arb* is likely one of the key events that have caused the rapid diversification of sexual characteristics in teleost species (Ogino et al., 2016, 2023; Crowder et al., 2018; Tang et al., 2018; Yu et al., 2018; Alward et al., 2020). Teleosts account for nearly half of all extant vertebrate species (Ravi and Venkatesh, 2018), and the evolutionary acquisition of diverse sexual characteristics driven by sexual selection may have contributed to the radiation of teleosts.

In this review, we provide a comprehensive understanding of *ar* gene function in the context of the development of sexual characteristics in teleost fishes, by summarizing recent findings on the molecular evolution and functional diversification of *ar* genes. This review also emphasizes the involvement of Ar regulation in immunity of teleost fishes because the immune system is closely associated with androgen signals due to the expression of *ars* in immune cells. The *ar* gene duplication may have contributed to wider variations in the immune response in teleost fish, which affect the survival and reproductive success of individuals according to environmental factors.

Evolutionary history of *ar* gene in vertebrates

Steroid hormone receptors are thought to have undergone molecular evolution through multiple gene duplications, including two whole genome duplication processes that occurred during early vertebrate evolution (Thornton,

2001). *ar* has not been identified in lamprey; however, genes showing ligand responsiveness almost identical to that of tetrapods are present in emerged cartilaginous fish (Ogino et al., 2009). Thus, it is thought that the *ar* gene emerged after the divergence of the jawless fish lineage, at least by the divergence of cartilaginous fishes through duplication of the gene encoding the progesterone receptor (Thornton, 2001; Ogino et al., 2018).

Most tetrapod species have one copy of *AR*, whereas most teleost fish have two distinct *ar* ohnologs generated by TSGD (Fig. 1). Medaka *ara* and *arb* are mapped to chromosomes 10 and 14, respectively, with a conserved synteny relative to a single region located in the *AR* gene on human chromosome X, suggesting that teleost *ar* gene duplication occurred as a result of TSGD (Ogino et al., 2009). TSGD is an evolutionarily recent whole genome duplication that occurred approximately 350 Ma, which is after the split of the non-teleost actinopterygian lineage (namely, bichir, sturgeon, gar, and bowfin) from the teleost lineage, but before the divergence of Elopomorpha (i.e., Japanese eel) and Osteoglossomorpha (i.e., silver arowana) (Hoegg et al., 2004; Jaillon et al., 2004; Pasquier et al., 2016). The fact that *ar* ohnologs are maintained in the genome approximately 350 million years after duplication suggests that these duplicated genes may have contributed to the evolution of the endocrine system and diverse reproductive functions in teleost fishes (Douard et al., 2008; Ogino et al., 2018). Indeed, the molecular evolutionary analysis of *ar* ohnologs in medaka and mosquitofish revealed that *ara* has a faster evolutionary rate than *arb*, with the accumulation of more novel substitutions in *ara* than in *arb* after the split of Elopomorpha (Douard et al., 2008; Ogino et al., 2009, 2018) (Fig. 1). The lineage-specific loss of *ara* likely occurred independently in Osteoglossiformes (Arowana), Cypriniformes (Zebrafish), Siluriformes (Catfish), and Salmoniformes (Rainbow trout) (Takeo and Yamashita, 1999; Hossain et al., 2008; Ogino et al., 2009; Huang et al., 2011).

Distinct molecular properties acquired in *ar* ohnologs in teleost fishes as assessed by in vitro functional analysis at the protein level

Ar is composed of three major functional domains: a hypervariable N-terminal domain (NTD), a central highly conserved DNA binding domain (DBD) consisting of two zinc finger motifs, and a COOH-terminal ligand binding domain (LBD) (Evans, 1988; Bertrand et al., 2004; Bridgham et al., 2010; Baker et al., 2015) (Fig. 2A). Testosterone (T) and 5 α -dihydrotestosterone (DHT) are effective ligands for mammalian Ars (Quigley et al., 1995), whereas 11-ketotestosterone (11KT) is known as a potent androgen in teleost fishes (Borg, 1994). However, a recent analysis showed the presence of 11KT in urodele amphibians (Bolaffi et al., 1979) and humans (Imamichi et al., 2016), suggesting that 11KT is a functional androgen in other vertebrates and teleost fishes.

The molecular properties of *ar* ohnologs have been extensively studied in medaka and mosquitofish using in vitro reporter gene assays. *Arb* in these fishes exhibits a ligand-dependent transactivation capacity similar to that of AR in tetrapods, whereas *Ara* exhibits higher ligand-dependent transactivation capacity and constitutive nuclear localization in COS-7 cells (Ogino et al., 2009) (Fig. 2B). Based

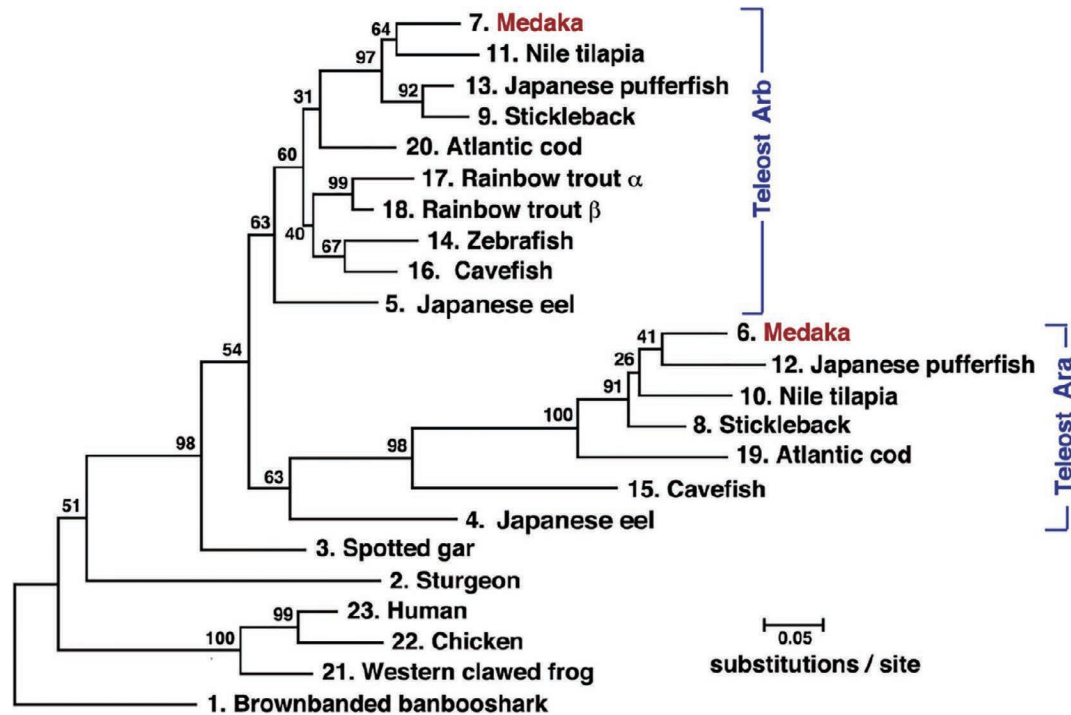


Fig. 1. Phylogenetic analysis of *Ar* genes. Molecular phylogenetic tree of vertebrate *ar* genes. This tree was constructed from the protein sequences of *ar* genes using the maximum-likelihood (ML) method combined with the JTT substitution model. The Brown-banded bamboo shark *ar* gene was used as an outgroup. The support values at the nodes represent bootstrap probabilities in the ML analysis. The GenBank and Ensembl accession numbers of the gene sequences used for this analysis are provided in Supplementary Table S1. Figures were modified from the previously published papers (Ogino et al., 2016, 2023) with permission for reuse (license number 5640600664159 from Oxford University Press).

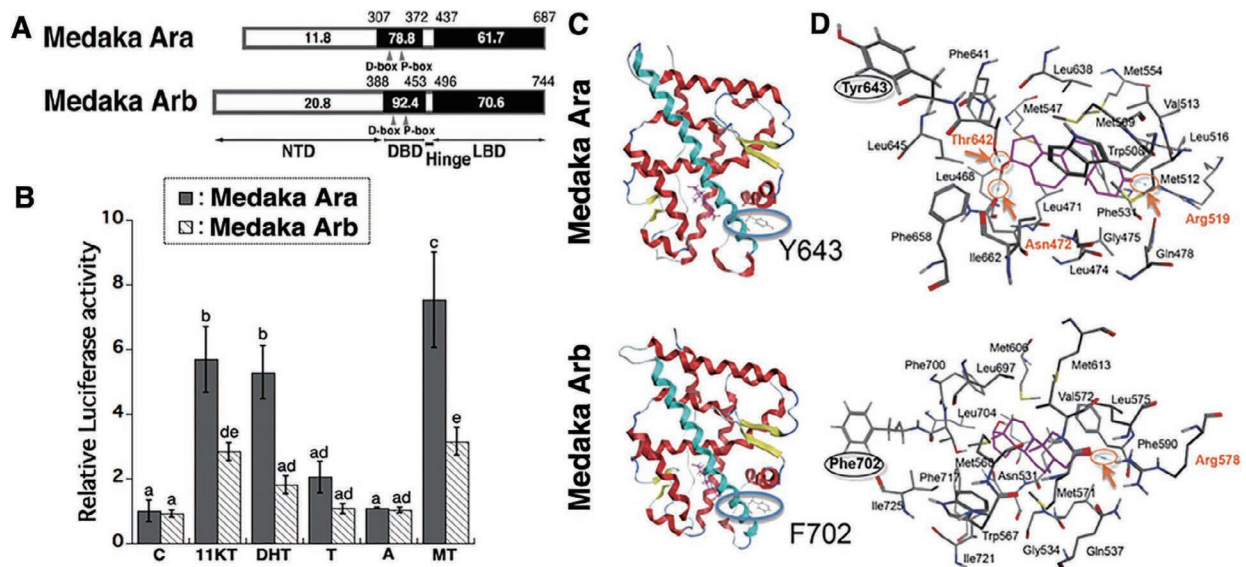


Fig. 2. Characterization of molecular property of medaka *Ar* ohnologs. **(A)** Structure of *Ar* ohnologs in medaka (GenBank accession numbers, Ara: AB252233 and Arb: AB252679). The numbers above each box refer to the amino acid positions in the putative DBD and LBD. The percentage of identity of the deduced amino acid sequences of each domain to the human AR (NM_000044.2) is shown in the boxes. **(B)** Ligand dependent transactivation properties of medaka *Ar* ohnologs in COS-7 cells. Transfected cells were treated with 10^{-9} M of various androgens, namely, 11KT, DHT, T, androstenedione (A), and 17α -methyl testosterone (MT), or vehicle only as a control (indicated as C). The relative transcriptional activity of *Ar* is shown as values normalized to pRL-induced activities. Vertical bars, Mean \pm SD. Different letters indicate statistically significant differences in luciferase activity ($P < 0.05$) (ANOVA followed by the Tukey-Kramer test). **(C)** 3D ribbon diagrams of medaka Ara and Arb. The helices 10/11 are labeled in blue. The key amino acid substitutions that determine *Ar* ohnolog-specific transactivation properties, Ara Y643 and Arb F702 in helices10/11, are indicated. **(D)** Predicted modes obtained from the docking simulation analysis of 11KT for medaka Ara and Arb. Orange arrows indicate the predicted hydrogen bonds that stabilize the receptor-ligand complex. Figures were modified from Ogino et al. (2016) with permission to reuse; license number 5640600664159.

on site-directed mutagenesis and computational prediction of protein-ligand interactions between medaka Ar LBDs and 11KT, two key substitutions generating the new functionality of Ara have been identified (Ogino et al., 2016) (Fig. 2C, D). Substitution of the possible importin-binding site in the hinge region (medaka Ara K375 and Arb G456) contributes to the unique intracellular localization of medaka Ara in COS-7 cells. The substitution of helices 10/11 in the LBD (medaka Ara Y643, Arb F702) modulates the hydrogen bonds that stabilize the Ar LBD-11KT complex, leading to the generation of hyperactive Ara. These non-synonymous substitutions in medaka Ara are highly conserved in the LBD in teleost fishes, except the Japanese eel, which represents an earlier branching teleost group (Inoue et al., 2003; Li et al., 2008) expected to have Ar ohnologs derived from their respective ancestral genes before functional diversification. Both Japanese eel Ar ohnologs maintain ligand-dependent nuclear localization and show no significant differences in their transactivation responses (Ikeuchi et al., 1999; Ogino et al., 2016). The insertion of Ara-specific substitutions into Japanese eel Ar ohnologs recapitulates the evolutionary novelty of medaka Ara in COS-7 cells (Ogino et al., 2016), indicating that the substitution generating the new functionality of teleost Ara was fixed in the teleost genome after the divergence of the Elopomorpha lineage.

Functional diversity of ar ohnologs in sexual characteristics development assessed by genome engineering

In mammals, the role of AR in sexual dimorphism in morphology and reproductive behavior has been extensively investigated by AR KO (Yeh et al., 2002; Matsumoto et al., 2003; Juntti et al., 2010), the testicular feminization mutation (Tfm) rodents which lack functional AR, and disorders of androgen insensitivity syndrome (AIS) in humans (He et al., 1991; Griffin, 1992; Quigley et al., 1995; McPhaul, 1999). AR KO male mice exhibit a female-type external appearance with abnormal external genitalia, and the absence of sex accessory organs but retain small testes with cryptorchidism and severely arrested spermatogenesis (Yeh et al., 2002; Matsumoto et al., 2003; Zheng et al., 2015). These findings indicate the essential role of AR in the development of male reproductive organs and spermatogenesis. Such pleiotropic expression in various tissues may have constrained the molecular evolution of the AR gene in mammals. As described above, the fundamental roles of AR in reproduction have been illustrated in mammals. However, few empirical studies have investigated the molecular mechanisms underlying the evolutionary acquisition of diverse sexual characteristics in vertebrates. The acquisition of two duplicated copies of *ar* could have contributed to the diversification of masculine sexual characteristics found in teleosts, owing to the reduction in their pleiotropic constraints.

Recently, the generation of *ar* KO fishes from zebrafish (*Danio rerio*) (Yong et al., 2017; Tang et al., 2018; Yu et al., 2018), African cichlid (*Astatotilapia burtoni*) (Alward et al., 2020), and Japanese medaka (*Oryzias latipes*) (Ogino et al., 2023) was reported. In both zebrafish and African cichlids, *arb* KO showed smaller testis size. Zebrafish *arb* KO males are infertile during natural mating due to defective spermatogenesis, although a small number of mature sperm that can fertilize oocytes by in vitro fertilization are produced (Tang et

al., 2018; Yu et al., 2018). Another possible reason for infertility is the reduced frequency of courtship-related behaviors, such as chases, zigzags, and tailnose, which are tactile behaviors related to spawning stimulation toward females and quivers (Yong et al., 2017). However, the zebrafish genome contains a single *ar* gene, possibly arising from the loss of a duplicate gene (Force et al., 1999), and genetic analysis of teleost fishes with both *ar* ohnologs is necessary to understand the contribution of *ar* gene duplication to the diversification of sexual characteristics.

The retention of the two *ar* ohnologs with distinct protein properties may have contributed to reproductive diversification in the teleost lineage. African cichlid and Japanese medaka are excellent model species for investigating the role of *ar* ohnologs in the development of sexual characteristics because they show social and reproductive behaviors and morphological traits such as coloration and fin elongation in the laboratory as in nature (Egami and Ishii, 1956; Yamamoto and Egami, 1974; Yokoi et al., 2015; Alward et al., 2020; Yamashita et al., 2020). Recent *ar* KO studies in African cichlid and Japanese medaka revealed that both *ara* KO males and *arb* KO males are fertile, but their frequency of reproductive success and fertilization rate has decreased because the two *ar* ohnologs have diverged in their functions for male sexual characteristics (Alward et al., 2020; Ogino et al., 2023). The African cichlid *ara* codes for reproductive and aggressive behaviors and *arb* for dominant bright coloration; either *ar* is sufficient for attacking males (Alward et al., 2020). Consistent with this, the Japanese medaka *arb* predominantly regulates external sexual characteristics such as fin morphology, pigmentation pattern, and sexual motivation (Fig. 3). The *arb* KO male medaka has shorter anal fin rays without any papillary processes which develop as branched bone nodules derived from the anal fin rays, as in females (Fig. 3). These masculine fin morphologies enable males to rub and prevent females from escaping during wrapping for spawning (Ono and Uematsu, 1957). However, in contrast to cichlids, medaka *ara* regulates not only reproductive behavior but also external sexual characteristics, such as tooth enlargement, which can be used in intra-male competition, suggesting that the functional contribution of *ara* varies among species (Ogino et al., 2023).

Recent technological advances in improving the resolution of androgen research have included the establishment of two knock-in medaka strains, *ara*^{FLAG-2A-mClover3} (Ara-KI) and *arb*^{FLAG-2A-mClover3} (Arb-KI), which express two distinct proteins, an epitope (3xFLAG)-tagged Ar and a green fluorescent protein (mClover3), from endogenous *ar* loci (Ogino et al., 2023). These strains enable the visualization of the expression patterns of Ara and Arb with green fluorescence and their intracellular localization by immunohistochemistry using an anti-FLAG antibody. For example, prominent green fluorescence and nuclear localization of Arb have been observed in the developing papillary processes of the anal fin. This is likely why *arb* KO males lack papillary processes (Ogino et al., 2023). Such differences in the expression patterns and the molecular property of Ar ohnologs indicate that they have distinct *cis*-regulatory sequences and substitution in protein coding sequences. In fact, the *cis*-regulatory sequences that are conserved in the 5' upstream regions of medaka, stickleback, and fugu *ara* genes are not conserved

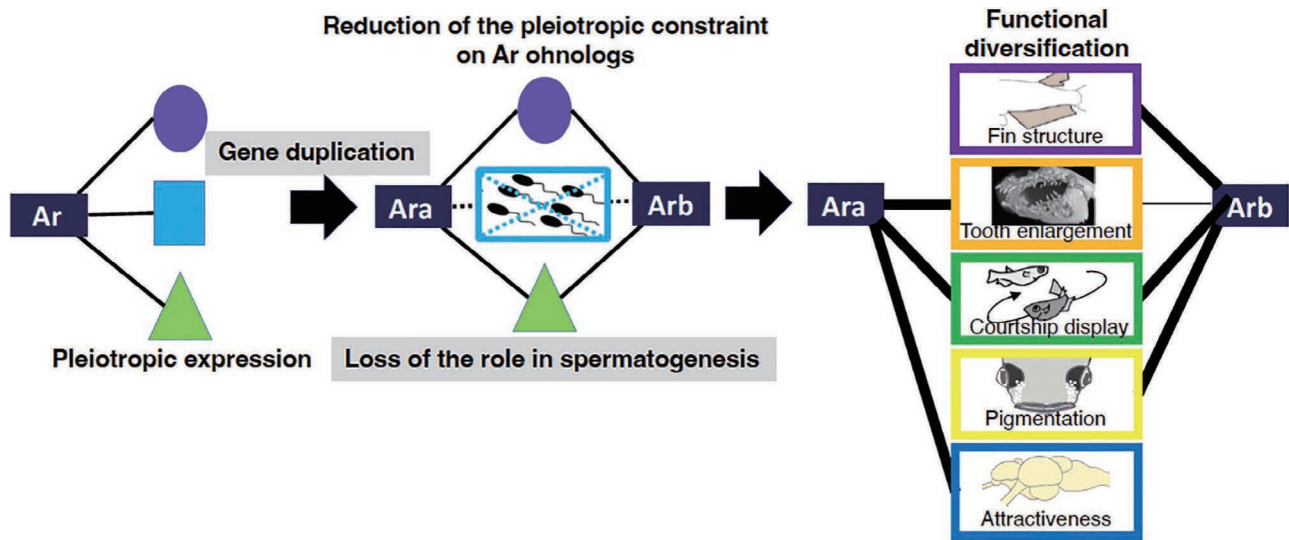


Fig. 3. Evolutionary scenario for the acquisition of male-specific sexual characteristics through *ar* gene duplication. It is thought that the increase in the copy number of the *ar* gene due to TSGD and the relaxation of evolutionary constraints due to the loss of its role in spermatogenesis serve as driving forces for the evolution of sexual characteristics in Japanese medaka.

in those of medaka *arb* gene and zebrafish *ar* gene (Ogino et al., 2023). An Ara-specific substitution has been identified in the nuclear localization signal (NLS) that contacts the NLS binding proteins such as the importin α proteins (Ogino et al., 2016). These findings indicate that differences in the regulation of both transcription and subcellular localization of Ars may result in the regulation of different target genes and determine functional differences in Ar ohnologs. Chromatin immunoprecipitation sequence analysis of target genes for each Ar ohnolog using these epitope-tagged Ar-KI medaka lines will provide a more detailed molecular mechanism of the functional differences of Ar ohnologs in vivo. Further analyses targeting the evolutionary acquisition of Ar-target genes as well as the changes in *ar* gene function will enable us to understand the mechanisms of the evolutionary diversification of sexual characteristics driven by *ar* gene duplication.

The evolutionarily conserved and diverged functions of *ar* genes affecting sexual characteristics among vertebrates

In Japanese medaka, not only single *ar* KOs (*ara* KO and *arb* KO) but also the double KO (*ar* DKO) has been established (Ogino et al., 2023), which enables the evolutionary comparison of *ar* function among vertebrates. Japanese medaka *ar* DKO males show a female-like appearance with shorter anal fin rays without any papillary processes or lack of tooth elongation. The *ar* DKO males could not breed successfully with females under natural mating, with mostly abolished courtship displays, whereas the single KO males displayed courtships, indicating the functional redundancy of *ar* ohnologs for courtship displays (Ogino et al., 2023). In rodents, *AR* KO resulted in the ablation of male-typical sexual and aggressive behaviors (Sato et al., 2004). These findings indicate that androgens play an essential role in male sexual behavior in vertebrates.

Unexpectedly, *ar* DKO can produce functional sperms. The frequency of sperm movement, average speed of

sperm, and in vitro fertilization rate were not significantly different from those of wild type males; moreover, total sperm number is higher in *ar* DKO than wild-type in Japanese medaka (Ogino et al., 2023). In contrast, *AR* KO mice exhibit spermatogenesis arrest at the pachytene spermatocyte stage (Yeh et al., 2002), and *ar* KO zebrafish exhibit a decreased number of mature sperms (Tang et al., 2018; Yu et al., 2018). Japanese eel spermatogenesis is stimulated by 11KT in cultured testes (Miura et al., 1991). Furthermore, previous studies in African cichlid showed that the *ar* DKO possess small testes (Alward et al., 2020; Hoadley et al., 2022) although it has not been investigated whether spermatogenesis proceeds normally. Given these situations, the essentiality of *ar* ohnologs in spermatogenesis has been lost at least in the lineage leading to medaka. The loss of their function in spermatogenesis and gene duplication likely resolved the pleiotropic function derived from their ancestral gene, which reduced the evolutionary constraints on *ar* ohnologs and accelerated the acquisition of exaggerated male-specific traits in medaka (Fig. 3). The medaka species are widely distributed in southern and southeast Asia and they have acquired diverse male-specific sexual characteristics such as fin outgrowth, pigmentation, and reproductive behavior (Ono and Uematsu, 1957; Yamamoto and Egami, 1974; Mokodongan and Yamahira, 2015; Nishiike et al., 2021).

Androgen-mediated immunomodulation in teleost fishes

It is widely known that vertebrates show sex differences in several aspects of immunity (Roved et al., 2017; Yang et al., 2022). For instance, the susceptibility of the immune system to sex steroid hormones is largely responsible for sex differences in fish immunity (Chavez-Pozo et al., 2018). Among teleost fishes, the expression of *ar* in the major immune organs, namely the head kidney, liver, and spleen, has been reported in salmonids, gilthead seabream, and zebrafish (Slater et al., 1995; Hossain et al., 2008; Aguila et

al., 2013). Teleost immune relevant leukocytes, namely acidophilic granulocytes and macrophages, have also been reported to express *ar* (Sanchez-Hernandez et al., 2014). These observations indicate that androgen signaling exhibits diverse effects on fish immunity.

Studies in various teleost species identified both positive and negative effects of androgen on immunity. In gilt-head seabream, enhanced phagocytic activity and accumulation of immune-related cytokines, peroxidases, and complement activity have been reported in response to T and 11KT (Chaves-Pozo et al., 2003; Cuesta et al., 2007; Aguila et al., 2013; Castillo-Briceno et al., 2013). These features represent enhanced innate immunity against diverse pathogens, some of which are possibly influenced by androgen signaling. In contrast, studies on other fish species have depicted androgens as immunosuppressors, as shown below. Leukocytes in salmonid species express *ar* and are sensitive to T and its derivatives, but respond negatively in that leukocyte populations decrease in response to direct exposure to physiological levels of T (Slater et al., 1995; Slater and Schreck, 1997). In addition, the intraperitoneal injection of androgen derivatives including 11KT to common carp suppresses phagocytosis and ROS activities of macrophages (Watanuki et al., 2002). Rainbow trout B lymphocytes, which are key mediators of humoral adaptive immunity, were also affected by T or 11KT treatment and showed reduced secretion of IgM against lipopolysaccharides in the liver and spleen (Hou et al., 1999).

The negative effects of androgen on the immune system are in agreement with the immunocompetence handicap hypothesis (ICHH), as stated by Folstad and Karter (1992). The ICHH states the existence of a trade-off between the development of secondary sexual characteristics and immu-

nity due to the immunosuppressive effect of androgens. In birds, individuals with more developed secondary sexual traits have a higher parasite load (Folstad and Karter, 1992). Similar examples have been observed in teleost fishes, such as arctic charr, stickleback, and cyprinids (Folstad and Karter, 1992; Liljedal et al., 1999; Kurtz et al., 2007; Rohlenova and Simkova, 2010).

However, some studies have questioned the ICHH. For example, the following results are inconsistent with this hypothesis. In the tench (*Tinca tinca* L.), T administration repressed the immune response, whereas the immune response stimulated by β -glucan did not affect plasma T levels (Vainikka et al., 2005). Also, tested immunological parameters had only weak or no correlation with T levels to support ICHH in humans, bluegill, or common carp (Saha et al., 2003, 2004; Loggie et al., 2018; Nowak et al., 2018). In the bluegill, 11KT implantation reduced the expression of immune-related genes (Partridge et al., 2014). However, the stimulation of immune response with vaccination composed of formalin-inactivated *Vibrio anguillarum* and *V. ordalii* did not decrease the circulating 11KT level (Loggie et al., 2018). These results imply that additional androgens could down-regulate immune-related gene expressions, while the immune response induced by infection does not influence circulating androgen levels.

These reports imply that there is no absolute enhancement or suppression of immunity solely due to the action of androgens. However, immunity encompasses a wide range of self-defense systems, and the above-discussed studies varied in the depiction of immune-related features, as well as the species. To gain comprehensive insight into the influence of androgens and their receptors on immune response, it is imperative to systematically dissect and classify the

In vivo testosterone derivative treatments

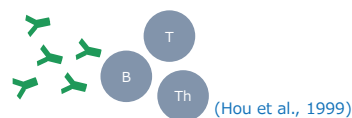


Reduced leucocytes
(Slater et al., 1997)

**Immune cell
activities**



**Humoral
adaptive immune response**



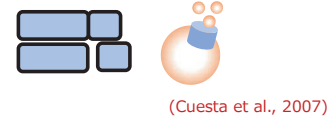
ROS response



IL1 β , TNF α , COX2...
**Cytokine
&
immune relevant gene expressions**

(Chavez-Pozo et al., 2003)
(Castillo-Briceno et al., 2013)
(Partridge et al., 2014)

Complement activities



Phagocytosis



No androgen effect observed

(Saha et al., 2003)
(Saha et al., 2004)
(Vainikka et al., 2005)
(Loggie et al., 2018)

Fig. 4. Androgen-mediated immune modulation. Schematic diagram of androgen-mediated immune modulation in teleost fish. In both in vivo and in vitro studies, the red letters represent enhanced modulation, whereas the blue letters represent suppressive modulation. The lists of references list previous studies.

diverse facets of the immune system. To the best of our knowledge, most studies on the effects of androgens on teleost immunity have focused on the innate immune system (Fig. 4). The *ar* ohnologs with distinct molecular properties could have contributed to the diversification of the immune system in teleost fishes. Further studies on the effect of androgens on teleost adaptive immunity, considering functional differences in *ar* ohnologs, are highly anticipated.

CONCLUSION

The diversity of the teleost fishes accounts for the majority of the diversity of currently existing vertebrates. TSGD was the key event that formed the foundation of teleost radiation. In addition to sex-linked genes, evidences showed that the *Ar* is responsible for sexual dimorphism by regulating the susceptibility to androgens. The emergence of duplicated genes with overlapping roles that allow organisms to be phenotypically stable may relax selection pressures and enable innovation. Thus, duplicated *ara* and *arb* ohnologs may have had a significant effect on the emergence of variations in reproductive traits. One representative example is the medaka *ar* ohnologs, wherein the *arb* is likely to have been biased to maintain ancestral function under the stronger pressure of sexual selection compared to *ara* which has functionally diverged in each species. Interestingly, the *ar* ohnologs of medaka lost their essentiality in spermatogenesis derived from their ancestral gene, which can be thought to resolve pleiotropic constraints on genes. The functional diversification of *ar* ohnologs could have been promoted by the loosened constraint on *ar* ohnologs by gene duplication and following the loss of the ancestral gene function.

To elucidate the whole function of *Ar*, further studies on other teleost species and non-teleost ray-finned fishes are required for comparison; studies should give deeper attention to the functional differences of *ar* ohnologs. Fortunately, most teleost fish lineages based on their phylogeny are present to date. The availability of wide lineages and recent advancements in genome information render teleost fish suitable models for genetic comparisons. Since genetic analysis methods such as KO and knock-in studies are available for many teleost fishes, cutting-edge molecular biology techniques could be applied to these models. Hence, teleost fish are ideal models for comparative studies to understand the molecular mechanisms underlying the evolutionary diversification of sexual traits. Studies using epitope-tagged *Ar*-KI medaka lines indicate that differences in the regulation of both the transcription and intracellular localization of *Ars* can be possible determinants of the functional differences of *Ar* ohnologs. Further studies to elucidate the gene regulatory mechanisms of *ars* with higher resolution, and chromatin immunoprecipitation sequencing analysis of their target genes for *Ar* ohnologs using *Ar*-KI lines will enable us to understand the genetic changes underlying the evolutionary novelty of sexual traits regulated by androgen signaling. The expression of *Ar* ohnologs in immune-related cells and the positive and/or negative effects of androgens on the immune system suggest that androgen signaling can cause sex differences in immune responses and possibly affect individual survival. In conclusion, from external phenotypes such as fin elongation to the internal phenotype exemplified by immune responses, varia-

tions in reproductive and survival strategies imply that *Ar* contributes to the evolutionary radiation of teleost fishes.

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COMPETING INTERESTS

The authors declare no competing interests.

AUTHOR CONTRIBUTIONS

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SUPPLEMENTARY MATERIALS

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Supplementary Table S1. Accession numbers of the sequences used for the phylogenetic analysis.

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