LABORATORY OF BIORESOURCES

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Medaka is a small egg-laying "secondary" fresh water fish found in brooks and rice paddies in Eastern Asia. This species has a long history as an experimental animal, especially in Japan. Our laboratory has conducted studies on the evolution of the sex determination system using medaka and relatives, adaptive significance of mate-guarding behavior, The molecular genetic basis of diversified sexually dimorphic traits in *Oryzias* species and the identification of causal genes for pigment cell mutants. In addition to these activities, our laboratory has stepped forward to lead the National BioResource Project Medaka (NBRP Medaka) from 2007.

I. Evolution of the sex chromosome and sexdetermining genes in *Oryzias* fish

Sex chromosomes harbor a primary sex-determining signal that triggers sexual development of the organism. In mammals, *Sry* is the dominant male-determining gene located on the Y chromosome, and has evolved from the neural gene *Sox3* on the X chromosome probably through a regulatory mutation. However, independent evolution of sex chromosomes is widespread in non-mammalian vertebrates, suggesting that sex determination mechanisms are regulated

			Sex chromosome		
		Species	System	Chr	Gene
1	atipes group	O. mekongensis	XY	2	
		O. latipes	XY	1	Dmy
	4-	O. curvinotus	XY	1	Dmy
javanicus grou		O. luzonensis	XY	12	Gsdf
	avanicus group	O. minutillus	XY	8	000000
	\neg	O. dancena	XY	10	OdSox3 ^Y
	- 4 -	O. hubbsi	ZW	5	
celebensis g		O. javanicus	ZW	16	
		O. wolasi	XY	24	
		O. woworae	XY	24	
L.	┥┌──	O. celebensis	XY	24	
	Ч —	O. matanensis	XY	24	
	- Ч.–	O. profundicola	XY	10	OmSox3 ^v
	<u> </u>	O. marmoratus	XY	10	OmSox3 ^Y

Figure 1. Phylogenetic relationships and sex determination mechanisms in *Oryzias* fishes.

by different genes and have evolved rapidly. Medaka fishes in the genus Oryzias have different sex chromosomes with different systems (XY and ZW), providing ideal conditions for investigating the mechanisms that lead to the rapid turnover of sex chromosomes (Figure 1). So far, different sex-determining genes, Dmy and Gsdf^Y, have been isolated from the Oryzias species, demonstrating that turnover of sex chromosomes is associated with the substitution of master sex-determining genes. Recently, we identified Sox3 as a novel sex-determining gene on the XY sex chromosomes in the marine medaka Oryzias dancena/melastgma by positional cloning. Sex reversed phenotypes in transgenic fish and loss-of-function mutants of the Y chromosomal Sox3 allele all point to its critical role in sex determination, suggesting that the neo-Y chromosome of O. dancena arose by co-option of Sox3. Furthermore, we found the Sox3 gene also on the XY sex chromosomes in distantly related Oryzias species, O. marmoratus and O. profundicola. Fine mapping and association analysis identified the Y chromosome-specific 430-bp insertion at the Sox3 locus, which appeared to be involved in its male determination function. The Sox3dependent sex determination system in Oryzias species is polyphyletic, and the Y-specific insertion has not been found in O. dancena, suggesting that Sox3 has evolved as the sex-determining gene independently in different lineages of Oryzias. These results suggest that Sox3 might have acquired the novel male-determining function repeatedly and independently during vertebrate evolution.

II. Identification of the causal gene of the medaka iridophore mutant, guanineless(gu)

The medaka has four pigment cell types: black melanophores, yellow xanthophores, white leucophores, and silvery iridophores. To date, causal genes of melanophore, xanthophore, and leucophore mutants have been elucidated, but the causal gene for the iridophore mutant remains unknown. Herein, we describe the iridophore mutant gu, which exhibits a strong reduction in visible iridophores throughout its larval to adult stages. The gu locus was previously mapped on chromosome 5, but was located near the telomeric region, making it difficult to integrate into the chromosome. We sought the causal gene of gu using synteny analysis with the zebrafish genome and found a strong candidate, purine nucleoside phosphorylase 4a. Gene targeting and a complementation test showed that pnp4a is the causal gene of gu. This result will allow the establishment of inbred medaka strains or other useful strains with see-through phenotypes, without disrupting the majority of the genetic background of each strain.

III. Adaptive significance of persistent mateguarding behavior in medaka

Males of various animals exhibit mate-guarding behavior to prevent rival males from mating with the female. Most of them, however, exhibit this behavior during only the mating period, because persistent mate-guarding is thought to have a high energy cost, which would reduce male survival rate. Previously, we reported that medaka males exhibit mateguarding irrespective of the mating period (Yokoi et al., 2015) and it remains unknown whether there is some benefit of the persistent mate-guarding, such as enhancement of male reproductive success, in medaka fish. In addition, medaka females tend to choose visually-familiarized males as their mating partner and the adaptive significance of this female mating preference is totally unknown. Recently, we found that mate-guarding led to familiarization with the female while at the same time blocking the female's visual familiarization with other males in medaka fish. We put three fish (female, male, male) separately in a transparent three-chamber tank, which allowed the male in the center (near male) to maintain a closer proximity to the female than the other male (far male). Placement of the wild-type male in the center blocked visual familiarization of the far male by the female via mate-guarding. In contrast, placement of an arginine-vasotocin receptor mutant male, which exhibits mate-guarding deficits, in the center, allowing for maintaining a closer proximity to the female by the far male and did not block familiarization of the far male with the female. This finding suggested that persistent mate-guarding allows males to gain familiarity with the female over their rivals, which may enhance female preference for the dominant male (Figure 2). We hope that this study helps us understand the evolutional origin of "pair-bonding".

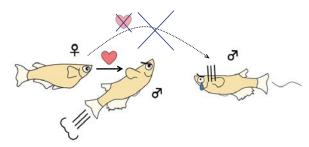


Figure 2. Persistent mate-guarding blocks familiarization between the female and the rival male, which may enhance female preference for the dominant male.

IV. The molecular genetic basis of diversified sexually dimorphic traits in *Oryzias* species endemic to Sulawesi, Indonesia

Sexual dimorphism is prevalent, but often differs remarkably between closely related species. However, we know little about which genetic changes can actually contribute to diversification of sexually dimorphic traits between closely related species. We therefore started to investigate the molecular genetic mechanisms underlying the diversification of sexually dimorphic body colorations in medaka (genus Oryzias) from Sulawesi, Indonesia. As a first step, we focused on an endemic species Oryzias woworae, whose males show red in the pectoral fins and blue in the lateral body. Quantitative trait loci (QTL) mapping in a F₂ intercross between a male of O. woworae and a female of O. celebensis, which is a close relative without such sexually dimorphic colorations, revealed that an autosomal locus controls red pigmentation in the pectoral fins. Subsequent gene expression analysis showed that upregulation of a gene on the QTL by the cis-regulatory mutation(s) would be responsible for the red fins. Further analysis with targeted genome editing technologies are underway to elucidate the molecular and developmental mechanisms underlying the red fin traits.

Publication List:

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[Original paper (E-publication ahead of print)]

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[**Review article**]

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