Meta-analysis of gonadal transcriptomes in protogynous fishes provides novel perspective into sex change machinery

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Abstract

Protogynous fishes can change sex from female to male; concomitantly, their ovarian tissue is completely replaced by testicular tissue. The high functional conservation of gonads across organisms suggests the existence of as-yet-undefined common and essential factors in the regulation of such gonadal transformation. To identify these factors, we conducted a meta-analysis of public and newly derived gonadal transcriptome data from seven species. Classical sex change-related genes were differentially expressed between the ovary and transitional gonads, which corroborated previous reports on protogynous fishes. Moreover, we identified novel factors not previously associated with gonadal sex change in fish. Notably, the expression patterns of acetoacetyl-CoA synthetase (*aacs*) and apolipoprotein Eb (*apoeb*), which are involved in cholesterol synthesis and catabolic processes, respectively, suggest that the levels of cholesterol, a precursor of steroid hormones crucial for sex change, are decreased upon sex change onset. Thus, cholesterol dynamics may influence gonadal transformation in protogynous fishes.

Introduction

Sequential hermaphroditism, a phenomenon in which individuals undergo sex change during their lifetime, has been extensively recognized in teleosts over the past several decades[1]. Specifically, protogyny (i.e., the transformation from female to male) is prevalent in 20 families[2]. Phylogenetic analyses have shown that this characteristic has been independently acquired in various evolutionary lineages[3,4]. On the other hand, the complete replacement of ovarian tissue with testicular tissue is commonly observed during protogynous sex change[5-9], the intricate regulatory mechanisms responsible for inducing these remarkable transformations in gonadal tissue remain incompletely understood. Furthermore, considering the high functional conservation of gonads across organisms, the existence of a regulatory mechanism governing gonadal transformation comprising common and essential factors across protogynous fishes is plausible; however, a comprehensive perspective of this process remains elusive.

Accordingly, elucidation of the molecular mechanisms underlying the gametogenesis switch in sex-changing fish has subsequently become a focus of research. In particular, the expression patterns of multiple sex-related genes during sex change within the family Labridae, which serves as a model for protogynous sex change, have been explored[10-13]. Recently, next-generation sequencing technology has enabled researchers to conduct comprehensive analyses of gene expression, allowing the identification of global gene expression profiles during gonadal transformation in protogynous fish belonging to Labriformes, Perciformes, and Synbranchiformes[14-18]. Thus, these results suggest the involvement of several pivotal genes in the ovary-to-testis transformation in sex-changing fish.

For example, a repertoire of sex-related genes, including cytochrome P450, family 19, subfamily A, polypeptide 1a (*cyp19a1a*), forkhead box L2a (*foxl2a*), folliculogenesis specific bHLH transcription factor (*figla*), anti-Müllerian hormone (*amh*), gonadal somatic cell derived factor (*gsdf*), doublesex and mab-3 related transcription factor 1 (*dmrt1*) were identified as

differentially expressed genes (DEGs) during sex change across protogynous fishes. Notably, the gonadal expression of *cyp19a1a* and *foxl2a*, which are key players in maintaining ovarian status, is reduced upon the onset of sex change in multiple species[13,19,20]. *cyp19a1a* encodes aromatase, an enzyme responsible for the conversion of androgens (e.g., testosterone) to estrogens (e.g., estradiol-17ß; E2), whereas *foxl2a* encodes a transcription factor that targets and up-regulates *cyp19a1a* in teleost fishes[21,22]. Furthermore, female-to-male sex change is triggered by a rapid decline in E2 levels[6]. The expression profiles of these genes coordinate well with the reduction in E2 levels upon sex change onset. Conversely, *amh*, *gsdf*, and *dmrt1* are crucial for testicular differentiation and development in teleost fishes[23-29]. In several sex-changing species, the upregulation of these genes coincides with the emergence of testicular tissue during transition, suggesting that these genes are involved in testicular formation during gonadal sex change[10-13,30].

Transcriptome analysis during gonadal transformation has also revealed differential expression of several genes not previously implicated in sex determination or differentiation pathways. In particular, upregulation of apolipoprotein Eb (*apoeb*), ectonucleotide pyrophosphatase/phosphodiesterase 2 (*enpp2*), and l-rhamnose-binding lectin CSL2 (*csl2*) expression, accompanied by downregulation of galectin-3 (*gal3*), was observed during the early phase of gonadal sex change in the protogynous Asian swamp eel *Monopterus albus*. These findings suggest that these factors are involved in gonadal transformation, particularly during the initiation of sex changes[14,17]. However, verifying their direct involvement in the sex change process remains challenging. Therefore, a novel approach is required to obtain additional evidence.

The recent exponential growth of high-throughput sequencing data available in public databases has opened new avenues for the effective utilization of meta-analysis. By amalgamating transcriptome data from multiple studies, meta-analysis has attracted attention as a powerful tool capable of providing novel insights overlooked by traditional

hypothesis-driven research methods. Indeed, several reports have described the discovery of previously unrecognized gene expression profiles through meta-analysis of publicly available transcriptome data[31-35]. Moreover, the commonalities revealed by meta-analytical approaches not only provide more solid evidence than that from individual studies but also serve as valuable launching points for data-driven research.

Therefore, the objective of the present study was to identify the shared factors involved in gonadal transformation across species using a meta-analysis of publicly available transcriptome data from multiple experiments and species. Moreover, to improve the performance of the meta-analysis, we included data (*de novo* genome assembly data and RNA sequencing (RNA-Seq) data from gonads undergoing sex change) generated in-house from an additional well-studied species, the three-spot wrasse, *Halichoeres trimaculatus*, a protogynous species belonging to the family Labridae[10-12]. Through meta-analysis of RNA-Seq data encompassing seven protogynous species from three orders (Fig. 1), we identified 168 DEGs between the transitional gonads and ovaries. Using bioinformatics and gene set enrichment analyses, we reevaluated the relationship between these factors and gonadal sex change, providing a novel perspective regarding the mechanisms underlying this process.

Results

De novo genome assembly and transcriptome of gonadal tissue in the three-spot wrasse.

High-throughput genome sequence data were obtained from a locally obtained female three-spot wrasse from Okinawa, Japan. The obtained HiFi data, which comprised approximately 32 Gb and encompassed approximately 1.9 million DNA sequences, were assembled using the hifiasm program[36]. Subsequently, the acquired Hi-C data were used for scaffolding, resulting in the generation of 227 scaffolds. The longest scaffold measured 44.2

Mb, with an N50 length (the shortest of the lengths covering 50% of the genome) of 37.9 Mb, contributing to a total assembly length of approximately 849.9 Mb. Assessment using BUSCO[37] revealed a completeness > 98%, indicating a high level of coverage and contiguity in the *de novo* genome assembly of the three-spot wrasse (Table 1).

The RNA-Seq reads obtained from transitional gonads and ovaries of additional females (n=2 each group) were mapped to the genome assembly, and the obtained mapping results were used to assemble the transcriptome for the annotation file ("merged.gtf"). This process yielded 27,573 transcript sequences (Table 2). Subsequently, 24,695 coding sequences (protein sequences) were predicted from the set of transcript sequences using TransDecoder[38].

Data curation of public RNA-Seq data and genomic information. We downloaded Sequence Read Archive (SRA) data from six fish species for which sex changes have been reported:[2] bluehead *Thalassoma bifasciatum* (order Labriformes); orange-spotted grouper *Epinephelus coioides*, Hong Kong grouper *E. akaara*, and black seabass *Centropristis striata* (order Perciformes); and Asian swamp eel *Monopterus albus* and zig-zag eel *Mastacembelus armatus* (order Synbranchiformes). Furthermore, using the metadata associated with the SRA data, we curated the RNA-Seq data into comparable sample pairs of intersexual (transitional) gonads and ovaries (a total of 31 paired data, including three-spot wrasse). The data pairs analyzed in this study are listed in Supplementary Table 1.

The genome sequences of five of the seven species utilized in this study are publicly available (Table 2) and served as reference genomes for read mapping. The genome sequences of *T. bifasciatum* (GCA_008086565.1), *E. coioides* (GCA_900536245.1), *M. albus* (GCF_001952655.1), and *M. armatus* (GCF_900324485.2) were retrieved from the National Center for Biotechnology Information (NCBI) Genome Database (accessed on October 2022). We also referenced the genome information of *E. akaara* reported by Ge et al.[39].

Transcriptome assembly and inference of ortholog relationships. For the five species with public reference genomes, the number of transcript sequences obtained using StringTie[40] with the "--merge" option is shown in Table 2. For black sea bass, (without a reference genome), the number of transcriptome sequences assembled using Trinity[41] was 594,726. Among these, 95,941 transcript sequences corresponding to the predicted coding sequences (CDS) were specified as references for expression quantification using Salmon[42]. The number of protein sequences predicted using TransDecoder is shown in Table 2. Orthology inference and consolidation of orthologs within the three-spot wrasse identified 7,289 orthologs that were common to all species used in this study (Table 2), and thus were considered as candidate sex-change factors.

Identification of differentially expressed transcripts. The total intersexual gonad and ovary score (IO-score) was calculated for these 7,289 factors (Supplementary Table 2). Among these, 99 factors were upregulated (Fig. 2a, Fig. 3, Supplementary Table 3) and 69 factors were downregulated (Fig. 2a, Fig. 4, Supplementary Table 4). Whereas the total IO-score of these factors was occasionally derived from a single species (up: *cep97*, *zmat2*, *tmem237a*, *supt5h*; down: *znf16l*, *lrrc8db*, *sh2b1*, *tmem263*, *cyldb*, *manea*, *nol11*), in most cases, the total IO-scores were based on contributions from two or more species. Notably, the upregulated genes included *amh* and *gsdf*, which have been previously reported to play important roles in gonadal sex change, particularly in testicular formation and development, in some protogynous fish. Conversely, the downregulated genes included *cyp19a1a*, *hsd17b1*, and *foxl2a*, which are crucial for the onset of sex change (Table 3).

Enrichment analysis of DEGs. Sequence homology search of the three-spot wrasse proteins using ggsearch36[43] against the reference zebrafish proteins (Ensembl Release 108)[44] resulted in the identification of 90 homologs among the 99 upregulated factors (Supplementary Table 3).

No corresponding zebrafish orthologs were found for the remaining nine factors that were common to all species analyzed in this study. The results of enrichment analysis using the 90 factors that could be converted to zebrafish orthologs are shown in Fig. 2b. The Gene Ontology (GO) terms “homologous chromosome pairing at meiosis” and “germ cell development,” which are related to reproduction, were significantly enriched among the upregulated factors. The specific genes annotated with these GO terms included *hormad1*, *terb2*, *si:ch211-199g17.9*, *gsdf*, and *sycp3* (Table 3).

We successfully obtained the corresponding zebrafish homologs for all of the 69 downregulated factors. The results of enrichment analysis are shown in Fig. 2c. Among the downregulated factors, GO terms related to the regulation of steroid hormone levels, including “regulation of hormone levels” and “steroid metabolic process,” were significantly enriched. Specific genes annotated with these enriched GO terms included *cyp19a1a*, *aacs*, *hsd17b1*, *ece1*, *amacr*, and *sdr42e1* (Table 3).

Discussion

In this study, we conducted a meta-analysis of gonadal RNA-Seq data from seven protogynous fish species using a unified analysis pipeline and threshold. The aim was to compare the transcriptomes of ovaries and early sexual transition gonads, with the goal of identifying common factors involved in protogynous gonadal sex change. Toward this end, we first assembled the *de novo* genome of the three-spot wrasse. The genome assemblies of various species from the family Labridae are listed in the NCBI genome database (accessed May 2023). The assembly statistics of the three-spot wrasse (Table 1) were comparable to those of other Labridae species, such as humphead wrasse (*Cheilinus undulatus*, GCF_018320785.1), ballan wrasse (*Labrus bergylta*, GCF_900080235.1), and New Zealand spotty (*Notolabrus celidotus*, GCF_009762535.1), previously deposited in the NCBI RefSeq database. These results

indicated that the *de novo* genome assembly of the three-spot wrasse exhibited high quality, enabling us to perform expression analysis and orthology inference with confidence.

Through this meta-analysis, we successfully identified sex change-related factors including *cyp19a1a*, *foxl2a*, *hsd17b1*, *amh*, and *gsdf*, that had been previously reported to play a role in sex change in various protogynous fish species[10,13,15,17]. Furthermore, our enrichment analysis of downregulated factors highlighted a term related to the “regulation of steroid hormone production.” This finding is consistent with those of previous reports, which indicate that a rapid decrease in estrogen levels is crucial for female-to-male sex change[6,45,46]. Thus, by pooling data across species, we were able to identify common factors involved in gonadal sex change. Notably, our meta-analysis demonstrates the potential of utilizing transcriptome data from multiple experiments to gain insights regarding the mechanisms underlying sex change in fish.

Through the enrichment analysis, we identified several factors that have not been previously associated with gonadal sex change. Among the up-regulated factors, we observed the inclusion of "*hormad1*," "*terb2*," "*si:ch211-199g17.9*," and "*sycp3*," which are annotated with a GO term related to "germ cells" (Table 3). Interestingly, *hormad1* and *sycp3* have been reported to exhibit higher expression levels in the testis compared to the ovary in zebrafish[47]. Based on these facts, the increased expression of these factors may indicate the progression of spermatogenesis during gonadal sex change. The timing of spermatogenesis during gonadal sex change can vary among species. In Serranidae, spermatogenesis is observed early phase in the sex change process, representing a histological characteristic at the onset of sex change [9,20,48]. Conversely, in Labridae species such as the three-spot wrasse and bluehead, the histological characteristic at the onset of sex change is the degeneration of ovarian tissue, and spermatogenesis is histologically observed in the later stages of sex change [6,15,49,50]. In our study, the RNA-seq data from Labridae species were obtained from gonads at an early stage of sex change. Therefore, the unexpected increase in the expression of multiple factors involved

in spermatogenesis suggests that testicular formation including spermatogenesis may commence early during gonadal transformation, even if it is not histologically recognizable. This characteristic appears to be common to protogynous sex change.

Our findings demonstrate that *aacs*, annotated with the GO term "regulation of hormone levels," is downregulated during sex change. Notably, no previous reports have suggested the involvement of *aacs* in sex change, indicating that the encoded protein (acetoacetyl-CoA synthetase; AACS) may represent a novel factor associated with this process. Typically, AACS plays a critical role in cholesterol supply. Studies in mice have shown that AACS knockdown decreases total serum cholesterol levels[51]. Additionally, in rat adrenal glands, inhibition of AACS expression through hypermethylation suppresses cholesterol supply and steroid synthesis[52]. Moreover, apolipoprotein Eb (encoded by *apoeb*, listed among the upregulated factors), has been suggested to participate in cholesterol catabolism[53]. These observations strongly support the hypothesis that the downregulation of *aacs* and the upregulation of *apoeb* during sex change contribute to suppression of the cholesterol supply.

Cholesterol serves as a precursor for steroid hormones, including estrogens, androgens, and glucocorticoids[54-56], which play crucial roles in protogynous sex change. Previous studies have shown that a decline in endogenous estrogens, particularly E2, triggers the transition from ovary to testis in protogynous fish[6,45,46]. E2 is synthesized from testosterone via an aromatase enzyme, encoded by *cyp19a1a*. Downregulation of *cyp19a1a* expression at the onset of sex change leads to reduced E2 production. Studies on *M. albus* and *T. bifasciatum* have revealed higher DNA methylation levels of the *cyp19a1a* gene upstream region in the testes than those in the ovaries, suggesting that epigenetic modifications may contribute to the suppression of *cyp19a1a* expression during gonadal sex change[15,19]. Our present findings introduce an alternative hypothesis, suggesting that the decreased E2 production at the initiation of sex change may be attributed not only to the downregulation of aromatase activity but also to suppression of the cholesterol supply, the precursor of steroid hormones. Although this

hypothesis requires further investigation and an understanding of cholesterol dynamics during sex change, additional exploration is warranted. Notably, a study on medaka (*Oryzias latipes*) subjected to starvation conditions implied a potential link between masculinization and lower cholesterol levels[57]. Specifically, female-to-male sex reversal was observed in starved medaka larvae, a gonochoristic fish, together with decreased cholesterol levels in the starved samples. However, the precise pathways underlying masculinization and cholesterol dynamics remain unknown. In general, cholesterol is synthesized not only in the liver and adrenal glands but also in the gonads[58-60]. Therefore, gaining a comprehensive understanding of the lipid metabolic mechanisms in fish gonads, including cholesterol synthesis and degradation during sex change, may provide valuable insights regarding the mechanisms underlying gonadal transformation. To clarify this perspective, the remaining challenge lies in providing experimental evidence regarding whether it is possible to control gonadal transformation by actually regulating cholesterol levels within the body.

In summary, we conducted a comprehensive meta-analysis by integrating transcriptome data from multiple protogynous fishes spanning three orders. Our aim was to compare the transcriptomes of sex-transitional gonads with those of ovaries using a unified pipeline to identify the factors involved in gonadal sex change. Through this analysis, we identified 168 differentially expressed factors between the two gonadal states. These factors are likely to play a universal role in gonadal sex change across diverse taxa of protogynous fishes. Notably, we identified novel factors that were not previously associated with gonadal sex change. In particular, we identified cholesterol dynamics as an important factor regulating the sex change process. Moreover, this finding highlights the potential of transcriptomics meta-analysis as a valuable approach to uncover overlooked mechanisms underlying conserved biological processes including sex change. We anticipate that further data-driven research utilizing these novel sex change-related factors will lead to new horizons in sex change research.

Methods

Animals. The adult female three-spot wrasse specimens collected in the field by local fisherman in the northern region of Okinawa, Japan were purchased and employed for genome and RNA sequencing. These specimens were subsequently cultivated in 1000 L tanks receiving a continuous supply of unregulated seawater, and were subjected to natural photoperiod conditions until sampling.

The maintenance and handling of fish in this study were conducted in accordance with the "Guidelines for Animal Experiments of the Okinawa Churashima Foundation," with the same consideration for animal care and welfare as that for higher vertebrates, including reptiles, birds, and mammals. Animal ethical review and approval were not required for the present study because the guidelines stipulated that approval from the Institutional Animal Care and Use Committee of Okinawa Churashima Foundation is required for "higher" vertebrates, and is waived for "lower" vertebrates including fish.

Genome sequencing and assembly for the three-spot wrasse. Muscle tissue from a mature female individual was used for genome sequencing. The specimen was randomly selected from cultivated tank. After anesthetizing the fish with 0.05% v/v 2-phenoxyethanol (FUJIFILM Wako Pure Chemical), the muscle tissue was dissected, immediately frozen in liquid nitrogen, and stored at −80 °C until genomic DNA extraction. High-molecular-weight DNA was extracted from muscle using a NucleoBond AXG column (Macherey–Nagel), followed by purification with phenol–chloroform. The concentration of the extracted DNA was measured using Qubit (Thermo Fisher Scientific Inc.), and its size distribution was first analyzed with a TapeStation 4200 (Agilent Technologies) to ensure high integrity, and subsequently analyzed via pulse-field gel electrophoresis on a CHEF DR-II system (BioRad) to ensure a size range of 20–100 kb.

To obtain long-read sequence data, a SMRT sequence library was constructed using the SMRTbell Express Template Prep Kit 2.0 (PacBio) and sequenced on a PacBio Sequel II system. The sequencing output was processed to generate circular consensus sequences to obtain HiFi sequence reads. Adapter sequences were removed from the HiFi reads using HiFiAdapterFilt[61]. The obtained HiFi sequence reads were assembled using the hifiasm (v0.16.1) assembler[36] with default parameters. The obtained contigs were first scaffolded with the P_RNA_scaffolder[62] and further scaffolded using Hi-C data as follows. The Hi-C library was prepared with the in situ method using the muscle tissue of the individual used for DNA extraction according to the iconHi-C protocol[63], employing the restriction enzymes DpnII and HinfI, and sequenced on a HiSeq X sequencing platform (Illumina). The obtained Hi-C read pairs, amounting to 232 million read pairs, were aligned to the HiFi sequence contigs using the Juicer program[64], and the HiFi sequence contigs were scaffolded via the 3d-dna to be consistent with the chromatin contact profiles through manual curation on JuiceBox[65]. The continuity and completeness of the resulting genome assembly were assessed using the webserver gVolante[66], in which the pipeline BUSCO (v5.4, reference datasets: vertebrata_odb10) was implemented[37].

RNA-Seq of gonadal tissue in the three-spot wrasse. Based on previous studies[10,45], we triggered a sex change in three-spot wrasse 5 females (body length; 8.0–9.3 cm, body weight; 12.4–20.9 g) to obtain transitional gonads through treatment with an aromatase inhibitor (AI), which exerts inhibitory effects on the enzyme responsible for estrogen synthesis. The collected gonads were cut into small pieces, one piece was immersed in TRIzol reagent (Invitrogen) and the rest was fixed in 4% paraformaldehyde/1× phosphate-buffered saline (PBS) for histological observation. Total RNA in each sample was extracted promptly in accordance with the TRIzol instruction manual. The extracted total RNA was dissolved in RNase-free water and stored at −80 °C until RNA-Seq analysis. We selected two treated and two control samples for

RNA-Seq analysis on the basis of histological observation (Supplementary fig. 1).

Beads with oligo (dT) were used to isolate poly(A) mRNA after the total RNA was collected from the samples. Fragmentation buffer was added to disrupt mRNA into short fragments. Using these short fragments as templates, a random hexamer primer was used to synthesize the first-strand cDNA. Second-strand cDNA was synthesized using buffer, dNTPs, RHase H, and DNA polymerase I. Short fragments were purified using the QiaQuick PCR extraction kit (Qiagen) and resolved with EB buffer for end reparation and adding an "A" base. Subsequently, the short fragments were connected to sequencing adapters. Following agarose gel electrophoresis, suitable fragments were selected as templates for PCR amplification. Finally, the library was sequenced using an Illumina HiSeq 2000 as 2 × 90 bp paired-ends. The acquired reads were subjected to the quality control procedures described below and used for downstream expression analysis.

Retrieval and acquisition of RNA-Seq data in protogynous fishes from public resources. To obtain RNA-Seq data from the gonads of protogynous fishes in public databases, we accessed SRA[67] (accessed in October 2022) to search SRA data containing the following keywords: "bony fishes (AND ovary OR gonad)." SRA data were converted into FASTQ files using the Fasterq-dump program of the SRA Toolkit (v3.0.0).

Quality control of RNA-Seq data. To ensure the integrity of the RNA-Seq reads, trimming and quality control procedures were performed. Specifically, we used Trim Galore (v0.6.7)[68] with the option "--quality 20 --paired" to eliminate low-quality bases from paired-end reads.

Read mapping against the reference genome. For species with available genomic information, RNA-Seq reads were mapped to the reference genome sequences using HISAT2 (v2.2.1)[69] with the parameter "-q -dta -x". The resulting SAM files were sorted and converted

into BAM files using SAMtools software (v1.15.1)[70].

Generating General Transfer Format (gtf) files based on genome sequence and RNA-Seq reads for reference gene annotation when quantifying expression values. To ensure consistency in the use of annotation information for expression quantification in species with available reference genomes, we employed the merge function of StringTie (v2.1.7)[40] to generate a gtf file that served as a guide for annotations. The transcriptome assembly for each fish was conducted using StringTie with default settings based on the mapping results (BAM file). The resulting gtf files were then merged using StringTie with the "--merge" option, producing a unified file as the "merged.gtf". This "merged.gtf" file contained a non-redundant set of assembled transcripts for each species. Generated "merged.gtf" files in each species were designated as the reference annotation files for quantifying transcript expression.

Quantification of transcripts expression and detection of differentially expressed transcripts. When reanalyzing high-throughput data from multiple experiments, it is crucial to consider batch effects[71]. In the present study, we calculated the transcript per million (TPM) value for each transcript and utilized the difference in TPM values between the paired data as an indicator for identifying differentially expressed transcripts.

Transcript expression was quantified in species with available genome annotation using StringTie, specifying the parameters as "-G merged.gtf -e". The resulting gtf file for each sample provided the TPM values, which were used for downstream analysis.

TPM values were computed for species lacking reference genomes using Salmon (v.1.9.0)[42] with the parameters "quant -i index -l A". To generate the transcriptome sequences required for Salmon, we performed transcriptome assembly using the Trinity (v2.13.1) assembler[41] with default settings. Open reading frames (ORFs) and CDS were predicted from the transcriptome assembly using TransDecoder (v5.5.0)[38] with the same settings as described

below. The resulting gff3 file obtained from the TransDecoder run was used to extract transcript sequences corresponding to the predicted CDS from the transcriptome assembly. The extracted sequence set was then utilized as the reference transcriptome after eliminating duplicate sequences using seqkit (v2.3.0)[72] with the “rmdup -s” command.

To assess changes in transcript expression, the expression ratio was determined using TPM values obtained from intersexual gonad and ovary transcriptomes (referred to as the IO-ratio). The IO-ratio for each transcript was calculated using Equation (1).

$$\text{IO ratio} = \log_2(\text{TPM}_{\text{intersexual}} + 0.01) - \log_2(\text{TPM}_{\text{ovary}} + 0.01), \quad (1)$$

This calculation was performed for all pairs of intersexual gonad and ovary transcriptomes. To convert zeros to logarithms, a value of “0.01” was added to the TPM of each transcript. Transcripts with an IO-ratio > $\log_2(5)$ (indicating a 5-fold expression change) were classified as “upregulated,” whereas transcripts with an IO-ratio < $-\log_2(5)$ (representing a 0.2-fold expression change) were considered “downregulated.” Transcripts outside these thresholds were deemed “unchanged.” To determine differential expression between the intersexual gonad and ovary, an IO-score was calculated for each transcript by subtracting the count of “downregulated” pairs from that of “upregulated” pairs, as shown in Equation (2).

$$\text{IO-score} = (\text{count number}_{\text{upregulated}}) - (\text{count number}_{\text{downregulated}}), \quad (2)$$

Using orthology inference as described below, the total IO-score for each transcript was calculated by summing the IO-scores of all species. Total IO-score thresholds of 7 and −7 were employed to identify transcripts that were differentially upregulated and downregulated, respectively. All calculations for IO-ratios and IO-scores were performed using R (v 4.2.1)[73].

Orthology inference among species. GFFread (v0.12.1)[74] was utilized along with the generated “merged.gtf” file to extract transcript sequences from the reference genomes. For species without reference genomes, transcript sequences were obtained via assembly using Trinity, as described previously. TransDecoder was used to identify the coding regions and

translate them into amino acid sequences for all species. ORFs were extracted from the transcriptome sequences using TransDecoder Longorfs with the parameters “-m 100”. CDS were then predicted using TransDecoder Predict with default settings, and the protein sequences converted from the predicted CDS were acquired. Subsequently, a reciprocal homology search was conducted between the predicted protein sequences of the three-spot wrasse and those of other species, and the reciprocal best hit (RBH) was identified as the ortholog. The program Diamond (v2.0.15)[75] was used for the RBH search using the parameters “--ultra-sensitive -e 1e-3”. To extract the orthologs shared among all species, we consolidated the RBH results with the three-spot wrasse-predicted protein IDs.

Gene set enrichment analysis. Differentially expressed gene sets were analyzed using the web tool Metascape (v3.5)[76], which enables gene set enrichment analysis. However, Metascape only supports the analysis of zebrafish among teleosts. Therefore, prior to analysis, the predicted protein sequences of the three-spot wrasse were mapped to the corresponding zebrafish Ensembl protein IDs. To obtain orthologous information, we utilized the ggsearch36 program from the FASTA package[43] to globally align the predicted protein sequences of the three-spot wrasse with the proteome sequences of zebrafish (Ensembl Release 108)[44].

Data availability. All sequencing data, including assembled sequences and raw sequence reads, were deposited in the DNA Data Bank of Japan (DDBJ) under the umbrella BioProject accession number PRJDB15835. The genome assembly was deposited in the DDBJ under accession numbers BSYP01000001–BSYP01000227. Additionally, raw sequence reads were deposited in the DDBJ under the following accession numbers: DRR466686 (PacBio HiFi reads), DRR486910 (Illumina HiC reads), and DRR483512-DRR483515 (Illumina RNA-Seq reads).

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Author contributions

RN and HB conceived and designed the study. MK and SK performed genome sequence and de novo genome assembly of three-spot wrasse. RN & MN RNA-seq data production of three-spot wrasse. RN performed RNA-seq data analysis and orthology inference. RN, MN, SK and HB wrote a draft manuscript. All authors read and approved the final manuscript.

Competing interests

The authors have no conflicts of competing interest to declare that are relevant to the content of this article.

Additional information

All supplementary information is accessible in figshare repository (https://doi.org/10.6084/m9.figshare.c.6704160)

Supplementary figure 1. Histological sections of control ovaries and transitional gonads treated AI for 7 days in the three-spot wrasse, *Halichoeres trimaculatus*.

Supplementary table 1

Supplementary table 2

Supplementary table 3

Supplementary table 4

Figure legends

Fig. 1. Schematic diagram of the analysis pipeline in this study.

Fig. 2 Scatter plot of the IO-score and gene set enrichment analysis of up- and

downregulated genes. a Scatterplot of total IO-scores for the 7,289 factors in descending order. Blue circles indicate 99 upregulated factors; red circles indicate 69 downregulated factors. Gray circles (which have the appearance of lines because they overlap each other) indicate unchanged factors (6 ≤ total IO-score ≤ −6). **b,c** Results of enrichment analysis for 99 upregulated (**b**) and 69 downregulated (**c**) factors

Fig. 3 Composition of total IO-scores for upregulated factors (n=99). Numbers in parentheses indicate the number of RNA-Seq data pairs for each species used in this study. Asterisk indicates a gene for which the total IO-score is derived from a single species.

Fig. 4 Composition of total IO-scores for downregulated factors (n=69). Numbers in parentheses indicate the number of RNA-Seq data pairs for each species used in this study. Asterisk indicates a gene for which the total IO-score is derived from a single species.

Table 1. Statistics of genome assembly in Three-spot wrasse (fHalTri1.1) and other Labidae fishes listed in NCBI Genomes.

	fHalTri1.1	***Cheilinus undulatus* (humphead wrasse)**	***Notolabrus celidotus* (New Zealand spotty)**	***Labrus bergylta* (ballan wrasse)**	***Semicossyphus pulcher***	***Tautogolabrus adspersus* (cunner)**
Assembly accession	BSYP01000001–BSYP01000227	GCF_018320785.1	GCF_009762535.1	GCF_900080235.1	GCA_022749685.1	GCA_020745685.1
Total seq length (Mb)	849.9	1173.4	846.7	805.5	794.1	723.6
Max length (Mb)	44.2	59.6	42.4	9.1	38.5	37.1
Num of scaffolds	227	45	467	13,466	178	347
Scaffold N50 (Mb)	37.9	51.5	37.1	0.8	32.1	31.7
Scaffold L50	11	11	11	252	12	11
Num of seqs > 1 Mb	25	24	24	197	35	24
% of seqs > 1 Mb	97.3	99.7	97.6	43.9	97.1	99.9

Num of gaps	117	284	1,133	257	8	283
Complete BUSCO (%)	98.7	99.0	97.1	98.9	98.9	98.1

Table 2. Statistics of orthology relationship among species.

Common name	Scientific name	Order	Reference genome	*Num of transcripts seqs obtained based on the RNA-seq data from gonadal tissue	Num of protein seqs predicted by TransDecoder	Num of RBH (vs Three-spot wrasse)
Three-spot wrasse	*Halichoeres trimaculatus*	Labriformes	Assembly in this study	27,573	24,965	24,965
Bluehead	*Thalassoma bifasciatum*	Labriformes	GCA_008086565.1	57,699	43,195	13,871
Hong Kong grouper	*Epinephelus akaara*	Perciformes	Ge et al., 2019	26,507	24,752	11,619
Orange-spotted grouper	*Epinephelus coioides*	Perciformes	GCA_900536245.1	30,867	34,191	12,507
Black seabass	*Centropristis striata*	Perciformes	NA	** 95,941	95,941	12,591
Asian swamp eel	*Monopterus albus*	Synbranchiformes	GCF_001952655.1	53,472	50,693	12,765
Zig-zag eel	*Mastacembelus armatus*	Synbranchiformes	GCF_900324485.2	48,724	40,908	13,095

* Based on the annotation file (merged gtf file), the extracted transcripts sequences from the genome by gffread

** Among transcriptome sequences (594,726 seqs) assembled by Trinity, transcripts sequences corresponding to coding seqences predicted via TransDecoder

Table 3. List of genes that contributed to GO term enrichment.

Up/Down	GO ID	Category	GO term	*Genes
Up	GO:0007129	Biological Process	homologous chromosome pairing at meiosis	*hormad1, terb2, si:ch211-199g17.9*
Up	GO:0007369	Biological Process	gastrulation	*zeb1b, tmem237a, col12a1b, pfn1, enpp2*
Up	GO:1902531	Biological Process	regulation of intracellular signal transduction	*cep55l, psd3l, arhgef18b, ccl19a.1, sh3bp1, enpp2, pik3r6b*
Up	GO:0005929	Cellular Component	cilium	*septin6, prom1a, tmem237a, si:ch211-66i15.4, flr*
Up	GO:0007281	Biological Process	germ cell development	*hormad1, gsdf, sycp3*
Down	GO:0010817	Biological Process	regulation of hormone levels	*cyp19a1a, aacs, hsd17b1, ece1*
Down	GO:0006413	Biological Process	translational initiation	*eif4g2b, eif4eb, eif4e1c*
Down	GO:0019752	Biological Process	carboxylic acid metabolic process	*lpl, ldha, aacs, amacr, acaca, dars2*
Down	GO:0008202	Biological Process	steroid metabolic process	*hsd17b1, amacr, sdr42e1*
Down	GO:1904888	Biological Process	cranial skeletal system development	*nog3, cep55l, cyldb, ece1*
Down	GO:1901362	Biological Process	organic cyclic compound biosynthetic process	*tbx5a, hsd17b1, alad, acaca, sdr42e1, adcy6a*

* Gene symbols follow the zebrafish gene nomenclature in Ensembl.

Fig. 1.

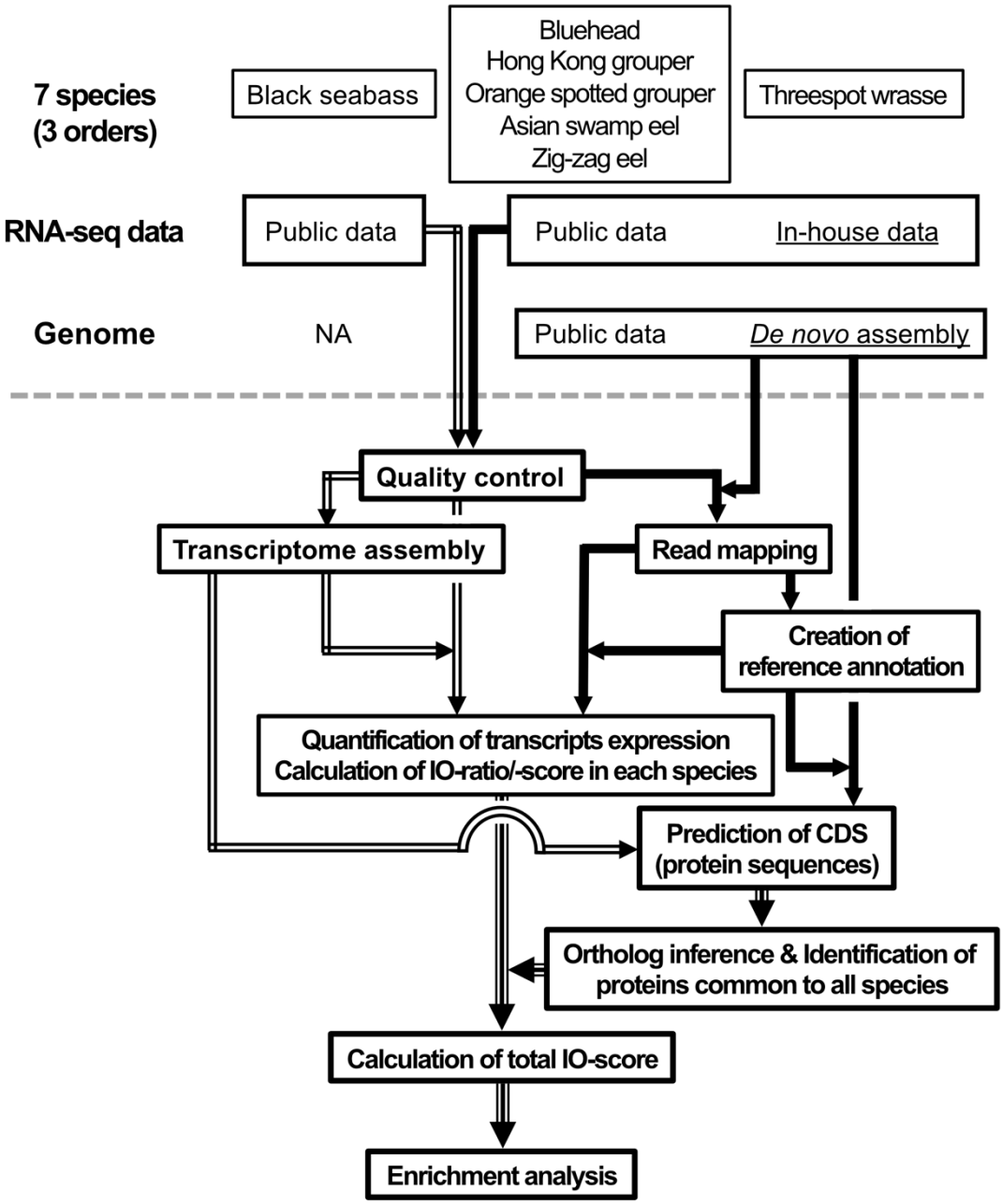

7 species
(3 orders)
Black seabass
Bluehead
Hong Kong grouper
Orange spotted grouper
Asian swamp eel
Zig-zag eel
Threespot wrasse
RNA-seq data
Public data
Public data
In-house data
Genome
NA
Public data
De novo assembly
Quality control
Transcriptome assembly
Read mapping
Creation of
reference annotation
Quantification of transcripts expression
Calculation of IO-ratio/-score in each species
Prediction of CDS
(protein sequences)
Ortholog inference & Identification of
proteins common to all species
Calculation of total IO-score
Enrichment analysis

Fig. 2.

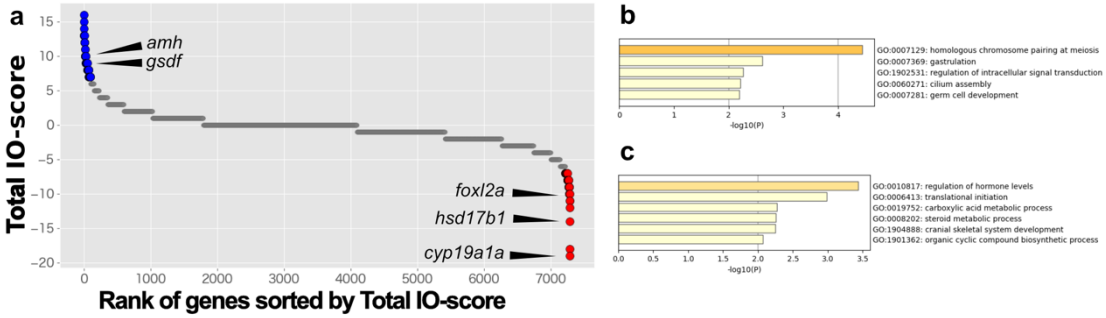

a
Total IO-score
Rank of genes sorted by Total IO-score
amh
gsdf
foxl2a
hsd17b1
cyp19a1a
b
GO:0007129: homologous chromosome pairing at meiosis
GO:0007369: gastrulation
GO:1902531: regulation of intracellular signal transduction
GO:0060271: cilium assembly
GO:0007281: germ cell development
-log10(P)
c
GO:0010817: regulation of hormone levels
GO:0006413: translational initiation
GO:0019752: carboxylic acid metabolic process
GO:0008202: steroid metabolic process
GO:1904888: cranial skeletal system development
GO:1901362: organic cyclic compound biosynthetic process
-log10(P)

Fig. 3.

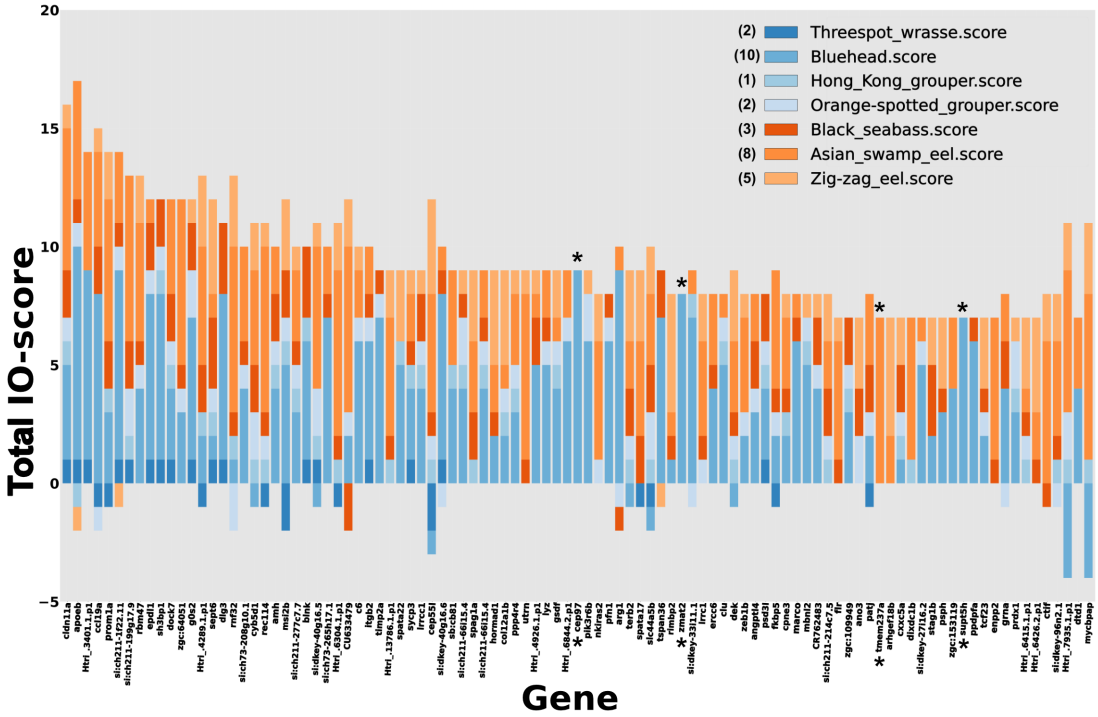
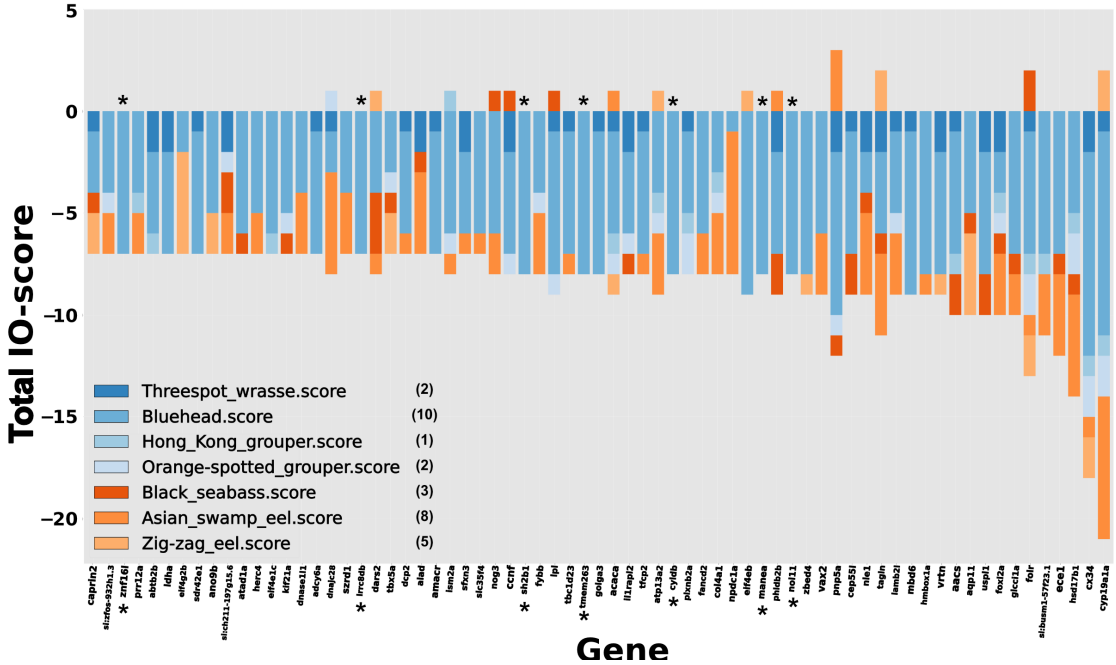

(2) Threespot_wrasse.score
(10) Bluehead.score
(1) Hong_Kong_grouper.score
(2) Orange-spotted_grouper.score
(3) Black_seabass.score
(8) Asian_swamp_eel.score
(5) Zig-zag_eel.score
Total IO-score
Gene
20
15
10
5
0
−5

Fig. 4.


Total IO-score
5
0
−5
−10
−15
−20
Threespot_wrasse.score (2)
Bluehead.score (10)
Hong_Kong_grouper.score (1)
Orange-spotted_grouper.score (2)
Black_seabass.score (3)
Asian_swamp_eel.score (8)
Zig-zag_eel.score (5)
Gene