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**Towards an advanced comprehension of bivalve  
sex determination through a comparative and  
evolutionary approach**

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# Chapter 1

## Introduction

### 1.1 Molecular mechanisms of sex determination and the evolution of sex-determining genes

The process of sex determination (SD) has been traditionally associated with the very first step of gonad differentiation, where an initial trigger activates the molecular pathway that establishes organism sex. According to this view, two alternative types of SD have been recognized at first: the environmental sex determination (ESD) and the genetic sex determination (GSD), depending on whether the very first cues are of environmental or genetic origin. Conversely, all the downstream events of gonad development (i.e., after SD) have been appointed as primary sex differentiation (PSD), which consists of the entire set of morphogenetic, molecular, and physiological events leading to the full maturation of testes or ovaries (**Uller and Helanterä, 2011; Beukeboom and Perrin, 2014**). Lately, however, the dichotomous views of ESD/GSD and of SD/PSD have been questioned. On the one hand, a growing number of studies on non-model organisms proved that ESD and GSD represent a continuum of mixed conditions rather than two mutually exclusive phenomena. On the other, the high evolutionary dynamics and the variable expression patterns of the genes involved in the processes of gonad commitment and development make the distinction between SD and PSD of unclear utility (**Beukeboom and Perrin, 2014**).

Considering this complex scenario, **Uller and Helanterä, 2011** proposed a unified and broad-scope definition for SD, that is, “the processes within an embryo leading to the formation of differentiated gonads as either testes or ovaries”, without any actual distinction between environmental/genetic initial triggers or the downstream effectors. However, I argue that this

definition should be expanded to encompass not only the embryonic stage of the animal life cycle but also adulthood, since cases of sex reversals and sex changes (sequential hermaphroditism) legitimately express proper SD processes during post-embryonic life stages as well.

In its most intimate core, animal SD is the manifestation of complex gene regulatory networks where, in accordance with the Wilkins' theory (1995), the downstream actors appear to be nearly conserved both from functional and identity point of views, while the master top regulators (the commonly recognized sex determinants, such as the sex-determining region of chromosome Y [SRY] in therians or the ratio between sex and autosome chromosomes in *Drosophila*) are often the most variable part (**Beukeboom and Perrin, 2014**). As a matter of fact, this evolutionary pattern of animal sex-determining cascades has been observed in major animal clades, including vertebrates (e.g., **Marshall Graves and Peichel, 2010**), insects (e.g., **Verhulst et al., 2010**), and nematodes (e.g., **Stothard and Pilgrim, 2003**).

Sex-determination related genes (SRGs) are of particular interest not only from a regulatory point of view but also because of their patterns of molecular evolution. In fact, transcriptionally sex-biased genes (including SRGs) often tend to evolve faster than unbiased genes at the level of protein sequences. In particular, male-biased genes generally show higher rate of sequence evolution in comparison to both female-biased and unbiased counterparts (reviewed in **Parsch and Ellegren, 2013; Grath and Parsch, 2016**), as it has been repeatedly observed in well-studied organisms such as fruit flies (e.g., **Meisel and Connallon, 2013**), nematodes (e.g., **Cutter and Ward, 2005**), mice (e.g., **Kousathanas et al., 2014**) and primates (e.g., **Khaitovich et al., 2005**), and in other emerging model systems, such as *Daphnia pulex* (**Eads et al., 2007**), aphids (**Purandare et al., 2014**), and two wasp species of the genus *Nasonia* (**X. Wang et al., 2015**). Growing evidence is however showing cases in which instead female-biased genes have higher rates of sequence evolution than male-biased genes, such as in mosquitoes of the genus *Anopheles* (**Papa et al., 2017a**), and European and Manila clams of the genus *Ruditapes* (**Ghiselli et al., 2018**).

The pattern of molecular evolution of sex-biased genes is particularly evident in organisms with sex chromosomes (both in XY/ZW and X0 systems), such as fruit flies, birds and mammals, where the so-called fast-X (or fast-Z) effect has been extensively reported for sex-chromosome associated genes (**Vicoso and Charlesworth, 2006; Mank et al., 2007; Meisel and Connallon, 2013**). This high rate of sequence evolution in sex-biased genes and sex chromosomes (SCs) can be the result of both adaptative and non-adaptative processes, since the observed

higher ratio between non-synonymous and synonymous mutations (dN/dS) can be caused by natural selection, sexual selection or sexual antagonism, as well as genetic drift (**Vicoso and Charlesworth, 2006; Meisel and Connallon, 2013; Parsch and Ellegren, 2013; Grath and Parsch, 2016**).

## 1.2 Sex determination in bivalves: a long-standing enigma

Bivalves are the second largest clade in molluscs, counting more than 18,000 species (Catalogue of Life) distributed at all depths and in all marine environments, as well as in some freshwater habitats. Thanks to their high diversity and biological peculiarities, they have been proposed as promising model organisms for investigating a wide array of biological, ecological and evolutionary issues (**Milani and Ghiselli, 2020; Ghiselli et al., 2021**). However, despite their socio-economic and scientific importance, the knowledge concerning the molecular basis of bivalve reproduction and SD is still quite limited (**Breton et al., 2018**). Clues from various works seem to suggest that both genetic and environmental factors (e.g., temperature, food availability, and steroids) are involved in SD, and that heteromorphic sex chromosomes (HeSCs) are absent (**Breton et al., 2018; Han et al., 2022**). However, the exact process by which sex is determined and gonad commitment is established is, currently, still unknown. Actually, bivalves represent a dazzling example of how the traditional dichotomies between ESD/GSD and SD/PSD can sometimes hamper scientific research, as many bivalve species exhibit various forms of hermaphroditism and because a master environmental or genetic sex determinant inducing PSD may just not exist.

In the attempt to identify SRGs, many differential gene expression analyses have been recently performed on a variety of species covering most of the phylogenetic diversity of bivalves (e.g., **Milani et al., 2013; Zhang et al., 2014; Chen et al., 2017; Capt et al., 2018; Ghiselli et al., 2018; Y. Shi et al., 2018**). Some of the genes that were found to be differentially expressed between gonads of different sex were systematically retrieved across species, such as those belonging to the *Dmrt*, *Sox*, and *Fox* families, which act in concert in various animal developmental processes including the SD cascade (**Marshall Graves and Peichel, 2010; Beukeboom and Perrin, 2014**). To this regard, **Zhang et al., 2014** proposed a working model for the sex-determining pathway of the Pacific oyster *Crassostrea gigas* in which: *CgSoxH* promotes male gonad development by activating *CgDsx*, which belong to the *Dmrt*

family, and inhibiting *CgFoxL2*; *CgFoxL2*, when not inhibited by the pair *CgSoxH/CgDsx*, promotes female gonad development. Moreover, **Han et al., 2022** recently identified homomorphic sex chromosomes (HoSCs) in eight scallop species and appointed *FoxL2* as a putative SRG in *Patinopecten yessoensis* and *Chlamys farreri*. Though, much of the recent research effort on bivalve SRGs has been limited to their molecular cloning, differential transcription, and tissue localization (**Liang et al., 2019; Sun et al., 2022**). Furthermore, few works have directly investigated the biological functions of *Dmrt*, *Sox*, and *Fox* genes in bivalves so far, and most used post-transcriptional silencing of target mRNAs (RNA interference [RNAi]). **Liang et al., 2019** studied the role of *Sox2* in the spermatogenesis of the Zhikong scallop *Chlamys farreri* and found that it likely regulates proliferation of spermatogonia and apoptosis of spermatocytes, since its knockdown resulted in the loss of male germ cells. **G. Wang et al., 2020** proposed that in the female gonads of the freshwater mussel *Hyriopsis cumingii*, *FoxL2* might be related to the *Wnt/ β-catenin* signaling pathway, which takes part in ovarian differentiation also in vertebrates. **Sun et al., 2022** found instead that in *C. gigas*, *FoxL2* and *Dmrt1L* mRNA knockdown results in the size reduction of female and male mature gonads, respectively.

In this sense, bivalve molluscs represent a striking example of the difficulty to reconcile the traditional view of a single sex determinant with an apparent multifactorial model in which many genes and environmental cues act in concert to establish the sexual identity of the individual (**Breton et al., 2018**). Lately, much effort has been put in the characterisation of bivalve SD and a general framework is eventually taking shape. Functional assays with RNAi and CRISPR-Cas9 techniques (e.g., **G. Wang et al., 2020; Sun et al., 2022; M. Wang et al., 2022**), as well as with *in-situ* localization and immunohistochemistry (e.g., **Perez-Garcia et al., 2011; Milani et al., 2013**), are making their way into the study of bivalve biology and have been proved essential instruments also for the investigation of sex-related traits. However, very few works have made extensive use of the comparative and integrative approach in bivalve studies so far, which hampers the possibility to infer general patterns for such a vast class of organisms (**Milani and Ghiselli, 2020**). The high evolutionary rates and plasticity of SRGs make the situation even harder, since phylogenetic and orthology inferences can lead to erroneous reconstructions in the presence of signal saturation and high sequence divergence (reviewed in **Natsidis et al., 2021; Lozano-Fernandez, 2022**).

# Chapter 2

## Bivalves as emerging model systems to study the mechanisms and evolution of sex determination: a genomic point of view

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**Abstract.** Bivalves are a diverse group of molluscs that have recently attained a central role in plenty of biological research fields, thanks to their peculiar life history traits. Here we propose that bivalves should be considered as emerging model systems also in sex-determination studies, since they would allow to investigate: (i) the transition between environmental and genetic sex determination, with respect to different reproductive backgrounds and sexual systems (from species with strict gonochorism to species with various forms of hermaphroditism); (ii) the genomic evolution of sex chromosomes, considering that no heteromorphic sex chromosomes are currently known and that homomorphic sex chromosomes have been identified just in few species of scallops; (iii) the putative role of mitochondria at some level of the sex determination signaling pathway, in a mechanism that may resemble the cytoplasmatic male sterility of plants; (iv) the evolutionary history of sex-determination related gene families with respect to other

animal groups. In particular, we think that this last topic may lay the foundations for expanding our understanding of bivalve sex determination, as our current knowledge is quite fragmented and limited to few species. As a matter of fact, tracing the phylogenetic history and diversity of sex-determination related gene families (such as the *Dmrt*, *Sox* and *Fox* genes) would allow to perform more targeted functional experiments and genomic analyses, but also fostering the possibility of establishing a solid comparative framework.

**Significance.** In this perspective, we provide an examination of the phylogenetic diversity of *Dmrt* genes, a sex-determination related gene family, to address the importance of bivalves in sex determination studies. By analyzing their taxonomic distribution and sequence diversity, we show how such a comparative study may set a common ground plan to settle down targeted functional experiments and essays. This kind of approach should be applied more extensively in future studies, especially when dealing with understudied organisms.

Bivalves are the second largest clade in molluscs, counting more than 18,000 species (Catalogue of Life, accessed 16/12/2022) distributed at all depths and in all marine environments, as well as in some freshwater habitats. Thanks to their high diversity and peculiar biological features, they have been proposed as promising model organisms for investigating a wide array of biological, ecological, and evolutionary issues, from mitochondrial biology and evolution to the physiological plasticity under fluctuating environmental conditions (**Milani and Ghiselli, 2020; Ghiselli et al., 2021**). In this context, bivalves may serve as a compelling model system to investigate the evolution and characteristics of sex determination (SD) as well, thanks to the diversity of their reproductive modes and genomic features. Nonetheless, this research field has been largely overlooked and many aspects of bivalve reproductive biology remain uncharacterized. In this perspective, we address the topic by first examining the relevant questions that bivalves may help to answer regarding processes and patterns of SD, and then providing a case study in the field of comparative genomics.

## 2.1 Open yet inspiring topics in bivalve sex determination

Despite the socio-economic and scientific importance of bivalves, the knowledge concerning the genetic and molecular bases of their SD system is quite limited and its study has been mostly neglected. Yet, bivalves may constitute a novel model system in SD studies that is as intriguing and valuable as other well-established models, such as vertebrates, insects and plants (**of Sex Consortium et al., 2014**), as they may provide complementary perspectives in many aspects of SD evolutionary studies. Topics such as (i) the transition between environmental and genetic SD, (ii) the evolution of sex chromosomes, (iii) the mito-nuclear interaction, and (iv) the evolution of SD related genes, can largely benefit from the integration with bivalve studies. But many others are likely to emerge as research in the field progresses.

### 2.1.1 Transitions between environmental and genetic sex determination

Clues from several works seem to suggest that both genetic and environmental factors are involved in bivalve SD, thus implying that a mixed system may exist (reviewed in **Breton et al., 2018**). The traditional dichotomy between environmental sex determination (ESD) and genetic

sex determination (GSD) seems inapplicable in most bivalve species, where ESD and GSD rather represent the two ends of a continuum of mixed and plastic conditions. A weak distinction between ESD and GSD is also found in amphibians, reptiles and teleost fish, three clades in which environment-dependent SD has been largely studied. Here, the interaction—or even the transition—between the two sexual systems have been reported in many species, suggesting that sex-determining mechanisms can be extraordinary plastic (**Bachtrog et al., 2014; Capel, 2017**). Adding a representative and diverse group of Lophotrochozoa (Protostomia) to those vertebrate taxa, can widely expand the comparative framework of the investigation, allowing to better understand the evolution of SD as a whole. In bivalves, ESD has been studied mostly in oysters, where hermaphroditic species show an effect of temperature on SD (reviewed in **Breton et al., 2018; Figure 2.1**). Oysters may indeed constitute a prolific model to examine how the SD pathways are shaped in the presence of different initial triggers and highly dynamic reproductive backgrounds. In fact, various sexual systems can be found in oysters, such as (i) strictly gonochoric population, (ii) the coexistence of simultaneous hermaphroditic with strictly gonochoric individuals in the same population, (iii) the possibility of sex change according to environmental conditions, and (iv) the presence of both parasitic dwarf males and free-living males in the same species (**Collin, 2013**). Consequently, oysters may be extremely useful to understand how epigenetic control is involved in sex change, how gene regulatory networks can sustain the occurrence of different hermaphroditic conditions within gonochoric populations, and whether certain SD systems are more labile than others (**Abbott, 2011**).

### 2.1.2 Evolution of sex chromosomes

So far, heteromorphic sex chromosomes (i.e., sex chromosomes showing strong morphological differentiation; HeSCs) have never been observed in bivalves (**Breton et al., 2018**), while the first evidence of homomorphic sex chromosomes (i.e., sex chromosomes showing little or no differentiation; HoSCs) comes from a very recent study on several scallop species, where a non-homologous origin of the SD system has been proposed for different subfamilies (**Han et al., 2022; Figure 2.1**). Theory predicts that, once originated, sex chromosomes (SCs) will eventually turn into HeSCs, because of the recombination arrest in the sex-determining region (**Bachtrog et al., 2014; Beukeboom and Perrin, 2014; Han et al., 2022**). Nonetheless, HoSCs are much more widespread in the animal kingdom than expected, sometimes also being of ancient age (**Bachtrog et al., 2014; Han et al., 2022**).

Species from the order Pectinida may thus be useful to investigate what determines the long-term maintenance of HoSCs and which genomic architectures and molecular dynamics prevent HeSCs from evolving in bivalves. Additionally, they may be taken as model systems to investigate the origin of SCs in relation to the sexual systems and the route by which molecular pathways have been reprogrammed in the transition between different SD mechanisms (**Han et al., 2022**).

Researchers have been addressing this topic mainly in snakes, ratites and sturgeons (**Bachtrog et al., 2014; Han et al., 2022** and references therein). Though, scallops currently hold the oldest HoSC pairs, which are dated back to about 350 million years. The system is thus of great importance to investigate the role of sex-biased gene expression and selection forces in the long-term stability of SCs (**Han et al., 2022**), as well as the intertwining between SD systems.

### 2.1.3 Mito-nuclear interactions

An additional pivotal topic in bivalve biology, tentatively connected to SD, regards the doubly uniparental inheritance (DUI) of mitochondria, a process in which two highly divergent mitochondrial genomes are transmitted uniparentally through the maternal and paternal lineages, respectively through eggs and sperm. This process, which has been reported in more than a hundred bivalve species from five different orders (**Figure 2.1; Gusman et al., 2016; Capt et al., 2020**), has been proposed to interact with the major nuclear pathways that primarily establish the sexual identity, in a way that can resemble the cytoplasmatic male sterility (CMS) of plants (**Ghiselli et al., 2013; Breton et al., 2022**). In CMS, specific mitochondrial chimeric ORFs cause the pollen to be sterile, while certain nuclear loci act in counterbalance to restore male fertility when occurring in the same individual. This Red-Queen scenario, in which balancing selection shapes the evolution of both CMS and restorer-of-fertility genes and keeps the two sexes viable, has been also hypothesized to be acting on bivalve DUI species (**Ghiselli et al., 2013; Xu, Iannello, et al., 2022**), where additional and effectively-transcribed ORFs have been observed in both the male-inherited and female-inherited mitochondrial lineages (**Milani et al., 2013, 2014**).

Clearly, if a functional interplay between DUI and SD in bivalves is proven, this will provide new research questions regarding not only bivalve biology itself but also broader evolutionary topics (e.g., are there any converging trait between DUI and CMS systems? What is the degree

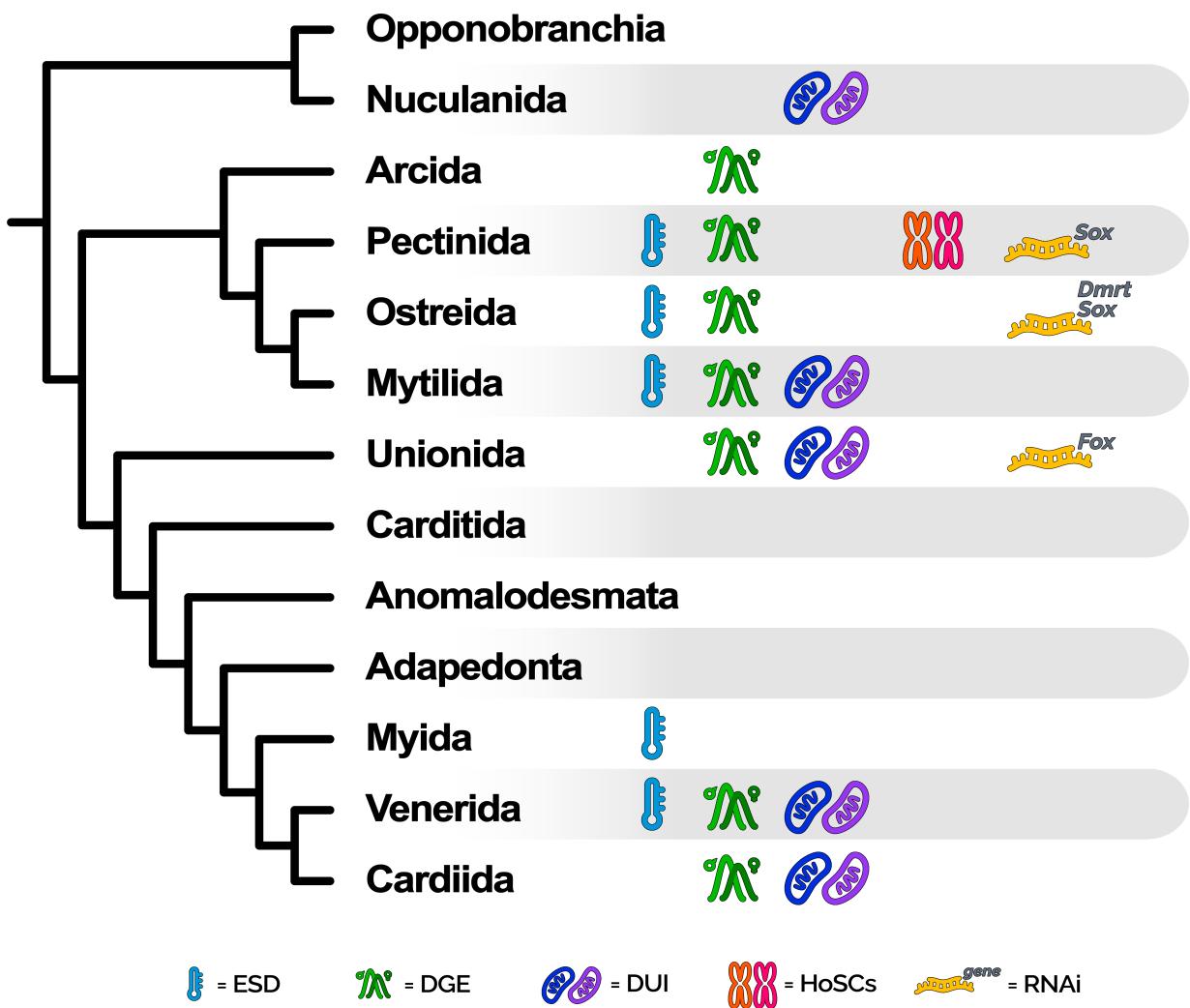


Figure 2.1: Graphical summary of the available knowledge and experiments concerning the genetic basis of SD in bivalves, at the level of major taxonomic orders (as reported in WoRMS; accessed before or on 14/03/2023). For each bivalve clade it is reported: (i) the availability of records of environmental-induced sex-determination (ESD) (ii) the availability of differential gene expression (DGE) experiments specifically intended to investigate sex-biased or sex-specific genes; (iii) whether the doubly-uniparental inheritance (DUI) of mitochondria has been reported in at least one species; (iv) whether homomorphic sex chromosomes (HoSCs) have been identified in at least one species; (v) the availability of RNAi experiments for genes belonging to the *Dmrt*, *Sox*, and *Fox* gene families. The phylogenetic tree on the left has been drawn on the basis of the most widely accepted topology for bivalves, according to analyses based on nuclear markers and morphological data. The tips of the tree correspond to major bivalve orders, except for Opponobranchia and Anomalodesmata, which represent higher-level taxonomic ranks. References for the availability of data and experiments can be found throughout the main test.

of plasticity of such mitochondria-related SD systems? Are mitochondria-related SD systems more widespread in eukaryotes than currently thought?).

#### 2.1.4 Evolution of sex-determination related genes

Considering this intricate scenario of SD mechanisms and the wide diversity of bivalves, in the last years many differential transcription analyses have been performed on several species with the attempt to identify the most probable SD related genes (SRGs; e.g., **Milani et al., 2013; Zhang et al., 2014; Chen et al., 2017; Capt et al., 2018; Y. Shi et al., 2018; Figure 2.1**). Interestingly, certain genes consistently emerged across different bivalve species as being substantially more transcribed in one sex (sex-biased) or exclusively transcribed in one sex (sex-specific), suggesting their potential involvement in the SD pathway. These genes mainly belong to the *Dmrt*, *Sox*, and *Fox* families, which play a role in various developmental processes (including the SD cascade) in most animals (**Marshall Graves and Peichel, 2010; Bachtrog et al., 2014; Beukeboom and Perrin, 2014**). Members of these three gene families are also included in the working model for the SD regulatory network proposed for the Pacific oyster *Crassostrea gigas* by **Zhang et al., 2014**, in which: *CgSoxH* (which belong to the *Sox* family) promotes male gonad development by activating *CgDsx* (which belong to the *Dmrt* family) and inhibiting *CgFoxL2* (which belong to the *Fox* family); *CgFoxL2*, when not inhibited by the pair *CgSoxH/CgDsx*, promotes female gonad development. Similarly, **Han et al., 2022** appointed *FoxL2* as a putative SD gene in the two scallop species *Patinopecten yessoensis* and *Chlamys farreri*. If their pivotal role in SD of bivalves is confirmed, an evolutionary genomic analysis may help in better understanding why members of the above-mentioned gene families appear particularly prone to be recruited in the SD cascade also in distantly related species, as it is observed for *Dmrt1* and *Sox3* homologs in vertebrates (**Marshall Graves and Peichel, 2010; Bachtrog et al., 2014**; and the following section). Furthermore, considering the occurrence of mixed SD systems in bivalves, *Dmrt*, *Sox*, and *Fox* genes may provide new perspectives on the influence of different environmental cues on the molecular evolution of animal SRGs. However, to date, experiments have been limited to molecular cloning, differential transcription, and tissue localization of such genes (**Liang et al., 2019; Sun et al., 2022**), while only a few have directly investigated their biological functions in bivalves, for example through post-transcriptional silencing of target mRNAs (RNA interference [RNAi]; **Figure 2.1**; e.g., **Liang et al., 2019; G. Wang et al., 2020; Sun et al., 2022**).

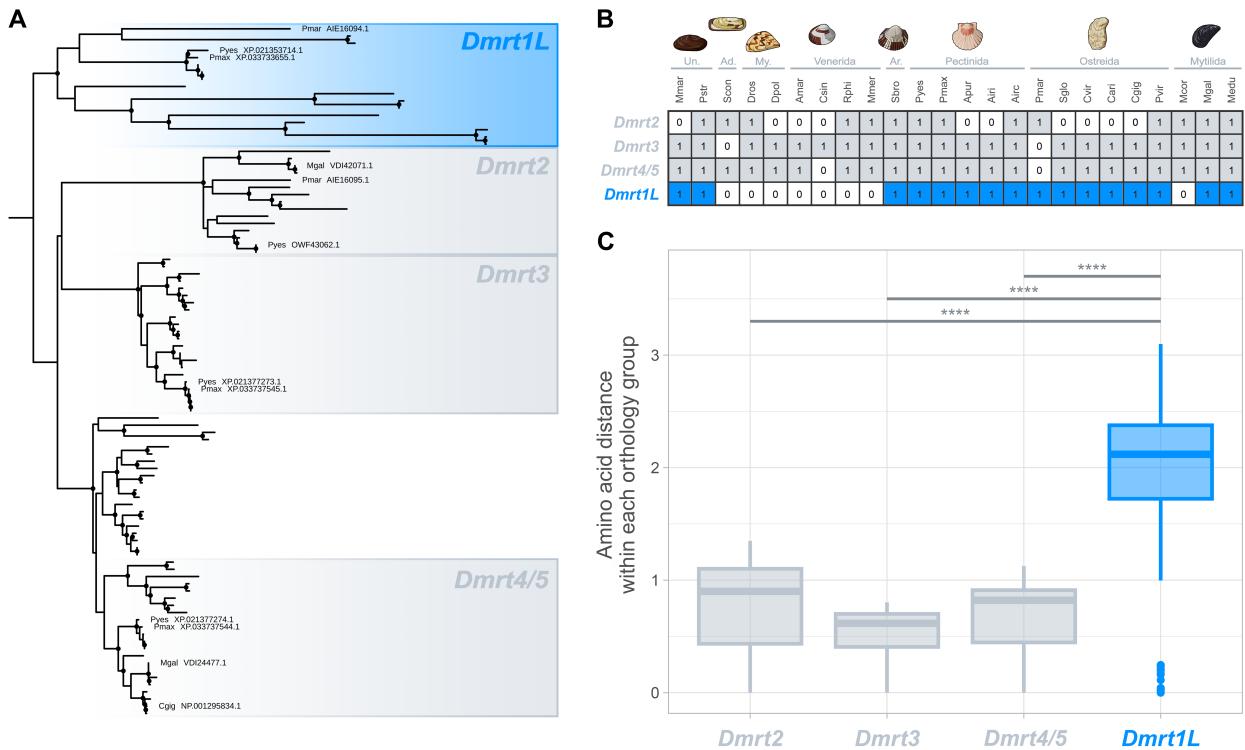
Overall, *Dmrt*, *Sox*, and *Fox* genes are highly interesting targets to be investigated in the framework of bivalve SD and have indeed obtained much more attention than the study of SCs or the role of environmental cues. However, much work is still to be done in order to understand their function in the SD signaling pathway and their evolutionary history.

## 2.2 The case of the *Dmrt* gene family in bivalves

Among the SRG candidates identified in bivalves, *Dmrt* genes (named after doublesex [*dsx*] from *Drosophila melanogaster* and male abnormal-3 [*mab-3*] from *Caenorhabditis elegans*) are of particular interest. As a matter of fact, in vertebrates, besides their role in placode neurogenesis and somite patterning (reviewed in **Mawaribuchi et al., 2019**), *Dmrt* genes are also involved in the development of male gonads and the maintenance of the testicular function (**Sun et al., 2022**). Their role in the specification and organization of male sexual characters seems indeed to be common across Metazoa, suggesting that a similar function may have been already present in the Bilateria common ancestor (**Kopp, 2012; Beukeboom and Perrin, 2014**).

The first attempts to dig inside the phylogenetic history and diversity of bivalve *Dmrt* genes have been provided by **R. Li et al., 2018** and **Evensen et al., 2022**: besides retrieving all the canonical genes (i.e., *Dmrt2*, *Dmrt3* and *Dmrt4/5*), their inferences brought to light a monophyletic *Dmrt* group (named *Dmrt1L*, which stands for Dmrt1-like) which appears to be private to molluscs and present in several bivalve species. The *Dmrt1L* monophyletic group is confirmed also when expanding the analysis by mining genomes from a wider range of bivalve taxa (**Figure 2.1**; **Figure 2.2A**), suggesting that *Dmrt1L* genes are widespread in bivalves and were likely present in their common ancestor (Evensen et al., 2022). In particular, *Dmrt1L* genes can be successfully retrieved in species of the orders Mytilida, Ostreida, Pectinida, Unionida, and from *Scapharca broughtonii* (Arcida), while the opposite holds for Venerida, *Sinonovacula constricta* (Adapedonta), and *Dreissena* spp. (Myida; **Figure 2.2B**). Clearly, the absence of *Dmrt1L* genes demands further investigations, as it may derive from errors in genome assembly and annotations.

The present analysis also supports a higher amino acid sequence divergence of the *Dmrt1L* orthology group with respect to the other *Dmrt* orthology groups (**Figure 2.1C**), which may be explained by a higher rate of sequence evolution related to their sex-biased expression in certain species (**Zhang et al., 2014; J. Shi et al., 2015; R. Li et al., 2018; Evensen et al.,**



**Figure 2.2: Phylogenetic tree (A) and taxonomic distribution (B) of *Dmrt* genes in bivalves, and comparison of amino acid pairwise distances within *Dmrt1L* and the other *Dmrts* (C).** (A) *Dmrt* orthologs from bivalve genome assemblies were obtained with HMMsearch (HMMER toolkit; Eddy, 2011) with the Pfam HMM profile of the DM domain (PF00751). Amino acid alignment was obtained with MAFFT-DASH (Rozewicki et al., 2019), and manually inspected to remove poorly aligning sequences, and trimmed with trimAl (gap threshold of 60%; Capella-Gutiérrez et al., 2009). The phylogenetic analysis was carried out using IQ-TREE 2 (Minh et al., 2020) with default parameters. Nodes with bootstrap values greater than 84 are marked with filled black circles. The tree was rooted according to Evensen et al., 2022. *Dmrt* genes analysed by Evensen et al., 2022 were used as reference to annotate the various orthology groups, and accession numbers are reported in the tree. The phylogenetic tree with all annotated tips and nodes can be accessed on supplementary material online. (B) Taxonomic distribution of identified *Dmrt* genes in bivalve genomes. Orders as reported in WoRMS (accessed before or on 14/03/2023) and in Figure 2.1 are specified. (C) Pairwise amino acid distances were computed for amino acid sequences within each *Dmrt* orthology group identified in the tree, with the R package ‘phangorn’ (Schliep, 2011) under the JTT substitution model. After checking for normality with the Shapiro-Wilk test ( $W = 0.88544$ , p-value  $\approx 2.2e-16$ ) and for group effect with the Kruskal-Wallis test (p-value  $\approx 2.2e-16$ ), the pairwise Wilcoxon rank-sum test was used to compare the distributions of pairwise amino acid distances of *Dmrt1L* and the other *Dmrts*. Horizontal bars mark the significative results with  $p < 2.2e-16$  (\*\*\*\*) (Bonferroni correction for multiple test was applied). The list of genome assemblies used for these analyses and species identifiers can be found in Figure 2.1. Un.: Unionida; Ad.: Adapedonta; My.: Myida; Ar.: Arcida.

2022). This is consistent with what has been already observed for the SRGs *Dmrt1* and *dsx* in vertebrates and *Drosophila*, respectively (e.g., **Bewick et al., 2011; Baral et al., 2019**). In fact, sex-biased genes (including SRGs) often tend to evolve faster than unbiased genes at the level of protein sequences, either when considering male-biased (reviewed in **Parsch and Ellegren, 2013; Grath and Parsch, 2016**) or female-biased genes (e.g., **Papa et al., 2017b; Ghiselli et al., 2018**). Another possible explanation for the higher amino acid divergence of *Dmrt1L* genes may lie on their expression breadth, that is, genes with a narrow tissue-specific expression tend to evolve faster than more ubiquitous genes (**Parsch and Ellegren, 2013; Xu, Martelossi, et al., 2022**). As a matter of fact, *Dmrt1L* genes have been found to be significantly more transcribed in the gonadic tissue (particularly in testes) in *P. yessoensis* (**R. Li et al., 2018**) and *C. gigas* (**Yue et al., 2021**).

Understanding the role and molecular interactions of *Dmrt1L* genes in bivalve SD and gonad development would greatly enhance the possibility of outlining the evolutionary causes and consequences of their high amino acid divergence (**Figure 2.2C**), for example by linking the molecular evolution to the degree of pleiotropy. However, most of our knowledge on *Dmrt1L* biology is currently limited to the temporal and tissue localization of transcripts in a few species of bivalves (e.g., **R. Li et al., 2018; Yue et al., 2021**). In fact—apart from the work by **Sun et al., 2022**, which confirmed the role of *Dmrt1L* in the gonad development of *C. gigas* through non-invasive RNAi and found that the knocked-down phenotype results in size reduction of male gonads—no other experiments intended to elucidate the function of *Dmrt1L* genes in bivalves have been carried out so far (**Figure 2.1**). This clearly hinders any possible integration between molecular data with functional assays. If the role of *Dmrt1L* as major sex determinants was confirmed, bivalves would become an intriguing clade in which investigate why, in Metazoa, certain genes (namely, the *Dmrt* gene family) appear particularly prone to being recruited at the top of the SD cascade. To date, this phenomenon has been widely examined in vertebrates, where *Dmrt1* genes have independently gained a primary role in male SD in fish, amphibians, and birds, and are considered candidate sex-determining genes also in monotreme mammals (**Marshall Graves and Peichel, 2010; Beukeboom and Perrin, 2014; Mawaribuchi et al., 2019**). Bivalves may provide an alternative evolutionary scenario to study the selective forces and molecular modifications that support *Dmrt* genes in repeatedly taking over the SD process. In fact, since *Dmrt1L* genes seem to be restricted to molluscs (**Figure 2.2A**), it would be intriguing to clarify if the putative involvement in the SD cascade of extant bivalve species

is the result of shared ancestry or convergent evolution, which would establish a study system for the evolution of *Dmrt* genes parallel to that of vertebrates (see **Capel, 2017**).

Obviously, *Dmrt1L* should not be expected to be the sole sex-determining gene. In fact, *FoxL2* has already been appointed as the female sex-determining gene in *P. yessoensis* and *C. farreri* (**Han et al., 2022**). Consequently, we should expect that other primary genetic determinants exist, consistently with the extremely high species diversity of the clade. Thus, bivalves may additionally serve as a valuable model system to study how genes from different families take over the SD cascade and are shaped by selection.

## 2.3 Conclusions: bivalves as new models in the study of sex determination

SD is undoubtedly a fascinating biological and evolutionary topic as much as it is challenging to investigate. Our understanding of the causes and consequences of the SD mechanism diversity strongly relies on the study of different systems and non-model model organisms (**Bachtrog et al., 2014; Milani and Ghiselli, 2020**), which provide the foundation for depicting a comprehensive evolutionary and comparative framework in which new and coherent research perspectives can be grounded.

In recent years, bivalves have been achieving growing importance in many fields of biology, from ecology to genomics, and from environmental biomonitoring to mitochondrial studies (**Milani and Ghiselli, 2020; Ghiselli et al., 2021**), but they can be a valuable model to address also SD studies. The diversity of their life history traits provides indeed a challenging, yet extremely fascinating framework, to put the SD processes into an evolutionary context.

Bivalves can help us explain how ESD and GSD interplay with each other in response to the environmental conditions, as a mixed system of both has been proposed to act in the establishment of bivalve sexual identity (reviewed in **Breton et al., 2018**). Moreover, the occurrence of the many existing variants of hermaphroditism and gonochorism even in closely related species, or within the same population, strongly suggests that the basic SD pathway (whether genetic, environmental, or mixed) should be plastic enough to sustain the existence of individuals of both sexes, thus providing the opportunity to study how SD gene regulatory networks are shaped and selected throughout evolution and how epigenetic regulation may

influence SD. The unique DUI system further poses an undeniable challenge in SD studies since it may represent an SD-linked mechanism which relies on the non-nuclear portion of the genome and may unfold many new research paths (**Milani and Ghiselli, 2020; Ghiselli et al., 2021**). Nonetheless, much of the research effort on bivalve SD has been devolved to specific groups of socio-economic importance, such as Mytilida, Ostreida, Pectinida, and Unionida, while the other lineages of the bivalve phylogeny have been neglected (**Figure 2.1**). Our understanding of the SD processes of bivalves is thus restricted and is mainly lacking a broad comparative framework in which to draw comprehensive evolutionary inferences.

Genes from the *Dmrt*, *Sox* and *Fox* families, which are involved in SD also in other Metazoa, may be considered excellent genomic targets to study the processes and patterns of molecular evolution in sex-biased genes, as well as of the recurrent recruitment of genes in the SD cascade. Also, identifying the major genetic regulators of SD in bivalves would burst the functional study of the interaction between ESD and GSD, by providing genetic targets that can be manipulated through RNAi and/or genome editing techniques to understand the role of environmental cues in SD. In the same way, knowing the main genetic actors of SD would allow researcher to identify SCs not only on the basis of in-silico techniques (such as k-mer based or SNP methods) but also by less-expensive wet lab protocols (such as fluorescence in situ hybridization on metaphase chromosome plates). Furthermore, it would help to understand whether and how the mitochondrial additional ORFs of DUI species interact with the SD system, by performing thorough gene expression essays.

In conclusion, we strongly urge researchers to invest more resources in the integrative study of bivalve SD to unravel the many underlying mechanisms and expand our understanding of this biological process. Given our limited knowledge in the field, one of the first routes that should be undertaken may rely on the comparative study of SRGs of bivalves from a genomic perspective, as this kind of data is nowadays growing at a rate faster than ever. Establishing such a genomic ground plan for understudied organisms will in fact allow researchers to develop evolutionary-aware experiments with better selected genetic targets.

Table 2.1: **List of bivalve genomes from which *Dmrt* genes have been extracted.** For each species, the accepted name and the most-common synonym (in parentheses) are reported. NCBI accession numbers are provided, when available, as well as BUSCO scores of the predicted proteomes against the metazoa\_odb10 dataset (Manni et al., 2021).

Species	ID	Order	Assembly level	BUSCO score	Reference	NCBI Acc. No.
<i>Anadara (Scapharca) broughtonii</i>	Sbro	Arcida	Chromosome	C:91.2% [S:85.6%,D:5.6%] F:2.6% M:6.2%	Bai et al., 2019	NA
<i>Simonovacula consticta</i>	Scon	Adapedonta	Chromosome	C:92.5% [S:80.4%,D:12.1%] F:3.4% M:4.1%	Ran et al., 2019	GCA_007844125.1
<i>Dreissena polymorpha</i>	Dpol	Myida	Chromosome	C:86.9% [S:75.1%,D:11.8%] F:6.4% M:6.7%	McCartney et al., 2022	GCA_020536995.1
<i>Dreissena rostriformis</i>	Dros	Myida	Scaffold	C:75.2% [S:73.2%,D:2.0%] F:15.2% M:9.6%	Calcino et al., 2019	GCA_007657795.1
<i>Mytilus unguiculatus (coruscus)</i>	Mcor	Mytilida	Chromosome	C:80.0% [S:79.1%,D:0.9%] F:7.7% M:12.3%	Yang et al., 2021	GCA_017311375.1

Table 2.1 continued from previous page

Species	ID	Order	Assembly level	BUSCO score	Reference	NCBI Acc. No.
<i>Mytilus edulis</i>	Medu	Mytilida	Scaffold	C:83.7% [S:64.5%,D:19.2%] F:5.2% M:11.1%	Corrochano-Fraile et al., 2022	GCA_905397895.1
<i>Mytilus galloprovincialis</i>	Mgal	Mytilida	Scaffold	C:80.3% [S:47.5%,D:32.8%] F:8.8% M:10.9%	Gerdol et al., 2020	GCA_900618805.1
<i>Perna viridis</i>	Pvir	Mytilida	Scaffold	C:99.4% [S:99.0%,D:0.4%] F:0.2% M:0.4%	Inoue et al., 2021	GCA_018327765.1
<i>Magallana (Crassostrea) ariakensis</i>	Cari	Ostreida	Chromosome	C:94.6% [S:90.9%,D:3.7%] F:0.9% M:4.5%	A. Li et al., 2021	GCA_020567875.1
<i>Magallana (Crassostrea) gigas</i>	Cgig	Ostreida	Chromosome	C:98.5% [S:67.6%,D:30.9%] F:0.3% M:1.2%	Peñaloza et al., 2021	GCF_902806645.1

Table 2.1 continued from previous page

Species	ID	Order	Assembly level	BUSCO score	Reference	NCBI Acc. No.
<i>Crassostrea virginica</i>	Cvir	Ostreida	Chromosome	C:98.1% [S:58.6%,D:39.5%] F:0.3% M:1.6%	Gómez-Chiarri et al., 2015	GCF_002022765.2
<i>Saccostrea glomerata</i>	Sglo	Ostreida	Scaffold	C:88.9% [S:85.3%,D:3.6%] F:5.1% M:6.0%	Powell et al., 2018	GCA_003671525.1
<i>Argopecten irradians concentricus</i>	Airc	Pectinida	Scaffold	C:94.8% [S:93.9%,D:0.9%] F:3.7% M:1.5%	Liu et al., 2020	GCA_004382765.1
<i>Argopecten irradians irradians</i>	Airi	Pectinida	Scaffold	C:94.8% [S:93.9%,D:0.9%] F:3.7% M:1.5%	Liu et al., 2020	GCA_004382745.1
<i>Argopecten purpuratus</i>	Apur	Pectinida	Scaffold	C:89.2% [S:88.5%,D:0.7%] F:5.0% M:5.8%	Liu et al., 2020	NA

Table 2.1 continued from previous page

Species	ID	Order	Assembly level	BUSCO score	Reference	NCBI Acc. No.
<i>Pecten maximus</i>	Pmax	Pectinida	Chromosome	C:98.5% [S:74.7%,D:23.8%] F:0.4% M:1.1%	Kenny et al., 2020	GCF_902652985.1
<i>Mizuhoppecten (Patinopecten) yessoensis</i>	Pyes	Pectinida	Scaffold	C:98.6% [S:75.2%,D:23.4%] F:0.4% M:1.0%	S. Wang et al., 2017	GCF_002113885.1
<i>Margaritifera margaritifera</i>	Mmar	Unionida	Scaffold	C:92.6% [S:82.3%,D:10.3%] F:3.2% M:4.2%	Gomes-dos-Santos et al., 2021	GCA_015947965.1
<i>Potamilius streckeroni</i>	Pstr	Unionida	Scaffold	C:74.7% [S:73.8%,D:0.9%] F:7.0% M:18.3%	Smith, 2021	GCA_016746295.1
<i>Calyptogena (Archivesica) marissinica</i>	Amar	Venerida	Chromosome	C:82.0% [S:80.0%,D:2.0%] F:6.1% M:11.9%	Ip et al., 2021	GCA_014843695.1

Table 2.1 continued from previous page

Species	ID	Order	Assembly level	BUSCO score	Reference	NCBI Acc. No.
<i>Cyclina sinensis</i>	Csin	Venerida	Scaffold	C:94.0% [S:83.8%,D:10.2%] F:1.9% M:4.1%	Wei et al., 2020	GCA_012932295.1
<i>Mercenaria mercenaria</i>	Mmer	Venerida	Chromosome	C:95.4% [S:70.9%,D:24.5%] F:0.5% M:4.1%	Song et al., 2021	GCF_014805675.1
<i>Ruditapes philippinarum</i>	Rphi	Venerida	Chromosome	C:83.4% [S:74.5%,D:8.9%] F:8.8% M:7.8%	Xu, Martelossi, et al., 2022	GCA_026571515.1

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## **2.5 Data Availability**

Analyzed data and R scripts used to generate plots can be accessed in supplementary material online deposited at the following GitHub repository: [filonico/bivalve\\_sex\\_perspective](https://github.com/filonico/bivalve_sex_perspective).

# Chapter 3

## Identification of putative sex-determination related genes in bivalves through comparative molecular evolutionary analyses

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***In preparation.***

# Chapter 4

## Expression patterns of three sex-related genes and the germline marker *Vasa* in early developmental stages of *Mytilus galloprovincialis* embryos

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### 4.1 Materials and Methods

#### 4.1.1 Time-series gene expression

Miglioli et al., 2024 recently produced one of the very first detailed developmental transcriptome of *M. galloprovincialis*, spanning from the unfertilized oocyte to the larval stage at 72 hpf, with time points sampled every 4 hpf. A total of 30 different mRNA libraries was sequenced,

consisting of fifteen developmental time points per two technical replicates. These data are very useful to thoroughly investigate the transcription patterns of genes throughout the first three days of development in *M. galloprovincialis* and to obtain hints on the expected outcomes of mRNA-ISH experiments.

Raw reads were downloaded from the Sequence Read Archive (SRA) in NCBI (BioProject: PRJNA996031) and trimmed using Trimmomatic v0.39 (**Bolger et al., 2014**; LEADING:5 TRAILING:5 SLIDINGWINDOW:4:15 MINLEN:65). Read quality was checked using FastQC v0.12.1 (**Andrews et al., 2010**). Trimmed reads were mapped against the *M. galloprovincialis* annotated genome (GCA\_900618805.1; **Gerdol et al., 2020**) using STAR v2.7.10b (**Dobin et al., 2013**) in alignReads mode with default parameters. The resulting gene count matrix was extracted with StringTie v2.2.1 (**Pertea et al., 2015, 2016**) in expression estimation mode followed by the python script prepDE.py (-l 99).

The resulting matrix was processed in R. Raw gene counts were normalized using the built-in function `vst` of the package DESeq2 (**Love et al., 2014**). The function `plotPCA` was then used to run a principal component analysis (PCA) on read mapping counts and visualize the corresponding results. Normalized gene counts were also used to plot expression values of target genes (i.e., *Vasa*, *Dmrt1L*, *SoxH* and *FoxL2*), as well as in maSigPro (**Conesa et al., 2006**) to run a differential gene expression analysis in a time course experiment.

The entire pipeline was automated through custom python and bash scripts, which are available in a private repository on GitHub.

#### 4.1.2 Sample collection, MitoTracker staining and fixation

Adult Mediterranean mussels (*M. galloprovincialis*) were hand collected from various locations surrounding the AltaSea institute at the port of Los Angeles (CA, USA). Sampling took place during the late spawning season of the species in California, i.e., from October 2023 to early January 2024. Specimens were checked for species and sexual maturity before usage.

Selected mussels were thoroughly cleaned from epibionts and placed in ice for approximately 30-60 minutes, then transferred in filtered artificial sea water (FASW) at 16°C and acclimatized for 30 minutes. All the individuals were then placed in a common tank and spawning was induced by cyclical thermal shock, that is, by exposing mussels alternatively to FASW at 24-26°C and 14-16°C for 30-40 minutes. As soon as individual mussels started spawning, they

were promptly removed from the common tank, carefully washed and then allowed to continue spawning in isolated containers of about 250 ml 16°C FASW.

Sperm from six males and oocytes from six females were separately mixed to increase the number of crosses. An hour after the spawning started, oocytes were filtered through a 75 over a 30 µm mesh and aged in 1 L of FASW for 40-60 minutes to let them assume a proper circular shape. Oocyte abundance was estimated under a stereo microscope, by counting the number of gametes in five aliquotes of 1 mL and then calculating the mean value. Sperm mitochondria were labeled with MitoTracker™ Red CMXRos (Thermo Fisher Scientific) at a working concentration of 500 nM for 30 minutes. MitoTracker is a vital and fixation-resistant mitochondrial dye and was used to be able to detect the sex of developing embryos (as early as the two-blastomere stage) according to the distribution pattern of sperm mitochondria (**Cao et al., 2004; Obata and Komaru, 2005**). From this step onward, samples were always kept in the dark.

Fertilization was performed by mixing oocytes and sperm at a ratio of 1:10. Fertilization success was checked after 20-30 minutes by the formation of polar bodies. The suspension was then carefully washed to remove excess sperm and brought to a concentration of 250 zygotes/mL. The resulting suspension was transferred into cell-culture flasks of 40 mL and embryos/larvae were reared at 16°C in the dark. Water was changed every 24 hours. After 48 hpf, larvae were fed with *Isochrysis galbana* at a final concentration of ~100,000 cells/mL following **Helm et al., 2004**.

Embryos/larvae were sampled at 1, 2, 3 and 4 hpf, and then every 12 hours until 72 hpf, every time after checking for proper development and vitality. After concentration in a mesh of proper size, embryos/larvae were fixed in 3.2% paraformaldehyde (PFA) in 1× PBS at 4°C overnight under constant and gentle shaking. Fixed samples were washed 3 × 20 minutes in 1× PBS 0.1% Tween 20 (PBST) and then dehydrated 3 × 30 minutes in absolute methanol at room temperature (RT). Dehydrated samples were stored at -20°C until usage.

#### 4.1.3 Hybridization Chain Reaction (HCR)

##### HCR probe design

*Vasa*, *Dmrt1L*, *SoxH*, and *FoxL2* spliced-transcript nucleotide sequences of *M. galloprovincialis* were obtained from previous analyses with OrthoFinder v2.5.5 (**Emms and Kelly, 2019**) and

Target	Amplifier	Fluorophore	No. of probe pairs
<i>Vasa</i>	B1	ALEXA-488	33
<i>Dmrt1L</i>	B2	ALEXA-647	18
<i>SoxH</i>	B3	ALEXA-546	22
<i>FoxL2</i>	B4	ALEXA-700	28

Table 4.1: List of genes targeted through HCR, with the corresponding amplifiers, fluorophores and number of generated probe pairs.

30 annotated bivalve genomes (see **Chapter 3**). Accession numbers of spliced transcripts are 10B017427, 10B093608, 10B014180, and 10B094018, respectively. The `insitu_probe_generator` script from Ozpolat Lab (**Kuehn et al., 2022**) was used to generate pairs of probes specifically designed for third-generation HCR (**Choi et al., 2018**). The built-in BLASTN search against the annotated *M. galloprovincialis* transcriptome was employed to check for putative off-target bindings of probe pairs. B1-488, B2-647, B3-546, and B4-700 pairs of HCR amplifiers and fluorophores were chosen as in **Table 4.1**. Resulting probes were synthetized by Integrated DNA Technologies (IDT™) in different oligo pools.

### Fluorescent *in-situ* hybridization through hybridization chain reaction and microscope imaging

HCR mRNA-FISH was performed following **Miglioli et al., 2024**. All the steps were carried out in the dark to prevent MitoTracker from fading. Probe hybridization buffer, probe wash buffer and amplification buffer were manufactured by Molecular Instruments, Inc.

Dehydrated samples stored in methanol were washed 4 times per 5 minutes and 1 time per 10 minutes in PBST. Samples were then permeabilized for 30 minutes in a detergent solution (1.0% SDS, 0.5% Tween 20, 50 mM Tris-HCl, 1.0 mM EDTA, 150.0 mM NaCl) and washed again 2 times per 5 minutes in PBST. Samples were prepared for the HCR detection stage by incubation in probe hybridization buffer for 30 minutes at 37 °C. Detection stage was then performed with 4 nM of each probe set in hybridization solution overnight (>12 h) at 37 °C.

Excess probes was removed by washing 4 times per 20 minutes with probe wash buffer at 37 °C and 3 times per 5 minutes with 5× saline-sodium citrate Tween 20 buffer (SSCT; 5× SSC, 0.1% Tween 20) at room temperature. Samples were incubated for 30 minutes in amplification buffer at room temperature. Hairpins were heated at 95 °C for 90 seconds and then snap-cooled at room temperature for 30 minutes. The amplification step of HCR was performed with 6 pmol of each hairpin in amplification buffer overnight (>12 h) at room temperature.

Target	Dye	Excitation (nm)	Emission (nm)
dsDNA (nuclei)	DAPI	360	460
Sperm mitochondria	MitoTracker™ Red CMXRos	575	600
<i>Vasa</i>	ALEXA-488	499	520
<i>Dmrt1L</i>	ALEXA-647	653	670
<i>SoxH</i>	ALEXA-546	557	575
<i>FoxL2</i>	ALEXA-700	685	700

Table 4.2: List of dyes used for every target, together with the excitation and emission peaks as returned by the Las X software.

Excess hairpins was removed by washing 2 times per 5 minutes, 2 times per 30 minutes, and 1 time per 5 minutes with SSCT. If not immediately mounted on slides, samples were stored in SSCT at +4 °C. Otherwise, samples were immersed in 50% and 70% glycerol for 30-60 minutes each, and then mounted with VECTASHIELD® PLUS Antifade Mounting Medium with DAPI (H-2000). Slides were imaged on a Stellaris 5 Confocal Package system with the software Las X (Leica Microsystems). Each dye was imaged sequentially in a separate channel, to enhance the yield and avoid any crosstalks. **Table 4.2** summarises the excitation and emission peaks for each dye. Images were then manipulated and post-produced using Fiji v2.14.0.

#### 4.1.4 Immunolocalization of *Vasa*

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