Vietnam Journal of Biotechnology **24**(1): 1-11, 2026. DOI: 10.15625/vjbt-23543

Review Article

GENETICS AND BREEDING OF THE IVORY SNAIL (*Babylonia areolata*): CURRENT STATUS, CHALLENGES AND PROSPECTS

Van Sang Vu[1,✉], Thiyagarajan Vengatesen[3], Duc Long Nguyen[1], Thi Thao Vu[4], Thi Hoan Ngo[5], Thi Nhu Phuong Le[5], Thi Thuy Vu[4], Phuong Ha Vu[1], Kim Hyun Woo[6] and Huy Hoang Nguyen[2]

[1]*Faculty of Biology, University of Science, Vietnam National University, Hanoi, 334 Nguyen Trai, Thanh Xuan, Hanoi, Vietnam*

[2]*Institute of Biology, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet, Nghia Do, Hanoi, Vietnam*

[3] *Hong Kong Oyster Hatchery & Innovation Research Unit, The Swire Institute of Marine Science and School of Biological Sciences, The University of Hong Kong, Hong Kong, China*

[4] *Phuong Thuy Genomics Company Limited, Son Dong, Hanoi, Vietnam*

[5] *Faculty of Fisheries, Ha Long University, Vang Danh, Quang Ninh, Vietnam*

[6]*Faculty of Marine Science, Pukyong National University, Busan, South Korea*

✉To whom correspondence should be addressed. Email: vuvansangts50@gmail.com

Received: 29 September 2025; Accepted: 19 January 2026; Published online: 10 March 2026

ABSTRACT

The ivory snail, *Babylonia areolata,* is a high-value marine mollusc widely distributed in the Indo-Pacific and increasingly farmed in Southeast Asia, particularly Vietnam. Its fast growth, short farming cycle, and strong market demand have made it a promising aquaculture species for the coastal provinces in Vietnam. However, the *B. areolata* industry faces major challenges, including low seed quality and poor broodstock management. To achieve sustainable and rapid development, the establishment of high-quality breeding populations for long-term improvement is essential. This review synthesizes current knowledge of reproductive biology, genetics and selective breeding for *B. areolata*, highlighting advances in molecular tools for assessing population structure, genetic variation, and trait-associated markers as well as prospects for a selective breeding program in Vietnam. Selective breeding programs targeting growth rate and disease resistance are discussed, alongside challenges such as the lack of comprehensive genomic resources, high larval mortality, and inbreeding risks. To meet the high-quality seed demand for ivory snail industry, a selective breeding program was initiated in Vietnam in 2024, focusing on improving growth rate. However, no genes or molecular markers have been identified for this species yet. By integrating modern genomic technologies with traditional selection approaches, *B. areolata* aquaculture can achieve significant genetic gains, ensuring the fast and sustainable development of strains that meet both commercial and conservation objectives.

Keywords: *Babylonia areolata*, genetic improvement, genomic selection molecular markers.

INTRODUCTION

The ivory snail, *Babylonia areolata* (Neogastropoda, Buccinidae), is an economically important molluscan species distributed throughout the Indo-Pacific region and Southeast Asia, including Indonesia, India, China, and Vietnam (Fu *et al*., 2016). Hatchery technology for this species was first developed in the late 1990s (Chaitanawisuti and Kritsanapuntu, 1997), and recently *B. areolata* has emerged as a key marine aquaculture species in Vietnam. This is largely due to its rapid growth, short farming cycle, and strong market demand in both domestic and export markets.

In Vietnam, *B. areolata* is primarily cultured in coastal ponds, with an annual production of approximately 11,195 tonnes (Vietnam Ministry of Agriculture and Rural Development, 2024). Farm-gate prices range from USD 9.50 to 13.30 per kilogram, making the species economically attractive. As a result, ivory snail farming is increasingly viewed as an alternative to brackish-water shrimp culture, owing to its simpler management requirements, lower disease incidence, and higher market value (Vu *et al*., 2025).

Despite its rapid expansion, several challenges constrain the sustainable development of ivory snail aquaculture in Vietnam. These include: (i) inadequate broodstock management and poor pedigree recording, leading to genetic erosion and limited information for future breeding programs; (ii) ineffective distribution of high-quality broodstock, restricting genetic diversity within cultured populations; and (iii) declining effective population size, resulting in increased inbreeding, altered gene frequencies, and loss of genetic variation. To address these issues, many countries have invested in breeding research that integrates conventional selection with molecular genetic techniques. In Vietnam, the application of quantitative and molecular genetics has produced substantial gains in several major aquaculture species, including shrimp, tilapia, carp, sea bass, and Portuguese oysters, with average growth improvements of 5–8% per generation.

Production of *Babylonia areolata*

B. areolata is widely distributed in tropical seas of the Indo-Pacific region and inhabits sandy or sandy-muddy substrates. The species is gonochoristic and exhibits internal fertilization. Across its range, spawning times vary, but in Vietnam, peaks in spawning activity occur between March and July, although the species can be held in cement tanks with sand bottoms and conditioned with high-protein diets to allow year-round spawning (Hua *et al*., 2001; Figure 1).

The size at first maturity of wild *B. areolata* ranges from 40–50 mm shell height, with no significant difference between males and females (Nguyen *et al.,* 2004). Under artificial rearing conditions, *B. areolata* spawn for the first time at around 7–10 months of age (Hua *et al*., 2001; Nguyen *et al.,* 2004). During the spawning season, mating typically occurs in the late afternoon and at night before egg laying. The male transfers sperm through the penis into the female via the sperm duct, and the sperm is stored in the seminal receptacle (Nguyen *et al.,* 2004). Snails can be held as isolated pairs for mating, which can be used to facilitate selective breeding.

Figure 1. Broodstock conditioning of the ivory snail in cement tanks with a sand bottom. The ivory snails are being fed with high-protein fresh feed (Photo: Van Sang Vu, 2024).

Average fecundity under natural conditions is 56,424 eggs per spawning, depending on temperature. Fertilized eggs develop into trochophores, which remain within the egg capsules. The larvae then develop into veliger larvae (Figure 2), and after 5–7 days, the veligers hatch from the egg capsules. The larvae are free-swimming for 15-18 days, feed on unicellular algae, and undergo metamorphosis into crawling larvae, transitioning to a benthic lifestyle (Nguyen *et al*., 2004). After 23-25 days, juvenile ivory snails fully adopt a benthic lifestyle and begin carnivorous feeding, like adults, but they will readily accept formulated diets (Chaitanawisuti *et al*., 2011). After 25 days of nursery rearing, juveniles are transferred to grow-out ponds, where they are cultured for 6–8 months before harvest when they reach market size of 120-150 snails/kg (Nguyen *et al.,* 2004; Chaitanawisuti *et al*., 2009).

Genetics of *B. areolata*

Genetics plays a central role in the long-term domestication and improvement of aquaculture species and represents one of the most effective approaches for enhancing economically important traits. In *B. areolata*, genetic research has advanced substantially over the past decade, providing critical insights to support selective breeding and stock enhancement programs. Research has primarily focused on (i) characterizing genetic diversity and population structure, (ii) identifying molecular markers associated with growth, disease resistance, and reproductive performance (Fu *et al*., 2016), and (iii) developing breeding strategies that optimize productivity while minimizing the loss of genetic variation (Vu *et al*., 2025).

A range of molecular tools, including mitochondrial DNA sequencing, microsatellite markers, and high-throughput single nucleotide polymorphism (SNP) genotyping, has been applied to assess genetic diversity in both wild and cultured populations (Fu *et al*., 2016; Liu *et al*., 2024; Wei *et al*., 2024). These approaches have demonstrated that, although wild populations typically exhibit moderate to high genetic variability, cultured stocks often show reduced heterozygosity and allelic richness. Such declines in genetic diversity can lead to inbreeding depression, resulting in reduced growth rates and fecundity (Fang and Li, 2023a; Fang and Li, 2023b).

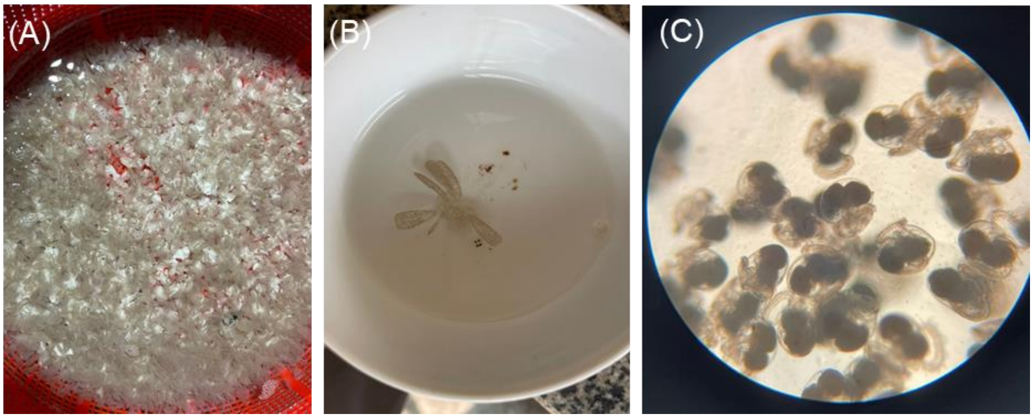

Figure 2. (A) Egg capsules of the ivory snail incubated in plastic baskets in aerated cement tanks; (B) egg capsules; (C) hatched larvae still inside the egg capsules (Photo: Vu Van Sang, 2024).

Genetic diversity and population structure

Assessment of genetic diversity and population structure represents a fundamental component of genetic research in *B. areolata* (Vu *et al*., 2025). Maintaining genetic variation is essential for sustaining breeding programs across generations, particularly in closed-cycle systems where limited broodstock numbers can rapidly erode diversity (Fu *et al*., 2016, Van In *et al*., 2017). Inbreeding depression remains a major concern under such conditions.

Recent advances in genome-wide SNP analysis and whole-genome sequencing have enabled more precise parentage assignment, identification of growth- and disease-resistance loci, and fine-scale population structure analysis (Guo *et al*., 2023; Zou *et al*., 2024; Zhang *et al*., 2024; Wu *et al*., 2025). These tools have strengthened understanding of genotype–phenotype relationships and improved the efficiency of selective breeding programs.

Genetic diversity in cultured stocks can be maintained through strategies such as periodic introduction of unrelated wild broodstock and continuous genetic monitoring to track allele frequencies across generations. These measures reduce inbreeding risk and enhance resilience to disease and environmental stressors. Moreover, knowledge of population structure facilitates the identification of appropriate management units and supports the selection of genetically compatible broodstock, thereby maximizing heterosis and long-term productivity (Vu *et al*., 2025).

Given the growing economic importance of *B. areolata* in Southeast and East Asia, further investment in molecular and genomic approaches, particularly genomic selection, will be essential for developing high-performance strains while preserving genetic robustness. These advances should be integrated with rigorous broodstock management frameworks to ensure sustainable aquaculture production.

Current state of selective breeding programs

The objective of breeding programs is to enhance one or more traits of economic importance, like growth rate, survival, shape, yield, shell or mantle color, temperature tolerance, and disease resistance. A common important commercial trait in mollusc species is growth, especially for the initial phase of a breeding program because the development of fast-growing strains can significantly lower production costs by decreasing the culturing time (Saillant *et al*., 2009; Vu *et al*., 2025; Boudry *et al*., 2025). Several genetic parameters, including heritability, genetic correlations, and selection responses, have been documented in molluscan species such as oysters, mussels, and snails (Vu *et al*., 2025). Examples of notable selection responses observed in different molluscan species are summarized in Table 1.

Table 1. Selection outcomes observed in various farmed molluscan species.

Species	Traits of selection	Selection method	Selection response (%/generation on average)	Number of generations	References
C. angulata	Whole weight	Family	6.8	3	Vu *et al.,* 2020
C. gigas	Whole weight	Family	2.26	5	de Melo *et al*., 2016
Saccostrea glomerata	Whole weight	Mass	9.0	2	Nell *et al.,* 2000
Ostrea edulis	Whole weight	Mass	23.0	1	Newkirk and Haley, 1982

Selective breeding and genetic improvement of *Babylonia areolata*

A high-quality chromosome-level genome assembly of *B. areolata* has recently been generated using PacBio, Illumina, and Hi-C sequencing technologies (Zou *et al*., 2024). The assembly comprises 35 chromosomes with a total length of 1.65 Gb and high completeness, providing a strong foundation for genomic research and breeding programs.

Selective breeding remains one of the most effective strategies for improving aquaculture performance, enabling cumulative genetic gains across generations (Jiang *et al*., 2024). In *B. areolata*, breeding efforts have primarily focused on growth and survival (Le *et al*., 2025; Vu *et al*., 2025). Faster-growing strains reach market size more rapidly, reducing production costs and improving farm profitability.

Selection indices can be used to improve multiple traits simultaneously, including body weight, shell growth, and feed efficiency (Falconer and Mackay, 1996; Lall *et al*., 2025). Integration of molecular markers enables marker-assisted selection, improving selection accuracy and shortening breeding cycles. However, to date, no large-scale structured genetic breeding program has been fully implemented for this species.

Genetic improvement must be accompanied by rigorous broodstock management to prevent inbreeding and loss of diversity. Recommended strategies include rotational mating, optimal contribution selection, and periodic introgression of wild genetic material. Crossbreeding between genetically differentiated populations may also generate heterosis in growth, survival, and stress tolerance (Jiang *et al*., 2025). Vu *et al.*

(2025) reported additive genetic, heterosis, and maternal effects in base populations, providing a foundation for future breeding programs.

Potential for genomic selection in *Babylonia areolata*

Alongside conventional selective breeding based on phenotypes and pedigrees, the integration of molecular and genomic tools has the potential to enhance selection responses (Martinez, 2007), particularly for traits that are difficult or costly to evaluate or display low heritability. This is especially relevant when markers are closely associated with major-effect quantitative trait loci (QTL) (Robledo *et al.*, 2017). Genomic selection (GS) represents a promising approach for such traits, for example, soft tissue mass at different developmental stages. Although whole-genome sequencing remains prohibitively expensive for routine genotyping of all pedigree individuals in non-model species, reduced-representation sequencing methods such as genotyping-by-sequencing (GBS) provide a relatively inexpensive means of obtaining partial genomic data. GBS offers low-cost genotyping while generating a substantial number of high-quality genetic markers, which are potentially suitable for GS. Nevertheless, this method often yields missing genotype data, necessitating imputation, and in *B. areolata*, a considerable proportion of missing data has been reported. Consequently, more comprehensive approaches, such as whole-genome resequencing with minimal missing data, may be preferable for GS applications.

Among restricted-site associated DNA sequencing methods, Diversity Arrays Technology sequencing (DArTseq) combines DArT-based complexity reduction with next-generation sequencing (Kilian *et al.*, 2012). Similar to earlier DArT approaches relying on array hybridizations, DArTseq is optimized for each organism by tailoring the degree of genome representation and the proportion of the genome targeted. The emergence of GS, extending marker-assisted selection (MAS) to a genome-wide level, has created new opportunities. Instead of focusing on the discovery of specific QTL, GS assumes that markers are distributed densely enough to ensure linkage disequilibrium with all QTL across the genome (Hayes and Goddard, 2001). In practice, GS requires a reference population with combined genotype and phenotype records to estimate marker effects, which are then used to predict genomic breeding values in genotyped but unphenotyped individuals (Hayes and Goddard, 2001). While MAS is most effective for traits governed by large-effect loci, GS is well suited to improving polygenic traits controlled by many small-effect loci (Robledo *et al.*, 2017).

To date, GS has not been widely implemented in genetic improvement programs for marine gastropods in developing countries. However, successful applications in other aquaculture species have demonstrated its capacity to increase the accuracy of breeding value estimation for growth and quality traits (Boudry *et al.,* 2021; Vu *et al.,* 2021) and for disease resistance (Bangera *et al.*, 2017; Robledo *et al.*, 2018). While there has been considerable progress in QTL discovery for molluscs, validation across populations remains limited. For *B. areolata*, the lack of species-specific SNP arrays has been a major constraint, largely due to the high costs associated with chip development. DArTseq technology offers a cost-effective alternative, generating genome-wide sequence data suitable for building genomic relationship matrices and estimating breeding values for complex traits. Recent studies applying DArTseq in molluscs have shown that this approach can deliver high prediction accuracy for commercial traits and meet the developmental demands of the aquaculture industry (Vu *et al.,* 2021). Importantly, genomic heritability estimates for traits such as growth, body composition, meat quality, and shell morphology were consistently higher when derived from genomic data than from pedigree information, a pattern also reported in other molluscs including *C. gigas* (Boudry *et al*., 2021) and *C. virginica* (McCarty *et al*., 2022). These findings suggest that similar approaches could be effectively applied to *B. areolata* to accelerate genetic gains in aquaculture.

Challenges and opportunities in breeding programs

One of the major challenges is the high variability in larval and juvenile survival rates observed in both hatchery and grow-out phases. Survival during early life stages is influenced by a complex interplay of genetic factors, maternal effects, nutrition, and environmental and disease factors. High mortality not only reduces production efficiency but also weakens the effectiveness of selection programs, as fewer individuals reach maturity for breeding. Improving larval survival therefore requires integrated research that combines quantitative genetics, molecular biology, and hatchery management to optimize rearing conditions and identify genetic determinants of early-stage robustness. Advances in high throughput sequencing technologies and genomic tools offer substantial opportunities to overcome these limitations. The application of genome-wide association studies and restriction site associated DNA sequencing can accelerate the discovery of markers linked to key traits, enabling the implementation of marker-assisted selection in *B. areolata*. Even more promising is genomic selection, which uses genome wide marker data to estimate breeding values and predict the performance of individuals before phenotypes are expressed. Genomic selection has already demonstrated significant efficiency gains in aquaculture species such as mollusc and fish species, reducing generation intervals and increasing selection accuracy (Yanez *et al*., 2023; Wang *et al.,* 2024; Vu *et al.,* 2021). The genome of *Babylonia areolata* was published to support research on genomic selection and the development of SNP chips for this species. In addition, the genome size of *B. areolata* is significantly smaller than that of other molluscan species, such as *Achatina fulica* and *Bellamya purificata*, suggesting that genomic selection may be more advantageous in this species due to the lower cost of sequencing. In the future, integrating genomic selection with optimized hatchery protocols, crossbreeding strategies, and effective broodstock management could revolutionize *B. areolata* breeding. This combined approach would enable the production of strains that exhibit not only superior growth and survival but also resilience to environmental variability and disease outbreaks traits that are increasingly critical in the face of climate change and intensifying aquaculture production.

Climate change represents one of the greatest challenges to the snail aquaculture industry in Vietnam, particularly due to anticipated increases in water temperature. Thermal conditions directly influence reproduction, larval rearing, and grow-out performance. Selective breeding offers a pathway to mitigate these impacts by improving traits such as tolerance to elevated temperatures and salinity (Parker *et al.,* 2015; Parker *et al.,* 2021). A critical step forward will be collaboration among large companies to reduce genotyping costs and to develop affordable SNP arrays that are accessible to farmers. The incorporation of genomic tools into existing breeding programs would ideally involve genotyping all potential broodstock and their progeny, thereby removing the need to maintain separate families at early life stages and reducing common-environment confounding effects. Genomic selection also enables evaluation at younger ages, thereby lowering operational and labor costs for farmers. An urgent research priority is the development of species-specific SNP chips for *B. areolata* to minimize genotyping expenses. Once available, genotyping costs could be reduced to approximately USD 2.5 per individual, a level considered affordable for commercial producers. The adoption of SNP chips would allow both farmers and researchers to select broodstock more efficiently using markers linked to traits of economic interest. In Vietnam, molecular genetics infrastructure is already available at universities such as Vietnam National University, providing capacity for genetic testing, estimation of breeding values, breeding program design, and SNP chip development.

CONCLUSION

The genetic and breeding improvement of *B. areolata* is a promising area of research that holds significant potential for enhancing its role in global aquaculture. The application of molecular genetics, selective breeding techniques, and a better understanding of its reproductive biology will be key to optimizing production and ensuring the sustainability of this economically important species. While challenges remain, the progress made in genetic research and breeding methodologies provides a solid foundation for the future development of *B. areolata* aquaculture. By integrating modern genetic tools with traditional breeding practices, it will be possible to develop robust, high-performance populations that meet the growing demand for this valuable marine resource.

ACKNOWLEDGMENTS

The authors also wish to express their gratitude to Professor Le Duc Minh; Dr. To Thanh Thuy of the University of Science, Vietnam National University, Hanoi, Vietnam; and Dr. Nguyen Thi Anh Thu of Nha Trang University for their valuable assistance during the experimental procedures.

FUNDING

Van Sang Vu was funded by the Postdoctoral Scholarship Programme of Vingroup Innovation Foundation (VINIF) under grant numbers VINIF.2024.STS.52 and VINIF.2025.STS.40. In addittion, this research was funded by VNU Asia Research Center (ARC) from grants source by CHEY Institute for Advanced Studies, code CA.25.06A.

CONFLICT OF INTEREST

There is no conflict of interest in this study.

REFERENCES

Bangera R., Correa K., Lhorente J. P., Figueroa R., and Yáñez J. M. (2017). Genomic predictions can accelerate selection for resistance against *Piscirickettsia salmonis* in Atlantic salmon (*Salmo salar*). *BMC Genomics 18*, 121. https://doi.org/10.1186/s12864-017-3487-y.

Boudry P., Allal F., Aslam M. L., Bargelloni, L., Bean T. P., Brard-Fudulea S., *et al.* (2021). Current status and potential of genomic selection to improve selective breeding in the main aquaculture species of International Council for the Exploration of the Sea (ICES) member countries. *Aquaculture Reports, 20*, 100700. https://doi.org/10.1016/j.aqrep.2021.100700.

Boudry P., Vengatesen T., Gheyas A., Khanh T. D., Nguyen T. M., Htoo H., *et al,*(2025). Genetic parameters for whole weight and survival rate of the Portuguese oyster, *Crassostrea angulata*, at different harvest stages after six generations of selection. *Aquaculture International*, *33*(3), 1-12. https://doi.org/10.1007/s10499-025-01925-w.

Chaitanawisuti N. and Kritsanapuntu A. (1997). Laboratory spawning and juvenile rearing of the marine gastropod: Spotted Babylon, *Babylonia areolata* Linn. 1807 (Neogastropoda: Buccinidae), in Thailand. *Oceanographic Literature Review, 11*, 1351.

Chaitanawisuti N., Kritsanapuntu S. and Santhaweesuk W. (2009). Growth, production and economic considerations for commercial production of marketable sizes of Spotted Babylon, *Babylonia areolata*, using a pilot abandoned marine shrimp hatchery and recirculating culture system. *International Journal of Recirculating Aquaculture*, *10*(1). http://doi.org/10.21061/ijra.v10i1.1335

Chaitanawisuti N., Kritsanapun S. and Santhaweesuk W. (2011). Growth, food efficiency, and biochemical composition of juvenile spotted babylon *Babylonia areolata* (Link) fed on conventional trash fish and a formulated moist diet. *Aquaculture International, 19*, 865–872. https://doi.org/10.1007/s10499-010-9406-8.

de Melo C. M. R., Durland E., and Langdon C. (2016). Improvements in desirable traits of the Pacific oyster, *Crassostrea gigas*, as a result of five generations of selection on the West Coast, USA. *Aquaculture*, *460*, 105-115. https://doi.org/10.1016/j.aquaculture.2016.04.017.

Falconer D. S. and Mackay T. F. C. (1996). Introduction to quantitative genetics, 4th ed. https://doi.org/10.1093/genetics/167.4.1529.

Fang J., and Li Q. (2023a). Examination of the effects of inbreeding on reproductive capacity in the Pacific oyster, *Crassostreagigas*. *Aquaculture*, *574*, 739689. https://doi.org/10.1016/j.aquaculture.2023.739689.

Fang J. F., and Li Q. (2023b). The effects of inbreeding on stress resistance of the Pacific oyster *Crassostrea gigas* at different temperatures and salinities. *Marine Biology Research*, *19*(4-5), 249-260. https://doi.org/10.1080/17451000.2023.2224025.

Fu J., Lü W., Li W., Shen M., Luo X., Kei, C., *et al*. (2016). Comparative assessment of genetic variation in selectively bred generations from two geographic populations of ivory shell (*Babylonia areolata*), *Aquaculture Research*, *48*(8), 4205-4218. https://doi.org/10.1111/are.13241.

Guo X., Puritz J. B., Wang Z., Proestou D., Allen Jr, S., Small J., *et al.* (2023). Development and evaluation of high-density SNP arrays for the eastern oyster *Crassostrea virginica*. *Marine Biotechnology*, *25*(1), 174-191. https://doi.org/10.1007/s10126-022-10191-3.

Hua N. P., Nguyen T. X. T., Mai D. M., Phan D. H. and Kieu T. Y. (2001). Spawning characteristics of *Babylonia areolata* (Neogastropoda: Buccinidae). *Phuket Marine Biological Center Special Publication, 25*(1), 167-165.

Jiang K., Chen C., Jiang G., Chi Y., Xu C., Kong L., *et al.* (2024). Genetic improvement of oysters: current status, challenges, and prospects. *Reviews in Aquaculture*, *16*(2), 796-817. https://doi.org/10. 1111/raq.12868.

Jiang K., Dou F., and Li Q. (2025). Crossbreeding of three selected strains of *Crassostrea gigas* reveals heterosis in survival and growth. *Aquaculture International*, *33*(2), 152. https://doi.org/10.1007/s10499-025-01835-x.

Kilian A., Wenzl P., Huttner E., Carling J., Xia L., Blois H., *et al.* (2012). Diversity arrays technology: a generic genome profiling technology on open platforms. In Data Production and Analysis in Population Genomics. *Methods in Molecular Biology*, *888,* 67–89. https://doi.org/10.1007/978-1-61779-870-2_5.

Martinez V. (2007). Marker-assisted selection in fish and shellfish breeding schemes. Marker-Assisted selection-current status future perspective in crops livestock forestry and fish. *Food and Agriculture Organization*, 329–362.

McCarty A. J., Allen S. K., and Plough L. V. (2022). Genome-wide analysis of acute low salinity tolerance in the eastern oyster *Crassostrea virginica* and potential of genomic selection for trait improvement. *G3 Genes Genomes Genetics, 12*(1). https://doi.org/10.1093/g3journal/jkab368.

Lall S., Chris M., and Benjamin d. B (2025). Family-based selection: an efficient method for increasing phenotypic variability. *G3: Genes, Genomes, Genetics, 15*(10), jkaf165. https://doi.org/10.1093/g3 journal/jkaf165.

Le P. T. N., Thiyagarajan V., Nguyen H. H., Han Z., Van Doan H., Van Vu I., *et al.* (2025). Crossbreeding of three wild populations of the ivory snail (*Babylonia areolata*) reveals hybrid vigor in growth and survival. *Aquaculture International*, *33*(8), 692. https://doi.org/10.1007/s10499-025-02358-1

Liu X., Tang X., Chen M., Ni G., and Yang Y. (2024). Development and application of molecular markers in fisheries, aquaculture, and industry of representative temperate and tropical sea cucumbers: a review. *Frontiers in Marine Science*, *11*, 1423096. http://doi.org/10.3389/fmars.2024.1423096.

Nell J. A., Smith I. R., and McPhee C. C. (2000). The Sydney rock oyster *Saccostrea glomerata* (Gould 1850) breeding programme: progress and goals. *Aquaculture Research*, *31*(1), 45-49. https://doi.org/10.1046/j.1365-2109.2000.00387.x**.**

Newkirk G. F., and Haley L. E. (1982). Progress in selection for growth rate in the European oyster *Ostrea edulis*. *Marine Ecology Progress Series*, *10*, 77-79.

Nguyen T. X. T., Hua N. P., Mai D. M., Nguyen T. B. N., Nguyen V. H., Phan D. H., *et al.* (2004). Study on the biological characteristics, artificial seed production techniques, and commercial farming of the spotted babylon, *Babylonia areolata* (Link, 1807). In: Compilation of Scientific and Technological Research Works (1984–2004). *Research Institute for Aquaculture No. 3 – Nha Trang*.

Parker L. M., O'Connor W. A., Raftos D. A., Pörtner H. O., and Ross P. M. (2015). Persistence of positive carryover cffects in the oyster, *Saccostrea glomerata*, following Transgenerational Exposure to Ocean Acidification. *PloS One* 10 (7), e0132276. https://doi.org/10.1371/journal.pone.0132276.

Parker L. M., Scanes E., O'Connor W. A., and Ross P. M. (2021). Transgenerational plasticity responses of oysters to ocean acidification differ with habitat. *Journal of Experimental Biology, 224*(12). https://doi.org/10.1242/jeb.239269.

Saillant E., Dupont-Nivet M., Sabourault M., Haffray P., Laureau S., Vidal M. O., *et al.* (2009). Genetic variation for carcass quality traits in cultured sea bass (*Dicentrarchus labrax*). *Aquatic Living Resources*, *22*(1), 105-112. https://doi.org/10.1051/alr/2009010.

Robledo D., Palaiokostas C., Bargelloni L., Martıńez P., and Houston R. (2017). Applications of genotyping by sequencing in aquaculture breeding and genetics. *Reviews in Aquaculture*, *10*, 670-682. https://doi.org/10.1111/raq.12193.

Van In V., O'Connor W., Van Sang V., Van P. T., and Knibb W. (2017). Resolution of the controversial relationship between Pacific and Portuguese oysters internationally and in

Vietnam. *Aquaculture*, *473*, 389-399. https://doi.org/10.1016/j.aquaculture.2017.03.004.

Vietnam Ministry of Agriculture and Environment (2024). Production report of mollusc species in Vietnam in 2024 at Khanh Hoa province, Vietnam.

Vu S. V., Knibb W., Nguyen N. T., Vu I. V., O'connor W., Dove M., *et al.* (2020). First breeding program of the Portuguese oyster *Crassostrea angulata* demonstrated significant selection response in traits of economic importance. *Aquaculture*, *518*, 734664. https://doi.org/10.1016/j.aquaculture.2019.734664.

Vu S. V., Knibb W., Gondro C., Subramanian S., Nguyen N. T., *et al.* (2021). Genomic prediction for whole weight, body shape, meat yield, and color traits in the Portuguese oyster *Crassostrea angulata*. *Frontiers in Genetics*, *12*, 661276. https://doi.org/10.3389/fgene.2021.661276.

Wang Y., Ni P., Sturrock M., Zeng Q., Wang B., Bao Z., *et al.* (2024). Deep learning for genomic selection of aquatic animals. *Marine Life Science & Technology*, *6*(4), 631-650. https://doi.org/10.1007/s42995-024-00252-y.

Wei Z., Qin Y., Liu H., Xing Q., Yu Z., Zhang Y., *et al.* (2024). Aquaculture performance and genetic diversity of a new [(*Crassostrea hongkongensis*♀× *C. gigas*♂) ♂× *C. hongkongensis*♀] variety of the oyster “South China No. 1” in Beibu Gulf, China. *Biology*, *13*(5), 297. https://doi.org/10.3390/biology 13050297.

Wu L., Huang H., Yang H., Ye Y., Guo B., and Wang W. (2025). The complete mitochondrial genomes of *Babylonia spirata* and *Babylonia zeylanica* (Neogastropoda: Babyloniidae) provide new insights into Neogastropoda phylogeny. *Biochemical Genetics*, *64,* 828-846. https://doi.org/10.1007/s10528-025-11055-w.

Yanez J. M., Barria A., Lopez M. E., Moen T., Garcia B. F., Yoshida G. M., *et al.* (2023). Genome-wide association and genomic selection in aquaculture. *Reviews in Aquaculture*, *15*(2), 645-675. https://doi.org/10.1111/raq.12750.

Zhang Y., Xu C., and Li Q. (2024). Whole-genome resequencing identifies candidate genes and SNPs in genomic regions associated with shell color selection in the Pacific oyster, *Crassostrea gigas*. *Aquaculture*, *586*, 740768. https://doi.org/10.1016/j.aquaculture.2024.740768

Zou Y., Fu J., Liang Y., Luo X., Shen M., Huang M., *et al.* (2024). Chromosome-level genome assembly of the ivory shell *Babylonia areolata*. *Scientific Data*, *11*(1), 1201. https://doi.org/10.1038/s41597-024-0400 1-9.