

Meta Analysis

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Genetic Variation and Genomic Selection Strategies for Growth Rate in Abalone

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Abstract Abalone (*Haliotis* spp.), as a high-value marine aquaculture species, has growth rate characteristics that are in direct relation to farm productivity and breeding improvement outcome. The biological basis and genetic variation features of abalone growth rate are systematically reviewed in this study, and the uses and limitations of traditional breeding methods in improving growth performance are discussed in detail. The review focuses on the fundamentals, approaches, and recent advances of genomic selection (GS) technology for enhancing abalone growth rate, as well as on practical case studies, and discusses the integration of GS and traditional breeding. It also discusses key challenges in the implementation of genomic selection, including phenotypic data quality, genotyping cost, model predictive ability, and genetic diversity maintenance. By combining high-throughput genotyping and machine learning, this review recapitulates the recent progress of GS strategies and their implications in increasing breeding efficiency. This review provides theoretical foundation and practical reference for building an efficient, precise, and sustainable modern abalone breeding system, promoting the healthy development of the abalone industry.

Keywords Abalone; Growth rate; Genetic variation; Genomic selection; Modern breeding

1 Introduction

Abalone (*Haliotis* spp.) is a very valuable sea aquaculture species of great industrial significance and significant economic value worldwide. Because of its superior meat and growing market demand, abalone aquaculture is of vital importance to coastal economies and the international seafood industry. Among various production traits, growth rate is a critical determinant of aquaculture efficiency that has a direct effect on production cycles, yield, and profitability. Quick-growing abalone species can lower the times and cost of cultivation, thus enhancing overall industry competitiveness (Swezey et al., 2020).

Identification of the genetic determinants of growth rate is required for the development of effective breeding programs for improving this trait. Gradual improvement has come through traditional selection breeding programs, but the complex genetic architecture of growth traits and environment are the limiting components. With advances in genomic technology, genomic selection (GS) opens new windows for achieving maximum genetic advance using genome-wide marker information for making more accurate and effective selection (Xiao et al., 2025).

This review systematically gathers existing information about genetic variation in abalone growth rate and discusses comprehensively genomic selection techniques applied in its improvement. Its objective is to provide theoretical foundation and practical recommendations for the optimization of breeding programs, ultimately contributing to sustainable development and modernization of abalone aquaculture.

2 Biological Basis of Abalone Growth Rate

2.1 Definition and measurement methods of growth rate traits

Growth rate parameters in abalone are optimally described by wet body weight, shell length, shell width, shell height, and corresponding tissue weights such as foot muscle and soft tissue weight. These parameters are measured with calipers and electronic balances at several stages of development, often at several time points to capture longitudinal growth patterns. Correlation and path analyses have been used most commonly to assess

relationships among these characters, and shell length and width were found to be highly positively correlated with body weight, which are thus good indicators of selective breeding. These are the fundamental measurements for genetic evaluation and improvement programs in both pure lines and hybrids (Huang et al., 2018; Kho et al., 2021; 2023) (Figure 1).

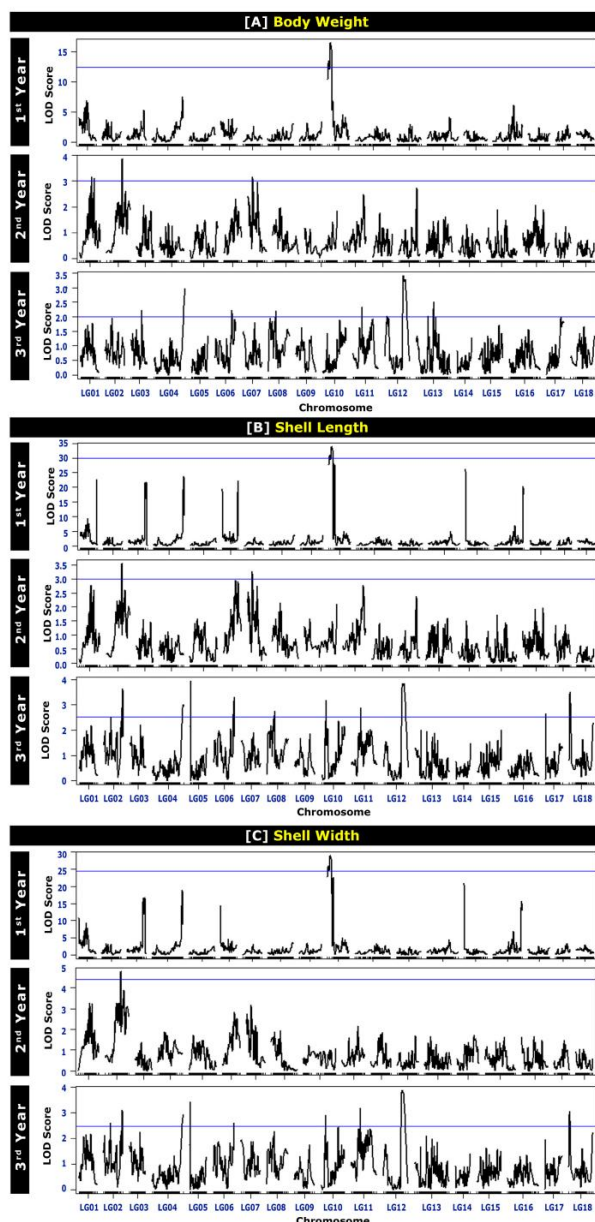


Figure 1 Logarithm of odds (LOD) profile of growth-related traits: (A) body weight, (B) shell length, and (C) shell width of abalone at different ages (Adapted from Kho et al., 2023)

2.2 Factors influencing growth rate

Abalone growth rate is under genetic, environmental, nutritional, and managerial control. Genetic effects are of greatest significance, with moderate to high heritability for valuable growth traits, indicating that genetic improvement of growth through selective breeding is feasible. Environmental effects of rearing mode, water temperature, and site conditions have large influences on growth, and genotype-by-environment interactions can cause reranking of phenotypes in different systems of culture. Nutrition, in terms of feed intake and feed conversion, is highly correlated with growth and optimizing them can achieve optimum performance. Stocking density and health protocols are also part of the management practices that affect growth outcomes (Zhou et al., 2022; Van Nguyen et al., 2023).

2.3 Growth differences and their genetic background among different abalone species/strains

Much growth variation occurs between abalone species, strains, and hybrids. Selectively bred "Huangxun No. 1" strains, for instance, grow faster than their wild relatives according to growth measurements. Interspecific and three-way cross hybrids have heterosis, in that hybrids are superior to purebreds in growth and survival. Growth characteristics are polygenic with multiple QTLs and candidate genes identified, with most being age- or environment-dependent. Molecular studies have demonstrated that growth variation is induced by gene expression, allele-specific expression, and microRNAs, and this is now being exploited for marker-assisted and genomic selection for breeding (Li et al., 2023; Huang et al., 2024).

3 Genetic Variation Studies on Abalone Growth Rate

3.1 Estimation of heritability and genetic parameters

Heritability estimation is central to revealing genetic control of abalone growth traits and breeding progress prediction. Current methods utilize genomic data and mixed models to estimate heritabilities and genetic correlations even for large samples. These methods blend equations of genomic prediction accuracy and number of independent chromosome segments to provide correct estimates of heritability and genetic correlations across generations and traits. Up-to-date right parameters is required to effective selection indices and avoid overestimation of genetic gain, especially since parameters can change very quickly under genomic selection (Yang et al., 2017; Misztal and Gowane, 2025).

3.2 Family-based selection and population genetic structure analysis

Family-based selection remains a cornerstone of abalone breeding, facilitating the identification of better families and individuals for growth rate improvement. Population genetic structure analysis, typically by the use of high-density molecular markers, is used to account for population stratification and relatedness, a requirement for both association studies and selection. Genomic relationship matrices and mixed models are used heavily to account for family structure and relatedness, improving the precision of genetic assessment and reducing false positives in marker-trait association studies (Sallam et al., 2020).

3.3 Molecular marker association analyses (QTL mapping, GWAS studies)

Quantitative trait loci (QTL) mapping and genome-wide association study (GWAS) are rich tools for the analysis of the genetic architecture of growth traits in abalone. GWAS capitalizes on dense marker information and recombination history to nominate genomic loci and genes that affect growth. Advances in methodology over the last decade, such as multi-locus and regional heritability mapping, have improved detection power and accuracy of mapping, especially in the analysis of moderately to highly heritable traits. These approaches also facilitate the construction of QTL-allele matrices, which can be applied in genomic selection as well as breeding design (Link et al., 2023).

3.4 Genetic diversity and utilization value of different germplasm resources

Genetic diversity within and between abalone germplasm resources is the basis for long-term breeding performance and responsiveness. High-throughput genotyping and diversity analyses expose population structure, levels of heterozygosity, and the presence of outstanding alleles. Diverse germplasm collections are a source of favorable alleles for growth and other traits, and characterization is imperative to broaden the genetic base and avoid inbreeding. Integrating genetic diversity information with association mapping enhances the identification and exploitation of valuable genetic material in breeding (Sallam et al., 2020).

4 Traditional Breeding Strategies for Improving Abalone Growth Rate

4.1 Practical cases of family selection and population selection

Family and population selection have been employed in extensive use in conventional abalone breeding programs for growth rate improvement. In family selection, the best growing individuals are chosen from families and utilized as broodstock for the next generation, while in population selection, the top-performing individuals are chosen from the whole population without regard to family. These operations have proved successful in increasing the mean rate of improvement from one generation to the next but depend on accurate phenotypic measurement

and competent management of genetic variation. Family and population structure can, however, affect considerably the accuracy of selection, which could lead to prediction accuracy values being spuriously high if they are not appropriately corrected for. This calls for understanding the genetic connections between breeding populations in order to yield reliable selection outcomes and permanent genetic progress (Werner et al., 2020).

4.2 Application of hybrid breeding to enhance growth performance

In hybrid breeding in abalone, genetic variation among different species, strains, or geographic populations is utilized to utilize heterosis to produce hybrid offspring with superior growth and overall production performance compared to parents. Methods of production and research have shown that, particularly under situations of large genetic disparity between parents, hybrid generations possess significant improvement in the major growth traits such as shell length, shell width, and body weight and even higher environmental adaptability and survival capability. During the recent years, the integration of hybrid breeding schemes with marker-assisted selection or genomics-based prediction methods has enabled early prediction of offspring performance, thereby accelerating superior combination identification and improvement in breeding program precision and effectiveness (Xu et al., 2018).

4.3 Limitations of traditional breeding

Although traditional mass and family selection programs have achieved remarkable progress in the growth performance of abalone, they are also beset with some serious drawbacks. For the first place, the extensive growth period and late sexual maturity of abalone hinder the slowing down of the process of selection and improvement for each generation and thus limit genetic progress. Secondly, traditional selection relies considerably on big and accurate phenotypic recording, whose validity can be greatly masked by extraneous factors such as farming conditions, quality of diet, and management practices. This is particularly a consideration when approximating breeding value of multifactorial and polygenic traits such as growth rate. In addition, traditional methods are unable to fully reflect the additive effect of small-effect genes and the complex interactions among genes, the scope of which optimal improvement is limited. In the recent past, the advent of new molecular breeding technologies such as genomic selection has the possibility of circumventing such limitations by allowing better genetic assessment and efficient breeding strategies for rapid improvement in elite abalone breeds (Xu et al., 2018).

5 Genomic Selection (GS) for Improving Growth Rate in Abalone

5.1 Principles and workflow of genomic selection

Genomic selection (GS) is a breeding technique that predicts the genetic value of individuals based on genome-wide molecular markers to facilitate early and accurate selection of polygenic traits such as abalone growth rate. GS models compute all loci effects, major- and minor-effect genes at once, resolving the absence of traditional marker-assisted selection. The standard process involves collecting phenotypic and genotypic data from a reference group, constructing statistical prediction models, and later predicting selection candidate breeding values from genotypes only. The genetic gain may be boosted and breeding cycles minimized significantly through the incorporation of GS in abalone breeding programs (Liu et al., 2022; Su et al., 2025).

5.2 Phenotypic and genotypic data acquisition

Accurate phenotyping of growth traits (such as body weight, shell length, and shell width) is the foundation for GS application. QTL mapping and LOD profile analysis of growth traits on 18 linkage groups of abalone revealed the genetic localization characteristics of total weight (A), shell length (B), and shell width (C) and also provided a reference for gene screening and marker development subsequently. Common genotyping technology that may be employed includes SNP arrays, GBS (genotyping-by-sequencing), and WGS (whole-genome sequencing) (Kho et al., 2021) (Figure 2). SNP arrays are of moderate cost and high throughput; GBS is of high marker density, can be used to identify new variants, and is suitable for non-model animals such as abalone, with missing data imputed to further improve data quality; WGS can precisely map QTLs and identify causal variants, enabling support of data in fine mapping and gene function analyses (Munyengwa et al., 2021; Čeran et al., 2024).

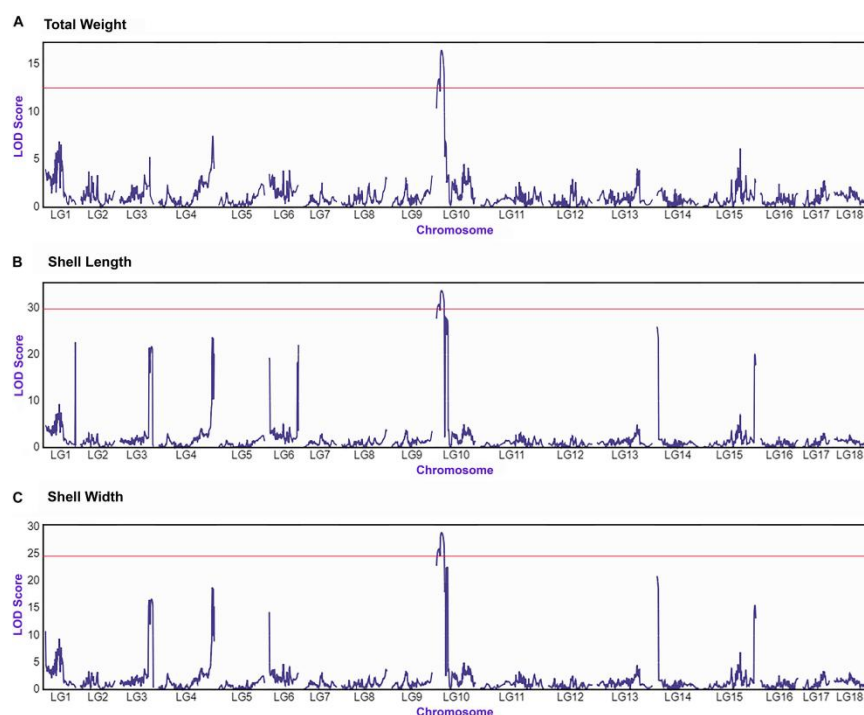


Figure 2 QTL mapping and LOD profiles of growth-related traits in abalone among 18 linkage groups: (A) total weight, (B) shell length, and (C) shell width. The red solid line indicates the chromosome-wide significance threshold (Adopted from Kho et al., 2021)

5.3 Statistical models and prediction approaches

GS employs advanced statistical models to estimate genomic estimated breeding values (GEBVs). A few of the popular models that are often employed include genomic best linear unbiased prediction (GBLUP) having equal marker effects and Bayesian methods (BayesA, BayesB, BayesR) where marker effects are different and prior knowledge is used. More recently, machine learning (ML) and deep learning (DL) techniques—e.g., support vector regression, random forests, convolutional neural networks, and ensemble learning—have also found potential to manage complex non-additive genetic structures and improve prediction precision of low-heritability traits in abalone (Abdollahi-Arpanahi et al., 2020; Wang et al., 2024; Su et al., 2025).

5.4 Research progress and case studies of genomic selection in abalone

Recently, research on abalone has demonstrated the utility and value of GS. As an example, GS was employed to improve heat resistance in Pacific abalone with moderate heritability and higher prediction accuracy through Bayesian models than GBLUP. GWAS-identified SNPs also improved prediction accuracy. The results show the potential of GS to speed up genetic improvement for growth and stress resistance characteristics in abalone breeding programs (Liu et al., 2022). While most GS applications in aquaculture remain to be seen, coupled high-density genotyping and advanced prediction models are poised to open the door toward practical implementation in abalone.

5.5 Integration modes of genomic selection with traditional breeding

GS may be combined with traditional family and population selection to achieve optimal genetic gain. Breeders can utilize the benefits of phenotypic and genomic information through the use of GEBVs as a second-tier selection aid. Hybrid approaches, such as GWAS-enhanced GBLUP and multi-trait models, improve selection accuracy and efficiency. The application of GS reduces intervals for generations, increases the intensity of selection, and enables the identification of high-quality broodstock at a younger age, complementing and augmenting traditional breeding schemes (Zhang et al., 2023).

6 Key Issues and Challenges in Implementing Genomic Selection in Abalone

6.1 Limitations in phenotypic data quality and quantity

Effective genomic selection (GS) for abalone requires large high-quality phenotypic data. Phenotyping is costly,

time-consuming, and not necessarily reliable, especially for thermal tolerance or growth rate. Low sample sizes and compromised data quality can reduce the predictive power and precision of GS models, and precise selection for complicated traits is difficult (Liu et al., 2023).

6.2 Cost and coverage issues of genotyping data

The increased availability of high-throughput genotyping technologies, such as SNP arrays and whole-genome resequencing, is still a considerable cost for large-scale breeding programs. Despite improving efficiency, new SNP arrays (e.g., Baoxin-I) and genotyping-by-sequencing technologies, data quality and marker density are still a balance concern, especially for non-model species like abalone (Liu et al., 2022; Li et al., 2024).

6.3 Prediction accuracy of models and cross-population application

GS model accuracy depends on the size and diversity of the training population, marker density, and the genetic architecture of the trait. Prediction accuracy varies between models such as GBLUP and Bayesian models, whose performance tends to decline when applied across populations or strains due to genetic background and allele frequency differences. This lowers GS model transferability among populations (Liu et al., 2023).

6.4 Genetic diversity conservation and inbreeding control

Intensive selection, like GS, can reduce genetic variation and increase inbreeding at the cost of long-term performance and adaptability. Maintenance of genetic variation and inbreeding control are essential to obtain sustainable breeding outcomes (Sandoval-Castillo et al., 2018; Dale-Kuys et al., 2020; Wooldridge et al., 2024).

6.5 Necessity of data sharing and international cooperation

Because of worldwide distribution and strong connectivity among abalone populations, international collaboration and exchange of data are necessary. Coordinated research among countries will improve reference panels, make predictions more accurate, and promote sustainable management and conservation across nations (Griffiths et al., 2025; Mares-Mayagoitia et al., 2025).

7 Current Status and Comprehensive Analysis of Genomic Selection Strategies for Abalone

7.1 Implementation status of genomic selection in abalone growth rate improvement

Genomic selection (GS) has also emerged as a popular method for abalone breeding, particularly in traits for growth rate and heat tolerance. There are new studies that show GS with high-density SNP genotyping and strong statistical models like BayesB and GBLUP have moderate to high accuracy for the prediction of complex traits. GS has been a successful strategy for improving heat tolerance in Pacific abalone, and BayesB has achieved up to 0.55 accuracy for breeding value prediction, which is higher than the traditional methods (Liu et al., 2022). Improved predictive accuracy is also obtained with the application of GWAS-identified SNPs, allowing the implementation of GS in practical abalone breeding schemes (Liu et al., 2022).

7.2 Integration of omics data and environmental factors in breeding program optimization

Multi-omics integration—genomics, transcriptomics, proteomics, and metabolomics—is improving in abalone breeding. These approaches allow for gene, pathway, and biomarker discovery regarding growth and environmental adaptation. Environmental data integration allows further insights into trait architecture and the ease of developing strong, environment-driven breeding programs. Such integration will also enhance multifactor trait selection and abalone yield under suboptimal environments (Nguyen et al., 2022).

7.3 Efficiency improvements in genomic selection supported by high-throughput genotyping technologies

High-throughput genotyping systems, including the Baoxin-I SNP array, greatly enhanced the cost savings and efficiency of GS in abalone. It is now possible to perform speedy, massive-scale genotyping with high accuracy and replicability by utilizing these technologies. The Baoxin-I array, for instance, exhibited greater call rates and abalone population polymorphism and application in GS had prediction accuracies for growth traits similar to whole-genome resequencing, confirming its suitability in selective breeding (Liu et al., 2022; Wang and Wang, 2024).

7.4 Practical effects of machine learning and AI-assisted breeding decision-making

Machine learning (ML) and artificial intelligence (AI) are being increasingly embraced in GS pipelines to enhance the accuracy of predictions and decision-making for breeding. ML models can identify sophisticated, non-linear genotype-phenotype relationships and are particularly well-suited when traits have multiple minor-effect loci or interactions with the environment. The utilization of these sophisticated computational techniques is poised to make abalone breeding programs even more precise and efficient (Alemu et al., 2024).

8 Concluding Remarks

Research on the genetic variability of growth rate in abalone has also made significant progress in the last several years, providing valuable information on heritability estimates, genetic parameters, and the genetic architecture underlying the traits. The establishment of molecular markers, QTL mapping, and GWAS has allowed a deeper understanding of the intricate traits defining growth performance in different abalone species and populations. All this information has established a solid foundation for introducing advanced breeding technologies.

Genomic selection (GS) is a new approach to abalone breeding that can greatly enhance selection accuracy and genetic gain. By utilizing genome-wide marker information and phenotype data, GS enables the estimation of breeding values more accurately than with traditional methods. Early applications and case studies demonstrate its potential for enhancing growth characteristics and overall production efficiency and economic viability in abalone aquaculture.

In the future, development of an effective and sustainable modern breeding program for abalone will need to create genomic selection in addition to traditional breeding, aided by multi-omics information and sophisticated computational methods such as machine learning. Genetic diversity, as well as pragmatic issues such as the accuracy and cost of phenotyping, will also need to be addressed. These integrated breeding methods will be key in addressing the demand for high-quality abalone commodities, enhancing business sustainability, and stimulating global aquaculture growth.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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