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Commentary

Genomic Selection Strategies for Advancing Genetic Improvement in Aquaculture

Mehdi Wargocki *

Department of Aquatic Systems, Technical University of Denmark (DTU), Lyngby, Denmark

DESCRIPTION

Aquaculture genetics is entering a phase where conventional genomic selection is being extended into extremely rare and emerging conceptual frameworks that go beyond standard breeding models. One of the least explored yet highly promising directions is epigenome-aware genomic selection under transgenerational aquatic stress memory systems.

Aquaculture production continues to expand globally, and genetic improvement remains central to enhancing traits such as growth, disease resistance, feed efficiency, and environmental tolerance. However, traditional genomic selection approaches often assume static gene effects across environments, which may not hold true in highly variable aquatic ecosystems.

Unlike conventional genomic selection, which relies on genome-wide Single Nucleotide Polymorphism (SNP) markers, this rare framework integrates multi-layered biological memory systems, including epigenomic marks that reflect past environmental exposures such as hypoxia, salinity shocks, pathogen pressure, and thermal fluctuations.

A genomic-epigenomic selection program in this context requires a tri-layer reference population structure. The first layer includes standard genotype and phenotype data. The second layer incorporates epigenetic profiles such as methylation landscapes obtained through bisulfite sequencing or nanopore-based detection. The third and most rare layer involves environmental exposure history encoding, where individuals are classified based on ancestral stress environments. This allows prediction models to capture not only genetic potential but also environmentally conditioned heritable responses.

In aquaculture systems, this approach is particularly rare but valuable for species exposed to extreme or fluctuating environments, such as estuarine fish, deep-water crustaceans, and high-density Recirculating Aquaculture System (RAS) populations. For example, offspring of fish exposed to chronic hypoxia may inherit altered metabolic regulation patterns that improve survival under low oxygen conditions, even without direct genetic mutation.

Disease resistance under this framework is reinterpreted as a multi-generational immune priming phenomenon, where genomic selection is combined with epigenetically trained immune responsiveness. Instead of selecting only for alleles associated with resistance, breeders may also select for stable immune memory signatures that persist across generations. This is extremely rare in current aquaculture breeding programs but has been observed in limited experimental fish populations.

Growth performance is also influenced by epigenetic regulation of metabolic pathways. Rare studies suggest that feed restriction or nutrient enrichment in parental generations can alter offspring growth trajectories through epigenetic programming. Genomic selection models that ignore these effects may underestimate true breeding values in fluctuating production systems.

Environmental tolerance becomes even more complex under this framework. Rather than selecting only for fixed tolerance thresholds, breeders can target plasticity-associated genomic regions, which allow organisms to dynamically adjust physiological responses. This includes rare genomic regions associated with stress-induced transcriptional flexibility, enabling fish to rapidly adapt to sudden changes in salinity, temperature, or oxygen availability.

Feed efficiency, traditionally measured through direct or indirect intake estimation, can also be influenced by epigenetic metabolic conditioning. Rare metabolic imprinting effects may alter mitochondrial efficiency and nutrient absorption pathways across generations. Incorporating these effects into genomic prediction models may improve long-term feed conversion outcomes in breeding populations.

A particularly rare aspect of this approach is the integration of microbiome-linked genomic selection, where host genetics are evaluated alongside heritable microbial community structures. Incorporating microbiome data into breeding programs may therefore improve the selection of aquatic species with enhanced health, productivity, and environmental adaptability. In aquatic species, gut and skin microbiomes can be partially transmitted

Correspondence to: Mehdi Wargocki, Department of Aquatic Systems, Technical University of Denmark (DTU), Lyngby, Denmark, E-mail: mehdi.wargocki@dtu.dk

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from parents to offspring through environmental and reproductive pathways. These microbial communities can significantly influence digestion, immunity, and stress tolerance, yet are rarely included in standard genomic selection frameworks.

CONCLUSION

Future aquaculture systems may evolve toward fully integrated adaptive breeding ecosystems, where genomic selection is continuously updated with real-time environmental and biological feedback. Automated phenotyping systems, environmental sensors, and multi-omic sequencing platforms will collectively enable selection decisions that respond dynamically to changing production conditions. While conventional genomic selection has already transformed aquaculture breeding, the incorporation of rare epigenetic, microbiomic, and environmental memory systems represents a next-generation frontier.