

Biotica Research Today



Article ID: RT1518

Phenomics: Potential Applications in Fisheries

V.L. Ramya¹, Jesna P.K.^{1*} and B.K. Das²

¹Regional Centre of ICAR-Central Inland Fisheries Research Institute, Bangalore, Karnataka (560 089), India ²ICAR-Central Inland Fisheries Research Institute, Barrackpore, Kolkata, West Bengal (700 120), India

Open Access

Corresponding Author Jesna P.K.

⊠: jesnamukundan@yahoo.com

of interest exists.

How to cite this article?

Ramya et al., 2023. Phenomics: Potential Applications in Fisheries. Biotica Research Today 5(12), 814-816.

Copyright: © 2023 Ramya et al. This is an open access article that permits unrestricted use, distribution and reproduction in any medium after the author(s) and source are credited.

Abstract

Phenomics is the study of phenome, which deals with the collection and analysis of phenotypic data. Phenotyping, being an integral part of phenomics, has been mostly studied in the case of plants and higher vertebrates, with limited studies on fish. Limitations in phenotyping make it more difficult to understand Conflict of interests: The author has declared that no conflict how genetics contributes to the transmission of quantitative traits. To enable the explicit and methodical investigation of the pleiotropic consequences of genetic variation, phenomics data is necessary. Fish phenotyping is still in its infancy and is confined to truss and classic morphometric investigations. This has sparked interest in creating high-throughput phenotyping techniques to evaluate the immense phenotypic plasticity of fish by integrating their genetic and phenotypic data.

> Keywords: Fish phenomics, Fisheries, High-throughput data, Information technology

Introduction

Global population growth is expected to bring the total number of people on Earth to 9.2 billion by 2050. Around 10% of the world's calorie intake is provided by fisheries and aquaculture products (FAOSTAT, 2009). But the recent climatic change is predicted to affect the future fish production. Fish production in either open water or aquaculture is influenced by abiotic stress such as temperature fluctuations, salinity, pollution and other physicochemical factors. Increasing the fish production in the altering environment is a globally challenging task. Hence the food security becomes one of the major concerns in the changing climate scenario. This can be solved only through the adaptation of emerging technologies in fisheries sector.

With the next-generation sequencing tools and improved biotechnology, determining the genetic makeup for largescale fish screening is no longer a difficult task. In order to take advantage of the vast amount of genetic data, quantitative fish performance or trait characterization is required. As a result, the phenotypic and functional data have not yet been thoroughly annotated. The definition of phenotype has changed significantly from conventional to molecular genetics; in the pre-genomic era, it was

described as the observable characteristics or attributes of an organism, taking into account the interaction of genotype and environment. But in recent decades, advances in the study of genomics have broadened our understanding of phenotype, which has been described as the variations and inheritance of an organism's appearance, physiology and behavior. The phenotype is a multi-scale description of observable qualities (Nachtomy et al., 2007).

The word "phenomics" was coined by Steven A. and is defined as the acquisition of high-dimensional phenotypic data on an organism on a wide scale. The process of linking genotype to phenome-level data is crucial for improving our understanding of how genetic structure influences phenotype (Houle et al., 2010). High-throughput phenomic research uses sophisticated robots, imaging techniques, high-tech sensors and high-power computation to assist in large-scale population screening for a particular trait. The latest bioinformatics tools and their advanced technology reduce the tedious process of multi-dimensional, high-resolution data generated through phenotyping. Gene function and environmental response can be well understood by the integrated approach in genotyping and phenotyping. The greatest deficiencies in phenomic data are

Article History

RECEIVED on 02nd December 2023

RECEIVED in revised form 06th December 2023

ACCEPTED in final form 07th December 2023

a shortage of annotators with a wide range of knowledge on fish physiology and disease traits. Hence, it leads to incorrect annotations and inadequate phenotyping, mainly due to the lack of knowledge in quantitative data generated through the tool and the morphological abnormalities.

Similar to genomics, phenomics should develop as a branch within biological science since it supports other omics indirectly and produces new technologies and human resources specifically for the phenomics area. Zebra fish having 70% of their genes orthologous to human genes are regarded as model organisms. Efficient phenotyping projects that yield multi-scale, high-resolution data for a variety of zebrafish phenotypes are anticipated to improve our knowledge of the relationships between genotype and phenotype as well as the genetic diagnosis of numerous diseases. The investigation of environmental effects on phenotypes associated with commercially important traits and production levels is mandatory for a deeper understanding of the interaction between genotype and environment and possible mitigation of negative effects. Phenomic studies led by large-scale phenotyping can also be useful for the discovery of 'climate change-adapted germplasm' and the identification of endangered species. Though there are some well-established phenotyping techniques used in fish, such as truss morphometry and recording of meristic traits, they fail to establish a link between genetic, transcriptomic and proteomic outcomes that would collectively contribute to studying a particular trait's expression and dynamism at all three areas. Therefore it becomes difficult to implement them in genetic improvement programs.

Forward and Reverse Phenomics

Forward Phenomics

Forward Phenomics is the study of growth, performance and characters of organisms by using phenotypic approaches. This method is used to filter the germplasm having valuable traits by subjecting the organism to abiotic and biotic challenges (Furbank and Tester, 2011). An automated imaging system can screen thousands of species for unique characteristics. After being chosen, the organisms with the desired features can be maintained to perform additional research and breeding.

Reverse Phenomics

It refers to a deep understanding of physiological and genetic processes controlling the expression of commercially important traits so as to have better control over trait expression patterns (Furbank and Tester, 2011). With the use of genetic transformation technology, reverse phenomics enables the exploitation of the mechanism underlying a trait or the candidate gene linked to it, which can then be introduced into novel strains or transplanted to different species.

Prospects and Constraints for the Fisheries Industry

Understanding Fish Physiology

Abiotic stressors that affect fish production include salinity, temperature extremes, limited rainfall and the inflow of waste water from industry or domestic and natural disasters. These factors are also the main causes of changes in fish ecology. Phenotyping for tolerance against various abiotic stimuli is a challenging task because of the intricate regulatory networks underlying tolerance against these stresses. Additionally, molecular markers are used to screen organisms for a desired characteristic, although sample collection from stressed species is challenging, time-consuming and expensive. However, the ability of reliable high-throughput phenotyping tools has made it possible to analyze the best trait in stressed organisms for large populations.

Applications in Fish Pathology

Globally, serious fish disease outbreaks result in large losses in the production of aquaculture. The physiological mechanisms underlying the host-pathogen interactions that link pathogen infection and the emergence of disease symptoms in the host can be better understood by developing a range of sophisticated and quantitative high-throughput image-based phenotypic methods. The host physiology altered by pathogen infection can be examined to enhance desired features and concurrently develop resistance lines by utilizing a wide range of imaging tools. Additionally, it would guarantee an accurate assessment of the disease's severity and, should it be discovered early on, allow for the implementation of suitable measures to impede the disease's advancement and prevent significant losses. The main limitation in phenotyping research is the use of imagebased phenotyping, which makes it difficult to accurately identify internal disease indications. Thus, for precise identification and characterization of disease phenotypes, early-warning systems for the detection of specific diseases and monitoring fish health in field circumstances, techniques such as enhanced imaging systems, remote sensors, or non-imaging-based phenotyping technologies need to be developed.

Perceptive to the Utility of Gene Action

The advancement of phenotyping, coupled with sophisticated data analysis frameworks and advanced imaging software, is necessary to bring novel perspectives to the field of fish genomics research. Without any uncertainty, phenomics would hasten our understanding of how genes function and react to their surroundings. Enhancing and maintaining sustainable fisheries may be rendered possible by highthroughput phenomic advancements that enable the analysis of mutant populations, the identification of quantitative trait loci (QTLs) and the finding of genes through environmental relations. It has enormous potential for deciphering the genetic makeup of intricate features and targeting the genes and particular alleles responsible for trait variation.

Advances in Fish Breeding

The development of novel varieties to increase productivity per unit area, yield potential, stress tolerance and quality of flesh are dependent on the application of efficient, quick and sophisticated phenotyping procedures. Using high-throughput imaging tools to capture field variability and continuously monitor the environment will surely



help identify the best progeny accurately and quickly by screening a large number of lines. Molecular breeding techniques like marker-assisted recurrent selection (MARS) and genomic selection, however, need an understanding of the genetic basis of complex trait variation and the utilization of phenotypic data. The organisms with the desired phenotypic traits may be screened and deliberately interbred with elite individuals to selectively propagate the organisms with desirable characteristics and produce new varieties and strains. Phenomic analysis could be used to evaluate the selection of acceptable genotypes in molecular breeding projects as well as to identify detailed issues related to fish growth, development and responses to their harsh environment.

Genetically Modified Organisms (GMOs)

The creation of transgenic fish is gaining attention, as this research targets novel gene transfer, improving the tenderness of flesh, increasing disease resistance and adaptation against environmental stress. The majority of gene transfer experiments are phenotype-driven, meaning that the degree of transgenic expression is determined by carefully examining the varied phenotypes that are induced by the transgene. Quantitative trait loci (QTLs) can be identified and genes of interest cloned under these QTLs using bi-parental recombinant inbred lines, doubly haploid sets, or genetically defined accessions for population genetics.

Indeed, a Bioinformatics Tool

High-throughput data, including numerous features in phenomic research, is produced from a large number of samples. In order to convert images into qualitative and quantitative data formats, highly skilled personnel, sophisticated statistical software and upscale facilities are needed. In addition to increasing characteristics, highthroughput phenotyping can also enhance sample size for improved comprehension and accuracy. Processing the analysis of the enormous amount of data takes days and it is a very difficult task. High-throughput phenomics needed information technologies and high-performance computation to derive the insights. A great deal of work and planning is required, from image to inference, in order to prevent misunderstandings and incorrect conclusions.

Conclusion

The gap between genomics and phenomics would be filled by accurate phenotypic predictions based on genetic composition and contribution, as current phenotypic techniques fall behind next-generation genotypic technologies. Investigating intricate relationships between the phenome, genome and environment could result in the bloom of the fisheries sector as well as the conservation of fishery resources.

References

- FAOSTAT, 2009. Food and agriculture data. Food and Agriculture Organisation of the United Nations. Rome, Italy. URL: http://faostat.fao.org/site/567/default.aspx.
- Furbank, R.T., Tester, M., 2011. Phenomics-technologies to relieve the phenotyping bottleneck. *Trends in Plant Science* 16(12), 635-644. DOI: https://doi. org/10.1016/j.tplants.2011.09.005.
- Houle, D., Govindaraju, D.R., Omholt, S., 2010. Phenomics: The next challenge. *Nature Reviews Genetics* 11, 855-866. DOI: https://doi.org/10.1038/nrg2897.
- Nachtomy, O., Shavit, A., Yakhini, Z., 2007. Gene expression and the concept of the phenotype. *Studies in History and Philosophy of Biological and Biomedical Sciences* 38(1), 238-254. DOI: https://doi.org/10.1016/j. shpsc.2006.12.014.

