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Fishery improvement in India – The genomics way

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ABSTRACT

Fishery is one of the most flourishing sectors under agriculture commodities in world as well as India. India has seen a sharp improvement in fishery sector in past ten years. This improvement is basically due to adoption of scientific improvements in traditional breeding practices. One such major advancement in breeding and selection methods that world has in last decade is the implementation of genomic values for selection of candidates – called Genomic Selection (GS). GS has been successfully implemented in livestock and plants breeding, and with the advent of NGS technologies it is now being utilized in fish and aquaculture breeding and selection too.

Key words: Fishery improvement, Genomic selection, fishery in India.

INTRODUCTION

Fishery is one of the most important components of agriculture activity(s) in India. Fisheries In India can be divided into marine and inland fisheries. India is the third largest fish producing nation in world and after China, it is the second largest aquaculture nation. Overall fishing employs about 14.5 million people throughout the country. Historically, fisheries as an employment found its mention in Kautiliya's "Arthashastra" (321-300 B.C.). A culture of small pond type fish rearing was very much prevalent in India from ancient times too. Due to its vast water resources and a marine coastline of 7,516 kms fishery sector has always played important role in livelihood and

nation development. Fishery sector in India has seen a 11-fold increase in from last six decades, and consists of 10% of global fish diversity.

Selective breeding has always played an important role in improvement of production parameters in livestock, poultry as well as fisheries. Advanced methods of mass selection, family selection, pedigree or progeny selection is now also possible in fishery sector due to betterment in infrastructural facilities. With increasing knowledge, now among 250 farmed fish species about 10% have been bought under intensive selection programmes, with about 60 specialised breeding programmes for different species of fish. Although these figures are ever increasing, there is substantial scope for fish breeding in India. In India, although scientific advancement has led to new methods of fish farming and product handling, most of the farming methods are based on traditional or cultural principles. There is a huge scope in application of genomic methods for species wise breeding of different species, which not only will improve the production parameters, but will also helps in maintaining proper seedstock for conservation of species. Judicious use of genomic methods for selection and breeding in fishery will thus not only improve the livelihood but may also reduce the practice of indiscriminate fishing.

Fishery statistics of India

With a coastline of 8118 kms and continental shelf area of 0.53 million square km, India is poised to have rich fishery production statistics. India has about 1457 landing sites and 3461 dedicated fishing villages. The total fish production has continuously risen from 10.76 MMT to 14.16 MMT in past 5 years, with an obvious increase in fish export rising from 30420 crore (in 2015-16) to 46442 crores (in 2019-20). Out of total fish production of India, marine fish production is 3.72 MMT and inland fish production is 10.43 MMT (Fig. 1. and Fig. 2). Fishery sector contributes about 1.24 % to total economy of India, and 7.28% in agriculture sector. In marine fish production, Gujarat is having maximum production followed by Tamil Nadu, Andhra Pradesh, Kerala and Maharashtra. In inland fish production, Andhra Pradesh is having maximum production, followed by West Bengal, U.P. and Odisha. Starting from 1985-86, total fish seed production has increased from 63220 lakhs fry to 521706 lakh fry in 2019-20. When consumption statistics are observed, Tripura is having highest fish consumption of 29.29 kg per capita per annum, followed by Kerala (19.41 kg per capita per annum), and then Manipur (14.10 kg per capita per annum). As per employment generation or person involved in fisheries sector, total 2,80,63,537 human resources are involved in fishery sector, with about 82% fisherman involved in inland fishery and 18% are involved in marine fishery. If the gender-wise distribution is observed, 56% are male and 44% of farmers are female, thus making fishery a family enterprise without any social / religious taboo (Handbook on Fishery Statistics, 2020).

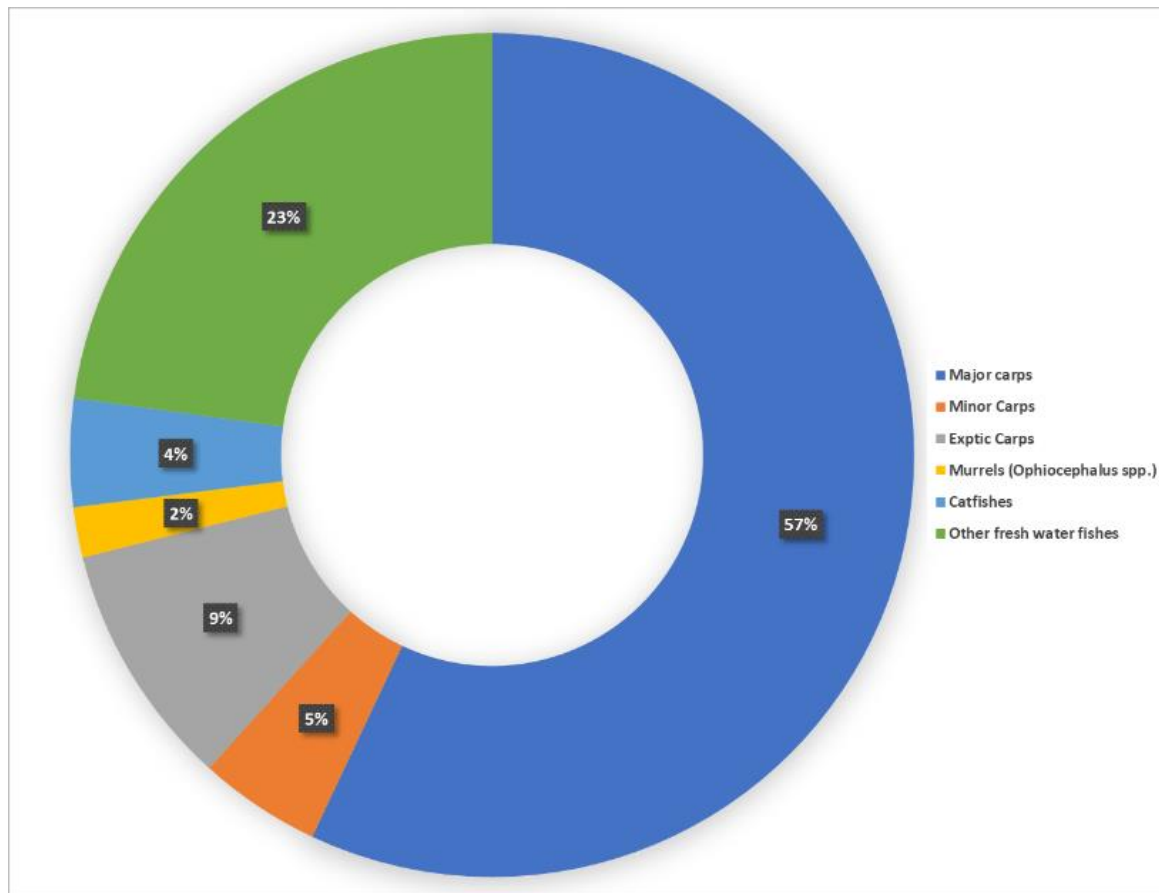


Fig. 1. Percentage production distribution/ landings of major inland fish species of India.

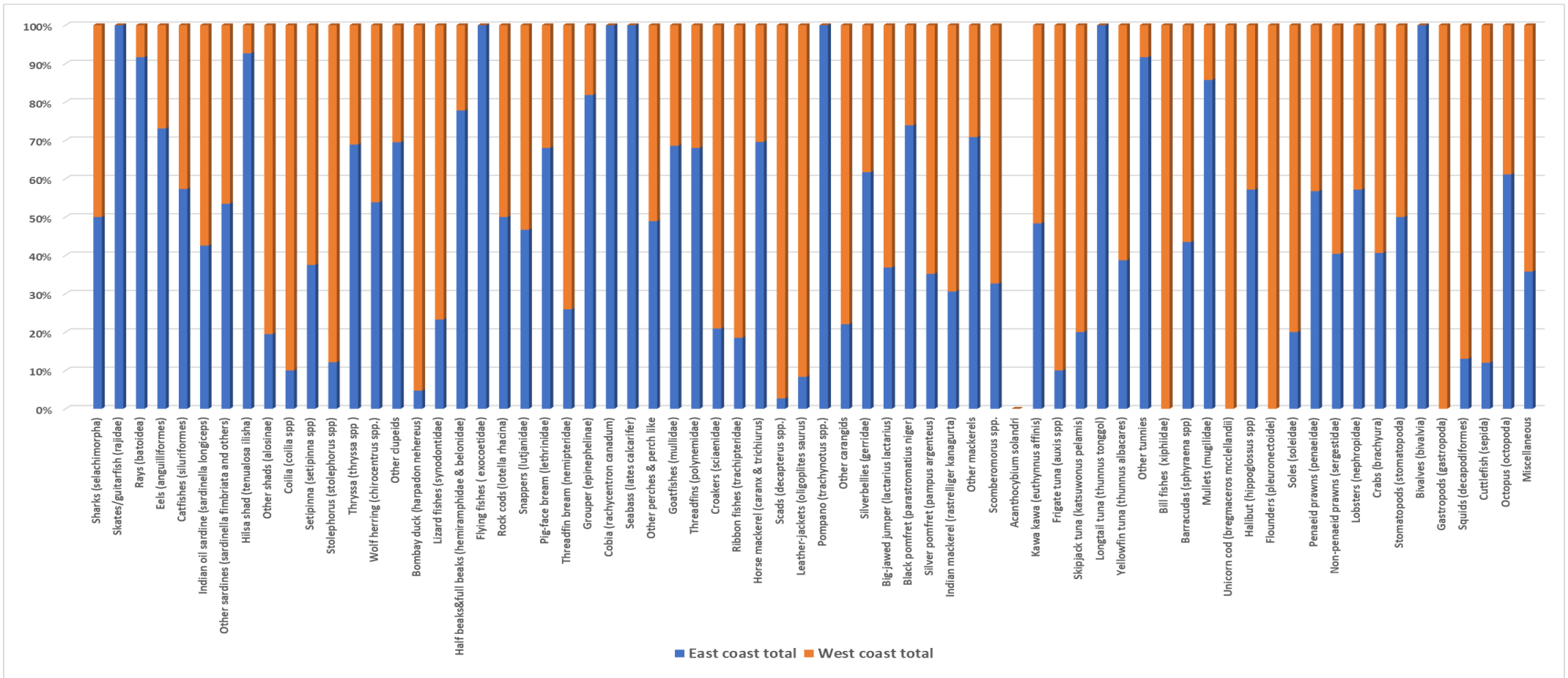


Fig. 2. Percentage production distribution/ landings of major marine fish species in east and west coast of India.

Genomics in fishery improvement

Traditional scientific methods of fishery improvement involve stock management and assessment models for improved production and maintaining enough diversity. Although, genomic methods of improvement existed since 1980s, but they have not gained much progress on global levels, especially India. This may be due to lack of initial understanding of genomic data, its cost and lack of consistency in results. However, with an increase in our understanding of genome and advent of new genotyping technologies, utilization of genomic values for enhanced productivity in livestock and fishes is not becoming a new normal. In view of fishery sciences, genomic information provide better way of stock management, can quantify species and stock level diversity and can differentiate between species in mixed stocks thus providing better identification methods. It also helps in identification of wild type of species that can be domesticated and aids in identification of better adapted/ resistance genotypes and their propagation (Yanes *et al.*, 2015). It helps in maintaining sufficient genetic diversity in fish farm as well as malicious mixing of threatened or non-edible species. Genomic information also allows better monitoring of adaptability of species in changing climatic conditions and act as biological monitor.

Massively parallel sequencing technologies have now made it possible to use genomic data for selection purpose. A scheme called “Genomic selection” is now widely practices in developed countries to bring significant change in production of domestic animals. The technique is now also used in fishery sector for improvement and better management of stocks. Introduced by Meuwissen *et al.* (2001), genomic selection is an extended form of marker assisted selection, where instead of few major marker alleles, whole genomic markers are used and genomic estimated breeding values are calculated. The utilization of dense markers allow better coverage of genome and hence smaller genetic variance can also be traced. Thus, this technique plays a major role in quantitative trait improvement where smaller genes are contributing for expression of desired character. The idea become more practicable with the advent of next generation sequencing technologies, which enable many subjects to be sequenced in parallel at a time, thus reducing the overall cost of genotyping (Fig. 3).

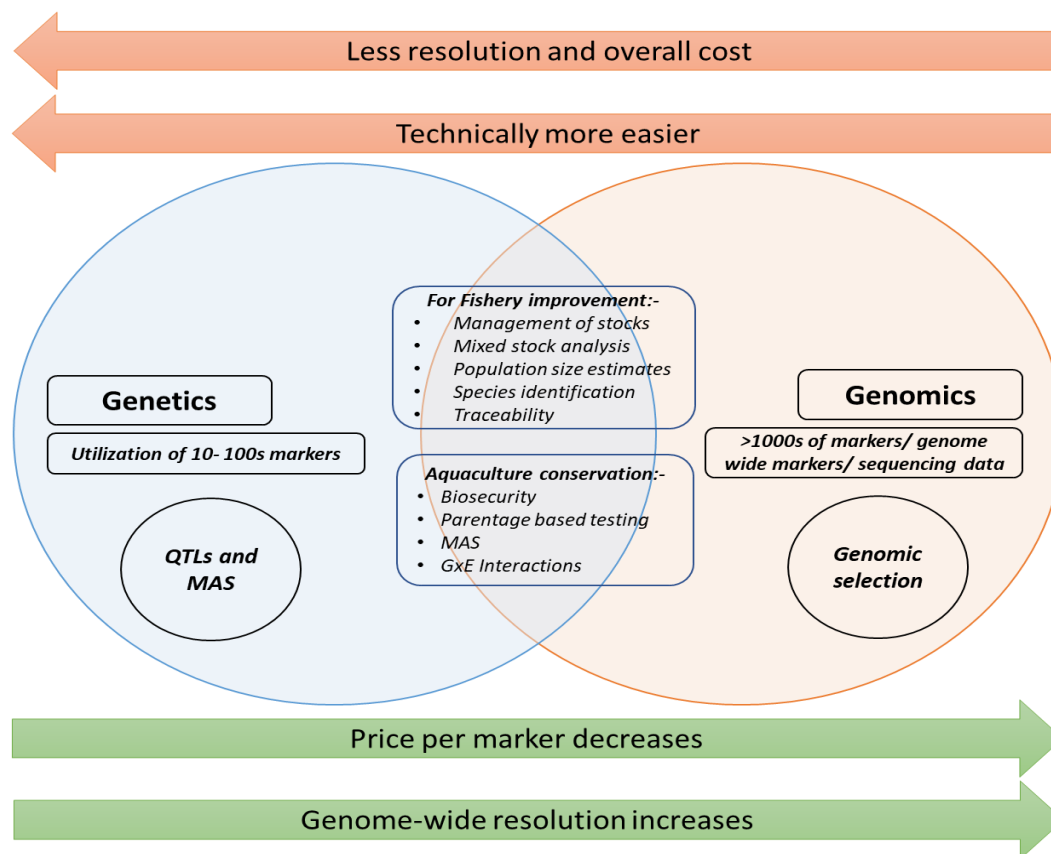


Fig. 3. Application of genetics and genomics in fishery sciences.

Genomic selection (GS) involves two basic steps. Classically the first step is to test the effects of various markers on a test population. The test population here may also be called as a reference population, the individuals in these population are genotyped on all the loci with concurrent trait recording. This is done to ascertain how the genomic “constitution” is responsible for change or variation in trait(s) of interest. The second step involves validation of the marker effects. This is generally done on subpopulation called training group. Once the marker effects are validated then selection can be practiced solely based on genotypes, rather than going for phenotypic trait recording. This process has been very well adopted in livestock and plants species but was lagging in fish and aquaculture species.

Recent advances in genomics have enabled better application of GS in aquaculture species. One such example is of Atlantic Salmon fish. The Atlantic Salmon fish or *Salmo salar*, is the 3rd largest fish from family Salmonidae. It is one of the most relished fish species around the world. The IUCN status of the is “least concerned”, however, recent human activities like over fishing has bought many local sub populations under threatened or even to endangered status at some places. Atlantic salmon is one of the few aquaculture species for which dense SNP chips are available. Traits like salmon lice resistance ($h^2 = 0.14$), fillet colour ($h^2 = 0.43$), weight ($h^2 = 0.14$) and length ($h^2 = 0.6$). Genomic breeding values in these traits provides better prediction

accuracy with a relatively lower density chip, when compared with livestock species. Higher density chips were only advantageous when genetic relationships between reference and validating populations were more distant. Hence, it was suggested that, for better accuracy the reference and validating populations should be more closely related genetically (Tsai *et al.*, 2016).

Another prominent example for genomic selection in fisheries is of large yellow croaker or yellow croaker or croceine croaker. It is from family Sciaenidae, and is a saltwater fish mainly from east Asian coastal areas. The population of this fish decreased from 1970s due to overfishing and genome was mapped in 2014. For traits like body weight, body length and meat quality, genomic techniques were applied. It was estimated that utilization of genomic value allowed for above 80 % prediction accuracy for complex traits too (Shepherd *et al.*, 2010; Dong *et al.*, 2016). Therefore, in general the accuracy of selection in genomic values, increased more than 20% specially for traits like growth and disease resistance.

The phenotyping – accuracy and cost effectiveness

Phenotyping or recording of trait is critical for every selection and breeding programme. Trait recording becomes more challenging in aquatic species. Errors in trait recording might over or underestimate the heritability estimates thus GEBV values might get biased or inaccurate. Therefore, high throughput technological advances need to be adopted for precise, accurate and bulk data recording in aquatic species. Problems in data recording hinder a effective selection programmes and it is one of the min constrains for effective deployment of genomic selection. The problems get augmented in aquatic species due to their high fecundity rates, a greater number of progenies per breeding pair and variable survival rates. Also, fish species still not have a standardized set of rules for trait generation and recording, as is present in livestock, especially dairy cattle. These constrains are now covered by using mechanized automation and imaging techniques, with high-speed data acquisition capabilities. Digital imaging or computer vision have now become most popular in fish species for data recording. Computer assisted imaging systems, 2D and 3D, are now being used effectively for trait recording in fish species. These have been applied to measure fish length in rainbow trout (Miranda and Romero, 2017), fish mass in Jade Perch (Viazzi *et al.*, 2015), with relatively, less mean errors. Furthermore, fish skin and colour traits can also be recorded as quantitative traits using ultraviolet-vis spectrophotometry measurements. These have been successfully applied in Atlantic salmon, pearls, rainbow trouts etc.

Another advancement in aquaculture phenotyping is the near infra-red (NIR) spectroscopy and hyperspectral imaging (HRI). These can identify and quantify the chemical and physical attributes of aquatic species with high accuracy. All these techniques can extract and analyse quantitative information from digital images by evaluating each image at pixel level and thus providing means for fast and accurate data recording. The biggest advantage of this technique is that they are non-invasive and automated hence animals need not to be removed from their rearing area. Every

machine vision system has two basic systems, first is the image acquisition system and data extraction system. The image analysis software are now upgraded with artificial neural network (ANN) algorithms and machine learning approaches. ANN approaches are highly advanced and these can mimic human brain like activities, thus they can differentiate between noise and real signals, based on which it can apply statistical models for accurate data interpretation (Zenger *et al.*, 2019).

Factors affecting utility of genomic selection

When a structured nucleus breeding programme is adopted, GS can have a rapid and significant impact on fishery improvement. However, potential of GS will vary as per the breeding structure, life cycle and fecundity of the species, effective population size and breeding objective. Among the factors affecting efficacy of GS, important ones are briefed below:

- a) Mating design - Adoption of right mating design is important to obtain long term genetic gain and to tackle the effects of inbreeding. Among the single pair, nested and factorial mating designs, factorial mating strategy gives highest selection response and lowest inbreeding. Whereas the single pair mating is worst in terms of response as well as level of inbreeding.
- b) Number of families – Number of families or breeders used in a selection programme are very important for response and selection intensity, increasing number of lines up to 100 may significantly reduce the inbreeding in population(s). However, when heritability of the trait in question is high, inclusion of a greater number of families for selection does not give any significant improvement in response to selection, when it is compared with the base population or a smaller number of lines. Simulation studies have shown that, family size of 200 with a SNP chip of 5000 SNPs allows more accurate predictions of breeding values.
- c) Marker density – Number of markers are an important criterion for any GS scheme. Increasing the number of markers to two-fold is shown to increase the total genetic gain by approximately 2% in generation 2 and 11% in generation 3. Also, if marker density is increased eightfold, it can increase the accuracy from 0.69 to 0.86. For an adequate intensity of selection, a family size of 100 and marker density of 24000 is needed.

CONCLUSION

In fisheries, yield of the harvested products is of prime economic importance. GS can be most beneficial when it is directed against such economically important traits. However, these can be difficult to apply directly on farm because in fisheries most of the GxE interactions are not clearly known, this, therefore, limits the validation of GEBV of testing populations and a genotype – environment correlation might bring unnecessary bias or inaccuracy in estimates. Secondly, implementation of GS may have infrastructural constrains, specially in developing nations, where costs of genotyping is a major factor. Under such situation it is necessary to look GS as a multi-stepped scheme. The first objective should be to make a centralized breeding structure for the

species in question, and then upgradation of infrastructural facilities for proper recording of the data/ phenotype that needs improvement in future. It will then be followed by development of genotyping methods and data analysis structure in the farm itself. When the genotyping and phenotyping in the farm/ nucleus breeding tier gets optimised, then the breeder may adopt to shift from traditional methods to GS method. However, caution should always be practiced in inclusion of traits, the traits which are economically viable and needs further improvement should only be targeted. When going for on farm analysis, it should be noted that objective of shifting from traditional method to GS is to have more economic return, and hence programme should be implemented keeping the objective in mind. It should be noted that although GS is a costly technique for developing nations, it can bring significant change in production as well as aid in conservation of species diversity, but these two applications are on different scales. As improvement on production efficiency is more market driven and conservation of species is of more of research/ academic interest, hence, both should be handled with their respective thrust domains.

REFERENCES

1. Dong L., Xiao S., Wang Q., and Wang Z. (2016). Comparative analysis of the GBLUP, emBayesB, and GWAS algorithms to predict genetic values in large yellow croaker (*Larimichthys crocea*). BMC Genomics, 17: 460.
2. Hosoya, S., Kikuchi, K., Nagashima, H., Onodera, J., Sugimoto, K., Satoh, K., Matsuzaki, K., Yasugi, M., Nagano, A.J., Kumagayi, A., Ueda, K., and Kurokawa, T. (2017). Genomic Selection in Aquaculture. Bull. Jap. Fish. Res. Edu. Agen. 45:35–39.
3. Shepherd R. K., Meuwissen T. H. E., and Wooliams J. A. (2010). Genomic selection and complex trait prediction using a fast EM algorithm applied to genome-wide markers. BMC Bioinformatics, 11: 529.
4. Tsai, H.Y., Hamilton, A., Tinch, A.E., Guy, D.R., Bron, J.E., Taggart, J.B., Gharbi K., Stear M.J., Matika, O., Pong-Wong, R., Bishop, S.C. and Houston, R.D. (2016). Genomic prediction of host resistance to sea lice in farmed Atlantic salmon populations. Genet. Sel. Evol. 48: 47.
5. Yanes, J.M., Newman, S. and Houston, R.D. (2015). Genomics in aquaculture to better understand species biology and accelerate genetic progress. Front. Genet. 6:128.
6. Zenger, K.R., Khatkar, M.S., Jones, D.B., Khalilisamani, N., Jerry, D.R. and Raadsma, H.W. (2019). Genomic Selection in Aquaculture: Application, Limitations and Opportunities with Special Reference to Marine Shrimp and Pearl Oysters. Front. Genet. 9:693.