CURRENT STATE OF REFERENCE FISH GENOMES AND PANGENOMES AND OPPORTUNITIES FOR AQUACULTURE BREEDING

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Abstract

In the last decade, drastic advances have been made in genome research. High-quality reference genomes are now available for major aquaculture species. These contiguous and accurate reference genomes set the foundation for genetic and genomic studies of aquaculture traits. In spite of such milestone achievements with reference genomes, only one or few genomes have been sequenced from any fish species, making them way behind for analysis of genomic variations relevnt to phenotypic variations. Pangenome is the complete set of genomes within a species, encompassing both genes and non-coding sequences of the genomes that may affect performance, diversity, evolution, and adaptation. Reference pangenomes include both core reference genome and dispensable genome segments representing mostly structural variations (SVs), which may contribute significantly to phenotypic variations among strains, isolates, and individuals. To date, pangenomes have been built only with few fish species such as Atlantic salmon. The lack of reference pangenomes limits the ability of association studies of phenotypic variations relevant to genomic variations, both within species and in related species where introgression is possible. This further hinders genomic selection or marker-asssisted selection, especially when considering integrating all phenotypic superiorty into synthetic breeds. In this paper, the current state of reference genomes and pangenomes will be reviewed. The current methods of producing reference pangenomes will be presented, and their pros and cons will be compared. A perspective of how the pangenome technologies can be adopted for aquaculture species, and opportunities for aquaculture genetics, genomics and breeding in the coming decade will be discussed.

Keywords: genome, pangenome, genomic variation, aquaculture

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