MBG -O6

CHROMOSOME-LEVEL GENOME ASSEMBLY AND GENOME-WIDE CHARACTERIZATION OF FOX GENE FAMILY IN THE ASIAN GREEN MUSSEL (*PERNA VIRIDIS*): INSIGHTS INTO EVOLUTION AND AQUACULTURE GENOMICS

V G Vysakh[1, 2]*, Sandhya Sukumaran[1], A Gopalakrishnan[1]
[1] Marine Biotechnology, Fish Nutrition and Health Division, CMFRI, Kerala
[2]Mangalore University. Mangalagangotri, Mangalore, Karnataka, India
*Email: vishakvg99@gmail.com

The Asian green mussel, *Perna viridis*, is an ecologically and economically significant bivalve species in aquaculture. We build a high-quality chromosome-level genome assembly of *P. viridis*, generated using PacBio SMRT sequencing, Illumina short-read sequencing, Hi-C scaffolding, and Bionano optical mapping. The final assembly spans 723.49 Mb with a scaffold N50 of 49.74 Mb, anchoring 99% of the genome into 15 chromosomes. A total of 49,654 protein-coding genes were identified. Using this genomic resource, we performed a comprehensive genome-wide characterisation of the Forkhead box (FOX) gene family, which plays a pivotal role in cellular regulation, development, and environmental adaptation. We identified 28 *PvFox* genes classified into 12 subfamilies, with lineage-specific losses of *FoxI* and *FoxQ1*. Gene duplication in *FoxL1*, *FoxB1*, *FoxH1*, and *FoxD2* suggests adaptive diversification in response to marine stressors. Structural analysis revealed exon-intron variations, with some *PvFox* genes exhibiting intron loss, potentially facilitating regulatory plasticity. Phylogenetic analysis confirmed evolutionary conservation, while selection pressure analysis indicated strong purifying selection. GO enrichment highlighted FOX involvement in apoptosis, oxidative stress, and immune responses, reinforcing their functional significance in stress tolerance and disease resistance. This study provides the first FOX gene landscape in *P. viridis*, advancing our understanding of its adaptive success and offering insights into the evolutionary dynamics of key regulatory genes in marine bivalves.

Keywords: *Genome assembly, Forkhead box genes, Perna viridis, Evolutionary adaptation*