



P0049: Draft Genome of the Anadromous Indian Shad, *Tenualosa ilisha* (Hamilton, 1822)

Vindhya Mohindra¹, Ratnesh K. Tripathi², Tanushree Dangi¹, Rajeev K Singh¹, Rakshit Chaudhary², Trivesh Mayekar¹, B. Kushwaha¹, Rajesh Kumar¹, Kuldeep K. Lal¹, J. K. Jena³, T. Mohapatra³

¹ICAR-National Bureau of Fish Genetic Resources, Canal Ring Road, P.O. Dilkusha, Lucknow - 226 002 INDIA

²Imperial Life Sciences (P) Limited, Gurgaon, Haryana 122001 INDIA

³ Indian Council of Agricultural Research (ICAR) , Krishi Anusandhan Bhawan - II, New Delhi - 110 012 INDIA

The Indian shad, *Tenualosa ilisha* (Hamilton, 1822) or Hilsa, an important anadromous tropical fish, is widely distributed in the Indo-Pacific region. It has high commercial value due to its delicious taste, nutritional content and high consumer preference. Hilsa forms major fishery component in the Ganga-Brahmaputra-Padma river system as well from the marine coasts. For generating draft genome sequence, estimated approximately 110X coverage of raw genomic sequences, generated using PacBio RSII platform, was assembled denovo using FALCON and polished with Quiver. The draft assembly of Hilsa comprises approximately 84% (763.19Mb) of the total genomic region and the assembled sequences were found to have N50 2.63Mb with largest contig length 17.43 Mb and L50 of 83 sequences. Genome completeness analysis with BUSCO against vertebrate lineage showed 95.8% genes as complete universal single-copy orthologs. The present Hilsa draft genome assembly shows highest similarity with *Clupea herrangus* assembly from Clupidae family, among those available in public domain. This high quality draft genome assembly of Hilsa will not only provide genomic resources to further arrange the contigs into scaffolds for generating high quality reference genome, but also fast track mining of important genes for salinity tolerance, higher productivity and disease resistance traits.

Author

Vindhya Mohindra

National Bureau of Fish
Genetic Resources

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