GENOME SEQUENCING AND DEVELOPMENT OF SINGLE NUCLEOTIDE POLYMORPHISM MARKERS FROM ROHU IN BANGLADESH

Aquaculture and capture fisheries are vital to food security and human nutrition. Aquaculture is expected to play a key role in meeting increasing human food and nutritional demands. Rohu (*Labeo rohita*) is primarily cultured in polyculture systems (those that cultivate more than one species) by small- and medium-scale farmers in Bangladesh. It is a highly preferred fish that is consumed by all income groups. The objectives of the Genome Sequencing project were to conduct stakeholder surveys to determine rohu carp aquaculture practices and profitability, sequence the rohu genome, and identify genome-wide single nucleotide polymorphisms (SNPs, which are variations at specific positions in the DNA sequence among individuals).

Farmers in Jashore District sample the rohu population. *M. Gulam Hussain*

STAKEHOLDER SURVEYS

The stakeholder survey results revealed that rohu-based carp polyculture was profitable where gross margin, net margin, and benefit-cost ratio were found to be positive. Results related to technical efficiency indicated that the farmers were efficient; nevertheless, the sample farmers operated well below the production frontier and, therefore, still had opportunities to achieve improved yields. The yield gap existed due to inefficient farming practices and technical biotic (e.g., diseases) and abiotic (e.g., flooding or drought) constraints. However, the results indicated that abiotic factors were more responsible than biotic factors for yield losses in the study areas. Productivity and efficiency were positively related, where small farms were more productive and efficient than large farms. The results also revealed that a considerable portion of farmers was young (18-35 years old) in the study areas, and young farmers were more productive and efficient than older farmers (≥ 51 years old). Most of the farmers preferred rohu as the main species in carp polyculture because of its higher production, high market demand, better feed conversion, and better taste and flavor. In terms of daily fish consumption, rohu alone contributed to more than half of total fish consumption among respondents and significantly contributed to their daily protein requirements. Since feed is the most costly aquaculture input, greater attention should be paid to feed price to promote carp polyculture. Farmers should be encouraged to apply the correct dose of inputs in their ponds to enhance productivity and ultimately reduce the yield gap.

SEQUENCING THE ROHU GENOME

After sequencing, the assembled rohu genome size is about 939.5 million base pairs (Mb) in length, a value less than half the previously reported size of the rohu genome as determined by Feulgen densitometry (1950 Mb), which is a common method used to determine DNA content. To explore this discrepancy, the project team used flow cytometry to determine the rohu genome size and found it is close to the assembled genome size (968 Mb on average for five male rohu with two determinations per fish). This suggests that the earlier Feulgen

densitometry determination of rohu genome size was likely flawed.The current assembly of the rohu genome is the most contiguous rohu genome available, composed of 6,175 scaffolded fragments, with more than half of the total genome in 26 fragments (L50), each of which is longer than 1.29 Mb (N50). Computational predictions indicated the rohu genome has 29,494 genes with 30,480 mRNAs.

IDENTIFYING SNPs

To identify SNPs, the project team compared the genome sequences of rohu carp collected from three different river systems (Padma, Jamuna, and Halda) to the genome assembly. About 99% of the carp sequences matched the genome assembly, and 1,033,085 SNPs were predicted. The SNP differences between fish correlated with the geographical distances between their rivers of origin. The predicted SNPs can be correlated with measured physical traits of rohu carp (such as growth rate) to enable the development of markers for beneficial or detrimental gene variants, accelerating and improving the effectiveness of breeding programs.

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CONCLUSIONS AND RECOMMENDATIONS

This study revealed that rohu-based carp polyculture in Bangladesh was profitable. The yield could be increased through maximizing efficiency, curtailing the yield gap, and increasing participation of young farmers. Fish farmers and their households consumed more fish than the national average, and rohu was preferred due to its better taste and flavor.

Availability of rohu genome and SNP markers provided much-needed genetic tools to initiate broodstock improvement programs for rohu. Linking SNP markers with better performing rohu would accelerate rohu genetic selection. Improved rohu broodstock would increase rohu aquaculture, profitability, and food security.

Based on the results of this study, the following recommendations are suggested:
1. The price of feed should be reduced while feed quality should be improved.
2. Cultural practices should be improved to reduce yield gaps.
3. Young entrepreneurs should be encouraged to participate in the aquaculture business.
4. Government and nongovernmental organizations should assist farmers in their economic decisions on aquaculture practices.
5. Research linking SNP markers with measurable physical traits should be supported.
6. Research developing superior broodstock through marker-assisted selection should be supported.
7. Once developed, superior broodstock should be provided to farmers.