Genomics of lumpfish (*Cyclopterus lumpus*)—towards marker-assisted selection

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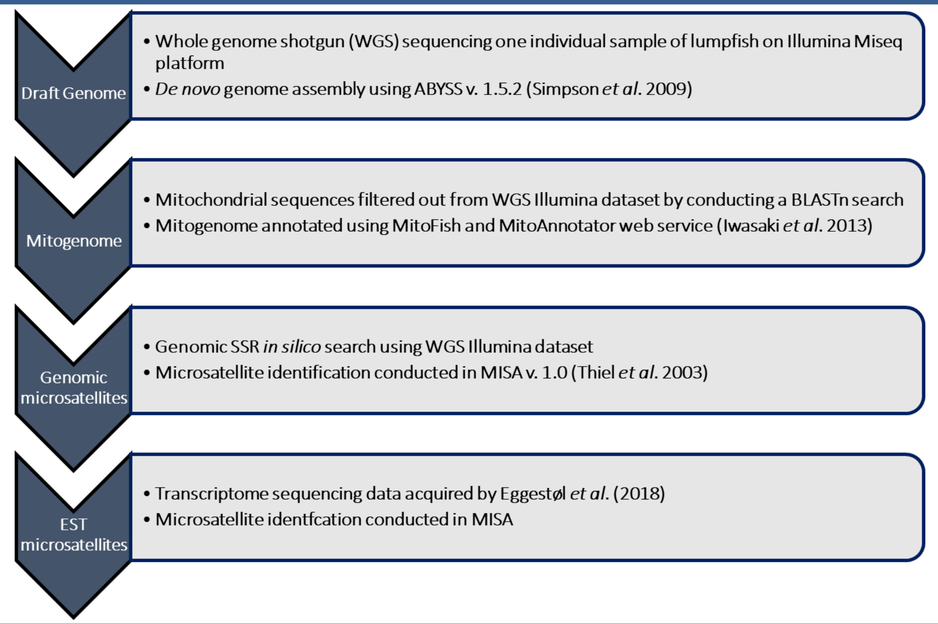
Abstract

Lumpfish *Cyclopterus lumpus* is a commercially important fish in several areas of its range in the North Atlantic Ocean. Despite the fishery and aquaculture importance of lumpfish, few genetic resources are currently available for the species. Here, a genomic approach using next-generation sequencing was used to develop genomic resource for lumpfish, which include a draft genome, mitogenome, genomic- and expressed sequence tag (EST) microsatellite loci. The extensive genomic information reported here will facilitate molecular ecology studies and many aspects of the selective breeding programme of lumpfish, especially for marker-assisted selection.

Introduction

- Lumpfish *Cyclopterus lumpus* (L. 1758) is commercially valued for its egg masses (roe) which serve as an alternative to sturgeon caviar
- This species also plays a vital role in salmonid aquaculture where it serves as a biological agent of sea lice control
- Recent investigations into the genetic diversity and population structure of *C. lumpus* along the Norwegian coastline and first-generation reared *C. lumpus* found no evidence of population differentiation; however, reported a decline in genetic diversity indices for the cultured *C. lumpus* (Jónsdóttir *et al*. 2018)
- Moreover, a recent investigations into the cleaning behaviour (sea lice grazing efficacy) and disease resistance in several families of *C. lumpus* showed significant difference among families (Imsland *et al*. 2016), of which, the genetic basis is yet to be investigated for selective breeding programmes
- The present study aims to develop genomic information for *C. lumpus* to facilitated marker-assisted selection for disease resistant and elite sea lice grazing families of the species.

Methods and Materials



Results

- Draft genome of *C. lumpus* is approximately 1.8 Gb in size with scaffolds consisting of 427.2 Mb (Table 1)
- The assembled mitogenome of *C. lumpus* is 17 188 bases in length and displayed synteny with other fish mitogenomes (Figure 1)
- A total of 85,940 genomic-microsatellite containing contigs were identified and, dinucleotide repeats were the most frequent (76,141 or 88.6%), followed by trinucleotide- (8,179 or 9.5%), tetranucleotide- (1549 or 1.8%), hexanucleotide- (57 or 0.7%) and pentanucleotide repeats (14 or 0.3%)
- While a total of 196,453 EST-microsatellite containing contigs were identified and, similarly, dinucleotide repeats were the most frequent (151,717 or 77.2%), followed by trinucleotide- (39776 or 20.3%), tetranucleotide- (3950 or 2.0%), hexanucleotide- (597 or 0.3%) and pentanucleotide repeats (413 or 0.2%)

Table 1. *Cyclopterus lumpus* L. genome assembly

Total scaffolded	427.2 Mb
Contig count	289,796
GC content	41.60%
N75	1,33 Kb
N50	3,01 Kb
N25	5,72 Kb
Minimum	200 bp
Maximum	39,4 Kb
Average	1,47 Kb

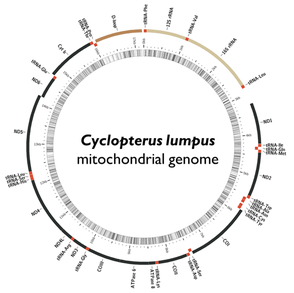


Figure 1. Mitogenome of *C. lumpus*

Discussion

- With only a limited set of 22 microsatellite loci available for *C. lumpus* (Skirnisdottir *et al*. 2013), the present study provides an extensive collection of genomic information for the species.
- This forms the basis for subsequent single nucleotide polymorphism (SNPs) detection, performing linkage- and quantitative trait loci (QTL) mapping in this economically important aquaculture fish.
- Additionally, the genomic information reported here will provide valuable insight into the impact of escapees from aquaculture farms on the genetic patterns of functional variation in wild population (*sensu* Jónsdóttir *et al*. 2018)

Conclusions

- The present study presents the first draft genome and mitogenome of *C. lumpus*
- A high-density novel set of genomic- and EST-microsatellite loci identified in *C. lumpus*
- These genome sequences bring *C. lumpus* breeding and molecular ecology into a genomic phase

Future Directions

- Functionally annotate the *C. lumpus* genome
- Characterize both type of microsatellite loci in *C. lumpus* and closely related species
- Develop SNPs using double-digest restriction a double digest restriction associate DNA sequencing (ddRAD) approach
- Construct high-density genetic linkage maps for QTL mapping in *C. lumpus*

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Acknowledgements

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