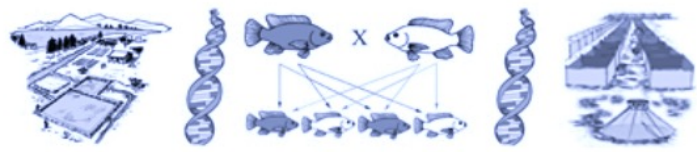


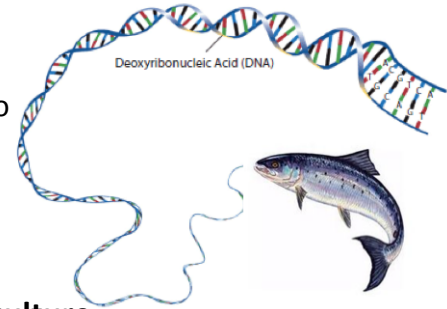
Cod do better...



Using Next Generation Sequencing to Improve Aquaculture

Aquaculture is one of the world's fastest growing food-producing sectors and accounts for half of the world's food fish (FAO, 2015-2016). Recent advances in next generation sequencing has led to the ability to produce massive quantities of sequencing data for non-model aquaculture species. Next generation sequencing can be used to identify and characterize genes of commercial interests, such as those regarding growth rates, reproduction, development, and disease resistance (Cerdeira & Manchado, 2013). This information can be used for better management and to sustainability optimize production (Cerdeira & Manchado, 2013).

Less than 9% of current farmed aquaculture species have been subjected to genetic improvement programs (FAO, 2015-2016). The lack of a reference genome and scarcity of transcriptome information has created challenges for whole genome sequencing.



The state of the world's aquatic genetic resources for food and agriculture

Conservation and sustainable use of aquatic genetic resources

Past, current, and planned exchange of aquatic genetic resources (FAO, 2015-2016)

Shifting from Sanger to Next Generation Sequencing

Species	Common Name	No. of Chromosomes	BAC	NGS Platform	Application
<i>Scophthalmus maximus</i>	Turbot	22	~40,000 clones of ~125 kb	454, solid	RNA-seq, de novo genome sequencing
<i>Hippoglossus hippoglossus</i>	Atlantic Halibut	24	35,328 clones of 100 kb	454	De novo genome sequencing
<i>Solea senegalensis</i>	Senegalese Sole	21	29,184 clones of 100-300 kb	454, Illumina	RNA-seq, de novo genome sequencing
<i>Solea solea</i>	Common Sole	21		Illumina	RNA sequencing

Modified from Cerdeira and Manchado, 2013

§miRNAs in the genome by transcriptome analysis with processes affecting development, metabolism, and disease (Rasal *et al.*, 2016)

§Expressed Sequence Tag to study gene expression (Zhang *et al.* 2012)

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§De novo Genome Sequencing

§Genetic Maps: identification of quantitative trait loci (Cerdeira and Manchado, 2013)

§Simple Sequence Repeat Markers or microsatellites: reveal genetic variability, strain and species identification, and parentage (Sundaray *et al.*, 2016)

