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Norwegian Team Completes Cod Genome Using 454 Sequencing System

Scientists from a consortium of Norwegian marine and aquaculture institutions announced this week that they have generated the first ever draft sequence and assembly of the Atlantic cod genome. The results, presented at the GenoFisk meeting in Oslo, Norway, include a high-quality genome assembly and preliminary annotation of the fish species, completed using only whole genome shotgun and paired-end data generated by the Genome Sequencer FLX System from 454 Life Sciences, a Roche Company (SIX: RO, ROG; OTCQX: RHHBY). By using the long-read GS FLX Titanium Series chemistry and the system's accompanying GS Assembler software, the consortium was able to produce a draft assembly at a fraction of the time and cost of traditional sequencing methods. The researchers hope to use this information and the fully annotated genome to identify genes and genetic variations underlying important traits for cod aquaculture.

The cod farming industry is of growing importance in northern latitude countries such as Norway due to the fish's high demand, declining wild stock, and relatively fast growth at low temperatures. In 2008, the Norwegian Centre for Ecological and Evolutionary Synthesis (CEES) was awarded the funds to complete the sequencing of the 0.9 Gb cod genome and the consortium turned to 454 Life Sciences to take on the project.

"The cod is a large and complex eukaryote with a number of highly repetitive regions in its genome. We understood the value of long 400-base sequencing reads to get the quality required for *de novo* assembly. In the end, we were able to generate 25x genome coverage and an assembly with few, large scaffolds, a major achievement given the diploid and non-inbred nature of our DNA source," explained Kjetill Jakobsen, Professor at the University of Oslo and consortium leader. "A preliminary transcriptome survey revealed that 95% of all sequenced transcripts are found in the current version of the assembly, confirming the quality of these results. With this project, we have made significant steps towards the creation of a highly annotated reference genome that can be mined for genes and genetic variations associated with important traits for cod aquaculture."

In the next phase of the project, the consortium plans to continue to sequence the cod transcriptome using the Genome Sequencer FLX System for genome annotation and to investigate specimens from various wild cod stocks. “In these follow-up studies we will be searching for SNPs and traits relevant to aquaculture, such as sexual maturity, temperature tolerance, oxygen uptake, as well as fishery related traits such as growth in response to harvesting,” explained Jakobsen. “Previous studies have shown that if the large cod are harvested from a population of fish, the subsequent offspring population tends to grow smaller. We plan to explore the genetic basis of this evolutionary response.”

“This study, along with other recently announced large genome project such as the oil palm, demonstrates that 454 Sequencing Systems have effectively replaced Sanger technology for *de novo* genome sequencing and assembly,” said Christopher McLeod, President and CEO of 454 Life Sciences. “We are extremely excited to continue to work with the cod genome consortium to analyze this important fish species.”

For more information on the 454 Sequencing System, visit www.454.com.

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