

Real-time genome-scale sequencing at sea

April 29 2014, by Cindy Spence

(Phys.org) —A University of Florida researcher has become the first scientist to achieve genome-scale sequencing and analysis of fragile marine creatures at sea aboard a ship and in real time.

The [genomic sequencing](#) of potentially thousands of marine species had been impossible until now because their fragile genetic material could not be stored or shipped reliably. Sequencing, too, used to take days. But using an at-sea full-equipped genomic laboratory and UF's powerful new HiPerGator supercomputer, Leonid Moroz has opened the floodgates to discovery.

The potential benefits are great: about 50 percent of drugs today are derived from natural products. The globe is 70 percent ocean, and scientists estimate 14 million to 20 million compounds remain to be discovered at sea.

"It is possible now to get the genomic blueprint of all animals in the sea," said Moroz, a distinguished professor of neuroscience, genetics, chemistry and biology at UF's Whitney Laboratory for Marine Biosciences, McKnight Brain Institute and College of Medicine. "And this is not science fiction.

"The real success of these two proof-of-concept trips is that we now know we can do high-throughput sequencing at any location on Earth," Moroz said. "And this is the perfect example of collaboration and synergy between public and private institutions such as Ocean Research Corp., International SeaKeeper Society, Florida Biodiversity Institute

and Ocean Expedition (OceanX) programs."

But science must make haste: the planet loses a species every six hours.

"We need to deploy a sequencing fleet," Moroz said. "There are potentially unique solutions in nature for medicine, but they are disappearing."

Moroz studies fragile marine pelagic organisms – [comb jellies](#) or ctenophores – for their ability to regenerate. Their wounds can heal in two to three hours and they can regenerate their elementary brains in three to five days. Another creature, sea slugs, may hold the key to the genomic basis for memory and neuronal evolution. While humans have learned to slow the progress of some diseases, Moroz said many sea creatures have already figured out how to reverse disease and injury. In a quest to speed the pace of discovery, Moroz went to sea.

Aboard the Copasetic in early February and later in March-April, within less than two weeks combined, Moroz's team was able to perform transcriptome sequencing of 22 organisms, among them rare comb jellies.

From the outset, each of these trips was a scientific adventure. Together with researchers at Bimini Shark Laboratory and Florida Biodiversity Institute, he planned to biopsy a hammerhead shark for cells, but on the first day no hammerheads showed up. More aggressive bull sharks did. As he was scanning the water he spotted a unique species of comb jelly, so as other crew members kept the bull sharks occupied, he jumped in to collect the comb jelly. The jelly was too fragile for tools, so he used a plastic bag to scoop it up. Two minutes later, he saw another species of comb jelly, not yet investigated rarely seen.

Back on board ship, the samples were immediately processed and sequenced using the Ion Torrent Personal Genome Machine System, which was linked via satellite to UF's new high performance supercomputer, HiPerGator, "and bingo, we had the data," Moroz said.

Moroz said he was motivated to prove direct sequencing and real-time genomic analysis in the middle of even a rough ocean would work because of past frustrations with field expeditions. The creatures that can be shipped to a lab often arrive in degraded condition. Oversampling to compensate for those errors is a problem, too, because it leads to "killing these beautiful creatures." But without enough samples to repeat experiments, researchers must undertake another costly field expedition.

The ideal, he decided, was to combine field work with lab work. UF alumnus and engineer Steven Sablotsky of Miami designed and donated the use of his 141-foot yacht for two trial runs, also supported by the Ocean Research Corp., the Florida Biodiversity Institute, LifeTechnologies, the Florida Museum of Natural History , International SeaKeeper Society, NASA, NIH and NSF. Moroz also teamed with Gustav Paulay, the leading expert in tropical biodiversity and a curator of the Florida Museum of Natural History, who joined the trips.

"This is the perfect example of symbiosis between public and private institutions," Moroz said, "Without such synergy, we will not be successful now and in the future."

The first results of the sequencing at sea (Moroz named it Ship-Seq) were presented at the international conference, Advances in Genome Biology and Technology, held at Marco Island in Florida in February.

"If you cannot bring the creatures to the lab, why not bring the lab to the sea?" asked Moroz. "Together with Ocean Research Corp., Florida Biodiversity Institute and Life Technologies, we turned a yacht into a

research vessel in two weeks. Unique Steven's design of his vessel paved the path to success."

"To learn from nature, we have to work in nature," Moroz said. "We can do genomic sequencing in extreme environments, from Antarctica to tropical seas."

While Moroz was delighted with the outing – "the science worked perfectly" – he was just as gratified by the success of the collaboration with multiple partners. The Gator flag flying from the mast was a conversation starter everywhere they docked, Moroz said, and led to opportunities to spread the word about the importance of research at sea. When he explained the high stakes, people often asked how to help.

"My hope is to seize the momentum and together with our colleagues at private organizations to develop a series of expeditions over a year or two. We could double our knowledge of the ocean," Moroz said.

Moroz said science, technology and computing power have all converged, leaving researchers on the brink of new discoveries. He points out that the 10-15 year Human Genome Project, which mapped all human genes, took \$3.5 billion and hundreds of sequencing machines. Today, the genome of one person will fit on a chip the size of a palm or less, and can be sequenced in 2-3 days for about \$1,000.

"We are in the midst of a genomic revolution," Moroz said. "Right now is the right time. We must take advantage of this great new computing facility. We are in a race to save species; in 20 years some won't exist. Losing them would be like losing the Sistine Chapel.

"We may not immediately cure cancer, but we can save our heritage, the heritage of the universe, and when you think of it like that, the price is not all that high."

Provided by University of Florida

Citation: Real-time genome-scale sequencing at sea (2014, April 29) retrieved 18 April 2024 from <https://phys.org/news/2014-04-real-time-genome-scale-sequencing-sea.html>

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