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Coelacanth Genome Informs Land Vertebrate Evolution

Apr. 17, 2013 — An historic fish, with an intriguing past, now has had its genome sequenced, providing a wealth of information on the genetic changes that accompanied the adaptation from an aquatic environment to land. A team of international researchers led by Chris Amemiya, PhD, Director of Molecular Genetics at the Benaroya Research Institute at Virginia Mason (BRI) and Professor of Biology at the University of Washington, will publish "The African coelacanth genome provides insights into tetrapod evolution" April 18 as the cover article in *Nature*.

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Coelacanth illustration. (Credit: iStockphoto/Sergey Mikhaylov)

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The coelacanth is critical to study because it is one of only two living lobe-finned fish groups that represent deep and evolutionarily informative lineages with respect to the land vertebrates. The other is the lungfish, which has an enormous genome that currently makes it impractical to sequence. The lobe-finned fishes are genealogically placed in-between the ray-finned fishes (such as goldfish and guppies) and the tetrapods – the first four-limbed vertebrates and their descendants, including living and extinct amphibians, reptiles, birds and mammals. A lobe-finned ancestor(s) underwent genomic changes that accompanied the transition of life in an aquatic environment to life on land. The coelacanth is undeniably a fish, however, phylogenetic analyses show that its genes are more like those of tetrapods than of ray-finned fishes. Additionally, coelacanth genes evolve at a considerably slower rate than those of tetrapods, a fact that is coincident with its apparently slow rate of morphological change.

"For evolutionary biologists the coelacanth is an iconic animal, as familiar as Darwin's finches on the Galapagos," says Toby Bradshaw, PhD, Professor and Chair, Department of Biology, University of Washington. "This paper by Chris and colleagues gives us our first comprehensive look at the coelacanth's place in our evolutionary history, and provides fascinating insights into the specific vertebrate genes involved in the critical transition from water to land – it seems that both loss and gain of gene function were required. I find the proposed gain-of-function changes in gene regulation for limb development particularly compelling, supported by experimental evidence that the lobed fins of the coelacanth really are akin to prototypical legs. Making legs from fins is a wonderful example of Francois Jacob's observation that 'evolution is a tinkerer, not an engineer.'" Adds Gerald Nepom, MD, PhD, Director of the Benaroya Research Institute, "This work represents a major accomplishment by a large and talented group of investigators, opening a new book of knowledge about

The coelacanth genome was sequenced by the Genome Center at the Broad Institute of MIT and Harvard, and analyzed by an international consortium of experts.

Sequencing the coelacanth genome has been a long-sought goal and a major logistical milestone, says Dr. Amemiya. He and scientists throughout the world have campaigned for sequencing of the fish for over a decade. "Analysis of changes in the genome during vertebrate adaptation to land has implicated key genes that may have been involved in evolutionary transitions," he says. These include those regulating immunity, nitrogen excretion and the development of fins, tail, ear, eye, and brain as well as those involved in sensing of odorants. The coelacanth genome will serve as a blueprint for better understanding tetrapod evolution.

"This is just the beginning of many analyses on what the coelacanth can teach us about the emergence of land vertebrates, including humans, and, combined with modern empirical approaches, can lend insights into the mechanisms that have contributed to major evolutionary

innovations," says Dr. Amemiya.

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adaptation that is now available to all scientists who want to better understand our complex genetic origins."

Genome sequencing is a laboratory and computational process that determines the complete DNA sequence of an organism's genome. Deciphering the genetic makeup of the coelacanth provides valuable clues for biologists studying the evolution of vertebrates. It was an international sensation when a living specimen of the coelacanth was first discovered in 1938 as this lineage of fish was thought to have gone extinct 70 million years ago. The living coelacanth has many anatomical similarities with its fossil relatives and seems to have undergone seemingly little morphological change since the Devonian period approximately 360 million years ago. It still possesses what many would consider to be a prehistoric appearance, and, as for many similar species that do not show much change over long evolutionary periods, is often dubbed a "living fossil." The relationship of the slow rate of evolution of its genes and its morphological appearance remains unknown and largely speculative. Today, coelacanths are on the endangered species list and biological tissues can only be obtained from expired animals that have been caught accidentally by fishermen.

In addition to this landmark genome paper in *Nature*, several companion papers are being edited by Drs. Amemiya and Axel Meyer for publication in a special open access coelacanth genome issue of the *Journal of Experimental Zoology (Molecular and Developmental Evolution)*.

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