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KU will be key donor of DNA samples to ambitious 'genomic zoo' project

LAWRENCE — For more than two decades, Ed Wiley has overseen collection and cataloging of fish specimens from all over the world in his role as curator-in-charge of the Division of Ichthyology at the University of Kansas' Natural History Museum and Biodiversity Institute.

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Natural History Museum and Biodiversity Institute

Now, frozen tissue from thousands of those collected fish will be source material for genetic sequencing in a huge new undertaking dubbed the "Genome 10K Project," a plan to map genomes from 10,000 vertebrates — species that possess backbones.

"There has been a lot of genomic work centered around humans, and that's very important," said Wiley. "But we need a much broader sampling of the diversity of genomes in order to understand many things. There are evolutionary and very practical reasons to sequence these genomes. Let me give you one example — sharks don't seem to get cancer. Is there something about their genome that is different from our genome that would explain this?"

Members of the Genome 10K Community of Scientists include representatives from major zoos, museums, research institutions and universities worldwide. Each will make a contribution to the project, but few as significant as the thousands of fish tissue samples KU will supply, which are expected to make up as much as 20 percent of the Genome 10K data.

"The KU Division of Ichthyology in the Biodiversity Institute has a large collection of fishes," said Wiley. "But our unique aspect is to have a very diverse collection of tissues that we've collected over the past 25 years. We have these tissues in an ultra-cold freezer, and they're associated with voucher specimens that we preserve in the regular, old-fashioned way. Almost half the total fish tissues that will be involved in this project will come from the KU collection."

For a quarter-century, Wiley's researchers have packed small tubes with muscle tissue from the backs of newly obtained fish specimens. Each tube then is frozen with a unique identification marker linking to its original specimen, which is preserved with formaldehyde and ethanol.

"We get requests from all over the world for little snippets of our tissue," Wiley said. "We do a very active program of gifting internationally, because everyone sees our collection as being a truly international resource for genetic studies of fishes."

The Genome 10K Project's quest to sequence DNA from species representing every vertebrate genus will be years in the making, Wiley said. Much will depend upon future cost reductions in DNA sequencing. If successful, the effort should yield what scientists call "an unprecedented resource for the life sciences."

"There may be features of the vertebrate genome that are so ancient that we can only stare in wonder at them," said Wiley. "The point of trying to sample broadly is to understand the commonalities of the genome. If there are certain parts of the genome of fishes that do exactly the same things that human genomes do, then you have an understanding of the origin — it has to be a very ancient thing as opposed to a very recent thing."

Wiley said that knowledge of such commonalities and differences in vertebrate genomes

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would lead investigators to a better grasp of evolution, morphology and disease in a host of creatures.

Wiley and 54 other scientists involved in the project met in April at the University of California-Santa Cruz and announced the project in early November. The KU researcher also co-authored an article describing the undertaking in the current issue of the Journal of Heredity.

“It’s going to be exciting,” Wiley said. “I’m really hoping that that the technological advances we saw at our meeting in Santa Cruz turn out to be industrial-strength. If they do, then sequencing of a genome per week is not out of the question.”

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