Tasmanian devil's genome sequenced

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Successful breeding efforts are underway in mainland Australia and Tasmania to preserve a captive population of Tasmanian devils that are free from Devil Facial Tumor Disease. Credit: Stephan C. Schuster, Penn State University

A revolutionary species-preservation approach based on whole-genome analyses of two Tasmanian devils -- one that had died of a contagious cancer known as Devil Facial Tumor Disease (DFTD) and one healthy animal -- has been used to develop a theoretical model to predict which individuals would need to be kept in captivity to maximize chances of preserving enough genetic diversity for the species to survive. The research helps to formulate one possible plan of action to prevent the extinction of the Tasmanian devil -- a marsupial found in the wild exclusively in the Australian island-state of Tasmania. The research

model also may be extended to other endangered species.

The team, led by Stephan Schuster, a professor of biochemistry and molecular biology at Penn State University; Webb Miller, a professor of biology and computer science and engineering at Penn State University; and Vanessa Hayes of the Venter Institute in San Diego, includes other scientists at institutions and universities in Australia, Denmark, and the United States. The results of the study will be published in the journal Proceedings of the National Academy of Sciences.

DFTD, which disfigures the victim and causes death from starvation or suffocation within months, is an unusual sort of cancer that first was observed on the east coast of Tasmania just 15 years ago, and since has spread rapidly westward, threatening the species with extinction. "The disease is like nothing we know in humans or in virtually any other animal. It acts like a virus but it actually is spread by a whole cancerous cell that arose in one individual several decades ago," Schuster explained. "This malignant cell is transferred directly from one individual to another through biting, mating, or even touching. Just imagine a human cancer that spread through a handshake. It would eradicate our species very quickly." The scientists explained that if a number of healthy Tasmanian devils were kept in zoos and other facilities in "protective custody" until the tumor ran its course and disappeared in the wild, then the captive animals could be released back into their former habitat and the population could begin to grow anew. "However, it's not just a matter of scooping up a few individuals at random and locking them away," Miller explained. "Our team developed a smarter, more calculated approach: We asked ourselves, which individuals would be the best candidates for 'protective custody,' and what criteria would we use to make those determinations? We soon realized that the answer was to compile genetic data and to analyze it in novel ways."

Zoo keeper and breeder Tim Faulkner holds a Tasmanian devil -- an endangered marsupial found in the wild in the Australian island-state of Tasmania. Credit: Stephan C. Schuster, Penn State University

The team approached the extinction problem on two fronts. The first was to sequence the complete genomes -- 3.2 billion base pairs each -- of two individual Tasmanian devils. One was a male called "Cedric," who had a natural resistance to two strains of DFTD, but succumbed after being infected with a different strain of the disease last year. The other was a female called "Spirit," who had contracted the vicious cancer in the wild. In addition, the scientists sequenced the genome of one of Spirit's tumors. Because the two animals had originated in the extreme northwest and southeast regions of Tasmania, respectively, they represented the maximal geographic spread of the species -- a measure that is used as an approximation of genetic diversity. The researchers then began an analysis of the genomic data from the two animals, and of the genetic characteristics of the tumor. Using these data, they created a model that could determine which individual animals should be selected for captive breeding programs, such as the ones currently underway in Tasmania and on mainland Australia.

Schuster explained that the genetic diversity of the Tasmanian devil population is low to begin with. For this reason, choosing the right individuals to represent the broadest genetic diversity possible is critical for successful species preservation. "It might seem you'd want to choose only those individuals that are genetically resistant to the DFTD cancer. However, that would defeat the purpose of maintaining genetic diversity because, by definition, you'd be selecting a tiny subset of the gene pool," Schuster said. "Instead, our model suggests a more balanced approach. You don't want to put out just the one fire -- the cancer. Instead, you want to develop a pool of diverse, healthy individuals that can fight future maladies or even pathogens that have not yet evolved."

The second aspect of the project was to learn how much genetic diversity had been lost since Europeans settled Tasmania in 1803. To do this, the scientists analyzed a large number of genetic markers from an additional 175 Tasmanian devils, some of which were museum specimens from the Smithsonian in Washington, D.C. and the Natural History Museum in London. Schuster explained that this approach to genomic research, which he has named "museomics," is truly unique and brimming with potential. "Museums are treasure troves of specimens collected in the last 250 years," Schuster said. "And, in fact, we can get DNA from hair shafts of a museum specimen." Schuster explained that DNA collection from hair is virtually non-destructive; that is, museum specimens are not damaged visually in the process of removing just a few hairs. Interestingly, after analyzing the 175 individuals, the scientists learned that the genomic diversity of the Tasmanian devil, while low, has not decreased much over the last century. "This is an important finding because it means that DFTD is not to blame for any lack of genetic diversity since the disease appeared only 15 years ago," Miller explained. "It's crucial that we act as responsible stewards for the species, helping maintain what little genetic diversity it had before the DFTD epidemic struck."

A team of Penn State University researchers have used genetic data to formulate a plan of action to prevent the extinction of the Tasmanian devil. Credit: Stephan C. Schuster, Penn State University

Schuster also said that a significant and defining part of the team's project was the ability to generate extra-long genetic sequences using a special genome-sequencing technology that, at the time the scientists performed the research, had not yet been released publicly. "This technology, developed by Roche Diagnostics and 454 Life Sciences, allowed us to assemble a mammalian genome from scratch," Schuster said. "The longer stretches of DNA or "long reads" were particularly critical to develop a full understanding of the genetic makeup of such a unique species."

Schuster and Miller hope that their novel strategies for tackling impending extinction will be applied to other endangered species. "We humans have contributed to the endangerment of many native species, so it's our responsibility to find a way to help fix things by giving nature a hand," Miller said. "Here's a way to think about it: If a driver causes a car accident, he is morally responsible for restoring any injured person

to the state of health that the person enjoyed before the accident. Likewise, our goal is to use museomics to inform efforts to restore the genetic health of endangered species to that which existed before humans came on the scene." Schuster added, "To plan for the future, you have to be willing to understand the past. It's important to examine museum specimens, as well as the population history of species over the last 10,000 to 50,000 years, and to use that genetic data to formulate a plan. The idea is to save a species, not to do a 'post-mortem' on it."

Schuster noted that the team's novel genomic concept at first was considered to be a "high risk/high gain" research strategy. "We are particularly grateful to the Gordon and Betty Moore Foundation since this organization had the foresight to support this research, which has resulted in a promising working regime for applying modern genomic methods to species conservation," he said. Additional private funding was obtained from GENEWORKS in Australia, the Allco Foundation in Australia, and Roche Diagnostics.

More information: Additional information about the team's research is posted at the project website, http://tasmaniandevil.psu.edu.

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