We are researchers at Johns Hopkins Medicine and NOAA studying how genetics can inform conservation. Ask us anything about the Hawaiian Monk Seal, genome sequencing and anything in between!

HopkinsMedicine$_AMA^1andr/ScienceAMAs^1$

[1]Affiliation not available

April 17, 2023

Abstract

Hi Reddit, We are Alan Scott, Ph.D., a geneticist and Associate Professor of medicine at the Johns Hopkins University School of Medicine in Baltimore, Maryland, and Stacie Robison, Ph.D., a research ecologist for the National Oceanographic and Atmospheric Administration's Hawaiian Monk Seal Research Program at the Pacific Island Fisheries Science Center in Honolulu, Hawaii. We are bringing you this coast-to-coast AMA to talk about how knowing the genome of an organism can tell us a lot about their biology and help inform conservationists who work to protect endangered animals. Hawaiian monk seals are an endangered species unique to the Hawaiian archipelago (there are only about 1,400 left, and they don't live anywhere else). Stacie works to increase our understanding of monk seals' biology, the things that threaten them and the effectiveness of conservation efforts. Stacie studies everything about monk seals from what they eat, to how they breed, to how disease impacts them, to where they travel. Alan led the collaborative effort to develop a faster way to sequence the DNA of organisms at 1/100,000th of what it originally cost to sequence the human genome and started with the Monk Seal. The genome was publically released on July 7 by NCBI. We plan to use these new genomics techniques to sequence the genomes of many more endangered species. We are excited to be working together to help scientists understand the evolutionary history, genetic diversity and population trends in this species. We'll be back at 1pm ET today to answer your questions.

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REDDIT

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CORRESPONDENCE:

DATE RECEIVED:
September 19, 2017

DOI:
10.15200/winn.150573.39036

ARCHIVED:
September 18, 2017

CITATION:
HopkinsMedicine_AMA , r/Science , We are researchers at Johns Hopkins Medicine and NOAA studying how genetics can inform conservation. Ask us anything about the Hawaiian Monk Seal, genome sequencing and anything in

Hi Alan and Stacie, and thank you for doing this AMA.

I read through your paper reporting the sequencing of the Hawaiian Monk Seal genome, Alan. It looks like most of the focus was on developing the technology to rapidly and cheaply sequence and assemble the genomes of organisms for which short-read assembly doesn't make much sense. There doesn't seem to be a lot of analysis of the genome itself, though.

I was hoping you and Stacie could comment on any notable features of this animal's genome - especially, what are you looking for in terms of conservation studies?

SirT6

Hi, Alan here. We are working on another paper that will discuss the interpretation of the genome. What we have seen so far is that the monk seal has about 1/10th the heterozygosity of the typical human. They are quite inbred. In terms of conservation studies, we hope the data we have from the three seals we have sequenced so far will allow us to develop a SNP-based test, which would look at the DNA signatures of the animals. Based on similarities or differences among the Monk Seals from island to island.

between!, *The Winnower* 4:e150573.39036 , 2017 , DOI: 10.15200/winn.150573.39036

Thanks for coming to talk with us today! For an endangered species, at what population level does lack of genetic diversity become a serious problem?

asbruckman

Hi, Alan here. Compared to other mammals the population is pretty inbred. Once you have a population that is below a few hundred animals, it is hard to escape an extinction spiral, but that is dependent on how variable they were to begin with. You could have what I like to call a fast bottleneck, like if you took 100 people from NYC, you would have a large amount of diversity. But, if you took the same number of people from a smaller town in eastern Iceland, you may not have that same level of variation. It just depends on the starting point.

Thank you for doing this AMA!

Because monk seals are an archipelago species, do they have any genetic diversity advantages over non-island endangered species, given their tiny remaining population? Do you see much genotypic/phenotypic variation from island to island?

neurobeegirl

Alan here! There are only about 1400 monk seals living in Hawaii. They are thought to have gone through a population bottleneck in the 1890's when their numbers may have been fewer than 100. I doubt if there is much variation from island to island, but that is not something we have investigated yet.

I appreciate the time taken to chat!

Stacie, how has conducting the research in Hawaii been for you? I read an article which featured you and another woman living or traveling to the island at a field station for weeks at a time just to count the seals every season. How is that? Did you develop any small emotional attachment to them? I know I would.

LaniMermaid

Stacie here! I feel pretty lucky to work with such an interesting animal in a beautiful place! While I spend my year based in Honolulu, we do have field teams that spend up to 3-5 months in camps in the remote Northwestern Hawaiian Islands - they are amazingly hearty and dedicated biologists! The seals, especially the young ones, are pretty charismatic - so it can be hard not to get attached, but we try.

You can get to know a little more about our field crews on our blog here:
https://pifscblog.wordpress.com/2017/05/23/team-french-frigate-shoals/
https://pifscblog.wordpress.com/2017/05/26/teams-laysan-lisianski/

And you can get a feel for the NWHI on our story map here:http://arcg.is/2p5BS4F

Welcome and thank you for taking the time to share your research with us! I'm going to struggle through asking my question, because I lack a lot of the basic framework for your field, so please be patient with me.

I know there are companies that offer genetic testing services that you can buy as a regular consumer. As I understand it, that just give you your results and they'll vary from individual to individual. That's different than the genome of a species, but I don't understand why.

What does it mean to sequence the genome of a species? What is a genome and how do we understand it?

PapaNachos

Alan here. Good question! A genome is the entirety of the DNA in a cell. So genetic tests are built by comparing your DNA against a reference genome. The human reference genome took 15 years and 3 billion dollars to build and is a representative DNA sequence for humans. We use it as a roadmap to study the human genome, but everyone has their own variation of this map. However, commercially available genetic tests only look at sections of DNA we know to vary from person to person, and don't necessarily sequence the the whole genome. Even in research, we hardly ever sequence the whole genome.

When we do genetic testing, we are comparing your differences to that of the reference. At Johns Hopkins Genomics, we compare people with the disease to the reference and other healthy people to find places in the genome that are associated with a disease. We can use that info to diagnose a disease and to design better treatments for people.

When we create a new genome for a species, we don't know ahead of time which genes are there and how they are arranged compared to one another. We've created a reference for the monk seal by using new technologies that allowed us to work with very long DNA molecules. If you think of the genome as a jigsaw puzzle, it's easier to assemble a puzzle with large pieces as opposed to many small pieces.

Hi Alan and Stacie, with respect to the Hawaiian Monk Seal or other species do you see any particularly conservation-useful information in endangered species genomes that is not available through other research means? Or is this more a way to acquire information in a less invasive or less costly way?

Do you expect there to be similarly useful genomic information for most endangered species?

Thank you for the work you both do.

TheArtOfShazzam

Hi, Alan here. Yes. Absolutely! Knowing the genomes of other species will be as valuable to their conservation as knowing the human genome is to helping with our health and disease. There are various projects now to try to sequence thousands of genomes. There is one called Genome 10K that hopes to sequence 10,000 mammalian genomes. And another called the Earth Bio Genome Project that hopes to sequence all living things on the planet. Zoos keep pedigree info on animals and they use that info when they decide which animals to use in their breeding programs. Now, they can do this more accurately because they can see, for example, if there is a mutation that causes a deleterious phenotype and attempt to breed that out of the population. The more information we have on the genes, the more precisely we can do this. We hope that this new technology can make this process faster, cheaper and better. We estimate that these methods cost about $15,000 to generate the monk seal genome vs. $3 billion for the human. This should make it much more accessible for conservation efforts and other fields and we're working on making it even cheaper.

What types of markers do you see in the genome of the monk seals that tell you things about their

evolutionary history and population trends?

kerovon

Hi Stacie here. This is the next step. Now that we have a complete genome for the monk seal, we can use that tool to look at variability in the population to get a better picture of their population history.

Hi guys, thanks for doing this AMA!

As someone not in the field of genetics I'm interested in what sort of impacts we could see from your work. Realistically, what could be affected long term? Are we talking about things like elimination of disease in certain population, or something along those lines? I apologize if this is an obtuse question. Thanks for your time!

Austion66

Alan here. That's a good question. Yes, for captive populations of endangered animals, we can and do use genetics to eliminate inherited disease.