Of Penguins and Polar Bears, Sponges, Shipworms, and Snails

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Ocean genome research advances evolutionary biology, medicine, sustainability.

It is summer in the Northern Hemisphere, but far, far to the south, austral winter has settled in. Life has gone into a deep freeze, including for what may be the Southern Hemisphere’s best-known diplomats, penguins.

The evolutionary history of penguins, most of which live in iceboxes, is a tale of success. Earth is home to 18 species of these waddling, flightless seabirds. Or so scientists thought. Now biologists are asking: when viewed through the lens of genomics, how many penguin species in fact exist?

Take gentoo penguins. Gentooos are most closely related to Adelie and chinstrap penguins, with two gentoo subspecies recognized: Pygoscelis...
papua papua (the sub-Antarctic gentoo) and Pygoscelis papua ellsworthi (the Antarctic gentoo).

After analyzing the genetic differences in gentoo populations, however, scientists at the University of Bath say the penguins should be reclassified as four species. The researchers suggest that the two current subspecies should be raised to species level and that the new species should be named Pygoscelis poncetti and Pygoscelis taeniata.

The field of genomics is giving scientists new insights into a host of marine organisms, from penguins to polar bears to seaweed. Genomics research is leading to a rethinking of taxonomy and is yielding new discoveries in pharmaceuticals and sustainable foods. As Sir Alister Hardy wrote in his 1965 book, *The Open Sea: Its Natural History*, “All the discoveries of the marine biologists, however remote they may now seem from practical issues, will be required in their different ways for a full understanding of the life in the sea and its more rational exploitation.”

The penguin study, published in October 2020, in *Ecology and Evolution*, looked at the genomes of gentoos on the Falkland (Malvinas) Islands and South Georgia Island, as well as gentoos on the South Shetland Islands and Kerguelen Islands. The biologists used genomic data to create an evolutionary tree, then combined that with measurements from museum specimens.

“These penguins are not only genetically distinct; they are physically different, too,” says Jane Younger of the University of Bath, who led the project. “Gentoos tend to stick close to their home colonies, and over hundreds of thousands of years have become geographically isolated from each other to the point that they don’t interbreed.”

The four possible gentoo species live in different latitudes—*P. ellsworthi* on the Antarctic continent, and *P. poncetti, P. taeniata*, and *P. papua* farther north, where conditions are milder. It is a similar story to that of giraffes, the biologists say, which in 2016 were revealed as four genetically distinct species.

As four gentoo species, the penguins would be better protected, the researchers believe. A decline in one species would change its threat status as defined by the International Union for Conservation of Nature Red List, which shows trends in extinction risk. “Currently gentoo penguins are fairly stable,” says Younger, “but there’s evidence that northern populations are moving south as climate gets warmer. We need to watch these changes closely.”

**Promise of the ocean genome**

Far beyond penguins, the sea is home to remarkable biodiversity. “The genetic biodiversity we see on land is a tiny fraction of that in the oceans,” says Rachel Wynberg, a member of the High Level Panel for a Sustainable Ocean Economy and an environmental scientist at South Africa’s University of Cape Town. Only 35 percent of major animal phyla are found on land, according to *The Ocean Genome: Conservation and the Fair, Equitable and Sustainable Use of Marine Genetic Resources*, a paper released in June 2020, by the High Level Panel.

Established in September 2018, the High Level Panel is an initiative of 14 heads of government from Australia, Canada, Chile, Fiji, Ghana, Indonesia, Jamaica, Japan, Kenya, Mexico, Namibia, Norway, Palau, and Portugal.

The ocean genome—the genetic material in all marine biodiversity, or the complete set of genes in every cell or organism in the sea—is the foundation on which marine ecosystems rest. “The ocean genome determines the abundance and resilience of biological resources, including fisheries and aquaculture, which collectively form a pillar of global food security and human well-being,” states the 2020 High Level Panel paper. Despite the contribution the ocean genome makes to life on Earth, it is threatened by overexploitation, habitat loss and degradation, pollution, impacts from a changing climate, invasive species, and other pressures.

Untold benefits are hidden in the sea’s genetic diversity, scientists
believe. For example, the COVID-19 pandemic has drawn renewed attention to the ocean genome, a source of hydrothermal vent bacteria that produce enzymes important in virus testing. “When it comes to the ways humans rely on the oceans, genetic biodiversity, what we call the marine genome, provides a treasure trove of helpful products such as food and medicines,” says Wynberg.

A paper Wynberg coauthored with Robert Blasiak of Stockholm University, Carlos Duarte of Saudi Arabia’s King Abdullah University of Science and Technology, and other scientists, published in Nature Sustainability in May 2020, states that “conserving [marine] genetic diversity helps foster the fitness of populations and their potential to recover from and adapt to threats ranging from disease to environmental changes.”

According to Duarte, “The ocean genome is the product of more than a billion years of evolution. It has produced an amazing diversity of tools marine organisms use to cope with the difficult conditions of life in the sea. It’s a largely untapped source of solutions to our challenges.”

The heyday of ocean genomics research may be on the horizon. Marine conservation initiatives based on genomics are “nascent but show tremendous promise,” states the 2019 report Ocean Genomics Horizon Scan. “While sequencing costs continue to plummet, it is expensive and difficult to mimic marine systems in laboratory settings. There is a great need to build genetic libraries and molecular toolkits to understand the processes driving the sustainability of ocean life.”

One year later in this fast-moving field, the 2020 document Microbial Genomics of the Global Ocean System reports that researchers are beginning to “wield a toolbox of ‘omics technologies and bioinformatic methods that allow them to probe the structure and function of microbial [and other] communities that form the foundation of marine ecosystems.” These technologies range from genomics to transcriptomics, proteomics to metabolomics, and are being used to study species from penguins to polar bears, sponges, shipworms, and snails.

**Polar bears: To go where no grizzlies can**

Polar bears (Ursus maritimus) and brown, or grizzly, bears (Ursus arctos) diverged less than 500,000 years ago when polar bears evolved unique traits to adapt to the Arctic, such as a camouflaging coat of pigment-free fur. Scientists at the University of Massachusetts Amherst, Vanderbilt University, and Clark University recently uncovered the genomic foundations of the polar bear’s adaptations by pinpointing rapid changes in the bear’s gene copy numbers. The changes happened in response to a diet that shifted to meat.

In a paper published in July 2019, in Proceedings of the National Academy of Sciences, David Rinker of Vanderbilt University and his colleagues characterized population-level, genome-wide patterns of copy number variation (CNV) in the polar bear and brown bear. CNV is the difference between individuals in the number of copies of a particular portion of a genome.

The researchers compared gene copy numbers among 17 polar bears, nine brown bears, and two black bears. The results suggest that CNV played an important role in the adaptation of polar bears to the Arctic.

The project was a test case in understanding the effect of diet on copy number variations, according to coauthor John Gibbons of the University of Massachusetts Amherst. Of the genes linked to olfactory receptors, 88% had lower copy numbers in polar bears than in brown bears and black bears. “Polar bears mainly have to hone in on two things: seals and mates,” says Gibbons. They are not sniffing out berries and grasses, like brown bears do, so they do not need the same number of genes for scent.

“Now that we have the technology to detect CNVs, this type of mutation should be examined” in more studies, says Gibbons. The team plans to build on its polar bear genome work with a study of another species: Homo sapiens. The next step, the biologists say, is to find out whether
human populations have similar differences in copy number variants, and if so, what that may tell us about our own evolution.

**COVID-19 fighter from the sea**

“Marine organisms from microbes to large vertebrates establish complex interactions mostly mediated by a variety of chemicals,” according to Blasiak and colleagues. “These chemicals serve multiple purposes, including communication, defense against predators, and many others.” Known as secondary compounds, they often lead to new drugs and other “natural” products from the sea. The 34,000 or so marine natural products discovered to date have fostered eight approved drugs, with 28 more in clinical trials and some 250 under preclinical investigation.

Off the Florida coast in the 1940s, for example, organic chemist Werner Bergmann found an undescribed sponge that was ultimately named *Tectitethya crypta*. Bergmann discovered that the sponge has compounds similar to two RNA building blocks, thymidine and uridine. When the sponge is attacked by a virus, these compounds are incorporated into a strand of replicating viral DNA, terminating its chain and preventing further infection, according to Timothy Bouley and Marie-Christine Imbert of Emergent Ocean, an organization that works to build companies that use and safeguard living marine resources.

The compounds in *Tectitethya crypta* became known as spongouridine and spongothymidine. Their characteristics led to new drugs that have helped fight viruses such as SARS-CoV-2. Remdesivir, for example, used to treat COVID-19, is a member of a class of antiviral compounds called nucleoside analogs that interfere with viral replication. Nucleoside analogs have also been used against viruses such as HIV, herpes, and chickenpox.

**Shipworms versus parasites**

Another secondary compound, this one discovered in the gills of wood-eating clams called shipworms, could be the solution to parasites responsible for some of the world’s most common infections. Tartrolon E is a metabolite of the symbiotic bacteria that help shipworms—marine bivalve mollusks—feed on wooden piers, docks, and boats.

Tartrolon E, according to Roberta O’Connor, a veterinary microbiologist and pathologist at Washington State University, kills the parasites that cause malaria, toxoplasmosis, cryptosporidiosis, babesiosis, and theileriosis. The latter only affects cattle. The results were published in *PLOS Pathogens* in May 2020 and build on shipworm research O’Connor conducted at Northeastern University’s Ocean Genome Legacy Center. The center is a marine research organization and biological specimen repository dedicated to exploring and preserving the information contained in ocean organisms’ DNA.

“There are compounds that work against individual parasites,” says O’Connor, “but to find one like Tartrolon E that works against an entire group of parasites is what makes this compound unique.”

The scientist is hopeful that Tartrolon E’s effectiveness against cryptosporidiosis, in particular, may lead to a new drug. *Cryptosporidium*, a waterborne parasite, is a major cause of diarrhea in children, immunocompromised patients, and newborn animals. The parasite annually infects millions of people, as well as animals important in agriculture. Tartrolon E fights *Cryptosporidium* in mice; the researchers are now conducting a study to find out if it will treat cryptosporidiosis in lambs.

The results could have a significant impact on human and veterinary medicine, say O’Connor and her collaborator Nicolas Villarino, a pharmacologist at Washington State University.
No tumors in sharks?
If the shipworm genome holds answers in parasitology, the shortfin mako shark genome may offer the same in oncology. Anecdotal reports claim that the incidence of cancer in sharks is extremely low. A study in the journal *Genomics* in November 2020 indeed shows that in the shortfin mako shark, *Isurus oxyrinchus*, 9 out of the 10 most expressed genes in the animals’ livers are related to tumor suppression.

Fishing boat observers from the Portuguese Institute for Sea and Atmosphere collected tissue samples from the organs of four shortfin mako sharks. Then Brazilian researchers genetically sequenced eye and liver samples from the sharks. Among the genes with above-normal activity in the liver, one known as HABP2 reduces cellular migration in thyroid tumors, according to Rodrigo Domingues of the Federal University of Sao Paulo, the paper’s lead author. Another gene, PON3, encodes an enzyme that acts as an antioxidant, protecting cells from oxidative stress, a major factor in the development of cancer.

The scientists also discovered that the genes NIT2, RMC1, and FGFRK1, potential tumor suppressors, are expressed in several mako shark tissue types. The first two relate to suppression of colon cancer cells; the third has a negative effect on cell proliferation in prostate cancer. Other genes are involved in cancer suppression in myriad ways: ITIH3 in stomach cancer; CBS and A1CF in colon, ovarian, and breast cancer; and CBS in the brain cancer glioma. SERPIND1 plays a role in cancer metastasis.

“To find out if compounds developed from sharks might work the same way in people, we need to make extracts from the sharks’ organs and test them on human tumor cells,” says Domingues. “If these bioactive compounds produce a significant benefit, they could lead to new drugs.”

Edible seaweed, sustainable through genomics
Genomic discoveries in plants as well as animals may lead to new therapies—and to sustainable foods. In seaweed farms on the islands of Okinawa, Japan, farmers cultivate the edible brown alga Okinawa mozuku (*Cladosiphon okamuranus*). Popular in Japanese cuisine, this superfood produces high levels of fucoidan, a substance that suppresses blood clots and tumors.

Okinawa seaweed farmers annually harvest more than 15,000 tons of mozuku, contributing billions of Japanese yen to local economies. But the plentiful seaweed is beginning to suffer from ocean warming and acidifying waters.

In 2016, researchers at the Okinawa Institute of Science and Technology decoded the genome of the alga’s S-strain. Now the scientists have deciphered the genomes of three more strains: the O-strain, C-strain, and K-strain. The findings, published in June 2020 in *BMC Genomics*, could help seaweed farmers adapt to increasing environmental stresses.

Climate change and increasing levels of ocean acidification are the driving forces behind the biologists’ investigations of the genetics of Okinawa mozuku, they say. Genomic information will help the researchers identify the Okinawa
mozuku strains that are heat tolerant and the genes responsible.

These genetic differences could lead to classifying each strain of Okinawa mozuku as a subspecies, according to Koki Nishitsuji, the paper’s lead author. That would allow farmers to market unique, genetically distinct brands of seaweed, Nishitsuji believes.

**Fishing quotas for Earth’s most abundant vertebrates**

In the Atlantic Ocean, scientists are using whole genome sequencing to characterize 53 herring populations. The biologists developed genetic markers to better monitor the herring. Results of the study were published in December 2020 in the journal *eLife*.

“Our project provides a ‘toolbox’ in the form of genetic markers for cost-effective screenings that can be applied to herring stocks throughout their life histories, from the larval to the adult stage,” says Arild Folkvord of Bergen University, a paper coauthor. “It’s now possible to distinguish different stocks when they are mixed on their feeding grounds, which will help set sustainable fishing quotas.”

The Atlantic herring is one of the most abundant vertebrates on Earth. Herring in the Atlantic Ocean and adjacent waters have been estimated at one trillion fish. Stocks are defined by where and when they spawn, but until now, no efficient genetic markers have been available for identifying different stocks. The researchers found variants for hundreds of genes important in how the fish respond to salinity and water temperature during the spawning season.

Atlantic herring are well suited to studies of the impact of global warming on fish populations, according to Leif Andersson of Uppsala University, who led the genetic analysis. Many gene variants the biologists discovered are linked with water temperature. Andersson expects the variants to become more common as the fish move farther north in warming waters.

**Snail in a suit of armor: Genomics in The Deep**

Far beneath the ocean surface, deep-sea hydrothermal vent environments—with their high pressures, high temperatures, and low oxygen levels—harbor significant biodiversity. Many hydrothermal vent species have potential in biomedical and other applications, scientists are finding. Among them is the scaly-foot snail (*Chrysomallon squamiferum*), also known as the sea pangolin.
The scaly-foot snail is the only gastropod alive today with armor-like scales, a common feature in gastropods more than 540 million years ago. The snail is also the only known organism to incorporate iron into its exoskeleton. Until recently, little had been discovered about its genome, because the creature was almost impossible to locate. Then Pei-Yuan Qian of the Hong Kong University of Science and Technology and colleagues managed to collect 20 scaly-foot snails from depths of 2900 meters in the Indian Ocean.

Contrary to scientists’ expectations that the species’ genes were linked to its bizarre morphology, the biologists discovered that all the snail’s genes exist in other mollusks, such as squid and pearl oysters. In fact, the snail’s gene sequence has remained almost unchanged throughout its evolution. The results were published in April 2020 in *Nature Communications*.

The 25 transcription factors (proteins that regulate gene expression levels) that contribute to the snail’s scale and shell formation are also responsible for other hard parts in mollusks—the operculum in gastropods, beak in squids, spicule in chitons, and chaetae in polychaetes.

“Although no new gene was identified, the study offers valuable insights into biomineralization,” Qian says. Biomineralization is the process by which living organisms produce minerals, often to harden or stiffen their tissues. “The scaly-foot snail mediates its scale biomineralization by supplying sulfur through nanoscale channel-like columns in the scales, which react with iron ions diffusing inward from the vent fluid to make iron sulfide nanoparticles,” state Qian et al.

Uncovering the scaly-foot snail’s genome, adds Qian, “lays the groundwork for biomineralization applications. For example, the snails’ iron-coated shells withstand heavy blows, which could lead to ways of making more protective armor.”

More than a half-century after the publication of *The Open Sea: Its Natural History*, Hardy could not have imagined ocean genomics as we know it today—and where it would lead: to possible new iron-based materials, sustainable food sources, and treatments for a virulent virus that is ricocheting around the globe.

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