revive & restore

GENETIC RESCUE OF ENDANGERED
AND EXTINCT SPECIES

OUR CATALYST SCIENCE FUND
Q1 2026 REPORT

The Catalyst Science Fund (CSF) provides resources for 5 active programs at Revive & Restore: Climate Resilience, GAIA, Advanced Coral Toolkit, Stem Cells, and Black-footed Ferret. It is the umbrella for all of our science funding. This report marks a new chapter in how we share our CSF work. We're bringing you closer to the research and the teams doing it: what they're learning, what surprises them, what challenges they're navigating, and what excites them about what's to come. The people driving this science forward have a lot to say, and we hope this report gives you a richer sense of the work unfolding across our programs.
- Ryan Phelan, Co-founder & Executive Director | ryan@reviverestore.org

FROM OUR PROGRAM MANAGERS

Q1 was a busy quarter, and we are proud of the scientists and teams who drove this work forward. From a first-of-its-kind cetacean stem cell partnership to coral larvae exchange across nine Caribbean nations, our program teams are advancing on multiple fronts. In South Africa, a newly completed shark genome is illuminating the evolutionary architecture of an entire taxonomic group. In the Caribbean, practitioners from nine countries are laying the groundwork for what could be a historic first in reef restoration.

Meanwhile, GAIA, our AI-powered genomics initiative funded by the Bezos Earth Fund, is taking shape in partnership with The Rockefeller University and Cornell. On Earth Day, we announced the inaugural cohort of our $4M Climate Resilience Fund, selected from a record 160 applications.

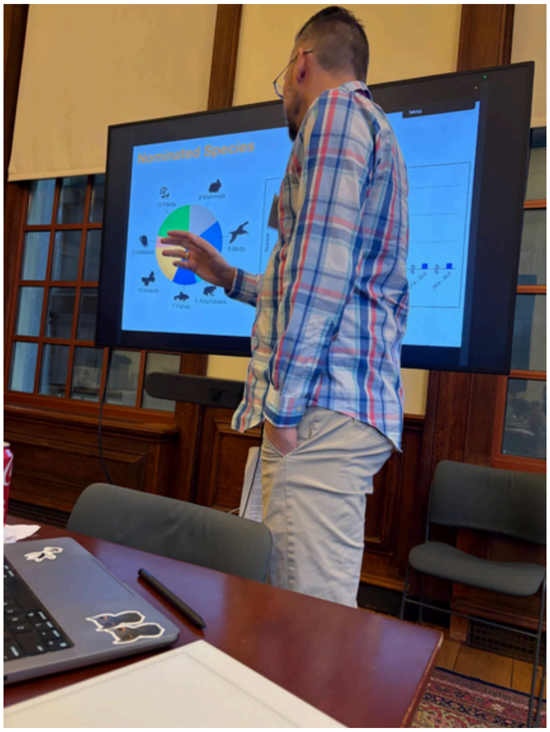
IN THIS REPORT

Detail of *Understory, 2007* by Isabella Kirkland

INTRODUCING GAIA
GENOMIC ARTIFICAL INTELLIGENCE APPLICATIONS

In October 2025, Revive & Restore announced that it had been selected as one of fifteen global teams awarded funding through the Bezos Earth Fund's AI for Climate and Nature Grand Challenge, competing against ~1200 other proposals, receiving $2 million for a two-year initiative to develop two breakthrough AI tools that will democratize advanced genomics for wildlife conservation. This new initiative for Revive & Restore is called GAIA: Genomic Artificial Intelligence Applications.

In the GAIA initiative, the first tool to be developed is called Jarvis, which will automate the time-intensive final steps of assembling complete genome sequences for endangered species, dramatically accelerating the pace at which scientists can decode an animal's full genetic blueprint. The second tool, Genera, will function as an AI-powered conservation advisor, analyzing genetic data to provide actionable recommendations for genetic rescue, identifying which populations need genetic intervention and how to implement it effectively. Together, these tools will enable any conservationist, regardless of genomic expertise, to make science-backed decisions that protect species for generations to come.



Ben Novak presenting at the GAIA planning kick-off in New York in January | ben@reviverestore.org

The GAIA team met at Rockefeller University to launch the initiative.

In addition to the GAIA objectives above, 50 new, high-quality reference genomes for US endangered species will be generated as part of this project. These genomes will serve as test cases for both the Jarvis and Genera tools, and will provide new resources for the conservation community. Cell lines will also be generated and biobanked when possible for these 50 species.

This project officially commenced on January 1, 2026. The GAIA team, led by Revive & Restore's Ben Novak as PI, along with co-PIs Erich Jarvis and Giulio Formenti from the Rockefeller University and Ayshwarya Subramanium from Cornell University, held a planning workshop in New York City in early January to launch the GAIA initiative, plan the technical development approach, and establish the two-year roadmap. Attendees included additional GAIA team members and subject matter experts from the Rockefeller University's Vertebrate Genome Lab and Data Science Platform, the Wellcome Sanger Institute, Google Research, Bezos Earth Fund, and Revive & Restore.

CLIMATE RESILIENCE FUND | FIRST AWARDED PROJECTS

On April 22, Earth Day, we announced the inaugural cohort of our $4M Climate Resilience Fund, selecting 10 from over 160 letters of intent representing more than $52M in demand. This fund marks Revive & Restore's strategic expansion into the climate space, applying the power of genetic rescue to strengthen, restore, and protect ecosystems on the front lines of climate change.

From marine microbes to blue carbon ecosystems, our goal was to build a portfolio that spans species, geographies, and genetic rescue approaches, all united by innovative biotechnology and clear pathways to real-world conservation. We are so excited to introduce the teams behind this work.

Selected Projects

- **Microbial genetic rescue for Malaysian mangroves:** Mapping resilience-associated microbial traits and pioneering CRISPR-based editing to build a Microbial Genetic Rescue Toolkit for mangrove restoration in Southeast Asia.
- **Red mangrove adaptation to strengthen restoration:** Using genomics and field phenotyping to match genetically suited mangrove propagules to restoration sites across the Bahamas, maximizing blue carbon and climate resilience.
- **California-wide kelp biobanking:** Building a statewide kelp biobank with linked genomic and thermal performance data across 300 lineages to enable climate-informed restoration at scale.
- **Pioneering assisted gene flow in Tasmanian Macrocystis:** Leveraging genomics and selective breeding to genetically rescue critically inbred giant kelp forests devastated by ocean warming.
- **Genetic engineering for climate resilience in kelp:** Using microalgal model systems and CRISPR/Cas9 to identify and introduce climate resilience genes into golden kelp (Ecklonia radiata) in Australia.
- **Culturing and engineering symbiotic algae:** Developing scalable, open-source tools to culture and genetically engineer symbiotic algae, with proof-of-concept applications in giant clams and anemones.
- **AI-guided microbiome tools for seagrass resilience:** Training graph neural network models to predict microbiome-restoration compatibility, improving eelgrass restoration outcomes on the US east coast.
- **Protoplast culture for fucoid seaweeds:** Pioneering cell culture and gene banking tools for foundation seaweed species underpinning Australia's Great Southern Reef.
- **Probiotics and AI-enabled micropropagation for salt marsh restoration:** Combining indigenous microbial probiotics with AI-assisted embryogenesis to produce stress-resilient Spartina alterniflora for marsh restoration across the US southeast.
- **Rapid sex identification test for sea turtle hatchlings:** Developing the first field-deployable, non-lethal CRISPR-enhanced rapid test for hatchling sex ID to monitor climate-driven sex ratio skew in sea turtles across Florida and Australia.

Learn more about all of the projects!

Among the awardees is a team developing the first rapid, non-lethal field test to determine the sex of sea turtle hatchlings — a critical tool for tracking how rising temperatures are skewing sex ratios in wild populations.

Another awardee team is working to culture and engineer symbiotic algae for the first time, using giant clams in Palau as a proof-of-concept host toward scalable restoration tools for photosymbiotic invertebrates.

ADVANCED CORAL TOOLKIT | HIGHLIGHTS

The Advanced Coral Toolkit (ACT) represents Revive & Restore's commitment to building a comprehensive suite of biotechnologies for coral conservation, from genomics and biobanking to probiotics, cryopreservation, genetic engineering, and beyond. As coral reefs face unprecedented pressure from warming oceans and disease, the urgency to develop, refine, and scale these tools has never been greater.

This year marks an exciting inflection point for ACT. We've established an official Advisory Council of experts from around the world, and look forward to leveraging their expertise to help us stay at the cutting edge of innovations for coral reef ecosystems. Several projects funded in our last cycle are reaching major milestones, including the field application of probiotic treatments in Colombia and the discovery of genes related to coral symbiosis, while others are embarking on their next phase of R&D. Meanwhile, a new wave of projects is under consideration, poised to push the frontier even further. Across the portfolio, teams are making meaningful progress on the tools that coral conservation will depend on for decades to come.

We're delighted to share a few highlights from this dynamic and growing program, and deeply grateful to the scientists driving this work forward.

- Dr. Liv Liberman, Director of Ocean and Climate and ACT Program Manager

Dr. Liv Liberman
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Caribbean Coral Larval Exchange | NEW PROJECT

Project Vision: Build the regulatory pathways, genetic protocols, and practitioner relationships needed to make responsible coral larvae exchange a standard tool in Caribbean reef restoration before genetic impoverishment closes the window on recovery.

Q&A with Dr. Liv Liberman, Program Manager, ACT

Funded through the Advanced Coral Toolkit program, this new project led by SECORE International brings together restoration practitioners from nine Caribbean countries and territories around a shared goal: moving coral larvae across international borders to rescue the genetic diversity of reef-building species in freefall. Decades of bleaching and disease have left many Caribbean coral populations with a fraction of their historical genetic diversity, and larval exchange has emerged as a more tractable genetic rescue strategy than moving adult corals, offering a pathway to break the bottleneck before the extinction vortex closes in.

In March 2026, SECORE hosted a pivotal four-day strategy and planning workshop in the Dominican Republic, bringing all nine network partners together for the first time. Dr. Liberman was in attendance and shares what the team has learned so far.

What have you learned this quarter?
One of the clearest takeaways from the workshop is something that practitioners across the Caribbean already suspected but hadn't fully reckoned with collectively: the shortage of local parent colonies is now hindering what restoration programs can accomplish. That bottleneck is, more than anything else, what motivated building this network in the first place. We've also had to confront a sobering data gap around some of the species we most need to help. For certain target corals, we simply don't have the population-genetic baseline across the region to design exchanges responsibly yet, which means foundational genetic sampling work will happen in parallel with the permitting and logistics within this project.

Has anything surprised you along the way?
As part of our workshop, participants with little to no prior molecular lab experience worked through a simplified DNA extraction protocol for elkhorn coral using a portable Bento Lab system, and several left feeling like genetic analysis was now within reach for their own restoration programs. That shift in what feels accessible for people going home to actually implement these exchanges matters.

The other surprise was how much the conversation evolved around intra-national exchange as a near-term on-ramp. The workshop identified opportunities for pilot transfers within national borders, between sites within the same country, that involve fewer regulatory hurdles and faster timelines. We're hopeful that successful domestic pilots can build the trust and precedent that international work will ultimately need.

Have you encountered any new barriers or challenges?
The regulatory landscape is complex and varies considerably across jurisdictions. CITES, national permits, and the Nagoya Protocol each operate differently across the Caribbean, and because moving coral larvae across borders for conservation purposes is so novel, many permitting authorities simply haven't encountered a request like this before. Navigating that complexity required developing shared tools and frameworks to help nodes understand how the process should flow, which we began during the workshop with the guidance of international wildlife trade specialist Steven Broad.

What's coming up that you're excited about?
We're finalizing standardized background materials that explain coral life history and the safety of the exchange process for local stakeholders and permitting authorities who may be entirely unfamiliar with coral reproduction. Spanish translation is the immediate priority, with French to follow as the network potentially expands. These resources won't just serve this network; once they exist, they become tools for the broader Caribbean restoration community.

At the same time, nodes are beginning to identify their regional pairing partners, permit applications are underway, and teams will collect gametes during the upcoming spawning season. If even one international larval transfer successfully clears regulatory hurdles and delivers larvae to a recipient site, it establishes a precedent that subsequent exchanges can build on.

Any new developments in your field worth highlighting?
It's worth being precise about what larval exchange does and doesn't do. Genetic rescue maintains evolutionary potential and buys time, but it has to be paired with ongoing demographic restoration and meaningful stressor reduction (e.g., addressing climate change) to actually move populations toward recovery. The network is clear-eyed about this distinction, and that framing matters for how we communicate the work to permitting authorities, funders, and the public.

Workshop participants (top); bred corals in Mexico (right top); extracting coral DNA (right bottom)

Photo credit: Paul Selvaggio

Coral Gene Knockouts | COMPLETED PROJECT

Project Vision: Build a functional genetics platform in cnidarian model systems to identify the genes underlying coral-algal symbiosis and thermal tolerance, laying the foundation for targeted conservation interventions

Q&A with Project PI, Dr. Philip Cleves

Dr. Phillip Cleves
Carnegie Institute (now UC Berkeley)

What have you learned this quarter, or over the course of the project?
Before we started, not a single gene was known to be involved in coral-algal symbiosis. We knocked down at least 100 genes and now have 12 bona fide phenotypes that tell us how the symbiosis works. And we've shown that genes important in our anemone model system are also important in corals. We did that most recently with a bicarbonate transporter that's critical for fueling algal photosynthesis. If you make mutations in that gene, you break symbiosis in both the anemone and the corals. That paper is currently under review at *Cell*. What we've been able to narrow down is a battery of genes that are downregulated *before* bleaching actually occurs, and we think that downregulation is the trigger. That's a massive contribution to the field because it provides targets for biomarkers: the expression of those genes could indicate more or less resistant animals.

Has anything surprised you along the way?
The HSF1 finding, honestly. HSF1 is the heat shock factor, a master regulator of the cellular heat stress response that controls how cells cope with stress from yeast to humans. We mutated it in Galaxea just to show that CRISPR works in that species, and we weren't really expecting to see anything interesting. But we found that Galaxea survived much longer without this key regulator than Acropora. It turns out Galaxea is one of the most thermally tolerant corals on the reef, while Acropora is generally much more sensitive. RNA sequencing revealed why: under the same heat stress, the sensitive species upregulates HSF1 far more than the tolerant one, as if it's desperately pulling every lever it has. This is the first time we've been able to functionally characterize a gene underlying variation in heat tolerance, and we're excited about whether HSF1 expression could become a diagnostic for how tolerant a coral is in the wild.

Have you encountered any new barriers or challenges?
We didn't hit our goal on the number of genes. We said we'd screen 250, and we didn't get there. When we say "screen," it's still pretty amateur relative to what you can do in human cell culture. We tried something really ambitious, and we didn't hit it. A lot of it turned out to be brute force. That said, it wasn't really much of a concern because every single thing we were doing was completely novel — every gene was completely new. Whether we did 100 genes or 200 genes, we were setting the stage. What I think would help now is pulling in automated image processing groups. There's a lot of money going into AI-driven imaging right now, and I think we could do something more sophisticated. It just was outside the scope of the project at the time.

What's coming up that you're excited about?
If I could do anything, I would buy a warehouse here in the Bay Area, fill it with coral spawning systems and more than a dozen people genetically engineering corals, and just run a true Coral CRISPR Institute. We'd be spawning corals every day, doing the genetics, pushing them toward thermal tolerance, and we'd learn an enormous amount through that process. I would love to do that. The dream team would be great geneticists, biochemists, molecular biologists, and ethicists all in the room. But I think the big question that has to anchor all of it is: *why do corals bleach?* If we knew that, we'd know which solutions are and aren't working, and we'd know whether corals are already adapting and what actually needs to be done.

Any new developments in your field worth highlighting?
I think the thing I'd point to is that the methods coming out of our lab are starting to get traction. Labs have reached out wanting the method, asking specific questions, and we're actively collaborating to get the technology into their hands. People are even asking to come to our lab to get trained. That to me is a sign that this platform has the potential to be step-changing, though it depends on how much it gets adopted and how many other people use it. But we went from a field where not a single gene was known to function in symbiosis to having a dozen, and a method that other people can build on. I think that sets the stage for finally bringing molecular biology into our understanding of both symbiosis and bleaching. That's a huge intellectual step.

STEM CELLS | HIGHLIGHTS

Dr. Ashlee Hutchinson
ashlee@reviverestore.org

In 2025, Revive & Restore announced the inaugural cohort of successful applicants to our Applied Stem Cell Conservation Fund. Now we are thrilled to announce the second round of awards, bringing this incredible portfolio to 10 funded teams, working toward crucial R&D that will enable the translation of stem cell technology from biomedical science to conservation.

Stem cell science is an essential component of Revive & Restore's Genetic Rescue Toolkit, enabling every level of our core suite of platform technologies. From our Biotechnology for Bird Conservation Program, to our Advanced Coral Toolkit, we've long been pushing the boundaries of cross-species stem cell technology to promote resilience, reproduction and adaptation in the face of environmental change.

Now, our Stem Cell Technologies Program is developing protocols across evolutionarily diverged lineages to deepen capacity within biobanking, reproduction, disease and AI-driven cellular technologies. The impact of this program will be a game-changing ability to protect species on the brink of extinction, enabled by pluripotent stem cells' capacity to become reproductive cells, embryos, or in vitro tools for engineered resilience. Here, two of our newest projects are highlighted, both exploring the development of cutting-edge reproductive tools. We are so excited to be driving the field forward and working with these phenomenal teams!

- Dr. Ashlee Hutchinson, Director of Stem Cell and Reproductive Technologies

Reviving the Bavarian Pine Vole: Integrating Advanced Reproductive Technologies for Conservation of a Critically Endangered Species | NEW PROJECT

Program Vision: Building a stem cell-to-offspring pipeline to rescue one of Europe's most critically endangered mammals from extinction.

A World-Class Team
Based at the Max Delbrück Centre in Berlin, the project is led by Dr. Sebastian Diecke alongside two of the most distinguished figures in reproductive biology: Professor Thomas Hildebrandt, a pioneer in wildlife reproductive technologies, and Professor Katsuhiko Hayashi, whose landmark research on deriving eggs and sperm from stem cells has fundamentally expanded what is scientifically achievable. Strengthening the transition to application, the team is working closely with the captive breeding program at AlpenZoo Innsbruck.

The Science
The team's goal is to establish a complete stem cell-to-offspring pipeline for the species. Beginning with genomic sequencing and biobanking of samples from both captive and wild individuals, the pipeline proceeds through cellular reprogramming, converting tissue samples into induced pluripotent stem cells (iPSCs), and ultimately to the derivation of functional gametes.

The final and most ambitious stage aims to produce viable offspring from stem cells using tetraploid complementation, a technique established in mouse research that would represent a paradigm-shifting first if successfully applied to an endangered species.

With no ongoing monitoring program and no confirmed wild populations, the Bavarian Pine Vole is known today from fewer than 30 individuals held across multiple zoos in Europe. Whether any wild populations persist remains unknown, but if they do, they likely face compounding pressures of habitat loss, reproductive challenges, and declining genetic diversity.

Learn more about the project

Super Cetaceans | NEW PROJECT

Program Vision: Developing the first iPSC protocols for cetaceans, opening new frontiers in genetic rescue for some of the ocean's most vulnerable mammals.

One of Revive & Restore's defining approaches as a funder is building communities of practice - connecting awardees across projects, encouraging open science, and assembling interdisciplinary teams to tackle the most difficult problems in conservation. When two exceptional research groups independently submitted proposals to derive induced pluripotent stem cells (iPSCs) from cetacean species, we were privileged to bring them together.

The result is the Super Cetaceans partnership: a collaboration between Professor Ralf Jauch's lab at the University of Hong Kong and Assistant Professor Li Fang Chu's group at the University of Calgary.

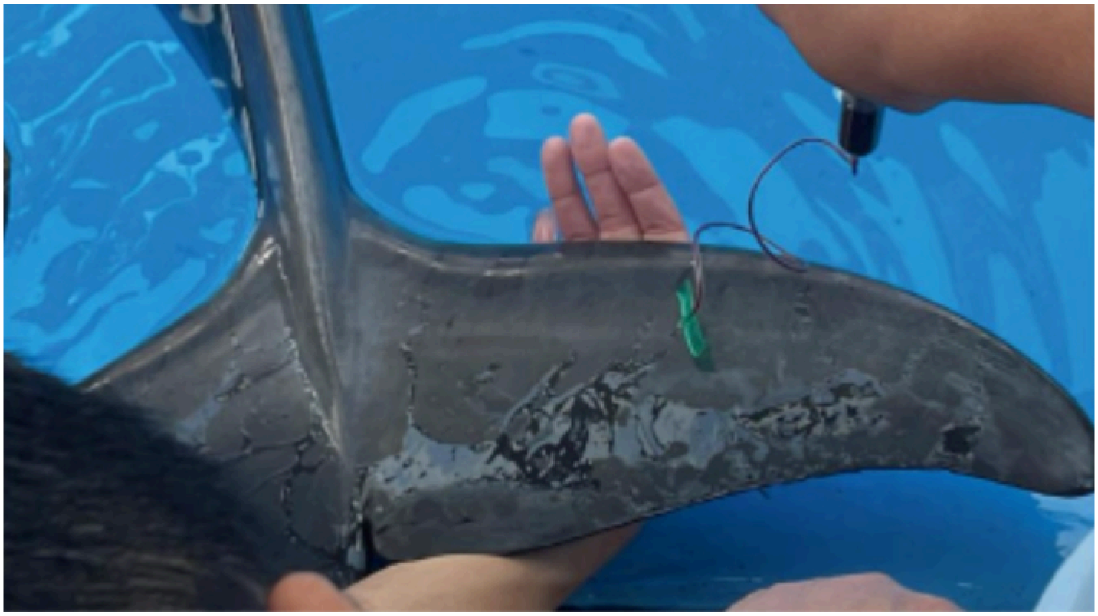
The Challenge

Stem cell and assisted reproductive technologies remain effectively out of reach for cetaceans - the group that includes whales, dolphins, and porpoises. While iPSC derivation is well established in mouse models, translating these methods across species is far from straightforward. Differences in genome regulation mean that protocols developed for one species often require substantial reworking before they function in another. The same challenge applies to the next frontier: using stem cells to derive functional eggs and sperm, which has been achieved in mice but remains elusive across most other species.

The Science

Working with two very different cetacean models - the Indo-Pacific bottlenose dolphin and the blue whale - this partnership aims to develop tractable iPSC derivation protocols across this taxonomic group, and to push further toward producing germline stem cell-like cells in vitro for cetaceans for the first time.

Their success will be a game-changer: preserved genetic diversity in a pluripotent form, new models for studying disease and environmental resilience, and a foundation for future reproductive technologies. Scaled, we hope to establish a template that marine biologists and conservation scientists can apply to some of the most vulnerable marine mammals on the planet.



The Jauch lab has partnered with Hong Kong Ocean Park to enable sampling and processing for the Indo-Pacific bottlenose dolphin. In the picture at left, small blood samples are taken as part of routine husbandry using a minimally invasive approach. Cells are isolated from this material and grown in incubators before reprogramming is trialed.

The reprogramming process involves transient non-integrative transfection with a core suite of transcription factors proven to induce pluripotency in a range of other species. When it works, cells change morphology and start growing in colonies, and the real work begins: validating pluripotency using a range of molecular assays.

Learn more about the project

WILD GENOMES | HIGHLIGHTS

Wild Genomes was built on a simple but powerful premise: put the fundamental tools of genetic rescue into the hands of the people who manage wildlife. Since launching, the program has invested $1.7M across 31 projects spanning 12 countries, generating reference genomes and sequencing resources for terrestrial, marine, kelp forest, and amphibian species that urgently needed them.

Now, as many of these projects reach completion and final results come in, we find ourselves at an inflection point. Teams across the portfolio are delivering on milestones, from published reference genomes to genomic data being integrated into species recovery plans, and we are actively connecting with PIs to understand the real-world impact of their work. This moment of reflection is also an opportunity to evaluate what Wild Genomes has accomplished, how we can better support this type of science going forward, and what the next chapter of the program looks like. We're proud of the breadth of science this program has catalyzed, and grateful to the field scientists, wildlife managers, and researchers who have carried it forward.

- Program managers Drs. Ben Novak, Liv Liberman, and Ashlee Hutchinson

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Pyjama Shark | COMPLETED PROJECT

Project Vision: Generate a chromosome-level reference genome for the Pyjama Shark (*Poroderma africanum*) to illuminate population connectivity, genomic diversity, and adaptive capacity across South Africa's kelp forest ecosystems, enabling science-based conservation management for this endemic, vulnerable species.

Q&A with project team member, Dr. Kelvin Hull, Postdoctoral Research Fellow

Postdoctoral Research Fellow
Dr. Kelvin Hull
Unversity of Pretoria

What is a big-picture takeaway that you learned during your project?
The size and complexity of elasmobranch genomes is staggering. Assembling this genome at 5.23 Gb, nearly double the size of the human genome, would have been nearly impossible without access to high-quality PacBio and Hi-C sequencing technology. From a South African perspective, we are still a long way from fully representing our endemic marine taxa on a genomic level, and these data are increasingly vital for resilience assessments and management. Genomics is a powerful tool, but it must be used alongside ecological data to understand not just where a species is going, but where it came from.

Has anything surprised you along the way?
Absolutely! Comparing the pyjama shark genome with close relatives revealed two striking patterns. First, sharks across orders have far more in common genomically than I expected: a core genome of 12,214 gene clusters was shared across eight species with wildly divergent life histories, meaning core genes evolve slowly while lineage-specific differences drive ecological adaptation. Second, the pyjama shark showed an overwhelming loss of genes relative to other species, with 1,774 gene families lost and only 49 gained. This pattern suggests substantial genomic streamlining to facilitate adaptation to its restricted, benthic niche, which has interesting implications for future population genomic work.

Have you encountered any new barriers or challenges?
In this project, the sheer size of elasmobranch genomes was the fundamental challenge, requiring extensive troubleshooting of existing analytical pipelines to ensure these analyses ran correctly or gave biologically meaningful information. As the field continues to expand, and more complex genomes are constructed, I'm sure that these shortcomings will be something that the new generation of scientists barely worry about. Overall, I am really excited about where the field of genomic research will go in the next 10 years.

What's coming up for this work that you're excited about?
The genome and annotation information that we generated are essentially the jumping-off point for future research into this species. Genetic studies of many non-model species are hindered by a lack of reference genome sequences. With this high-quality sequence, I am really looking forward to assessing populations along the South African coastline. I consider myself a population geneticist rather than a genome biologist, so the process of assessing these sharks to understand the overall genomic "health" of populations, whether they are connected or are actively diverging, and the mutations that are driving adaptation to different environments (and whether this will buffer these populations against future climatic changes) will be key to safeguarding this endemic shark.

Any new developments in your field worth highlighting?
We are in the process of publishing our work, and hopefully, this will be available soon. Outside of the work conducted here, our research group has several studies in the pipeline, focusing on unraveling cryptic population structure in important fisheries species (Gardiner et al., 2025), using genomic tools to assess how climate change is driving species distributional shifts (Pujolar et al., 2025), and understanding the impact of Marine Protected Areas on preserving genetic diversity in these species. We have also expanded our research scope to include terrestrial and marine plants, broadening the focus from marine genomics to include a bit of land as well. All of this research is being conducted on species that lack genetic data, many of which have had no prior research in this field, so the findings are sure to be informative for the continued management of these important taxa.

A Pyjama Shark (left) in a South African kelp forest (right). Photo credit: University of Pretoria

THANK YOU FOR YOUR SUPPORT!

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Detail of *Understory, 2007* by Isabella Kirkland