

# Seagrass Climate Resilience Project

*Teaching seagrass to withstand warmer seas — using epigenetics to switch on the heat tolerance it already carries in its own genome. No foreign genes, no GMO.*

~10%

OF GLOBAL OCEAN CARBON  
BURIAL

up to 35×

CARBON BURIED PER UNIT  
AREA VS. TROPICAL FOREST

5

TARGET SPECIES

6

GENOMES ANALYZED

## What We're Doing, and Why

*Seagrass is one of nature's most valuable assets — for carbon, for coastal ecosystems, and for the fisheries and coral reefs that depend on it — and it is dying. We are working to save it.*

Seagrass meadows bury carbon faster than tropical forests, anchor coastal food webs, and shelter an outsized share of marine life from a fraction of the seafloor. They are also a foundation of the coastal ecosystems that sustain coral reefs. And they are in serious peril: warming seas are driving mass die-offs faster than meadows can recover, and many of the plants that remain lack the heat tolerance to withstand what is coming.

The traits that let seagrass survive heat already exist within the species — the same plant carries both warm-adapted and cold-adapted populations. We read the heat tolerance out of the plants that have it and switch on those same traits in the plants that need it, working entirely within the plant's own genome. It comes down to teaching the non-adapted plants what the adapted plants already know.

Reversing seagrass decline will take a concerted, intentional effort. This project is built to be part of that effort.

## Why Seagrass

*Seagrass meadows are among the most productive and ecologically critical ecosystems on Earth — yet they are disappearing faster than tropical rainforests.*

### Carbon Powerhouse

Seagrass covers just 0.2% of the ocean floor but accounts for ≈10% of total ocean carbon burial. *Posidonia oceanica* alone stores ≈420 million tonnes of carbon in Mediterranean deposits.

### Biodiversity Foundation

Nursery habitat for commercially important fish and shellfish. Stabilizes sediment, hosts diverse epifauna, and supports entire coastal food webs.

### Climate Canary

Uniquely susceptible to warming and a cascade species — among the first to signal ecosystem collapse, triggering large downstream effects.

### In Crisis

Mass die-offs documented globally. Florida Bay lost >4,000 hectares of turtle grass in 1987; recovery took 17–23 years. Mediterranean *Posidonia* suffered five consecutive years of mass mortality (2015–2019).

*Declines of many seagrass species have been attributed to thermal stress associated with rising sea surface temperatures and extreme temperature events. Many seagrass species persist in low energy and shallow water environments such as coastal embayments, inlets and fjords. These environments are particularly susceptible to warming and extreme temperature fluctuations.*

"Seagrass Restoration Is Possible: Insights and Lessons From Australia and New Zealand"

## Market Opportunities

*Robust, climate-resilient seagrass connects to several established and emerging markets. These define the applied value of the biological work.*

### Blue Carbon

Seagrass meadows are among the most efficient carbon sinks per unit area. More durable, higher-fixation lines strengthen verified blue-carbon credits and coastal offset projects.

### Seagrass Restoration

A growing restoration sector needs planting stock that survives current and near-future conditions. Resilient material improves establishment rates and reduces replanting cost.

### Aquaculture

Healthy meadows support commercial species and sediment ecosystems — including sea cucumber and shellfish aquaculture that depend on seagrass-stabilized habitat.

### Beneficial Dredge Reuse

The U.S. Army Corps of Engineers targets 70% beneficial reuse of dredged sediment by 2030 (up from 30–40% historically), and seagrass establishment is a qualifying use — creating demand for plantable stock suited to placed sediment.

### Coral Reefs & Biodiversity

Seagrass meadows are nurseries and buffers for coral reefs — the ocean's biodiversity hotspots — filtering water, storing sediment, and sheltering juvenile reef fish. As a keystone foundation species, resilient seagrass underpins the reef, fisheries, and biodiversity programs that conservation funders care most about.

This is a funded federal priority, not a speculative one. A 2024 USDA/NOAA report to Congress places heat-tolerant seagrass inside an active government agenda, and the numbers behind it are concrete:

**\$325M+**

FEDERAL R&D INTO FARMED SEAGRASS & SEAWEED SINCE 2014 (7 AGENCIES)

**5**

NATIONAL SEASHORES FUNDING EELGRASS RESTORATION

**10,000 acres**

WASHINGTON PUGET SOUND RESTORATION GOAL

**→ 70%**

ARMY CORPS DREDGE-SEDIMENT BENEFICIAL-REUSE TARGET BY 2030 (FROM 30–40%)

### The government wants exactly this

The 2024 USDA/NOAA report names **heat tolerance** a priority breeding goal and is funding heat-tolerant eelgrass restoration across five National Seashores — the same trait, the same assisted gene flow our collection strategy follows.

### Our method already fits the rules

Federal escape-risk rules require staying within native genetic ranges. **Non-transgenic and locally-sourced**, RdDM meets them by default — no foreign genes, nothing moved outside its home range.

### Worth far more than carbon

≈**932,400 t of carbon** sits in NY–Maine meadows (≈447,000 homes/yr) — yet a Virginia study found carbon is **under half** the total value. Fisheries, clean water, and storm buffering make up the rest.

*Federal figures from the 2024 USDA/NOAA report to Congress (Farming Seagrasses and Seaweeds); full technical treatment, including the ReefGen planting robotics, in **Findings §9**.*

## Our Approach: Epigenetics First

*No seagrass has ever been genetically engineered. We're pioneering epigenetic triggering — a faster, non-GMO approach that works with the plant's own gene-regulation machinery.*

### What We Do

#### 1. Sequence

Genome + epigenome from multiple populations — typical habitats vs. heat-stressed environments.

#### 2. Publish

Open-access genomes and epigenomes for public science. Building the best publicly accessible seagrass genomic repository.

#### 3. Trigger

Switch on heat-tolerance traits with a targeted RNA signal — RNA-directed DNA methylation (RdDM) tunes the plant's own genes, with no foreign DNA required.

#### 4. Deploy

Treated seeds planted at scale by seafloor planting robots (ReefGen) that inject seed directly into sediment in degraded meadows.

### Why not just gene-edit it?

CRISPR would rewrite the plant's DNA to force heat tolerance — and for seagrass that path is both slow and unusable in practice. Editing requires tissue culture and whole-plant regeneration, which have never been established for seagrass, so the pipeline stalls before it starts. What comes out the other end is a **GMO**: a high regulatory bar, a decade-plus timeline, and the public resistance that has kept engineered plants out of conservation. Epigenetic triggering skips all of it — no cut to the genome, delivered as a seed treatment, non-GMO, and deployable in years rather than a decade.

	GENE EDITING (CRISPR)	EPIGENETIC TRIGGERING (RDDM)
Changes the DNA sequence?	Yes	No

	GENE EDITING (CRISPR)	EPIGENETIC TRIGGERING (RDDM)
Tissue culture + regeneration	Required — not established in seagrass	Not needed
Regulatory status	GMO (high burden)	Non-GMO (low burden)
Timeline	10+ years	2–5 years

### Why not just bring in a heat-tolerant plant from elsewhere?

The obvious alternative is to move a warm-adapted seagrass from a hotter region into the meadow you want to save. That trades one climate problem for an ecological one: **introducing non-native genotypes risks outbreeding, disease, and displacement of the local population** — the same harm conservation programs work to prevent, and a hard sell to the communities and regulators who protect these sites. Our approach keeps the **local genotype** and switches on the resilience that population already carries, so the meadow stays genetically itself.

### The traits already exist — we switch them on

Heat tolerance is not something we invent; warm-adapted seagrass ecotypes already carry distinct DNA methylation patterns that persist across generations. The task is to **identify those marks and switch them on in local plants**. Our 2026 analyses confirm the mechanism is available: the complete RdDM pathway is intact in *Zostera marina* and conserved across all four seagrass families (see Latest Findings).

## Latest Findings (2026)

*Results from computational analysis of 20 Zostera marina Nanopore methylomes (Decibel Bio sequencing). Full detail, figures, and downloadable data on the companion Findings page.*

[Read the full Technical Findings →](#)

The companion **Findings page** carries the complete analysis: the RdDM conservation heatmap across six genomes, the methylation landscape and feature-level maps, the transposable-element annotation, the collection-site and thermal-niche maps, the trait and deployment sections, and all downloadable data (figures, tables, reports).

**20 / 20**

RDDM PATHWAY GENES  
PRESENT

**~82M**

METHYLATION SITES / SAMPLE

**20**

DISTINCT GENOTYPES (NO  
CLONES)

**r = 0.77**

METHYLATION ↔ GENOTYPE  
COUPLING

### The RdDM toolkit is intact

All 20 core RNA-directed DNA methylation genes are present in the *Zostera marina* genome (13 strong, 6 moderate, 1 weak ortholog; none absent), and the full pathway is conserved across six seagrass genomes spanning all four seagrass families (*Zostera*, *Thalassia*, *Halophila*, *Cymodocea*, *Amphibolis*, *Posidonia*). The natural, non-GMO machinery this strategy depends on is an ancestral feature shared across the seagrasses, not something specific to *Zostera*.

### Promoters are the RdDM handle

Feature-level analysis shows promoters carry the highest CHH (non-CG) methylation of any gene region (3.3%) – higher than intergenic or repeat DNA. Because CHH methylation is maintained by ongoing RdDM, promoters are exactly where a targeted RNA trigger would act to tune a gene without altering its sequence.

### A methylation & genetic baseline

Across the 20 individuals, DNA methylation follows the canonical plant hierarchy (CG 70.5%, CHG 27.0%, CHH 1.44%) and is remarkably uniform. All 20 are genetically distinct (no clones), and methylation similarity tracks genetic similarity (Mantel  $r = 0.77$ ) – so genotype-linked marks must be separated from facultative ones when choosing targets.

## Research Pipeline

*From field collection to ocean deployment – an integrated pipeline connecting sequencing, analysis, and robotic planting.*



## Two Scientific Paths Forward

### Path A • Rigorous Discovery

Path A

Additional methylation sequencing across populations → epiGWAS association study → identify novel epigenetic factors → validate → target. More rigorous, builds the field.

### Path B • Rapid Deployment

Path B

Use published candidate genes (HSP70 family, known methylation marks) → go directly to epigenetic targeting on priority species. Faster, leverages existing literature.

## Target Species

Five deployment-target seagrass species spanning freshwater to marine, tropical to temperate – chosen for ecological importance, genomic tractability, and thermal vulnerability – plus one comparative reference species that anchors the heat-tolerant end of the spectrum.

Our species fall into two roles. **Deployment targets** are the species we aim to make more heat-resilient and eventually replant. **Comparative references** are species we sequence and analyze to learn from rather than to treat – a naturally heat-adapted seagrass shows us what thermal tolerance *looks like* at the sequence and methylation level, giving us the "answer key" for the marks we want to switch on elsewhere.

### Deployment Targets

SPECIES	COMMON NAME	HABITAT	GENOME	THERMAL OPTIMUM	LETHAL TEMP	REFERENCE GENOME	CARBON SEQ.
<i>Thalassia testudinum</i>	Turtle grass	Marine tropical	4,866 Mb	28–30°C	36–39°C	Chromosome-level	122 g C/m <sup>2</sup> /yr
<i>Halodule wrightii</i>	Shoal grass	Marine tropical	Unknown	23–32°C	>42°C	In preparation	~5–10 g C/m <sup>2</sup> /yr
<i>Zostera marina</i>	Eelgrass	Marine temperate	260 Mb	15–23°C	30–35°C	Chromosome-level	25 g C/m <sup>2</sup> /yr
<i>Posidonia oceanica</i>	Neptune grass	Marine temperate	3,192 Mb	15–25°C	~35°C	Chromosome-level	84 g C/m <sup>2</sup> /yr
<i>Vallisneria americana</i>	Wild celery	Freshwater	~3,600 Mb	28–36°C	>38°C	JGI draft in progress	Not quantified

### Comparative Reference

SPECIES	COMMON NAME	HABITAT	GENOME	THERMAL OPTIMUM	LETHAL TEMP	REFERENCE GENOME	ROLE
<i>Cymodocea nodosa</i>	Little Neptune grass	Marine temperate–subtropical	375 Mb	~30°C (up to 34–35°C)	>34°C	Chromosome-level	Heat-tolerant benchmark; 4th RdDM lineage

### Heat Tolerance Ranking

From most to least thermally tolerant – every species shows ecotype-dependent variation in thermal tolerance.

- 1 **\_Halodule wrightii\_** – Survives 42°C short-term; Fv/Fm unaffected at 34–35°C after 38 days
- 2 **\_Cymodocea nodosa\_ (reference)** – Highest thermal optima of any Mediterranean seagrass tested; optimum ~30°C, tolerates 34–35°C; may benefit from projected warming
- 3 **\_Vallisneria americana\_** – Chesapeake ecotypes thrive at 33–36°C; Wisconsin populations die
- 4 **\_Thalassia testudinum\_** – Tropical but vulnerable; chronic stress at 32–33°C; sulfide-mediated die-offs
- 5

***Posidonia oceanica*** — Photosynthesis inhibition at 27°C; five years of Mediterranean mass mortality

6 ***Zostera marina*** — Most vulnerable; O<sub>2</sub> flux declines 50% above 28.6°C; wasting disease amplified by warming

## Species Profiles

### ***Thalassia testudinum*** — Turtle Grass

Priority Sequence #1

Keystone Species

- Dominates both Culebra and Bocas del Toro meadows
- Primary Caribbean carbon sink: 0.3–1.2 Mg C m<sup>2</sup>/yr
- Sediment storage up to 150 Mg C/ha; 241 Mg organic C/ha in Colombia
- Kill mechanism is sulfide intrusion, not heat alone
- Thermal safety margin <3°C in Gulf of Mexico
- 4,866 Mb genome — largest seagrass genome sequenced
- **Our data:** complete RdDM pathway confirmed conserved (2026)

### ***Halodule wrightii*** — Shoal Grass

Priority Sequence #2

Most Heat-Tolerant

- Naturally colonizes warmer, shallower, more disturbed sites
- Highest phenotypic plasticity in temperature and salinity
- Short life cycle, smaller genome — experimentally tractable
- Existing RNA-seq data under thermal stress
- Recolonizing Florida Bay where *T. testudinum* died
- Viable candidate for epigenetic triggering of HSP and photoprotective pathways

### ***Zostera marina*** — Eelgrass

Primary Target Species

Sequenced + Analyzed

- Smallest genome (260 Mb) — best-studied seagrass genome
- **Our data:** ~82M methylation sites/sample across 20 individuals
- **Our data:** all 20 RdDM pathway genes present and intact
- **Our data:** promoters carry highest genic CHH (RdDM handle)
- Southern populations recover gene expression after heat; northern don't
- SF Bay populations provide warm-edge germplasm

### ***Posidonia oceanica*** — Neptune Grass

Largest Carbon Sink/Area

EU Priority Habitat

- ~420 million tonnes C stored in Mediterranean mat deposits
- Contains the oldest known living clones on Earth
- Thermal priming already demonstrated in seedlings

- Mediterranean warming at  $\sim 0.04^{\circ}\text{C}/\text{yr}$  — among fastest globally
- 3,192 Mb genome — chromosome-level assembly available
- Deployment complicated by extremely slow growth and EU regulation

### ***Vallisneria americana* — Wild Celery**

Freshwater Analog

No Genome Yet

- Dramatic ecotypic thermal variation (Chesapeake vs. Wisconsin)
- CAM photosynthesis provides carbon-balance buffer under heat
- Chesapeake Bay keystone species
- Good model for understanding thermal adaptation genetics
- Primary threat is salinity, not temperature
- $\sim 3,600$  Mb estimated genome; JGI draft in progress

### ***Cymodocea nodosa* — Little Neptune Grass**

Comparative Reference

Heat-Tolerant Benchmark

- Highest thermal optima of any Mediterranean seagrass tested — a projected 'climate winner'
- Growth/photosynthesis optima ( $24.5 / 31.0^{\circ}\text{C}$ ) far above *Zostera*'s ( $15.3 / 23.3^{\circ}\text{C}$ )
- Euryhaline: tolerates 10–50 PSU salinity, thrives in variable coastal conditions
- Chromosome-level genome in hand (375 Mb, 28 chromosomes; GCA\_036874045.1)
- Second-smallest genome in the repository — highly tractable
- **Role:** the warm-adapted 'answer key' for thermal-tolerance marks + a 4th lineage for the RdDM conservation story

## **Collection Sites**

*Samples from three biogeographic regions enable comparative sequencing between typical and heat-stressed populations.*

### Culebra, Puerto Rico

**Primary site** — Private island property. Multiple collection trips completed with Pati Mar and Sociedad Ambiente Marino volunteers.

*T. testudinum* *S. filiforme* *H. wrightii*  
*H. stipulacea* (invasive)

### Bocas del Toro, Panama

**Heat-tolerant populations** — Private island property. Shallow mangrove location with naturally heat-stressed seagrass for comparative sequencing.

*T. testudinum* (dominant) *S. filiforme* *H. wrightii*

### San Francisco Bay, California

**Warm-edge eelgrass** — Southern range limit populations. Successfully collected and sequenced (20 samples analyzed, 2026). Small genome makes it the most cost-effective for initial work.

*Z. marina*

## Genome Inventory

Chromosome-level reference genomes now exist for three deployment targets plus our comparative-reference species, *Cymodocea nodosa*. We are building the most comprehensive public seagrass genomic repository — four species held (*Zostera*, *Thalassia*, *Cymodocea*, *Posidonia*), two targets still awaiting assembly.

**Assembly note (corrected 2026):** the *Zostera marina* row previously conflated two assemblies. GCA\_001185155.1 (Olsen et al. 2016, Nature) is the **v2.1 scaffold-level** assembly. The **v3.1 chromosome-level** assembly used for our methylation analyses (6 pseudo-chromosomes, 260.5 Mb, 21,483 genes) is **Ma et al. 2021 (F1000Research)**, distributed via Phytozome and not deposited to NCBI GenBank. Both are listed separately below.

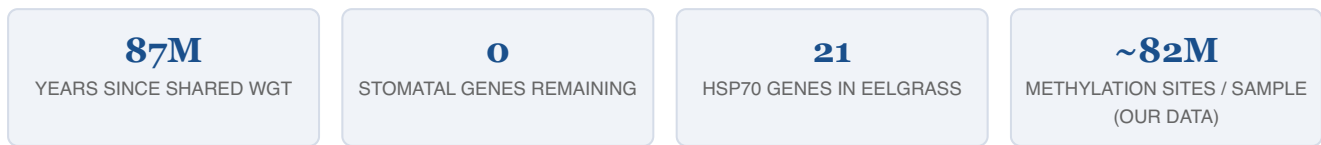
SPECIES	SIZE	CHROMOSOMES (N)	ASSEMBLY	KEY ACCESSION / SOURCE	REFERENCE
<i>Zostera marina</i> (v3.1)	260 Mb	6	Chromosome-level	Phytozome (PRJNA701932)	Ma et al. 2021
<i>Zostera marina</i> (v2.1)	204 Mb	scaffold	Scaffold-level	GCA_001185155.1	Olsen et al. 2016
<i>Thalassia testudinum</i>	4,866 Mb	18	Chromosome-level	Marine Angiosperm Genome Initiative	Ma et al. 2024
<i>Posidonia oceanica</i>	3,192 Mb	~20	Scaffold/Chr-level	GCA_037176725.1 (PRJNA1041560)	JGI 2024
<i>Cymodocea nodosa</i>	375 Mb	28	Chromosome-level	GCA_036874045.1 (PRJNA1041560)	JGI 2024
<i>Halodule wrightii</i>	Unknown	24–39	SRA data only	SRA runs (prep)	No assembly yet
<i>Vallisneria americana</i>	~3,600 Mb	20	JGI draft	PRJNA566556	JGI (raw reads)

## Our Sequencing Data

Genome + epigenome data available for *Thalassia testudinum* and *Zostera marina* from our sequencing runs with Decibel Bio. Twenty *Z. marina* Nanopore methylomes were fully analyzed in 2026 (see Findings page). Data location: **Google Drive** — Good Ancestor Shared Drive > Genome, with a dedicated Analysis folder for computed results.

## Shared Genomic Features

All seagrasses share an ancient whole-genome triplication (~87 million years ago) and remarkable convergent adaptations to marine life:



## Heat Tolerance Data

Comprehensive thermal tolerance profiles across the deployment targets plus our heat-tolerant reference (*C. nodosa*). Heat tolerance is ecotype-dependent in every species studied — meaning the alleles and epigenetic marks already exist within species.

PARAMETER	<i>V. AMERICANA</i>	<i>T. TESTUDINUM</i>	<i>H. WRIGHTII</i>	<i>Z. MARINA</i>	<i>P. OCEANICA</i>	<i>C. NODOSA</i> (REF)
Thermal optimum	28–36°C	28–30°C	23–32°C	15–23°C	15–25°C	~30°C
Photosynthesis inhibition	—	>33°C	Unaffected at 34–35°C	>25°C	>27°C	Tolerates 34–35°C
Chronic stress onset	—	32–33°C	—	25°C	27°C	>32°C
Upper lethal (sustained)	≈38°C	36°C (4 wk)	>42°C (short-term)	28–30°C	≈35°C	>34°C
Thermal safety margin	Large	<3°C (Gulf)	Moderate	Very small	Small	Large (warming winner)
Ecotypic variation	Yes	Limited data	Yes	Yes	Yes	Yes
Epigenetic data	None	Moderate (our data)	None	Extensive (our data)	Moderate	RdDM confirmed (our data)

## Molecular Basis of Heat Tolerance

### Epigenetic Evidence

- Warm-adapted ecotypes have higher global DNA methylation (Entrambasaguas et al. 2021)
- Methylation changes persist 5.5+ weeks post-stress in eelgrass (Jueterbock et al. 2020)
- Thermal priming creates persistent epigenetic memory in *P. oceanica* seedlings (Pazzaglia et al. 2025)
- HSP70 promoters act as methylation "rheostats" — CpG demethylation under heat triggers massive induction
- Clonal epigenetic memory persists 3–12 generations in aquatic plants
- **Our data:** the complete RdDM machinery that writes and maintains these marks is present in *Zostera* and *Thalassia*

### Key Engineering Targets

- **HSP70 family** — 6 thermosensitive genes in eelgrass
- **HSF transcription factors** — seagrasses have half of terrestrial plants
- **Antioxidant defense** — SOD, CAT upregulation
- **Carbon metabolism** — prevent respiration exceeding photosynthesis
- **Sulfide detoxification** — critical for *T. testudinum*
- **Meristem O<sub>2</sub> homeostasis** — compound stress protection

## Technology Partners

*Two technology partners enable our epigenetics-first pipeline: Decibel Bio reads and writes the epigenome, and Chris Oakes brings marine seed-delivery and pelletization for deployment at sea.*

### Decibel Bio — Epigenetic Triggering

Berkeley-based crop epigenetics platform. Reads, understands, and writes the plant epigenome using small RNA/DNA molecules that direct DNA methylation via the natural RdDM pathway. **Our 20 *Zostera marina* methylomes were sequenced by Decibel (Oxford Nanopore, 5mC).**

- \$12M launch financing (2025) · epigenome-driven trait models
- Foliar-spray or seed-treatment delivery that writes methylation without changing DNA
- Non-GMO · reversible · preserves genetic diversity · applied at planting or in-season

Breakthrough Energy Ventures

Leaps by Bayer

Syngenta

Spun out of Sound Agriculture

### Chris Oakes — Marine Delivery & Planting

Chris Oakes (former CEO/founder of ReefGen) brings robotic-planting and seed-delivery expertise to the marine deployment problem, including a pelletization technology for controlled seafloor release of treatments and seed.

- Robotic seed injection into the seafloor from a piloted underwater vehicle (developed at ReefGen)
- Pelletization approach for protected, localized delivery of RdDM trigger or treated seed
- Marine-deployment counterpart to Decibel's epigenetic write step

California

former ReefGen

## Team & Advisors

*Core team, science and industry advisors, and field collaborators.*

## Core Team

### Colby Thomson

Project Lead  
Good Ancestor Foundation

### Morgan Peterson

Co-Lead, Field Collection & Experimental Design  
UC Berkeley — Neuroscience & Epigenetics

### Parker Bonnell

Ecosystems Economist  
Good Ancestor Ag

### Chris Oakes

Marine Delivery & Planting  
former CEO/founder, ReefGen — California

## Science & Genetics Advisors

### Dr. Sean Yeldell

Chemical Biology & Genetics  
Senior Scientist, Silence Therapeutics

### Dr. Alexandra MacColl Garfinkel

Genetics — Metabolism, Development, Evolution  
Max Planck Institute (MPI-CBG)

## Industry & Technology Advisors

### Emily Hatas

Biotech & Funding Strategy  
Revive & Restore (formerly PacBio)

### Joel Dapello

Machine Learning for Genomics  
Senior ML Engineer, Altos Labs

### Eric Stackpole

Underwater Robotics  
Founder, OpenROV & Nat Geo Ocean Explorer

## Field Work & Ecosystem Advisors

### Pati Mar

Field Collection  
Coral reef protection — Puerto Rico

### Marion Prieler

Ocean Ecosystems Researcher  
Field work and collection

### Sociedad Ambiente Marino (SAM)

Local Marine Conservation  
San Juan, Puerto Rico

### Sam Rodriques

AI-Driven Scientific Discovery  
Founder, Future House — Co-creator of Kosmos AI Scientist

### Xiaoxi (Sofie) Wei, Ph.D

Coral & Sample Transport Technology  
CEO & Co-founder, X-Therma

## Coral Assisted-Evolution Advisors (via Marion Prieler)

Marion Prieler brings a coral assisted-evolution advisory network to the project; these advisors flow through her collaboration rather than advising the project directly.

**Prof. Iliana Baums**

Coral Assisted Evolution  
Helmholtz Institute for Functional Marine Biodiversity

**Prof. Chris Voolstra**

Coral Ecosystem Restoration  
Konstanz University

**Dr. James Guest**

Coral Assisted Evolution  
Newcastle University

## Computational Pipeline

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*The analysis tools used to produce the 2026 findings, and the autonomous-research tools we are evaluating for the next phase.*

### Tools used in the 2026 analyses

**miniprot — RdDM ortholog scan**

Protein-to-genome alignment used to map the 20 *Arabidopsis* RdDM machinery proteins onto six seagrass genomes, calling ortholog presence and confidence per gene. Basis of the conservation figure.

Orthology

**RepeatModeler2 + RepeatMasker**

De novo transposable-element discovery and genome masking. Produced the 68.9% repeat annotation and the LTR/DNA/LINE class fractions for *Z. marina* v3.1 (the RdDM substrate).

TE annotation

**bcftools + scikit-allel**

Per-sample VCFs merged and reduced to biallelic SNPs; IBS distances and clustering established that all 20 samples are distinct genotypes (no clones).

Genetics

**Python methylation stack**

pandas / numpy / scipy / matplotlib on the 20 Nanopore methylomes: weighted-methylation landscape, feature-level (promoter/exon/intron/TE) profiling, and the methylation↔genotype Mantel test ( $r = 0.77$ ).

Methylation analysis

**OBIS / GBIF + cartopy**

65,932 georeferenced occurrence records across the six species, joined to sea-surface-temperature envelopes and marine ecoregions to build the collection-site and thermal-niche maps.

Biogeography

## Future tools (under evaluation)

### Kosmos / Edison — Future House

Data-driven discovery agent. Accepts research objectives plus complex datasets (up to 5 GB): literature search, high-dimensional analysis, hypothesis generation. ~\$200/run; we have credits. Advisor: Sam Rodrigues.

Evaluating

Future House

### DeepScientist

Local-first autonomous research studio for long-horizon scientific work: git-native tracking, Bayesian optimization, research-map visualization. Open source.

Evaluating

Apache-2.0

## Current Status

Where we are as of mid-2026.

2

SPECIES SEQUENCED

2

EPIGENOMES MAPPED

20

Z. MARINA METHYLOMES  
ANALYZED

6

SPECIES GENOMES ANALYZED  
(ALL 4 FAMILIES)

### Completed

- Collected samples across multiple sites in Puerto Rico
- Sequenced *T. testudinum* genome + epigenome (PR collection)
- Sequenced *Z. marina* genome + epigenome (SF Bay, 20 samples)
- **Analyzed all 20 *Z. marina* methylomes** — landscape, feature-level, genetic structure (2026)
- **Confirmed complete RdDM pathway** conserved across six seagrass genomes spanning all four families — *Z. marina*, *T. testudinum*, *Halophila*, *C. nodosa*, *Amphibolis*, *P. oceanica* (2026)
- Partnership with Decibel Bio (UC Berkeley) and Chris Oakes (marine delivery, former ReefGen)
- Assembled a genome set spanning all four seagrass families — 4 held in-house (*Zostera*, *Thalassia*, *Cymodocea*, *Posidonia*) plus *Amphibolis* and *Halophila* analyzed for the conservation scan (6 total)
- **De novo TE annotation of the *Z. marina* v3.1 assembly** — 68.9% repetitive; LTR retrotransposons 45.5% of the genome, the RdDM substrate (2026)

### In Progress

- EDTA transposable-element cross-check of the RepeatModeler annotation (dedicated compute)
- Improved *T. testudinum* sample collection (PR)
- Building ~100 sample library across regions with Decibel
- Comparative analysis: heat-tolerant vs. heat-sensitive populations

### Experimental Plan

- **Library building:** ~100 samples from diverse regions, tagged for phenotypes
- **Controlled experiments:** different genotypes grown in aquarium trials
- **Epigenetic analysis:** control for genotype, identify thermal marks (baseline established: Mantel  $r=0.77$ )
- **Triggering:** targeted methylation of living seagrass or seeds (promoters = the CHH/RdDM handle)

- **Deployment:** treated seed as the low-risk anchor; loose and pelletized in-water delivery (Chris Oakes pelletization tech) as higher-value routes for established meadows

See the full 2026 analysis on the Technical Findings page →

## Key References

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Foundational literature and our own 2026 analyses. See the Findings page for the full RdDM literature review.

1. Olsen JL et al. (2016). The genome of the seagrass *Zostera marina* reveals angiosperm adaptation to the sea. *Nature* 530:331–335.
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