



Ocean Genomes: reference genome resources for marine vertebrates

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Overview



1. Acknowledgements
2. Ocean Genomes overview & progress
3. Reference genomes, so what?



Acknowledgement of Country



OceanOmics/Ocean Genomes operates on Whadjuk Noongar land.

The Noongar people remain the spiritual and cultural custodians of their land and sea country, continuing to practice their values, languages, beliefs and knowledge.

We pay respects to the first nations peoples, their elders and ancestors of the country where we live and work across Western Australia and Australia.



Team



Liam Anstiss ²



Philipp Bayer ^{1,2}



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Minderoo Foundation

We seek to uplift communities, support gender equality, protect natural ecosystems and respond to emerging threats and challenges.



OceanOmics



OceanOmics Centre



Genomics tools to transform marine biodiversity discovery & conservation.



Image credit: Giacomo d'Orlando / Ronin_Lab

eDNA biodiversity and reference genome datasets
Training, education & research opportunities

Ocean Genomes



Aim

- Accelerate and scale the production of reference genomes for marine vertebrates.

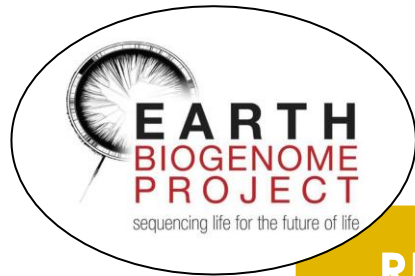
Purpose

- Facilitate breakthrough eDNA monitoring applications
- foundational resources to advance scientific research and inform conservation management.

Focus

- Native Australian and regional marine vertebrate fauna
- unique or high-conservation value species.

Ocean Genomes



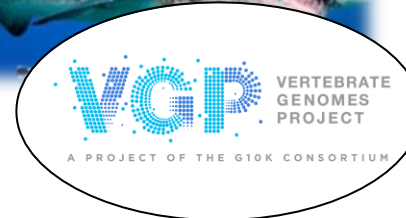
- Tiered approach to reference resource generation

REPRESENTATIVE

CATALOGUE

COMPREHENSIVE

reference genomes



Threatened species

'draft' genomes



Ocean Genomes



<https://bioplatforms.com/projects/australian-fish-genomics-initiative/>

The screenshot shows the website header with navigation links: Research Platforms, Projects, Partnerships, Bioinformatics, About Us, News, and Data Portal. The main content area features the Australian Fish Genomics Initiative logo, which includes a fish and a DNA helix. Below the logo, it states 'ENABLED BY' followed by the Bioplatforms Australia and Munderoo Foundation logos. A text block below the logo reads: 'Bioplatforms Australia and Munderoo Foundation are investing in the generation of referential biomolecular data to advance knowledge of Australia's fish species and support critical research and management strategies.' To the right of the main content is a 'Related Content' section with four links, each with a green arrow icon: 'Bioplatforms Australia Data Portal', 'The Australian Freshwater Fish Genomics Program', 'The Australian Marine Fish Genomics Program', and 'Request for Partnership 2024 - guidelines'.

Fish play a crucial role in Australia's environmental health and economy. As the largest and most diverse group of vertebrates, with over 34,500 species described globally, Australia hosts approximately 5,000 fish species, including around 400 native freshwater species. A significant proportion of Australia's freshwater fish are endemic, and many species are still being discovered or described due to the challenges associated with access and identification. Advancements in our understanding of how aquatic organisms adapt to and interact with their environments, coupled with improved population monitoring and environmental assessment, are facilitated by genomics-informed technologies. These technologies address a broad range of needs related to fish evolution and biodiversity, conservation, fisheries, aquaculture, and environmental biosecurity, including pest and disease management.

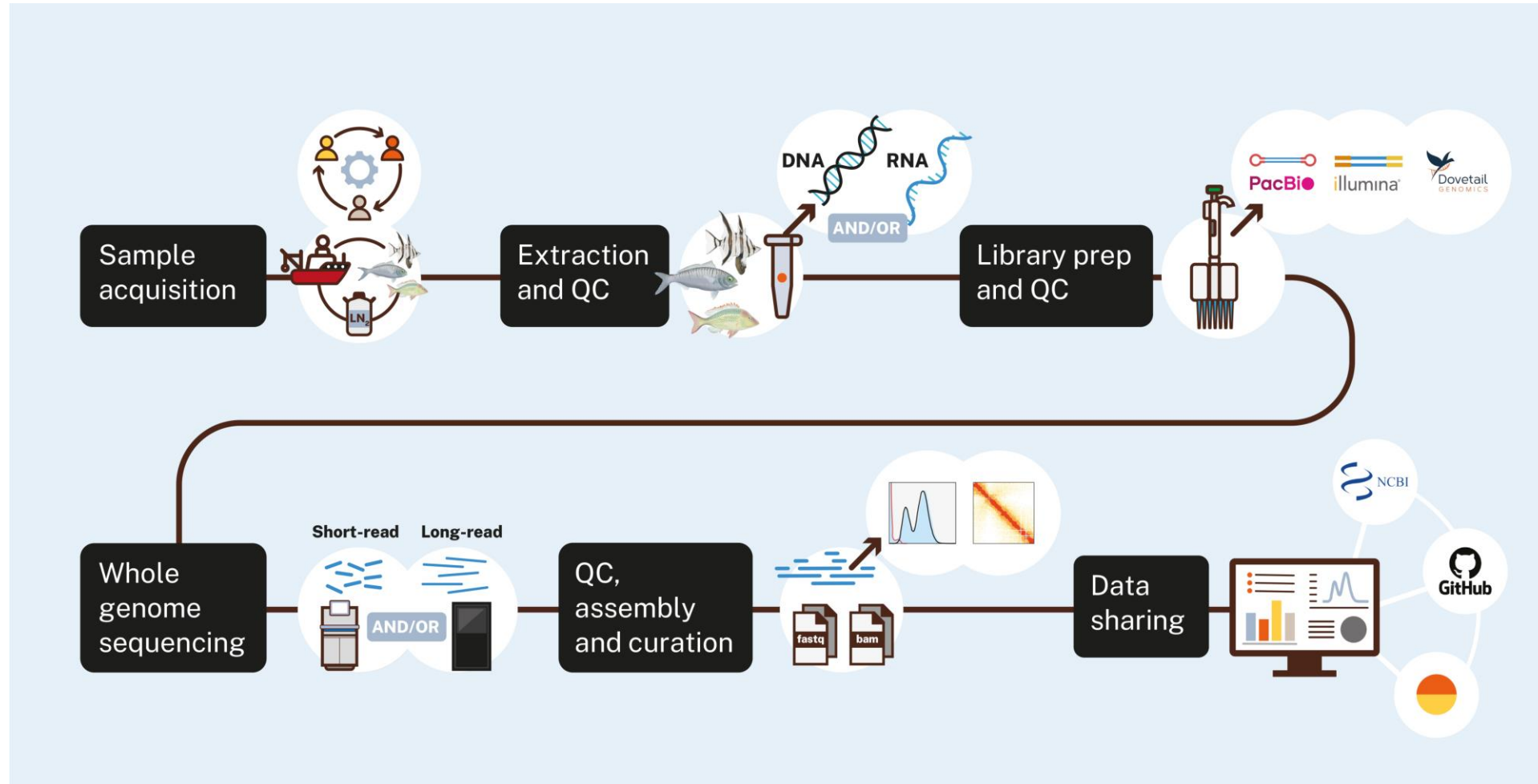
AIMS

The Australian Fish Genomics Initiative, in collaboration with the marine and freshwater research communities, aims to generate essential data for researchers and practitioners to accelerate the characterisation of Australia's fish species, enhancing our understanding of species adaptation, population dynamics, and evolutionary relationships.

Data types will include genomics, genetics (e.g., population genetics), transcriptomics, proteomics and metabolomics where required and include fish species from all major Australian habitats: freshwater, estuarine and marine environments. The Initiative will be progressing as two parallel themes:

- The Australian Freshwater Fish Genomics Program
- The Australian Marine Fish Genomics Program

Capabilities



Scaling



- **PacBio Revio** increase throughput 5×
- **ultra-low input protocols** unlocking access to more diverse sample types
- **automated preparations** on Biomek i7 liquid handler
- **scalable & reproducible pipelines** for reference, draft & mito- assembly

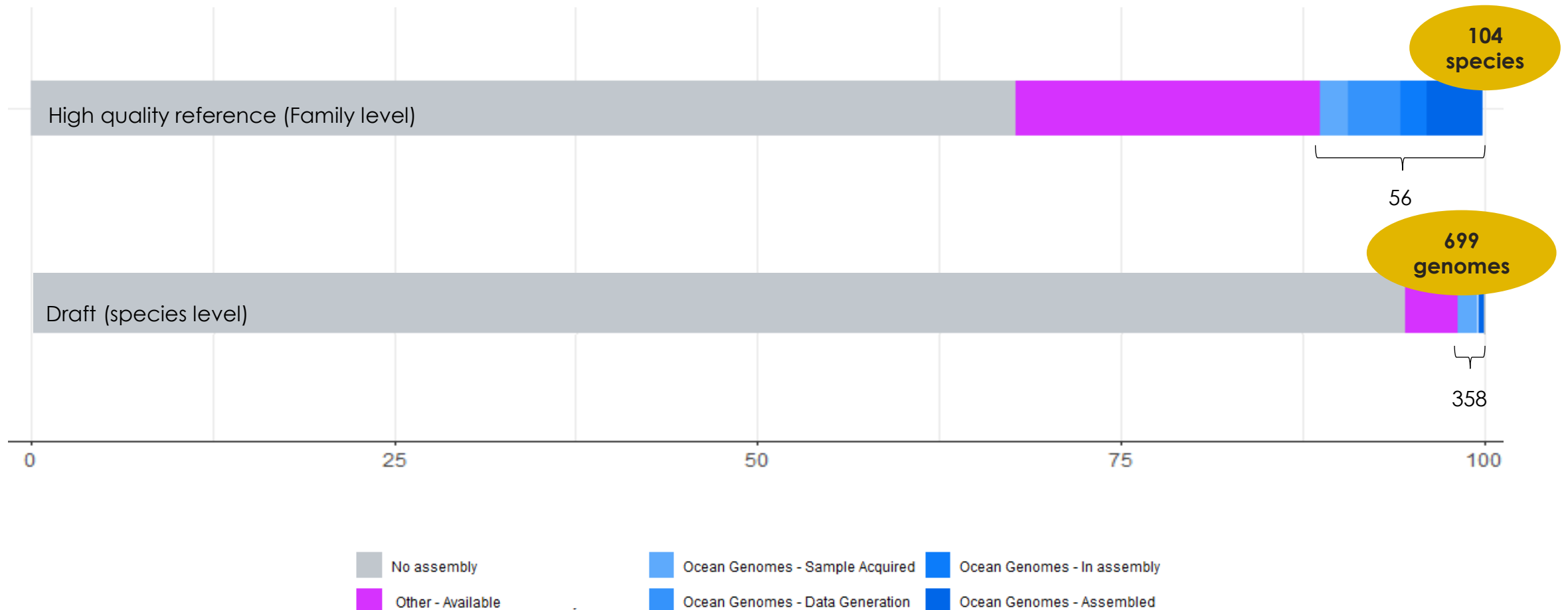
Workflow	# samples	Manual prep	Automated prep	Throughput
PacBio SMRT Bell	96	24 hours	6 hours	4×
Illumina DNA Prep	96	24 hours	6 hours	4×
Dovetail Omni-C & LinkPrep	24	27 hours	6 hours	4.5×



<https://github.com/MinderooFoundation/OceanOmics-OceanGenomes-ref-genomes>
<https://github.com/MinderooFoundation/OceanOmics-OceanGenomes-draft-genomes>



Reference genome progress

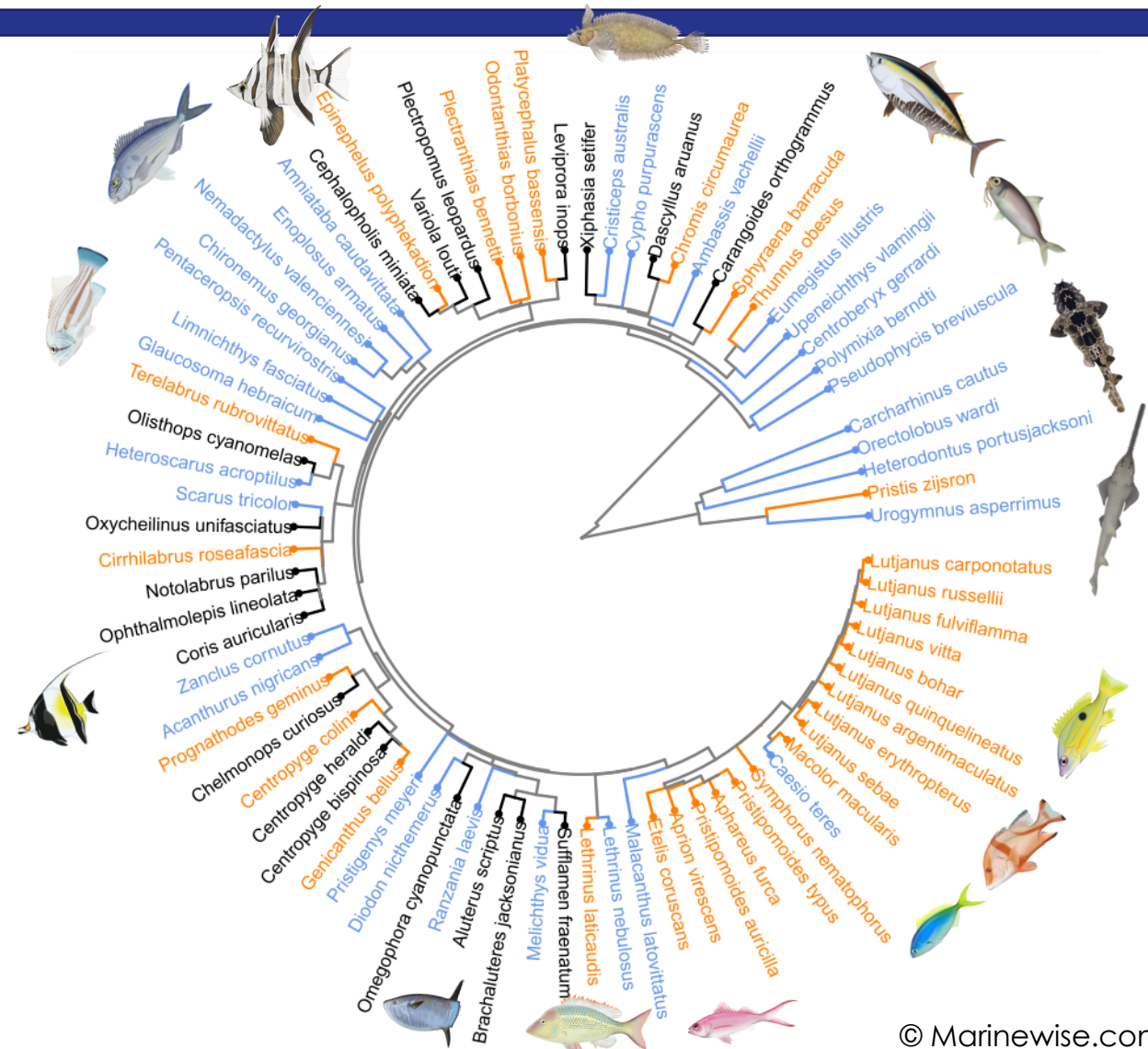


Capturing diversity

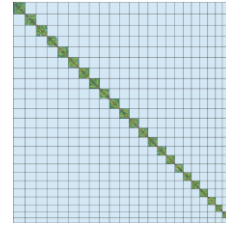
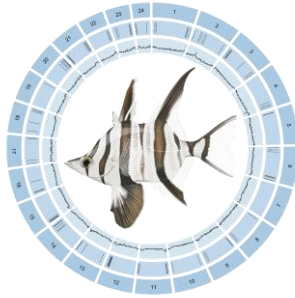


104 species, 56 families, 25 orders

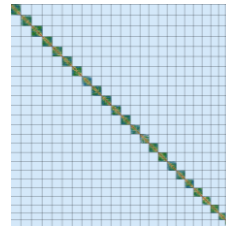
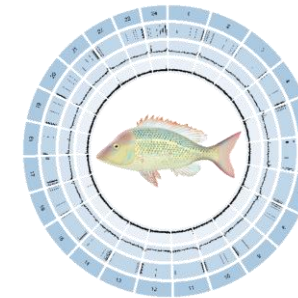
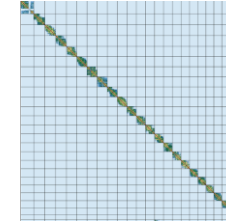
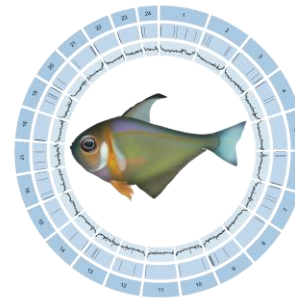
- ✓ Encompass marine vertebrate diversity
- ✓ previously not represented in reference databases
- ✓ **first representative of a family**
- ✓ **high conservation value.**



Reference genome quality



© Marinewise.com.au



	<i>Enoplosus armatus</i> (fEnoArm2.1)		<i>Pempheris klunzingeri</i> (fPemKlu1.1)		<i>Lethrinus nebulosus</i> (fLetNeb1.1)	
	Haplotype 1	Haplotype 2	Haplotype 1	Haplotype 2	Haplotype 1	Haplotype 2
Assembly size (Mb)	579		591		1093	
scaffolds	135	94	442	84	226	151
Scaffold NG50 (Mb)	25.6	25.6	27.8	28.1	24.0	20.8
Contig NG50 (Mb)	17.1	16.0	13.7	14.9	48.5	47.5
BUSCO (%)	98.9	99	99.3	99.3	99.3	99.4
Gaps	114	100	87	93	196	244
Assigned (%)	99.5	99.7	96.9	99	99	99.2
QV	61.2	60.2	59.4	62.4	61.2	61.2

Data sharing & accessibility



- Commitment to open science & equitable access to data & benefit sharing



<https://www.ncbi.nlm.nih.gov/bioproject/1046164>



<https://goat.genomehubs.org/projects/OG>



<https://edna.minderoo.org/>
AWS open data S3://minderoo-oceanomics

Talk to me!



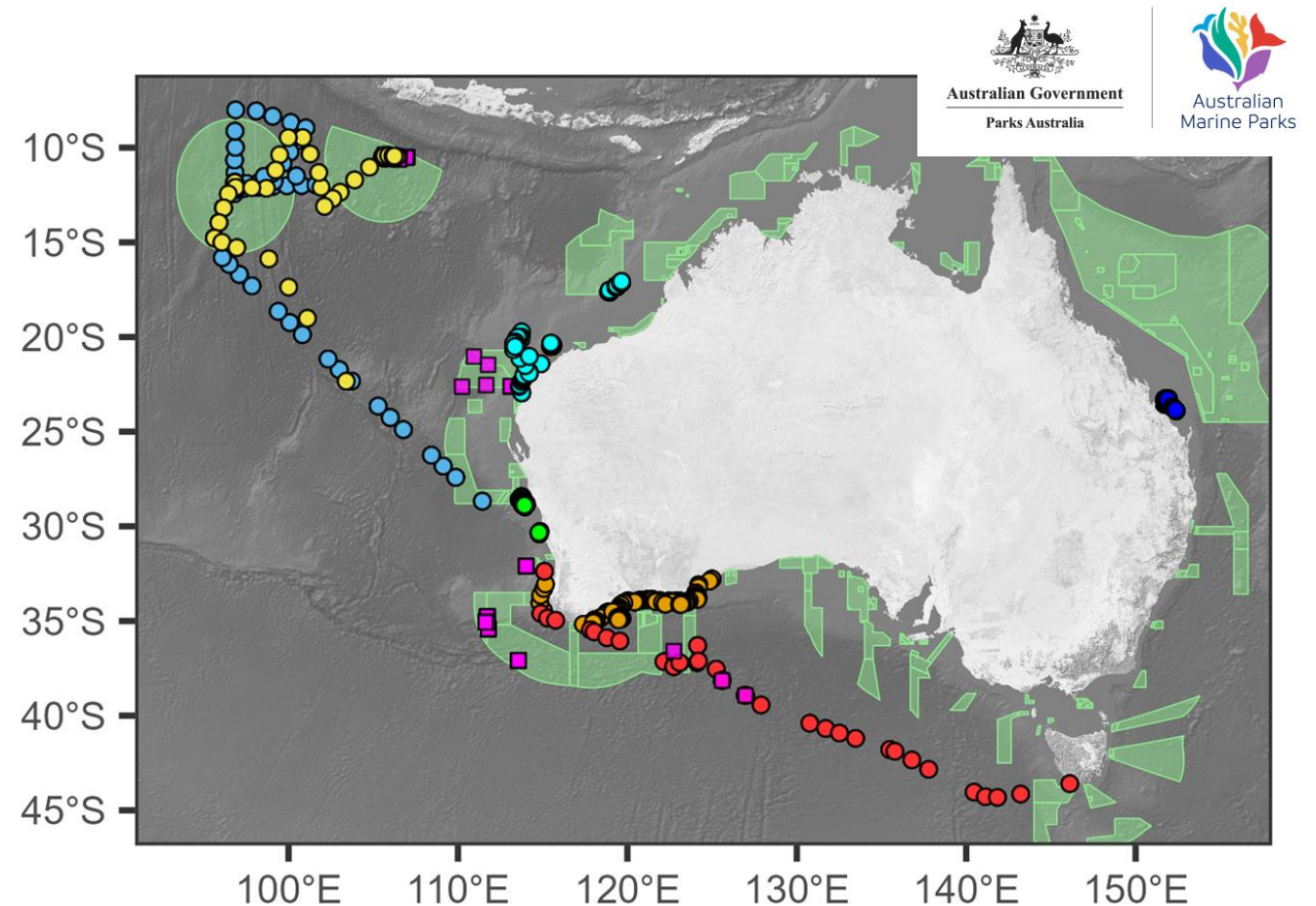
Philipp Bayer

eDNA biodiversity surveys



eDNA campaigns

- Indian Ocean Territories 2023
- Cocos (Keeling) Islands 2022
- Abrolhos Islands 2021, 2022, 2023, 2024
- Great Southern Reef 2022, 2023
- Ningaloo Reef, Rowley Shoals, Montebello Is 2019, 2021, 2023
- Great Barrier Reef 2020
- Southern Ocean transect 2024
- Deep-sea Discovery 2022, 2023
- Australian Marine Parks



SWWA sampling campaign



- Outstanding natural value
- high proportion of endemic species
- 100's of islands & reefs, many uncharted
- new marine park zones late 2026.



SWWA sampling campaign



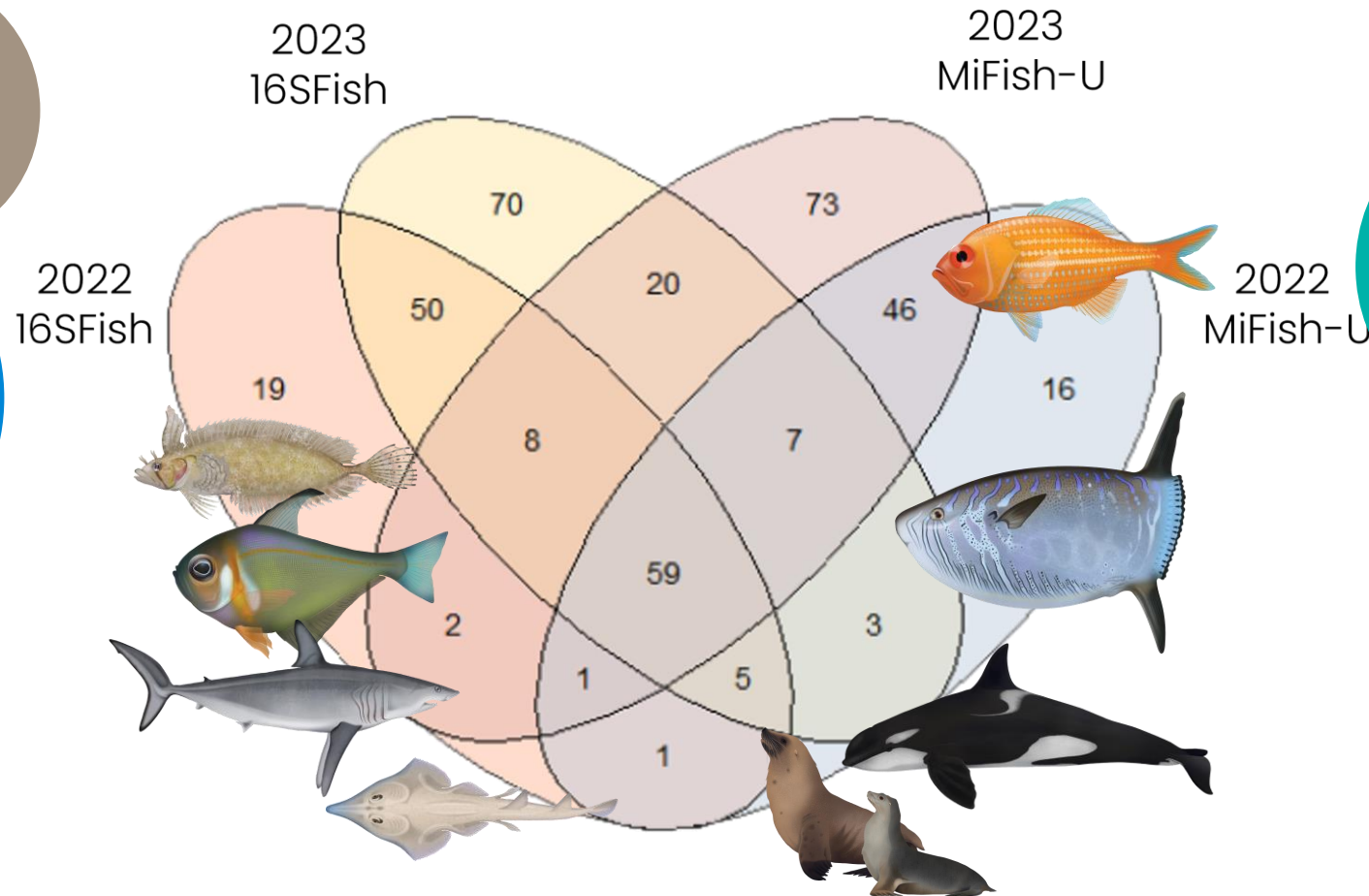
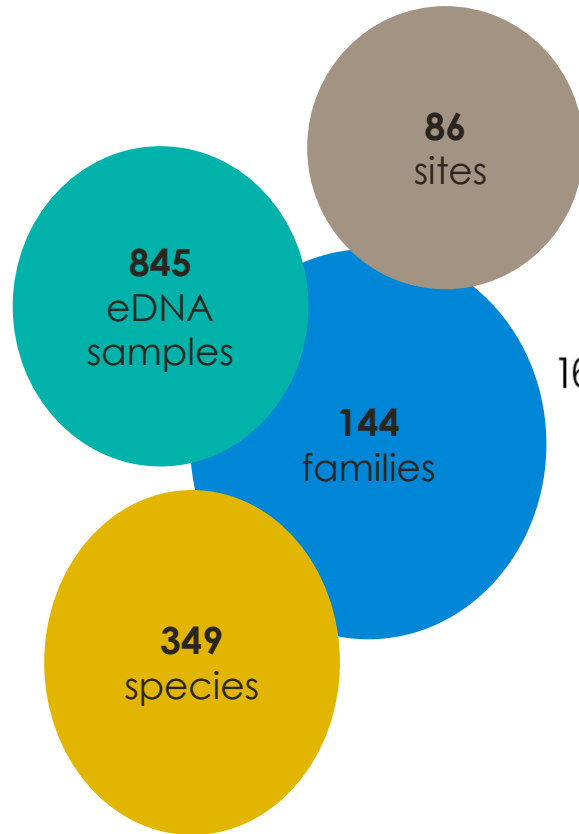
- Survey marine vertebrate fauna
- > 1000 km of coastline, spanning marine park boundaries
- 845 eDNA samples
- 162 tissue samples



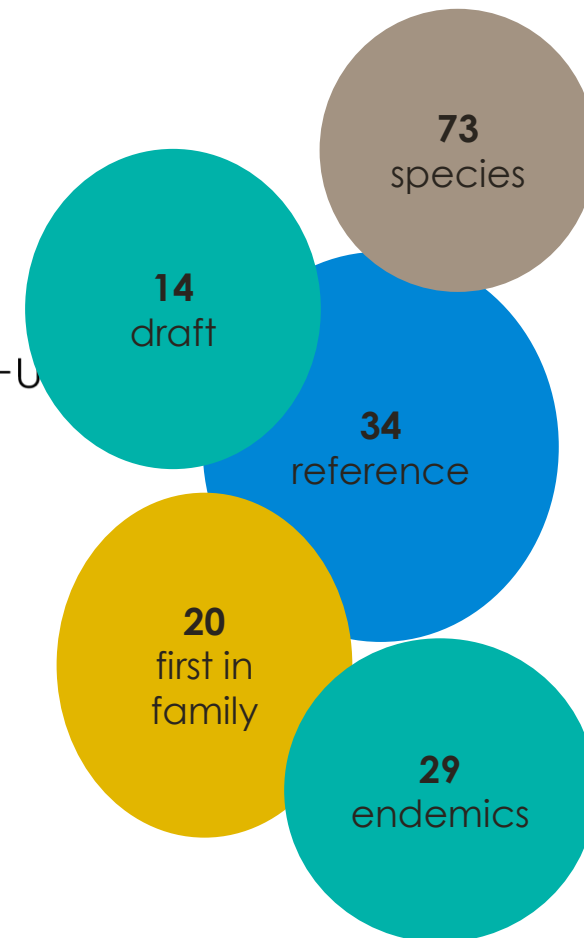
SWWA results summary



eDNA



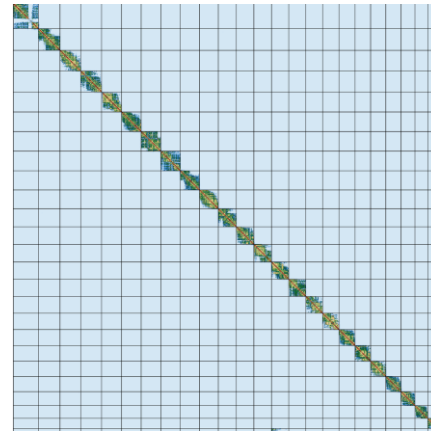
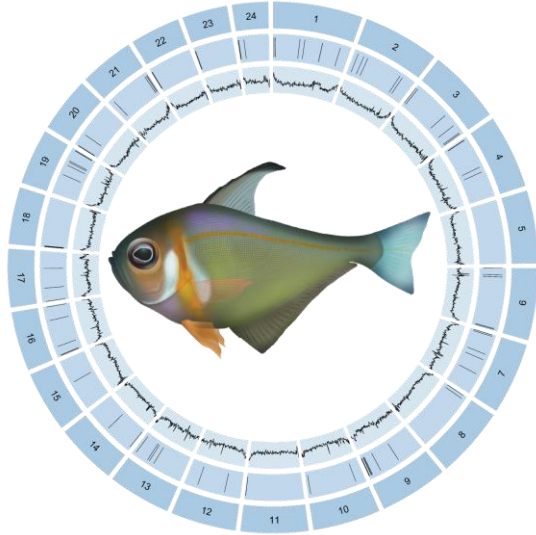
Genomes



Rough Bullseye, *Pempheris klunzingeri*



© Marinewise.com.au



- Australian endemic
- first high-quality reference for Pempheridae
- first publicly available genetic data for this species.

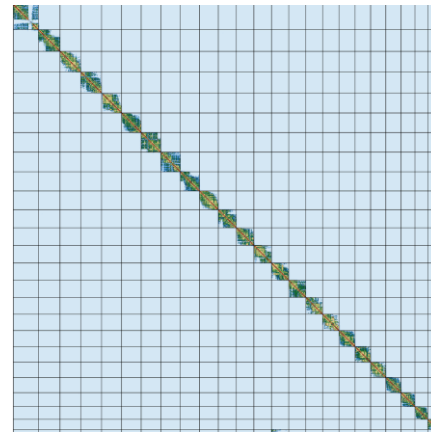
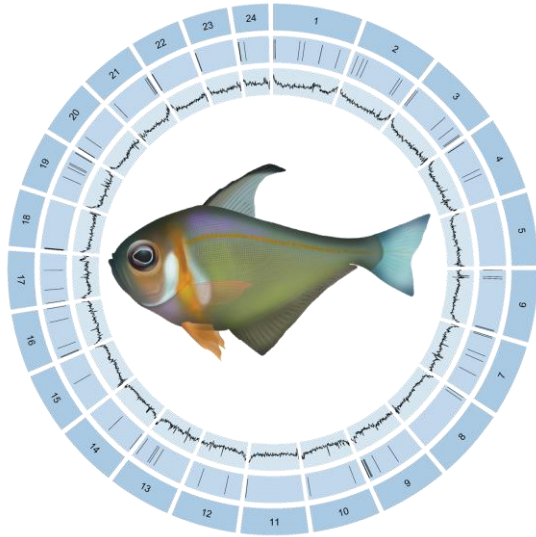
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Contig NG50 (Mb)	13.7	14.9
BUSCO (%)	99.3	99.3
Gaps	87	93
Assigned (%)	96.9	99
QV	59.4	62.4



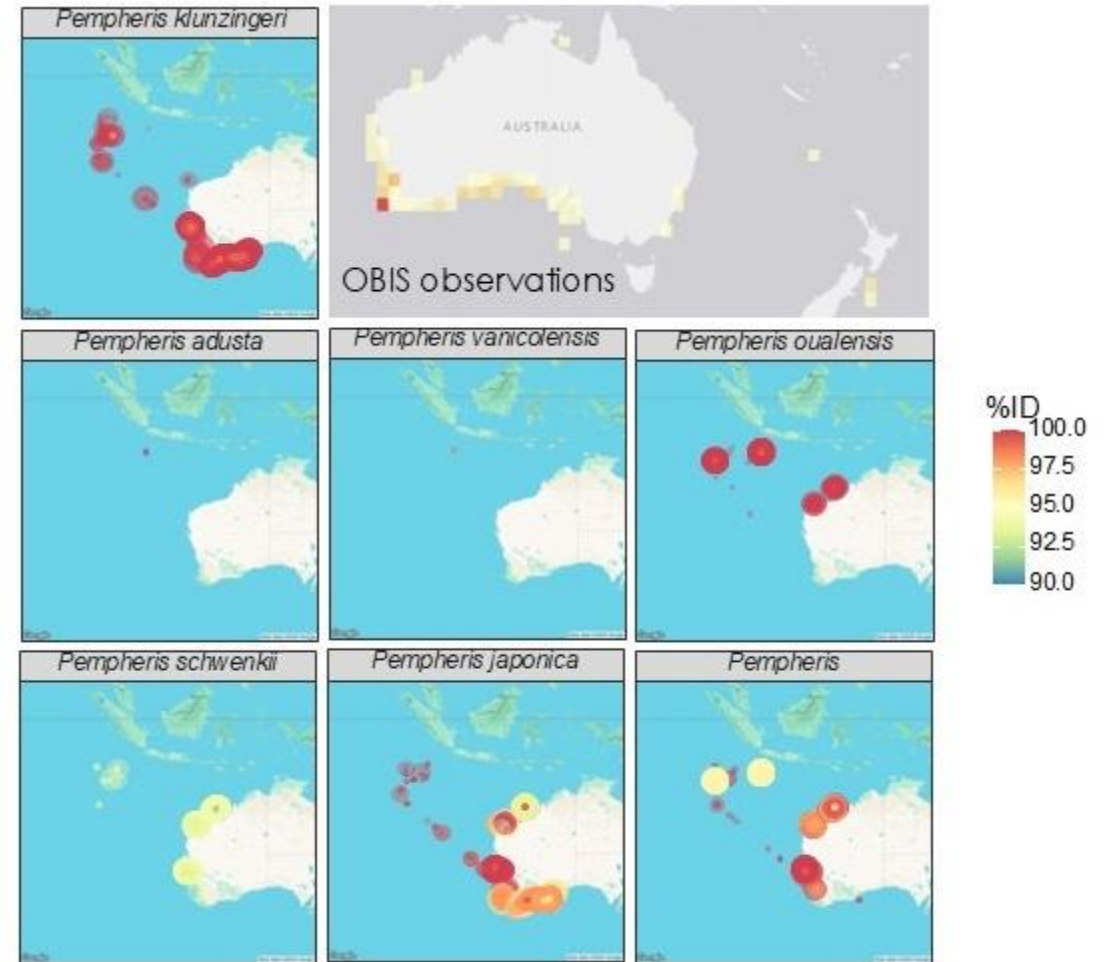
Rough Bullseye, *Pempheris klunzingeri*



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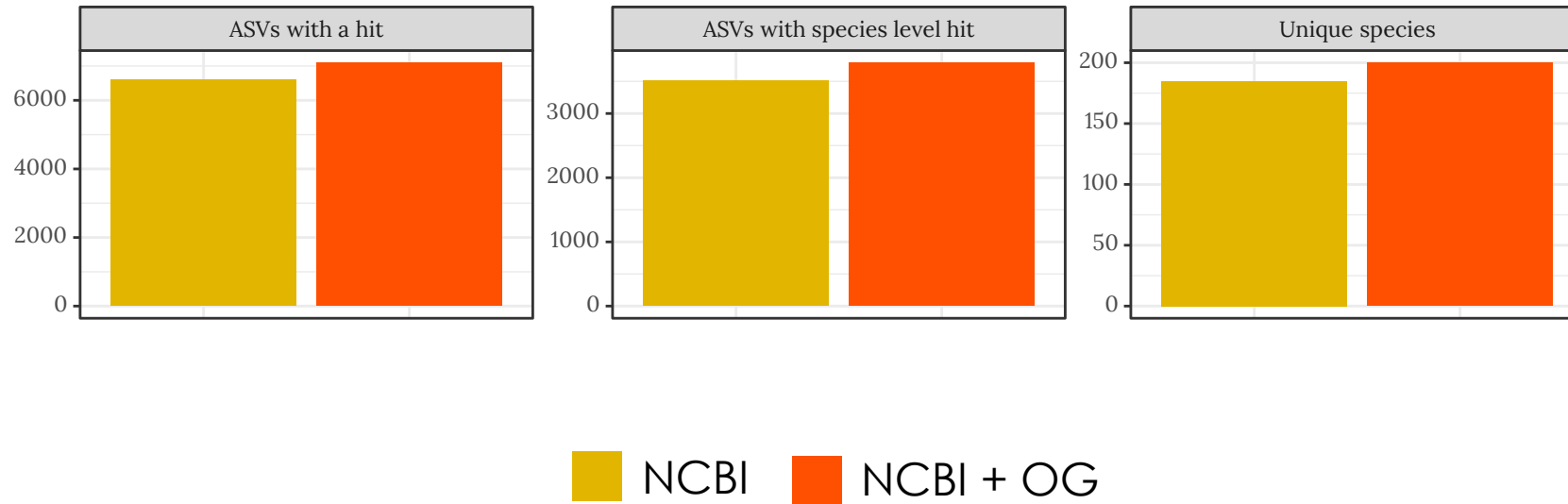


Impact



How much do we gain by adding new **mitogenome** references to databases?

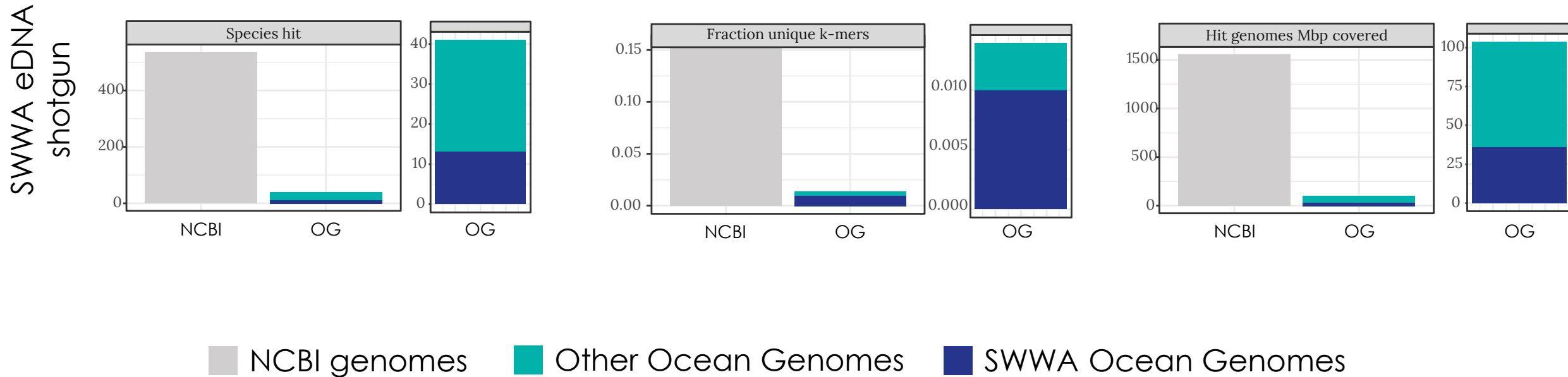
SWWA eDNA
12S/16S
metabarcoding



Impact



How much do we gain by adding new **whole genome** references to databases?



Capacity building



Image credit: Giacomo d'Orlando / Ronin_Lab

Call to action

- Facilitate specimen & sample collection to represent unique diversity in reference databases
- best practice sequencing in place of provenance
- future proof reference & eDNA biodiversity collections.



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Acknowledgements

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Emma DeJong	Sang Huynh	Ebony Thorpe
Anna Depiazzi	Anya Kardailsky	

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Special thanks to: Rich Edwards, Sequencing specialists Jahnvi Pflueger, Paul Gooding, James Miller, Angela Von, Myriam Elkhawand; automation specialist John Blinco, the Earth Biogenome Project, Vertebrate Genomes Project and Darwin Tree of Life staff and community members; and the many colleagues and collaborators that have contributed to sample acquisition including Craig Skepper, Sam Payet, Stephen Newman and Dan Gaughan (DPIRD WA Fisheries); Glenn Moore (WA Museum); Yi-Kai Tea (Australian Museum); Joseph Di Battista (Griffith University); Moreton Allentoft and Shane Herbert (TrEnD Lab and eDNA Frontiers, Curtin University); Shakirin Keegen and Shahrin Jamil (Sea Country Solutions); Alex Tomlinson, John De Majnik, Alexia Jankowski (Parks Australia); Floriaan Devloo-Delva, Bruce Deagle and Madie Green (CSIRO); Simon Goldsworthy and Roger Kirkwood (SARDI and Flinders University); Carolyn Hogg (University of Sydney); Karissa Lear (Murdoch University); Oliver Jewell (University of Western Australia); Alan Jamieson, Todd Bond, Paige Maroni (Minderoo-UWA Deep Sea Research Centre); Luke Thomas and Dean Tysdale (AIMS @ UWA); Matt McGee (Monash University); Culum Brown (Macquarie University), Jo Day (Taronga Zoo); Kyle Raina, Yamatji Southern Aboriginal Corporation, Yamatji Sea Rangers; Esperance Tjaltjraak Native Title Aboriginal Corporation; and the crews of RV Naturaliste, MV Pangaea Ocean Explorer, Immortalis.

