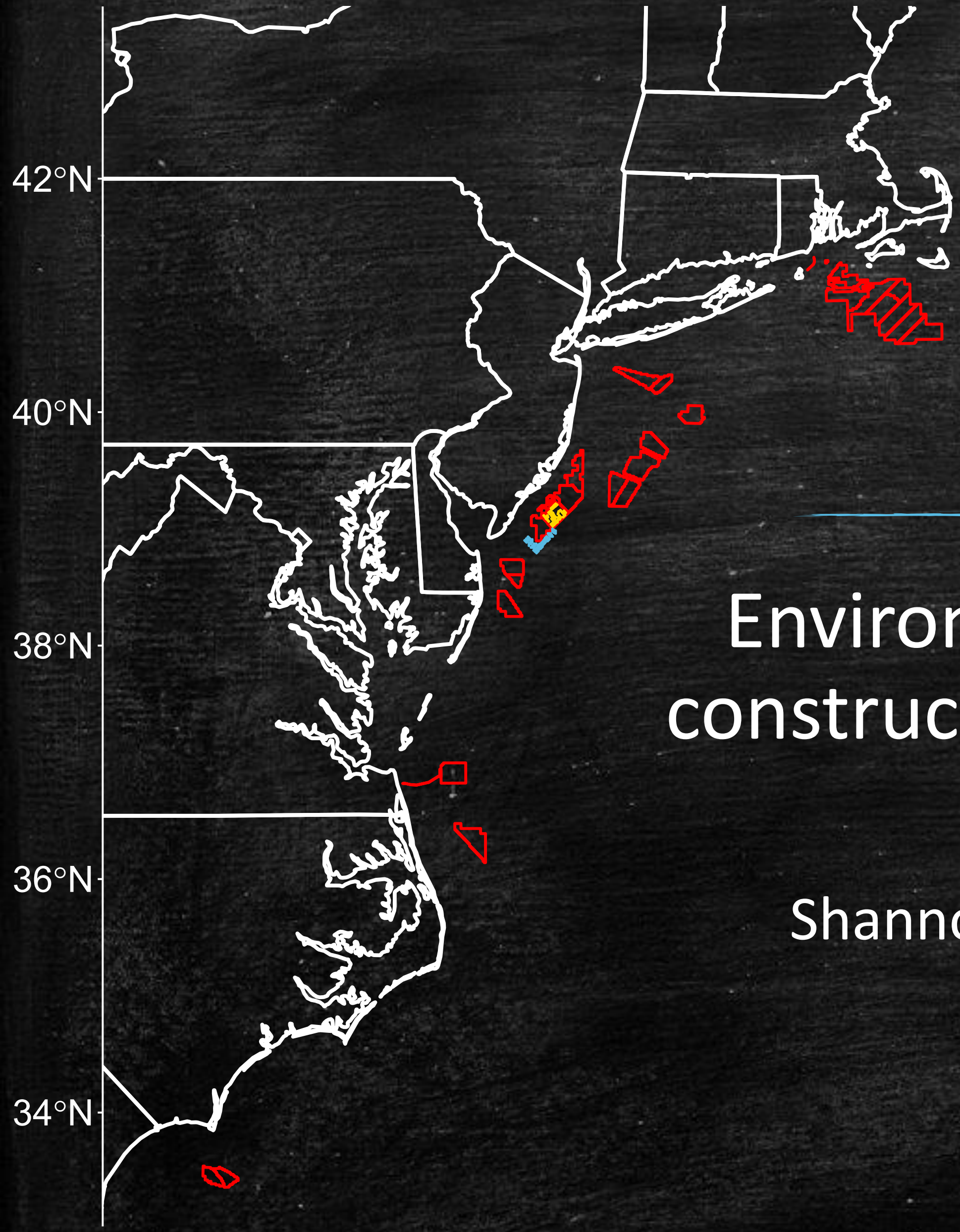
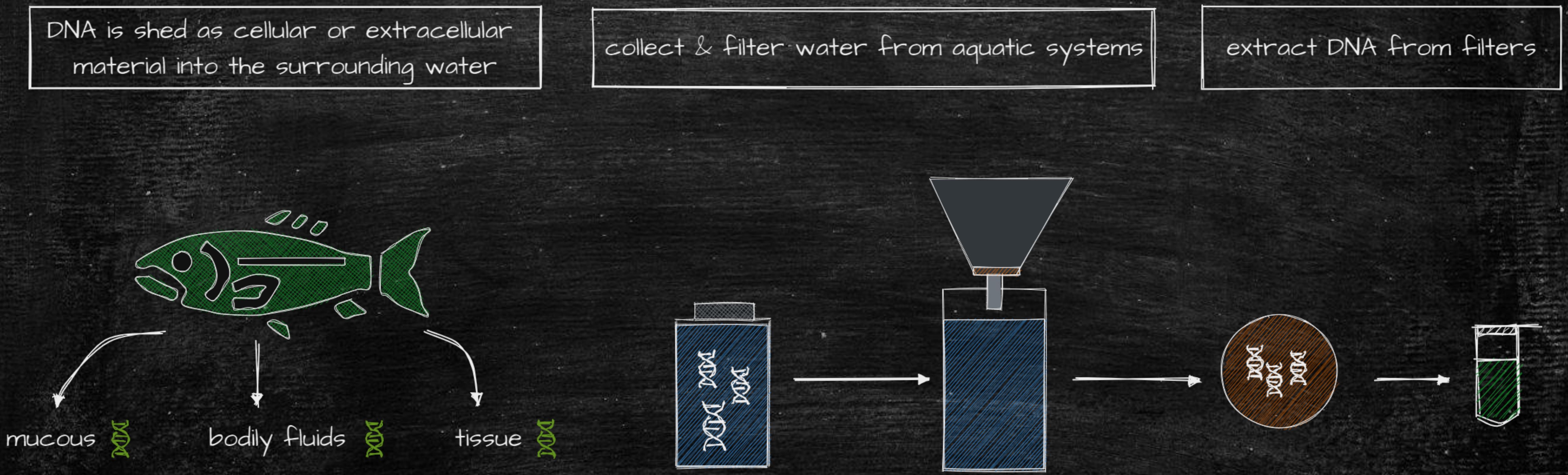
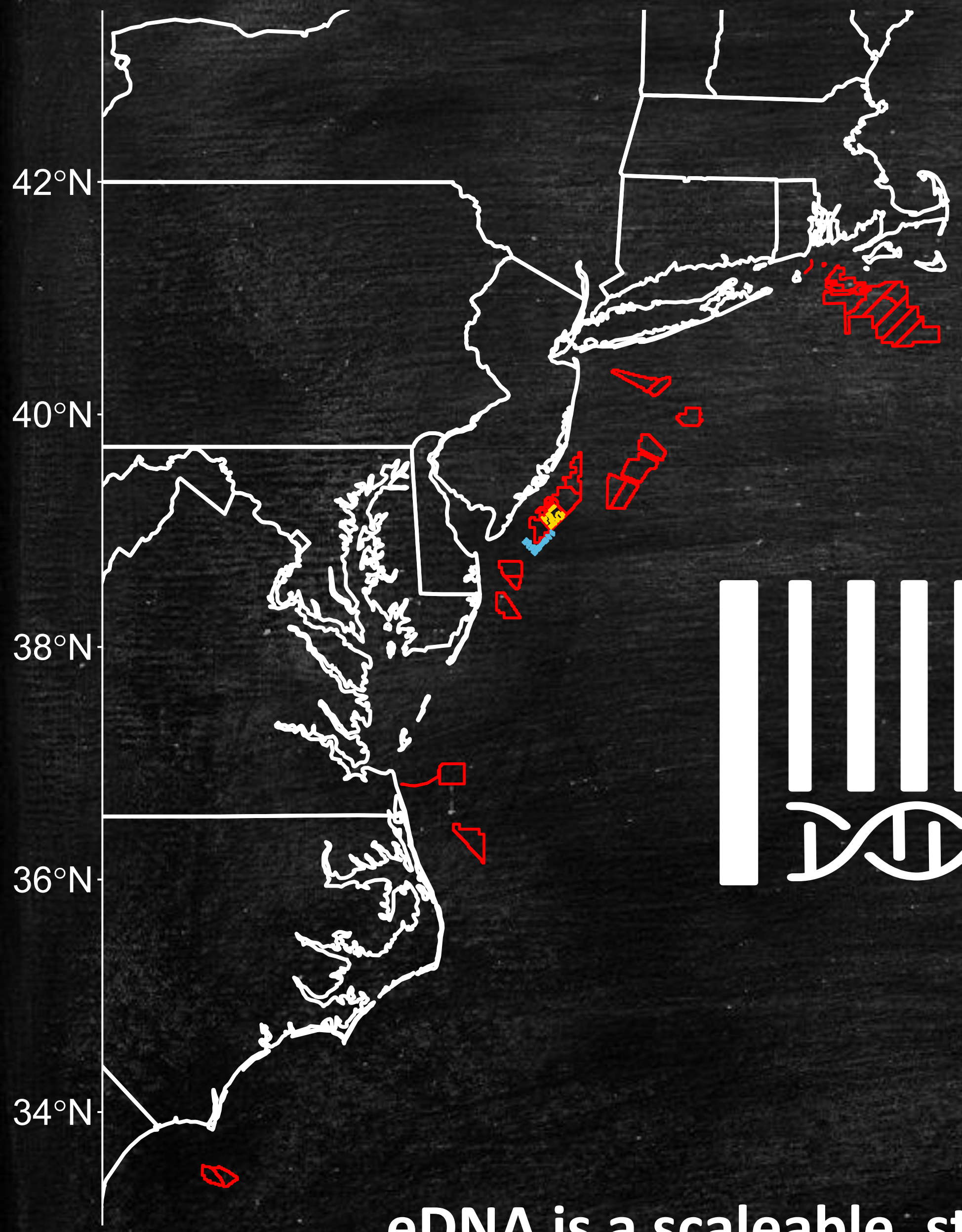


Environmental DNA effectively characterizes pre-construction fish communities at offshore wind sites

Shannon J. O'Leary, Sam Chin, Jason E. Adolf, Keith J. Dunton

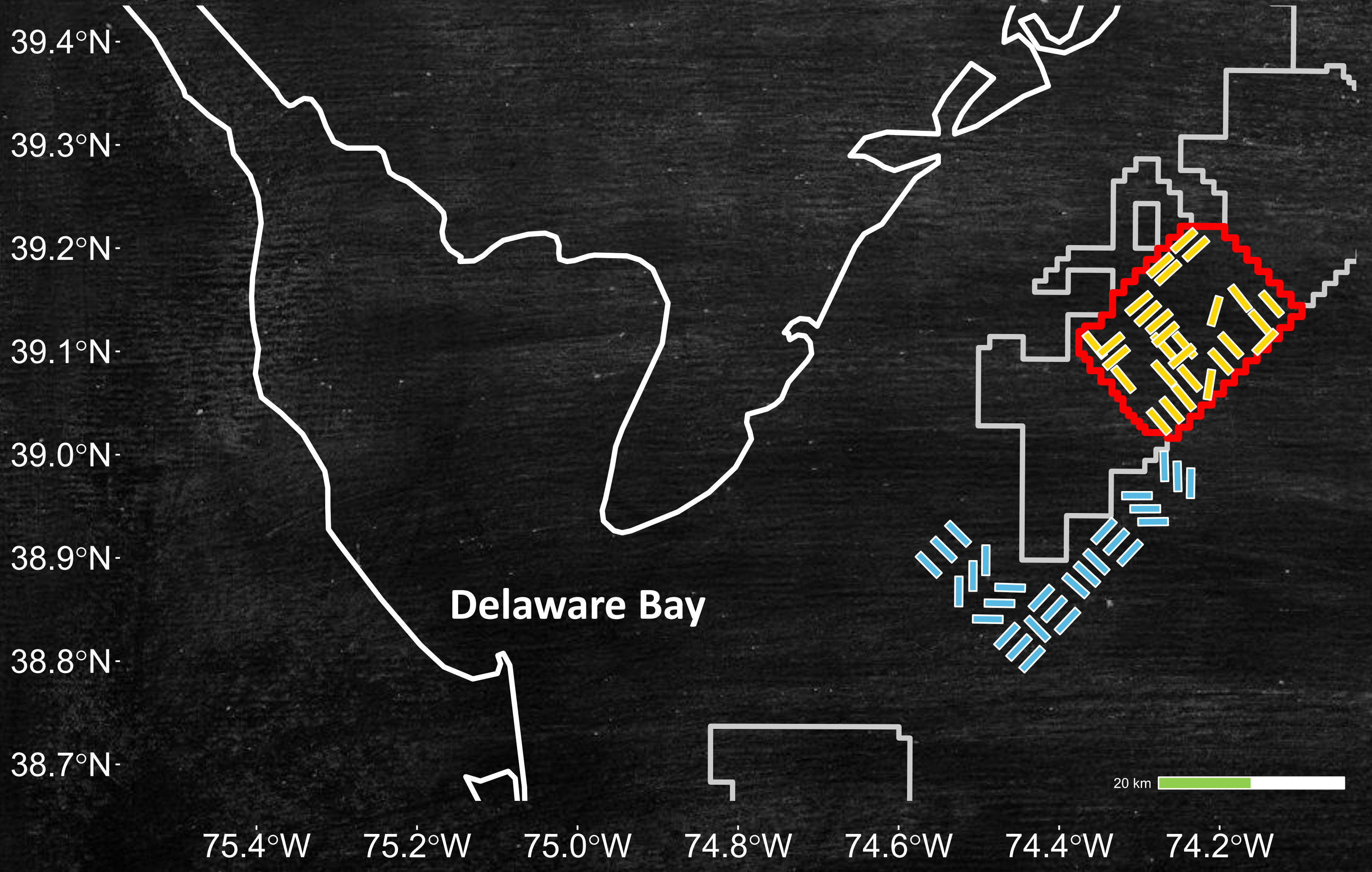


Environmental DNA is DNA captured from an environmental sample without the need for pre-isolating specific targets



- Low cost methods (scaleable)
- Simple sampling protocol (standardize across habitats)
- Easy access & few permitting issues
- minimal damage to habitat, target/bycatch species

eDNA is a scaleable, standardized, low-impact, low-equipment tool monitoring of the impact of large structures such as windfarms on ecosystems

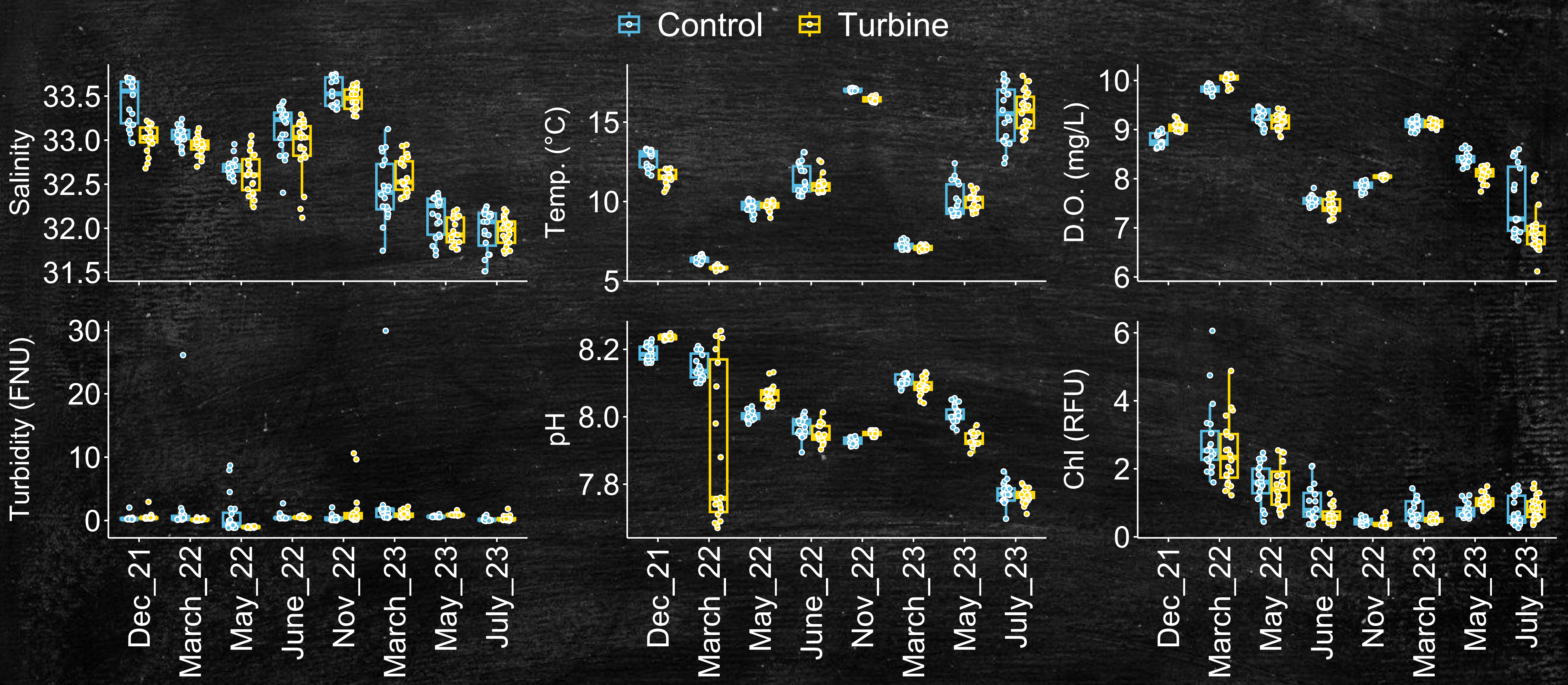


Offshore wind project with planned capacity of 1,100 MW to be operational in 2024

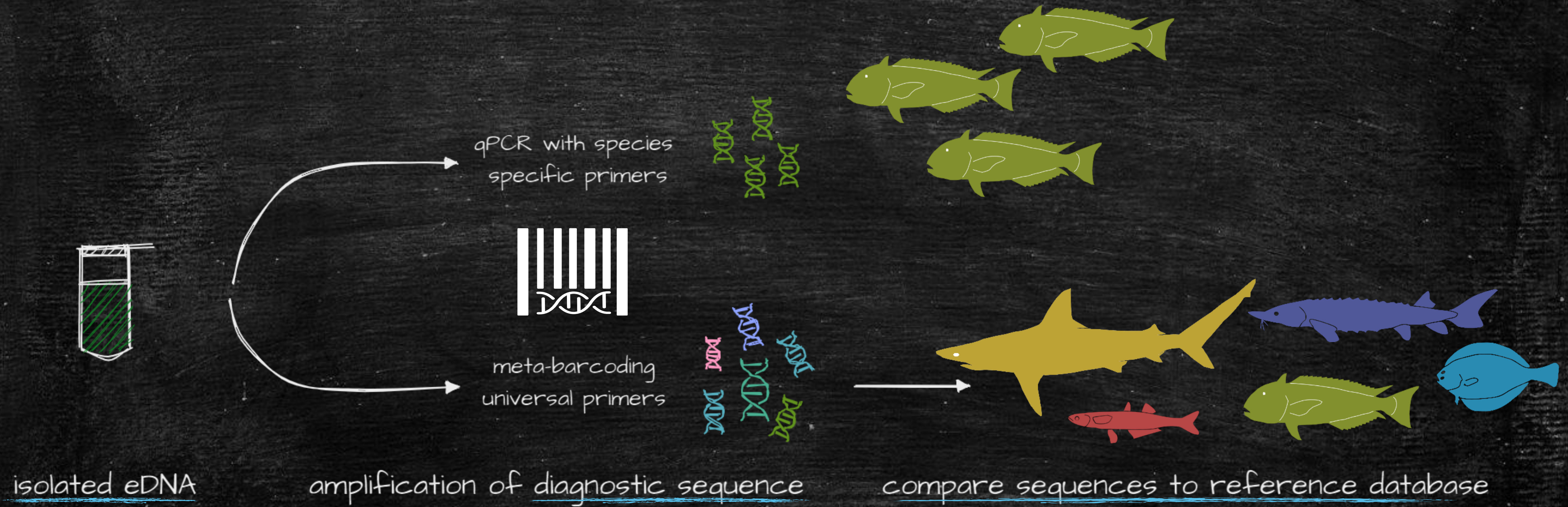
Turbine and **Control** sites consist of 28 stations

Quarterly **sampling bouts** for continuous monitoring of fish communities

Biomonitoring using environmental DNA to occur before, during, and after construction



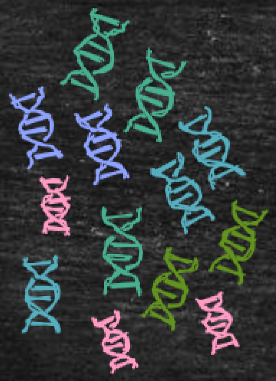
seasonal variability of environmental conditions is larger than between-site variation



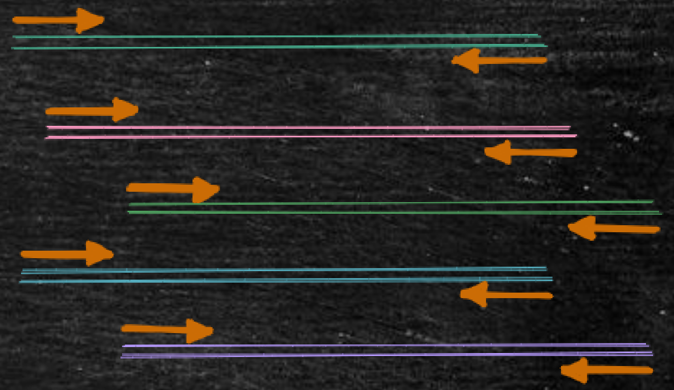
eDNA is useful for species-specific assessments and to characterize entire communities

even "universal" primers have bias that needs to be accounted for

e.g. Modified 16S primers (Riaz) amplified 2-3x more elasmobranchs compared to the standard set



isolated eDNA



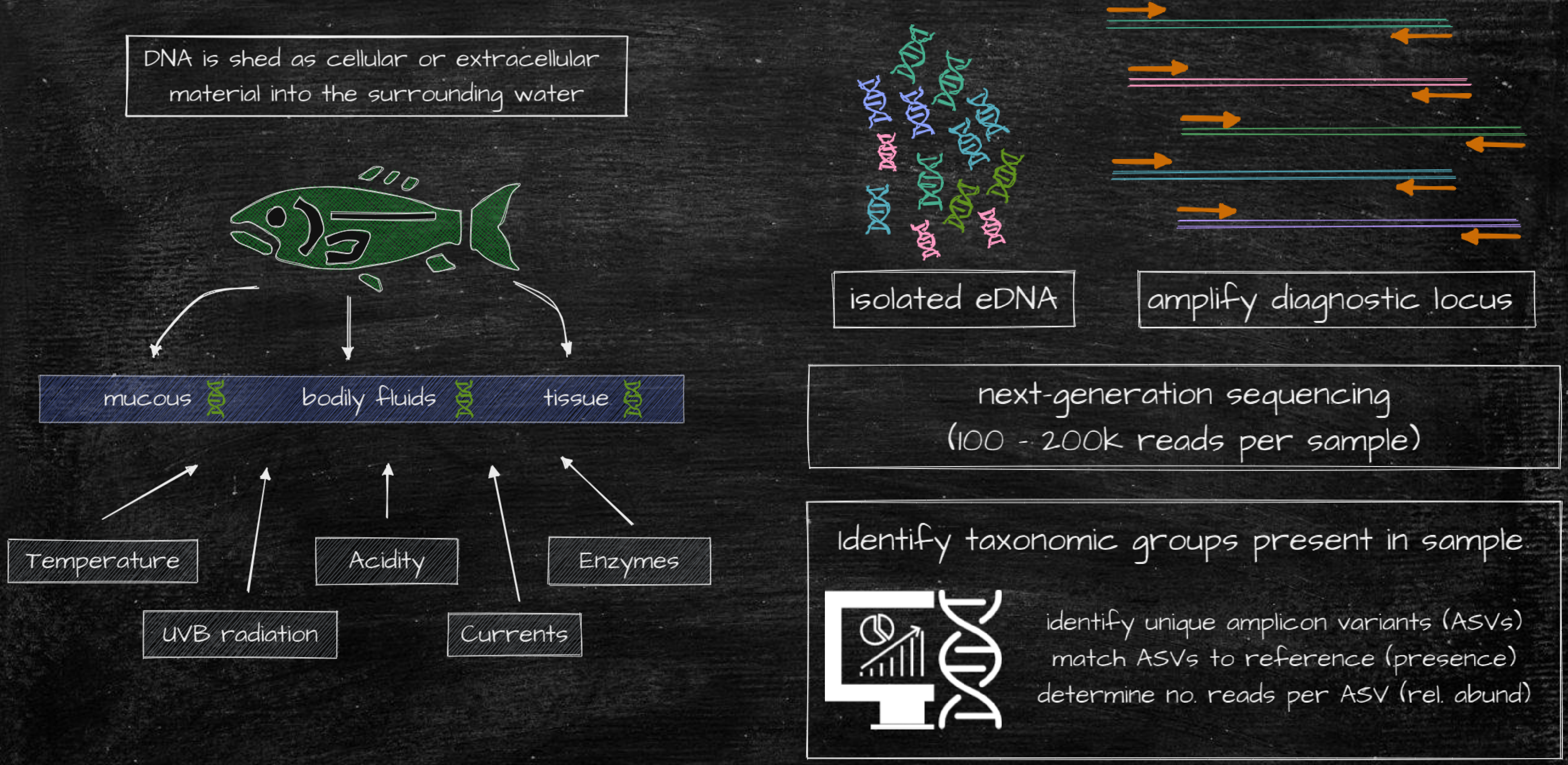
amplify diagnostic locus

next-generation sequencing
(100 - 200k reads per sample)

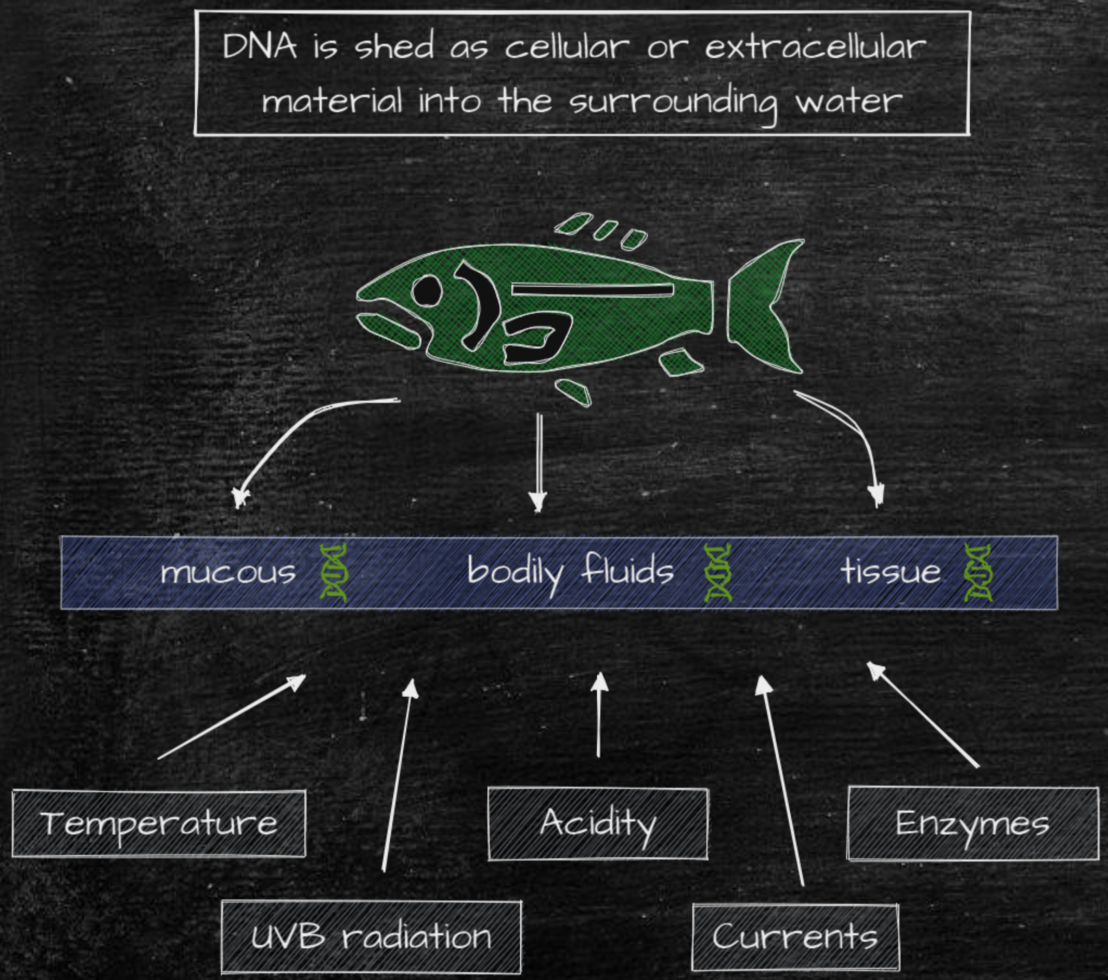
Identify taxonomic groups present in sample

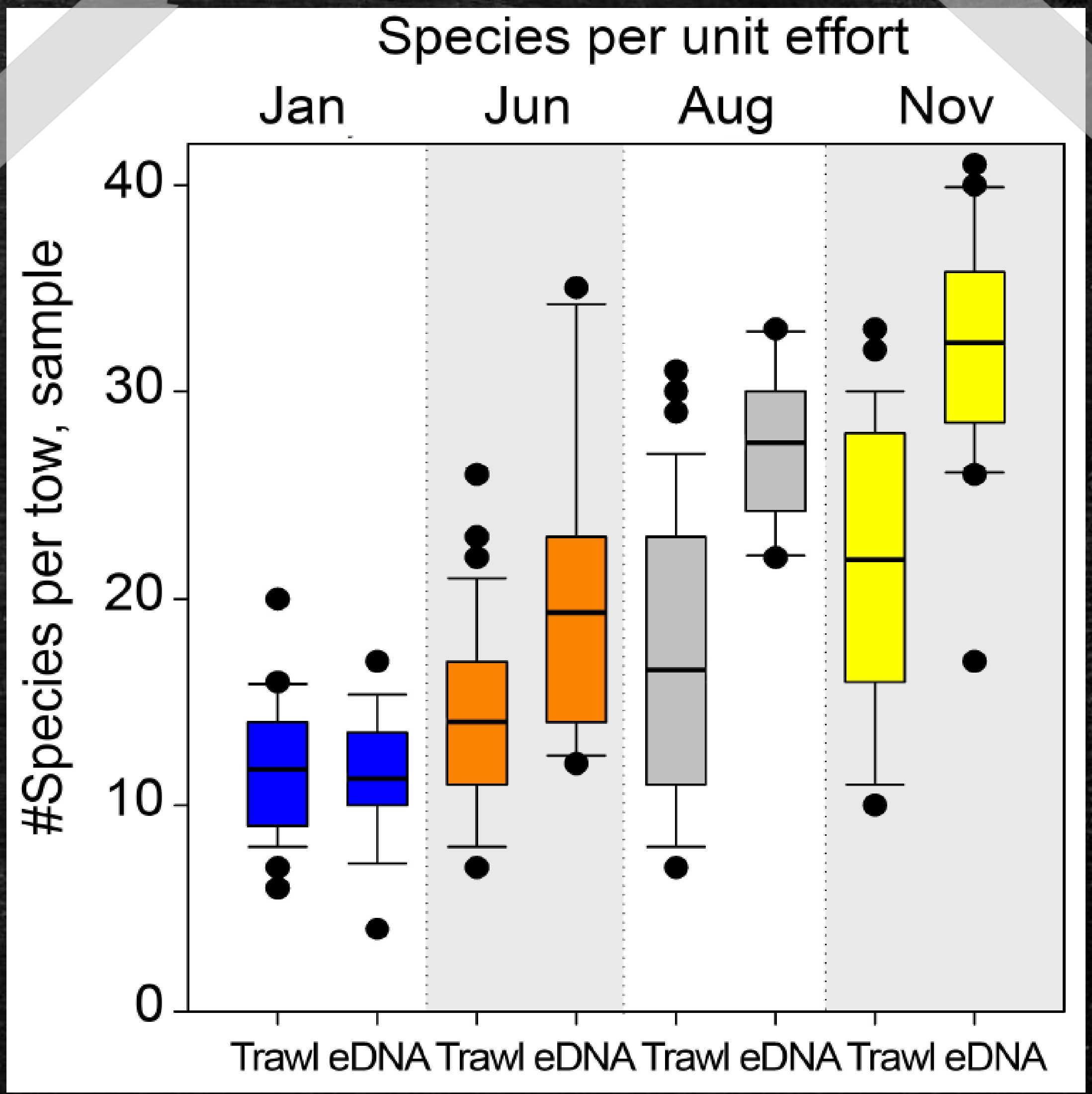
identify unique amplicon variants (ASVs)
match ASVs to reference (presence)
determine no. reads per ASV (rel. abund)

Metabarcoding can be used to characterize benthic fish communities



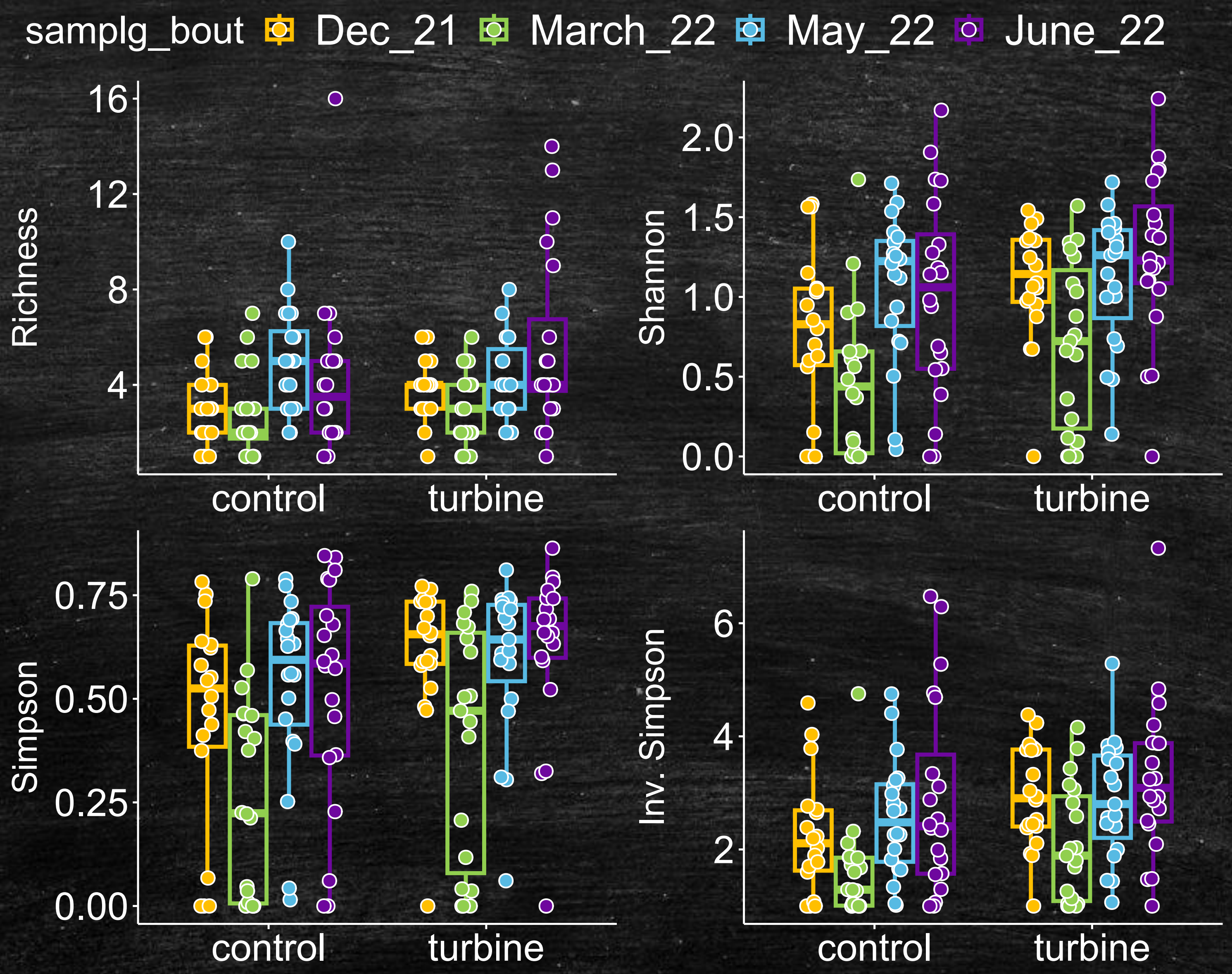
Metabarcoding is semi-quantitative: characterize presence & relative abundance



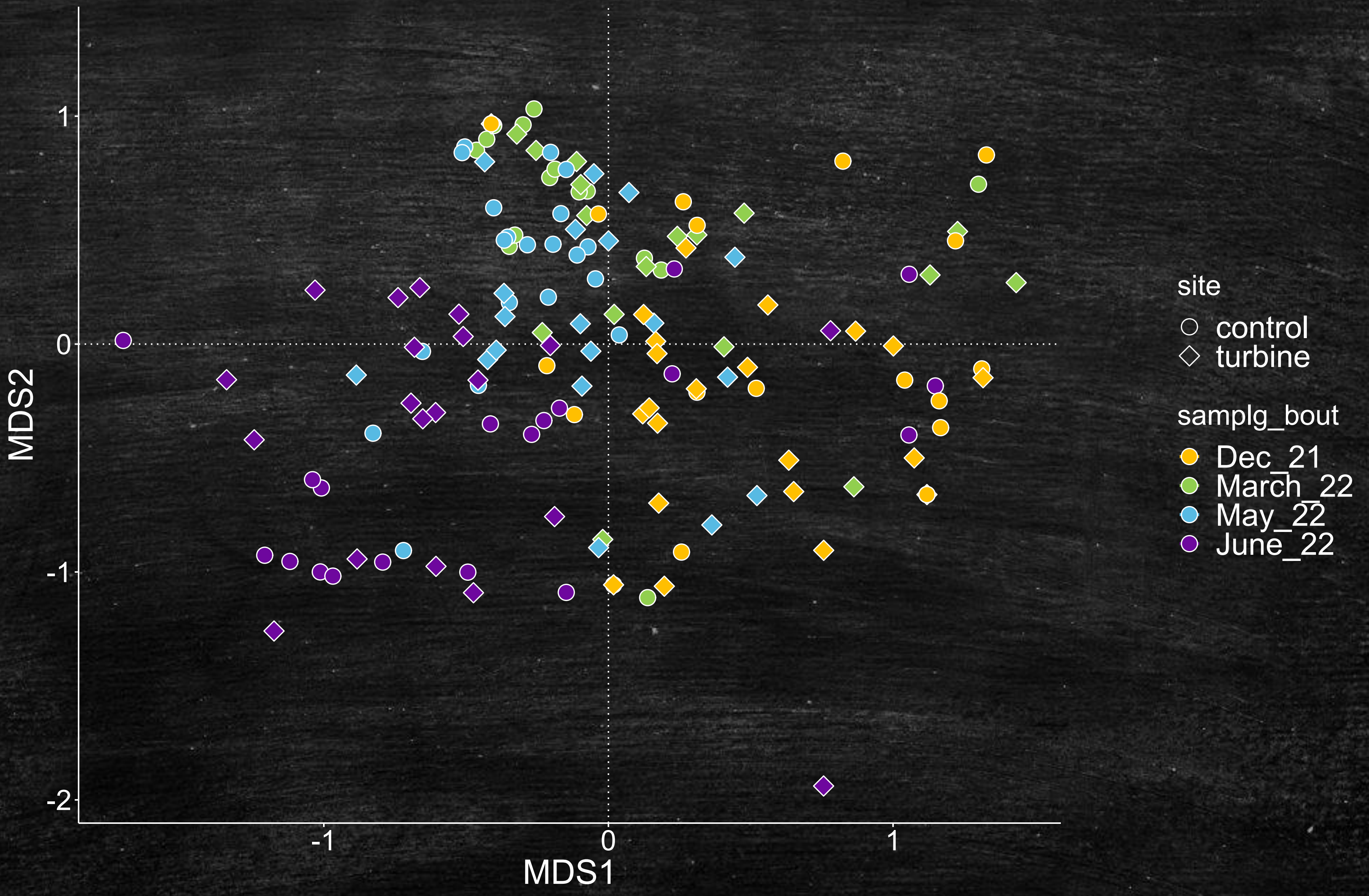


Stoeckle et al. 2020

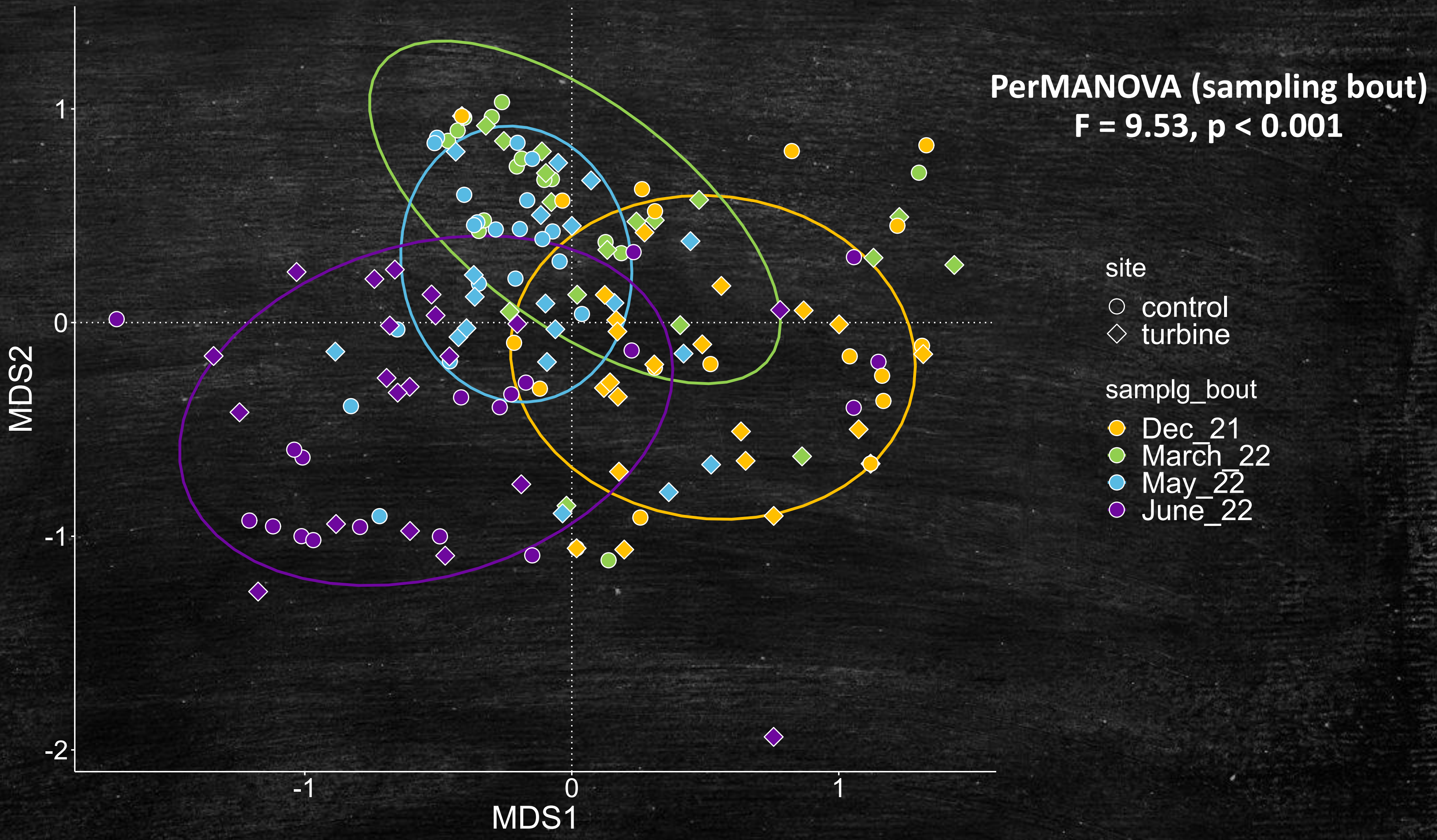
Metabarcoding is semi-quantitative: characterize presence & relative abundance



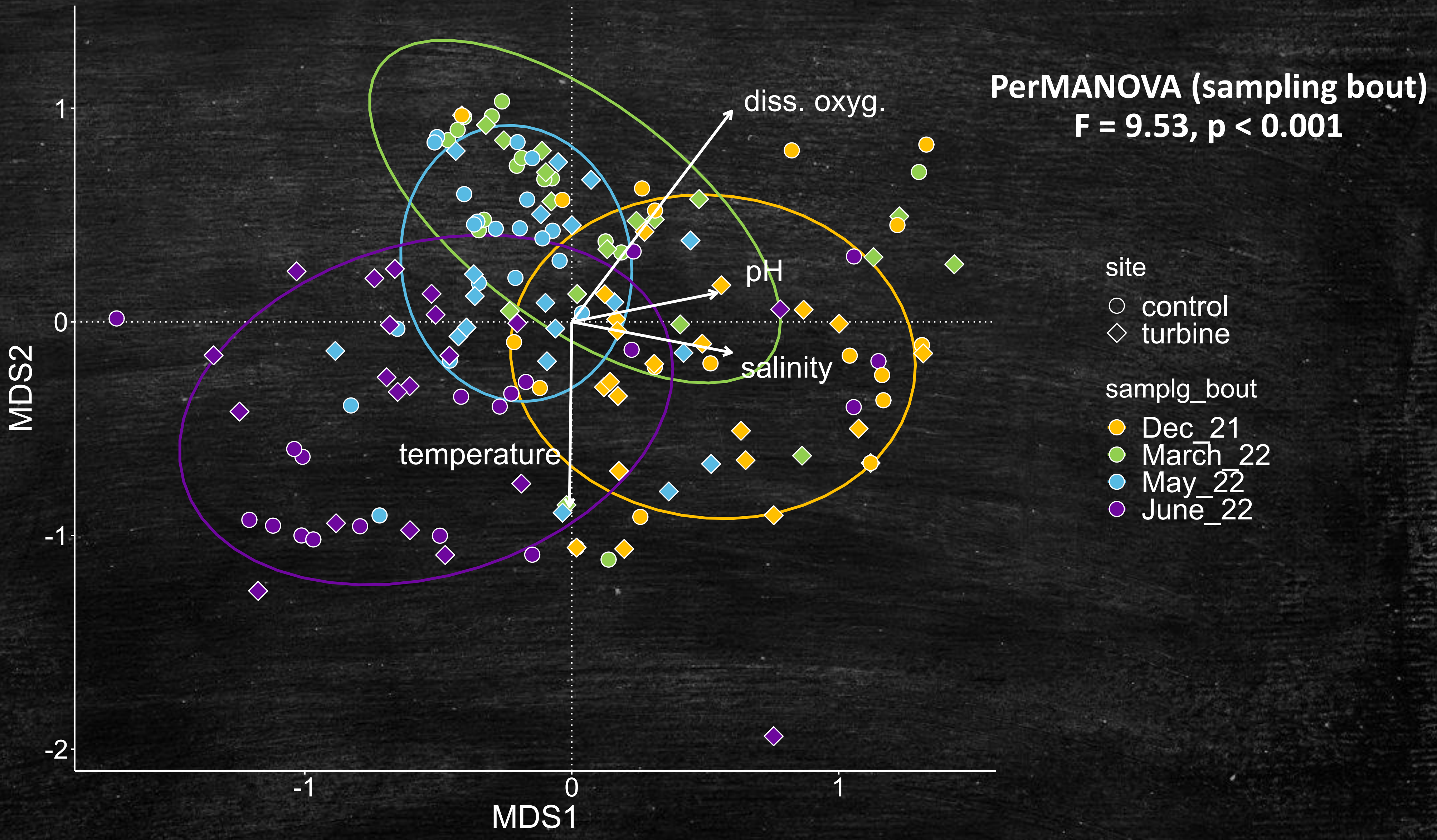
Differences in species abundance and diversity are driven by seasonal differences



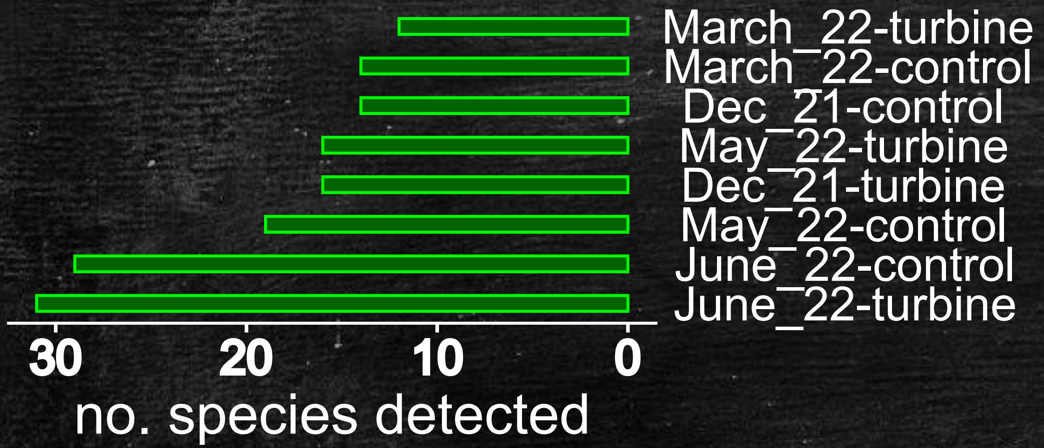
Structural diversity is driven by environmental variables and sampling season

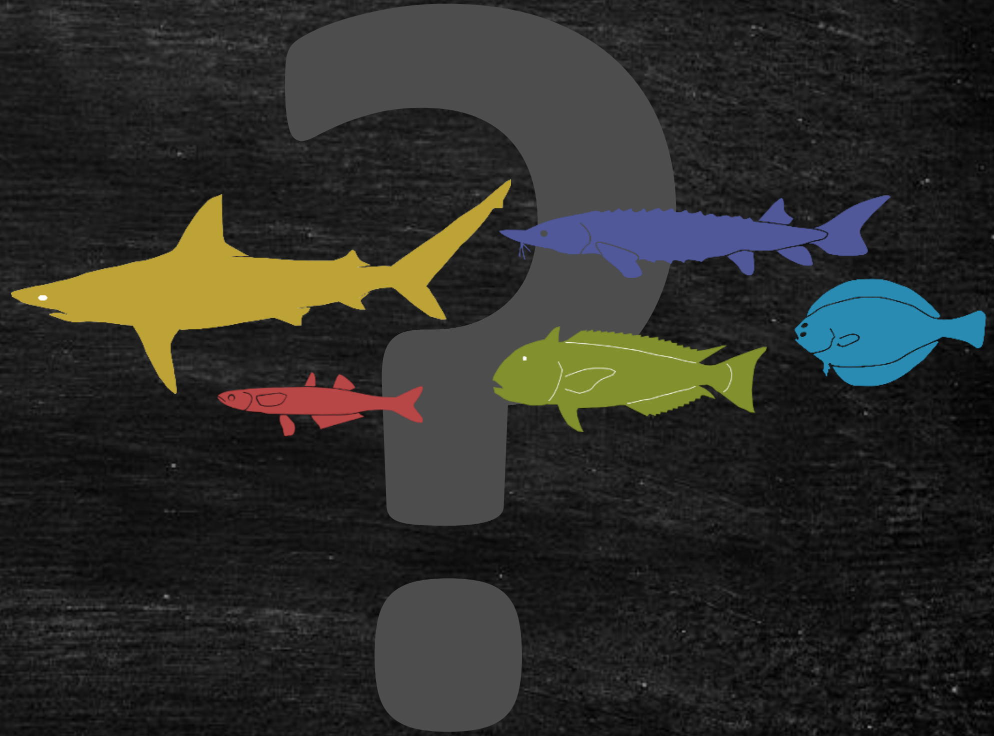


Structural diversity is driven by environmental variables and sampling season

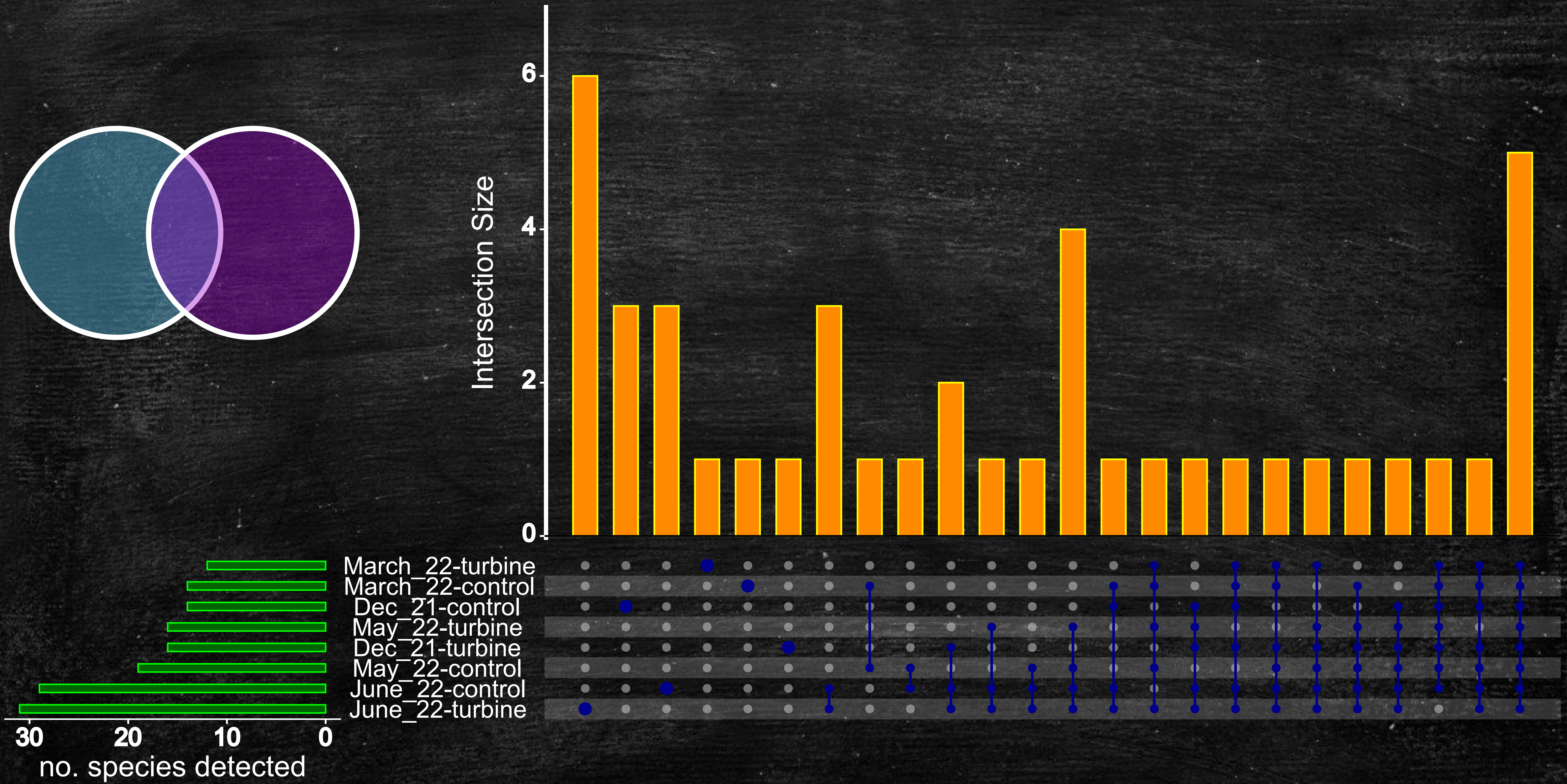


Structural diversity is driven by environmental variables and sampling season





A total of 43 species were detected across all stations and sampling bouts (mostly the usual suspects)



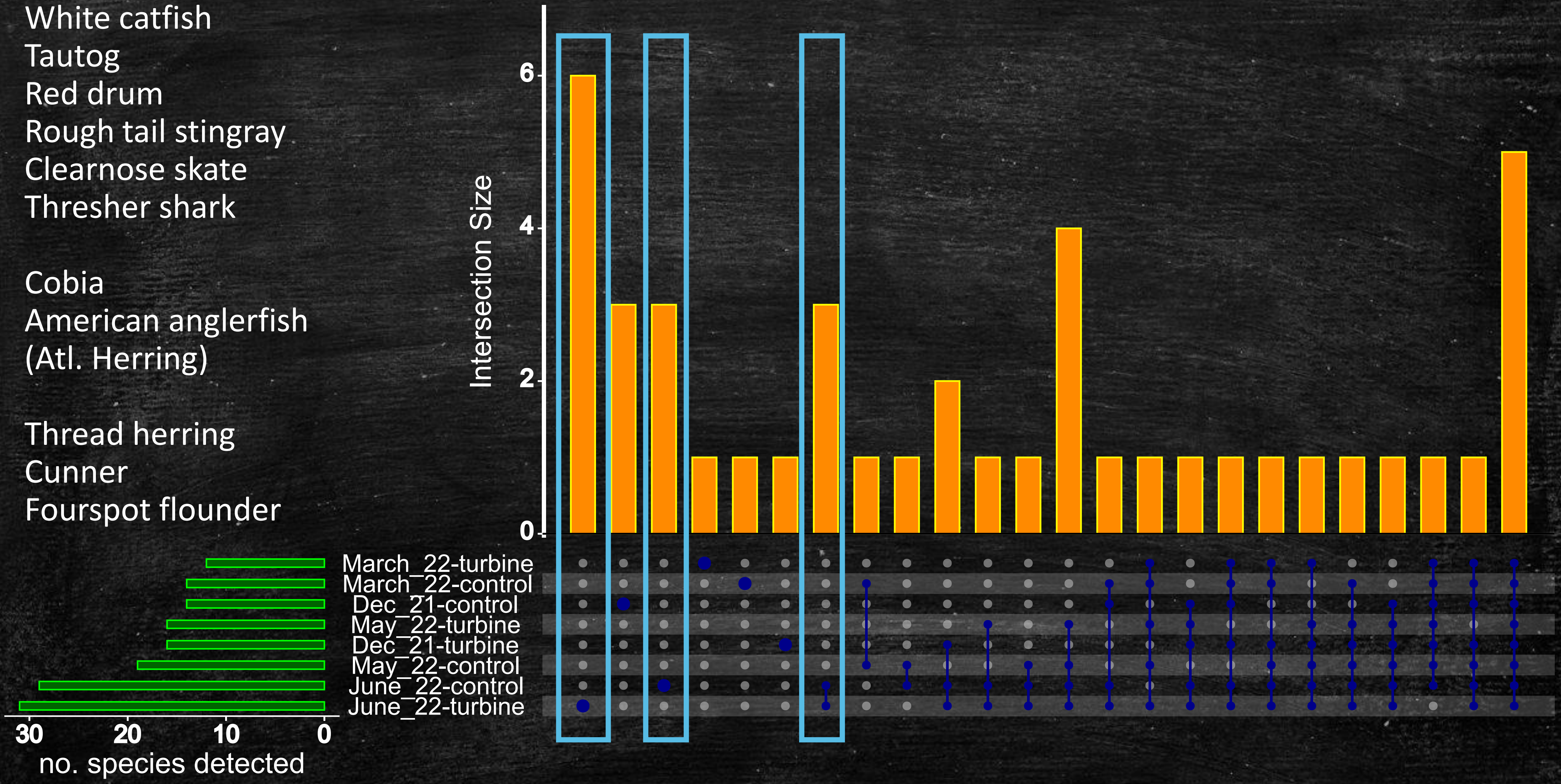
Five species were detected across all sampling bouts and seasons

June and December exhibit most unique species

White catfish
Tautog
Red drum
Rough tail stingray
Clearnose skate
Thresher shark

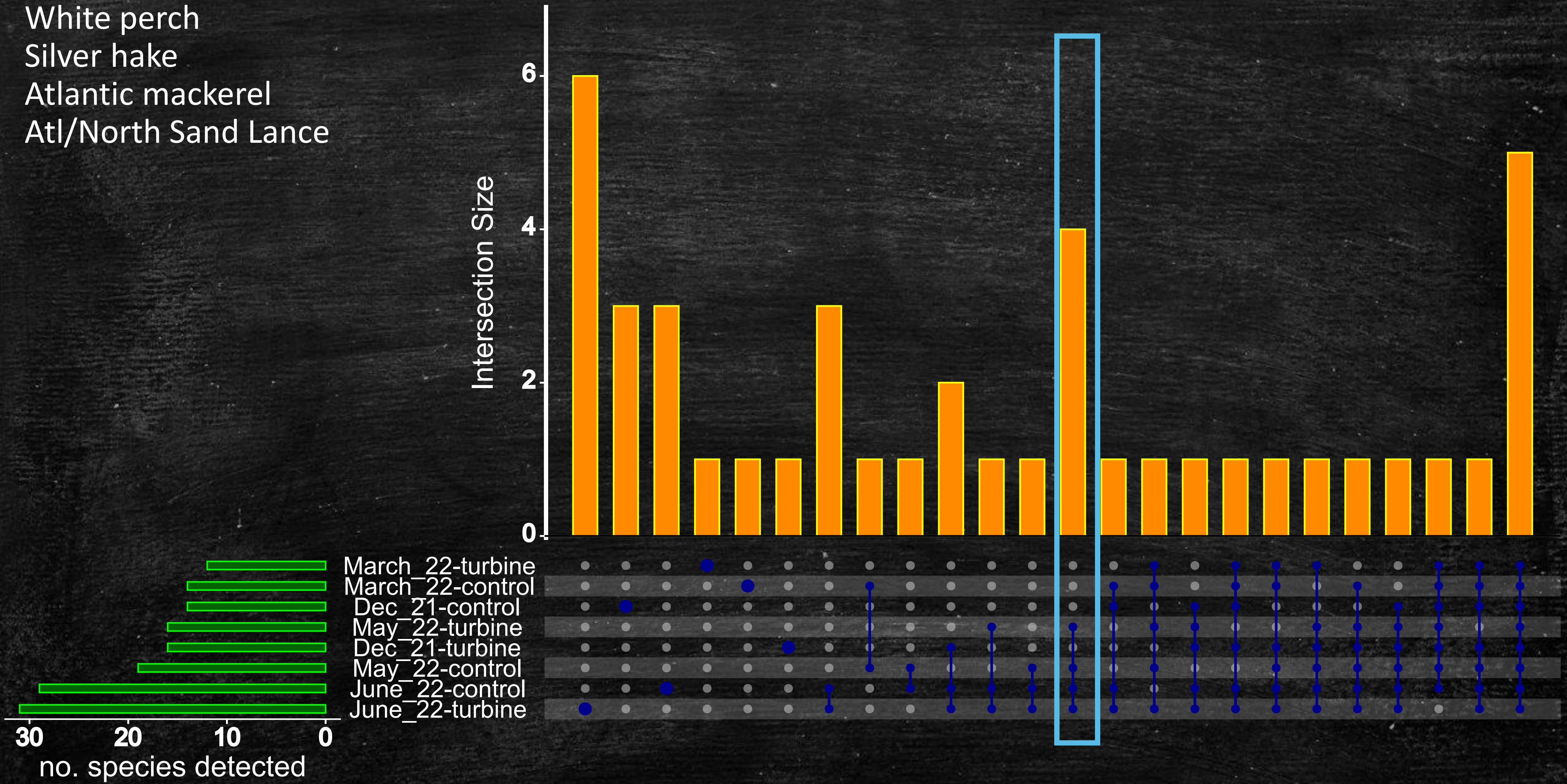
Cobia
American anglerfish
(Atl. Herring)

Thread herring
Cunner
Fourspot flounder



Five species were detected across all sampling bouts and seasons
June and December exhibit most unique species

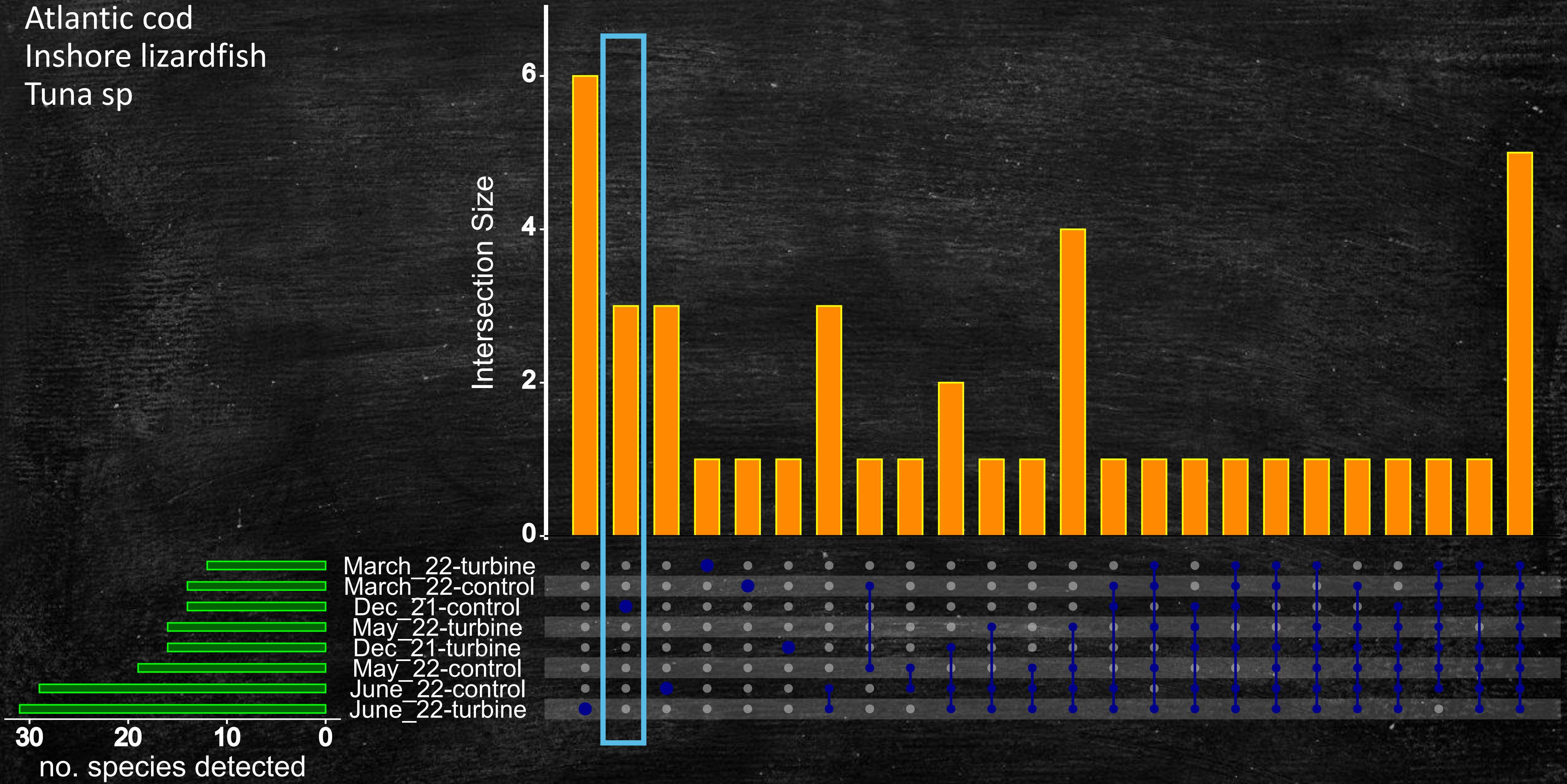
White perch
Silver hake
Atlantic mackerel
Atl/North Sand Lance



Five species were detected across all sampling bouts and seasons

June and December exhibit most unique species

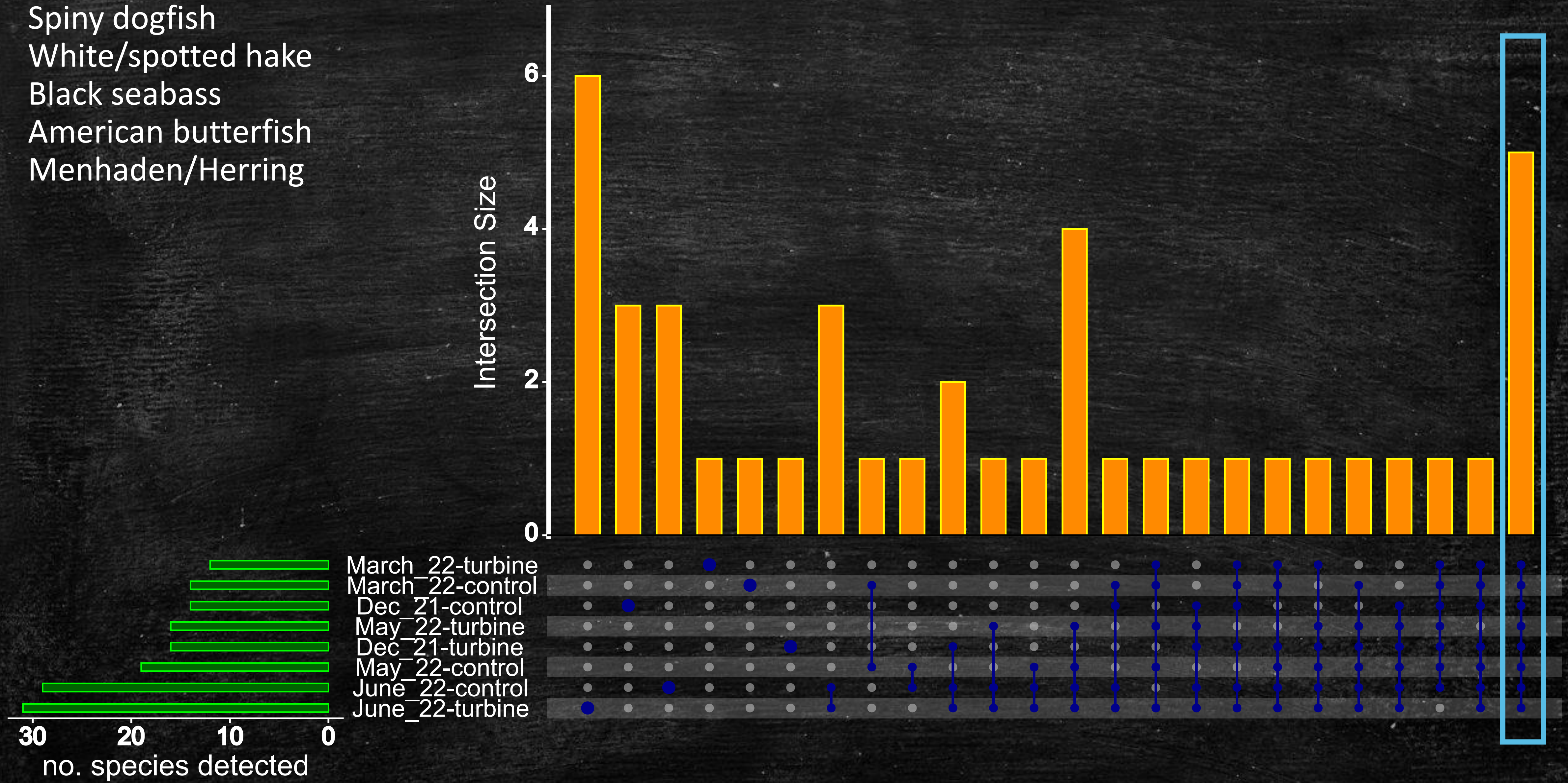
Atlantic cod
Inshore lizardfish
Tuna sp



Five species were detected across all sampling bouts and seasons

June and December exhibit most unique species

Spiny dogfish
White/spotted hake
Black seabass
American butterfish
Menhaden/Herring

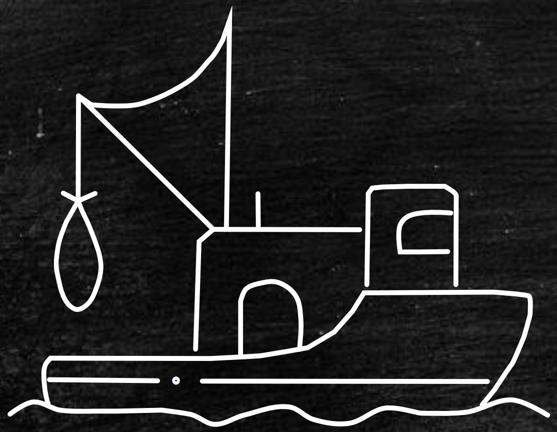


Five species were detected across all sampling bouts and seasons
June and December exhibit most unique species

Detections include species consistently caught at 35 – 65% of stations and those detected at only one or two during certain sample bouts

DNA captured from environmental samples without pre-isolating specific targets

- Low cost, simple, flexible sampling methods (scaleable)
- Standardize methods across wide range
- minimal damage to habitat, target/bycatch species
- few permitting issues
- Need more calibration studies to understand “gear bias” (DNA degradation, relative abundance estimates)



Specimen are extracted from their ecosystems with potential impact on habitat from fishing

- Biological data of captured specimen
- Existing long-term data sets
- Gear-bias well-understood
- Established methods for analysis & application to stock assessments

Potential and Pitfalls of using eDNA for biomonitoring compared to traditional sampling

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Questions?