Great Sandy Strait Seagrass Environmental DNA

Pilot study: November 2024

Queensland Government

Prepared by: Aquatic Ecosystem Health, Water Ecosystem Science, Department of the Environment, Tourism, Science and Innovation.

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Cover artwork by Navada Currie, Mununjali and Kabi Kabi woman at Gilimbaa.

April 2025

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Introduction

Following multiple flood events in 2022, seagrass habitats in the Wide Bay region, primarily the Great Sandy Strait (GSS) and Hervey Bay suffered major losses, which in turn had significant impacts on associated species, including those of conservation concern, such as dugong and turtles.

$1.5m was allocated to support marine species rehabilitation as part of the Disaster Recovery Funding Arrangements (DRFA) Category D 2021/22 Severe Weather Events Environmental Recovery Program. This funding supported post-flood monitoring surveys of seagrass habitats in the region, which were conducted in May and October/November 2022 (York et al., 2022; Bryant et al., 2023), and August to November 2023 (Bryant et al., 2024). Long-term monitoring at key intertidal and subtidal sites was recommended to continue to assess seagrass recovery (Bryant et al., 2023).

In November 2024, environmental DNA (eDNA) sampling was trialled at intertidal seagrass monitoring sites, and a seagrass site in proximity to the mouth of the Mary River. Key objectives were to test if key associated species were amenable to detection via these techniques, including those of conservation concern, such as dugong and turtles, and to characterise site specific differences in microbial groups that may be indicative of seagrass health and water quality.

Methods

Between 18 - 19 November 2024, seagrass locations at seven intertidal sites were sampled for eDNA, *in situ* water quality, and seagrass percentage cover estimated. Sampling locations are summarized in Figure 1.

At each sampling site, six replicate surface water (0.2 m) samples were filtered for eDNA analysis using Wilderlab wetland kits. Site water was filtered until filter blockage, with sample volumes ranging between 420 mL – 1140 mL (Table 1). Site water depth at the time of sampling was no greater than 3 m, with sites sampled on an outgoing tide, to maximise detections of biota associated with seagrass habitat.

Water quality indicators were measured *in situ* as per the Water Quality Monitoring and Sampling Manual (DES, 2018), with seagrass percent cover estimated based on camera drops at each site.

Environmental DNA samples were analysed via the Wilderlab comprehensive panel, which combines multiple assays for a universal tree of life approach. Noting that total detections are not directly comparable between sites owing to differing volumes filtered and therefore unit sampling effort. Detections include a range of taxonomic levels (i.e. species, genus, family, order). More technical detail on the analytical methods applied can be found at: Laboratory methods for Wilderlab ECOSCAN(TM) panels.

Water quality and eDNA data were analysed in PRIMER/PERMANOVA (v7.0.23). Water quality data was square root transformed and normalised. EDNA data was converted to presence/absence data, and distances between samples calculated with Euclidean distance.

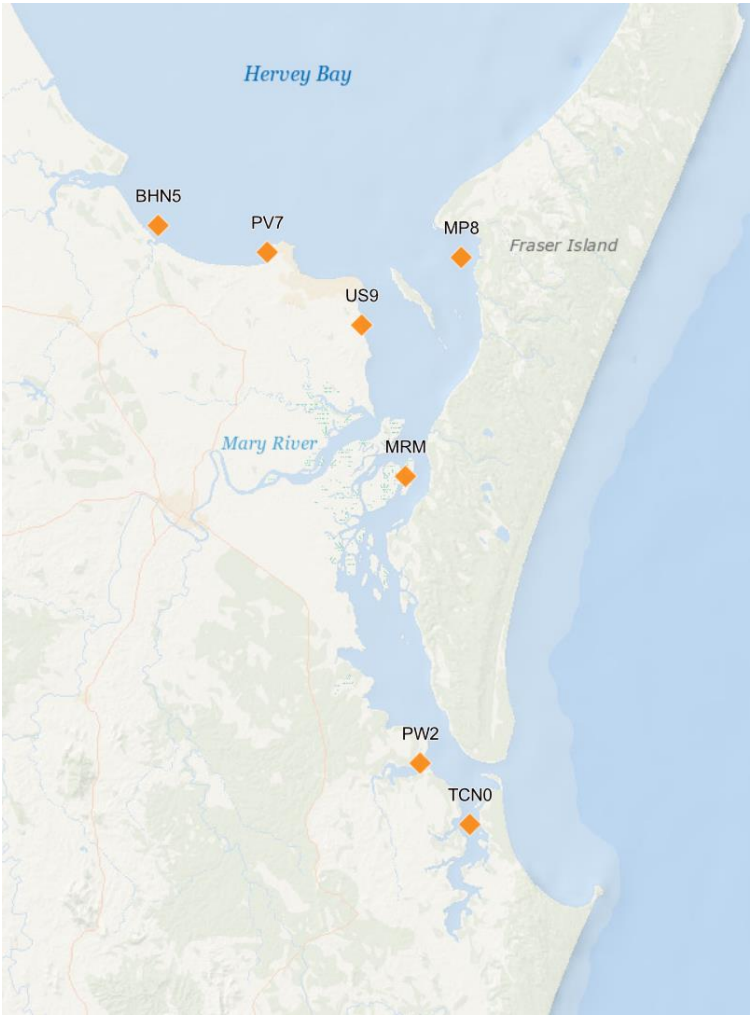


Figure 1 Environmental DNA and in situ *sampling locations, sampled between 18-19 November 2024*

Results

Water quality indicators and seagrass cover

Surface water quality data is summarised in Table 1. Sites ranged from more marine influenced sites (Moon Point, Point Vernon, Tin Can Bay), typified by higher specific conductivity (SpCond), water clarity, pH and lower turbidity, to those more exposed to more turbid and nutrient rich freshwater inflows (Burnett Heads, Mary River Mouth, Urangan and Poona).

The clearest waters were observed at Moon Point (secchi depth 6.5 m; 0.52 NTU), whereas the most turbid sites were further south at the Mary River Mouth (secchi depth 1 m; 6.07 NTU), and Poona (secchi depth 0.8 m; 5.83 NTU). Values for fluorescent dissolved organic matter (fDOM) were elevated at Poona (12.18 ppb), and to a lesser degree further south at Tin Can Bay (1.39 ppb). At Poona, the measured surface water pH was also low (pH 7.9), relative to other sites (pH 8.1 - 8.2), coupled with elevated indicators of *in situ* chlorophyll a (0.3 µg/L).

Photographs of the sampled seagrass locations are summarised in Table 2. Sites varied in terms of total estimated seagrass cover, ranging from 5% at Point Vernon, to 85% at Tin Can Bay, with patchy cover and epiphytic growth observed at the majority of sites. The most abundant genus was *Zostera*, which was observed at all sites (Table 2).

Site total seagrass cover was correlated to differences in water clarity, being lower at more turbid sites and higher at clearer water sites; negatively correlated with the water quality indicator for turbidity (-0.55); and positively correlated with pH (0.46) and secchi depth (0.44) (See Appendix, Table 4).

Environmental DNA detections

All eDNA data including photo and wheel of life summaries for this study are available at the Wilderlab site (https://www.wilderlab.co.nz/explore).

Seagrass eDNA was detected at all sampled sites. Three seagrasses were identified to species level, *Zostera muelleri ssp capricorni, Halophila decipiens*, and *Halodule uninervis*. These detections reflect the most abundant species observed at shallow seagrass sites during recent post-flood monitoring surveys in 2023 (Bryant et al., 2024).

Dugong (*Dugong dugon*) eDNA was detected at four sites, Burnett Heads, Moon Point, Tin Can Bay, and Poona. Only one dugong was observed during sampling, at the Moon Point site. Turtle eDNA, which included green sea turtle (*Chelonia mydas*), was detected at Moon Point and Poona, with multiple turtles observed at Poona during sampling. These sites all had total estimated seagrass cover above 20% at the time of sampling.

Other notable detections included, dolphin eDNA, including spinner dolphin (*Stenella longirostris*) at Moon Point, and at the Mary River Mouth site, and a reportable terrestrial invasive pest, brown marmorated stink bug (*Halyomorpha halys*), at Tin Can Bay, which has been reported to DPI for further investigation.

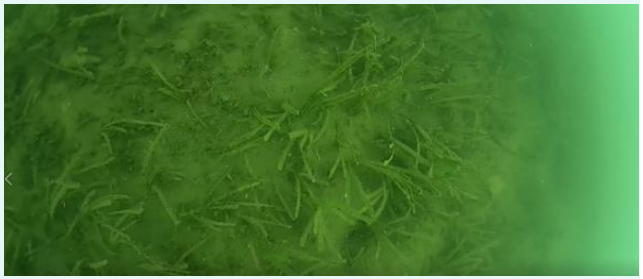
A diverse array of eDNA was detected at sampled sites, including species of sharks, rays and bony fishes, invertebrates, including corals, planktonic groups, and birds. A summary by site and identified group is provided in the Appendix in Table 5.

Table 1 eDNA sampling site in situ *surface (0.2 m) water quality data*

Site	Site code	Temp (°C)	Depth (m)	DO (%)	DO conc (mg/L)	pH	SpCond (mS/cm)	Turb (NTU)	fDOM (ppb)	Chl a (µg/L)	Secchi (m)	eDNA volume (mL)
Burnett Heads North	BHN5	28.7	0.8	112.7	7.16	8.2	53.66	2.76	0.01	0.13	2.5	840 – 900
Point Vernon	PV7	29.0	1.0	106.4	6.72	8.1	54.55	1.88	0.01	0.06	1.8	1080
Moon Point	MP8	26.7	1.8	100.9	6.61	8.2	54.09	0.52	0.01	0.01	6.5	1140
Urangan South	US9	27.6	2.8	105.2	6.80	8.2	54.12	2.97	0.01	0.04	1.55	780 – 840
Mary River Mouth	MRM	27.8	1.5	105.3	6.79	8.1	53.74	6.07	0.01	0.05	1.0	420 – 840
Poona West	PW2	29.5	0.9	106.1	6.65	7.9	53.93	5.83	12.18	0.30	0.8	420 – 840
Tin Can Bay	TCN0	29.0	0.8	125.9	7.98	8.2	53.41	1.72	1.39	0.12	1.7	840

Table 2 Seagrass site data

Site	Site code	Zostera cover (%)	Halophila cover (%)	Total seagrass cover (%)	Notes	Dominant substrate	Site photo
Burnett Heads North	BHN5	35 – 50	0	35 – 50	Patchy; Epiphytes	Sand	
Point Vernon	PV7	5	0	5	Patchy	Sand	
Moon Point	MP8	45 – 60	0	45 – 60	Consistent	Sand	

Site	Site code	Zostera cover (%)	Halophila cover (%)	Total seagrass cover (%)	Notes	Dominant substrate	Site photo
Urangan South	US9	30 – 40	25 – 40	55 – 80	Patchy; Epiphytes	Sand	
Mary River Mouth	MRM	5 – 15	0	5 – 15	Patchy; Epiphytes	Mud	
Poona West	PW2	20 – 35	0	20 – 35	Patchy; Epiphytes	20 – 35	

Site	Site code	Zostera cover (%)	Halophila cover (%)	Total seagrass cover (%)	Notes	Dominant substrate	Site photo
Tin Can Bay	TCN0	70 – 85	0	70 – 85	Patchy; Epiphytes	70 – 85	

Table 3 Notable eDNA detections by site (0 = not detected, 1= detected)

Group	Detection	Site						
		Burnett Heads North	Point Vernon	Moon Point	Urangan South	Mary River Mouth	Poona West	Tin Can Bay
		BHN5	PV7	MP8	US9	MRM	PW2	TCN0
Seagrass	*Zostera capricorni*	1	1	1	1	1	1	1
	Halophila	1	0	1	1	1	1	1
	Halophila decipiens	0	0	0	0	1	0	1
	Halodule uninervis	1	1	1	1	1	1	1
Mammals	Dugong, *Dugong dugon*	1	0	1	0	0	1	1
	Spinner dolphin, *Stenella longirostris*	0	0	1	0	0	0	0

Group	Detection	Site						
		Burnett Heads North	Point Vernon	Moon Point	Urangan South	Mary River Mouth	Poona West	Tin Can Bay
		BHN5	PV7	MP8	US9	MRM	PW2	TCN0
	Dolphins, *Delphinidae*	0	0	1	0	1	0	0
Turtles	Green turtle, *Chelonia mydas*	0	0	1	0	0	1	0
	Cheloniidae	0	0	1	0	0	0	0
Stony corals	*Acropora*	0	1	0	0	0	0	0
	Goniopora	0	1	0	0	0	0	0
	Micromussa	0	1	0	0	0	0	0
	Pocillopora	0	1	0	0	0	0	0
	Porites	0	1	0	0	0	0	0
Soft corals	Soft corals	1	1	1	1	1	1	1

Site eDNA community

All sites differed significantly in their overall eDNA community (PERMANOVA, P = 0.001), and in their microbial (bacteria and archaea) communities (PERMANOVA, P = 0.001).

Detected biota at each site were summarized into two major dimensions (MDS1, MDS2), MDS1 explaining the majority of data variation (20%) between samples. There greatest dissimilarity in site community composition was between communities at the lowest turbidity and nutrient site, Moon Point, relative to the highest turbidity and nutrient site, Poona.

Along the second dimension (MDS2, 10%), the greatest dissimilarity in composition was between the detected communities at the coastal northern sites, Point Vernon and Burnett Heads, relative to the enclosed sites further south at Tin Can Bay and Mary River Mouth (Figure 3).

The eDNA community at Moon Point site was most differentiated by the correlated group, echinoderms (sea urchins, sea stars and brittle stars), whereas bacteria were correlated with differences at the Poona site. Cryptomonads (a type of algae), fungi, and ciliates best characterised Tin Can Bay eDNA, whereas birds and fish groups best explained differences in the Point Vernon community (Figure 3).

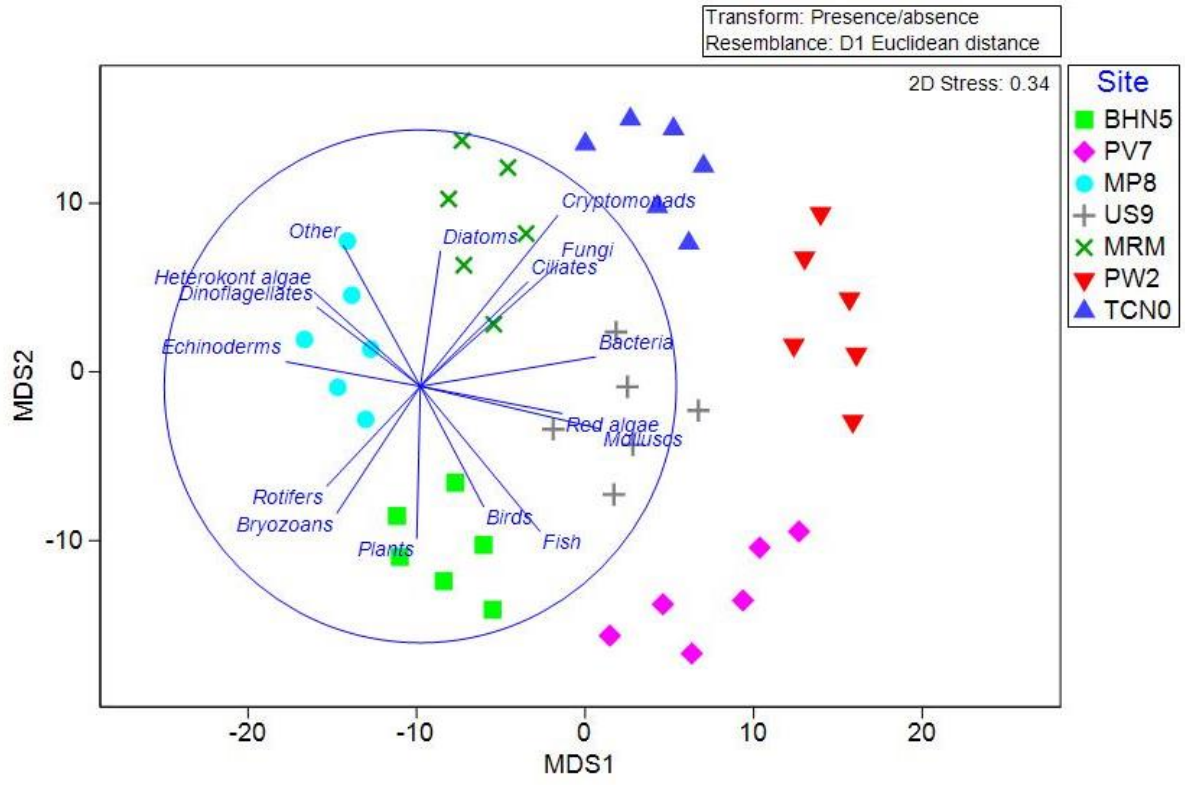


Figure 2 Metric Multi-Dimensional Scaling (MDS) plot of eDNA samples, coloured according to site. Vector overlay of correlated groups >0.5.

Considering only the microbial community (archaea and bacteria), less distinct site-specific separation was observed. However, the majority of the data variation (15%) was explained by differences between the microbial community at Poona, and to a lesser extent Tin Can Bay, and Urangan, versus the majority of other sites, primarily Mary River Mouth, Moon Point, and Burnett Heads. Differences at Poona were best characterised by *Flammeovirga* (chemoorganotrophic, deriving energy via the oxidation of reduced organic compounds), and *Spriochaetales* (free living or pathogenic, mostly anaerobes).

Environmental variables

Relating environmental variables to differences in the community composition observed across all sites, only temperature returned an overall significant result (DistLM, p=0.035). No individual water quality indicator significantly explained differences in microbial communities across all sites (DistLM, P>0.05).

Relating differences in measured environmental variables to site specific community composition (canonical analysis of principal coordinates, CAP), highly correlated variables included *in situ* chlorophyl, and to a lesser extent percent dissolved oxygen at Poona. Whereas at Urangan, Burnett Heads, and Tin Can Bay, differences in seagrass cover, and turbidly, were most highly correlated with differences in eDNA. In contrast at Moon Point, secchi depth was the most highly correlated variable with differences in community composition observed at this site (Figure 4).

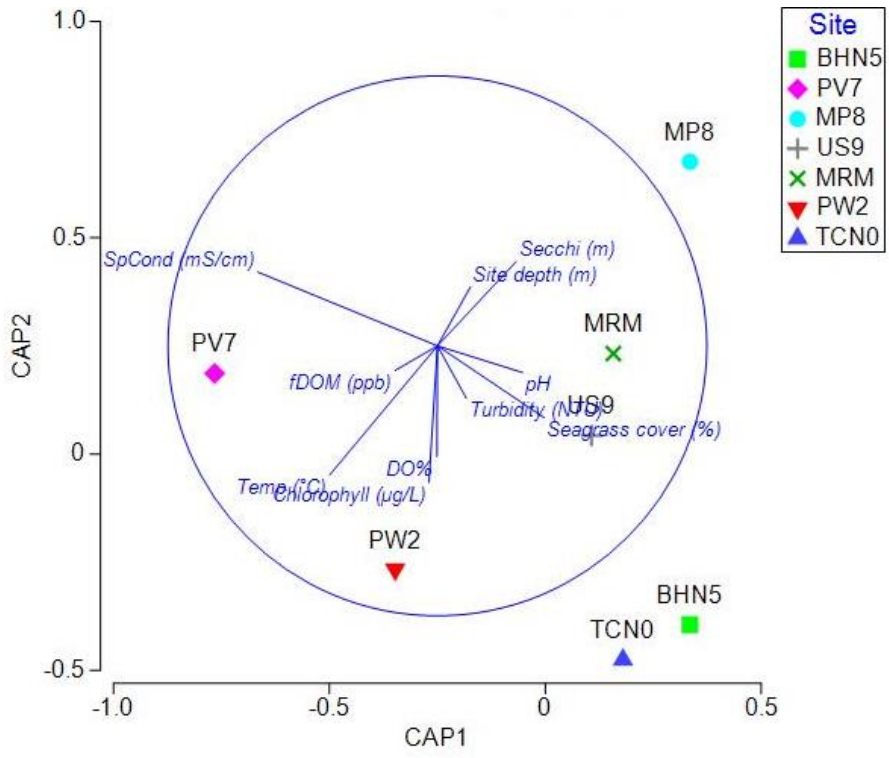


Figure 3 Canonical analysis of principal coordinates (CAP) of eDNA community by site, with vector overlay of environmental variables

Comparing site specific differences in environmental variables and observed microbial communities, differences in turbidity were most correlated with community composition at Poona, Burnett Heads and Mary River Mouth. Whereas at Moon Point, differences in seagrass cover, and secchi depth, were correlated with site specific differences in microbial communities (Figure 5).

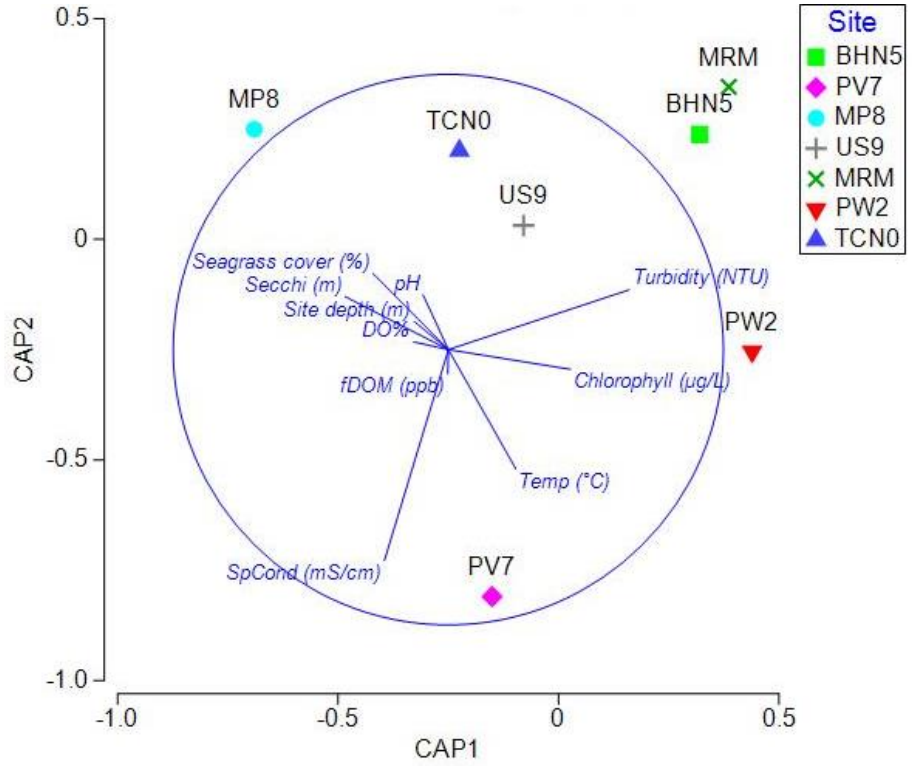


Figure 4 Canonical analysis of principal coordinates (CAP) of microbial community by site, with vector overlay of environmental variables

Conclusions

This pilot provides valuable insight into potential differences in community composition and water quality at recovering intertidal seagrass sites around the GSS and Hervey Bay. Sites sampled ranged from more marine influenced sites (Moon Point, Point Vernon, Tin Can Bay) to those exposed to more turbid and nutrient rich freshwater inflows (Burnett Heads, Mary River Mouth, Urangan and Poona).

Seagrass cover was dominated by the genus *Zostera,* and with exception of the clearest water site, Moon Point, cover was patchy, ranging from 5% at Point Vernon, to 85% at Tin Can Bay. Estimated total seagrass cover was correlated to differences in water clarity, typically with lower cover at more turbid sites, and higher cover at clearer water sites.

Environmental DNA successfully detected the presence of key intertidal seagrass species, species of conservation concern, and a possible notifiable terrestrial invasive species. However, it should be noted that the universal approach applied can lead to misidentifications at the species level, with database matching of closely related species. Targeted analysis is therefore required in order to confirm these possible detections.

Community composition detected via eDNA and correlated environmental variables were highly site specific. However, the biggest differences in detected biota were observed between sites across both a water quality and exposure gradient. Similarly microbial community composition differed according to site, though the two sites in closest proximity to freshwater influences showed the greatest similarity (Mary River Mouth, Burnett Heads), and were the most differentiated from the more marine influenced site (Moon Point).

Microbial indicators associated with heathy, and stressed seagrass were detected at all sampled sites. Indicators of healthy seagrasses included putative methylotrophic bacteria, iron cycling bacteria and nitrogen fixing bacteria, those associated with ‘stressed’ seagrasses include putative sulphur-cycling bacteria, both sulphide-oxidising and sulphate-reducing (Martin et al., 2020). Further analysis of the DNA extract may yield useful information into functional composition of the microbial communities at these sites and their relative abundances.

Given flooding has once again occurred in the area in March 2025, it would be beneficial to repeat this sampling to characterise change at these seagrass sites and their associated biota to monitor recovery.

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Appendix

Table 4 Correlation matrix of environmental data

	Temp (°C)	DO (%)	pH	SpCond (mS/cm)	Turb (NTU)	fDOM (ppb)	Chl a (µg/L)	Secchi (m)	Depth (m)
DO (%)	0.54								
pH	-0.56	0.20							
SpCond (mS/cm)	-0.17	-0.70	-0.10						
Turb (NTU)	0.41	-0.09	-0.65	-0.21					
fDOM (ppb)	0.62	0.14	-0.88	-0.19	0.45				
Chl a (µg/L)	0.88	0.39	-0.73	-0.35	0.57	0.85			
Secchi (m)	-0.66	-0.25	0.57	0.16	-0.85	-0.45	-0.63		
Depth (m)	-0.78	-0.57	0.30	0.35	-0.10	-0.41	-0.66	0.21	
Cover (%)	-0.25	0.43	0.46	-0.44	-0.55	-0.02	-0.11	0.44	0.20

Table 5 Environmental DNA detections by site and group

Group	Site						
	TCN0	PW2	BHN5	PV7	MP8	US9	MRM
Amoebae	2	2	0	0	0	0	0
Amphibians	0	1	0	0	0	0	1
Archaea	3	2	1	6	0	3	10
Bacteria	671	831	577	702	571	606	606
Birds	0	1	1	7	0	0	0
Bryozoans	4	3	13	8	8	5	4
Ciliates	213	307	202	169	204	221	220
Cnidarians	87	82	89	103	103	144	84
Crustaceans	129	176	148	215	170	129	173
Cryptomonads	67	68	35	42	43	47	52
Diatoms	111	118	85	103	101	98	142
Dinoflagellates	129	100	121	94	123	89	107
Echinoderms	5	0	6	0	7	1	1
Fish	143	260	205	274	169	180	96
Flatworms	7	5	5	5	0	0	0
Fungi	7	6	0	2	0	5	3
Green algae	81	83	73	74	83	79	78
Heterokont algae	84	58	72	33	90	65	56
Insects	5	3	0	8	1	0	0
Mammals	2	1	5	0	3	1	1
Mites and ticks	1	0	0	1	0	0	0
Molluscs	119	166	107	157	65	73	81
Oomycetes	10	8	7	0	3	0	1
Other	251	258	244	137	262	195	229
Plants	66	64	107	95	58	64	65
Red algae	38	30	15	42	16	42	19
Ribbon worms	13	15	14	13	21	19	19
Rotifers	1	0	6	1	1	0	0
Roundworms	1	3	0	0	0	0	0

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