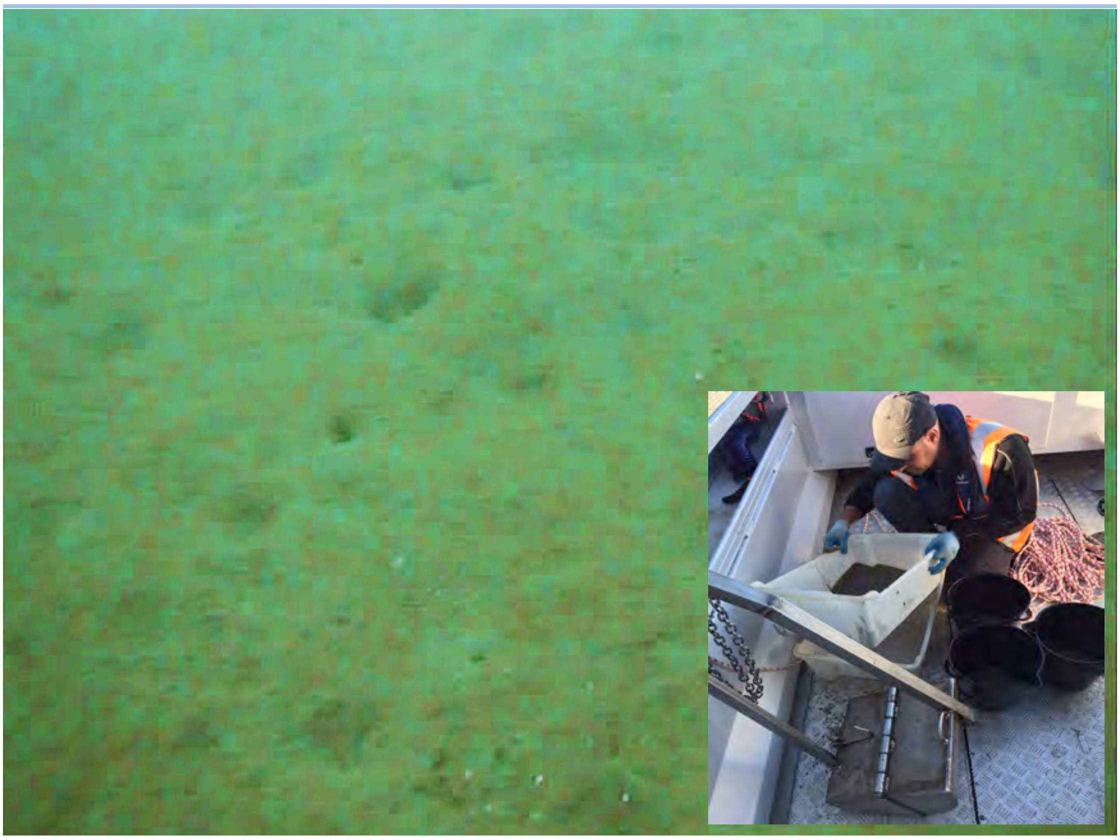
INFAUNA SURVEY – OFFSHORE DISPOSAL LOCATION

Eden Harbour – Breakwater Wharf Extension



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Cover Photo: Eden Breakwater Wharf, Snug Cove. NSW.

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1.0 Introduction

Department of Industry – Lands (DoI – Lands) is responsible for the management of approximately half of the land in NSW, encompassing the dry and submerged lands, up to 5.5 km offshore from the NSW coastline. The Department manage a range of built maritime assets, including 25 coastal harbours and 21 river entrances and maintains access to these assets, where appropriate.

Recently, the Port of Eden has seen increased activity from the cruise industry, however restricted by draft and length, cruise ships are currently unable to berth alongside land-based infrastructure (i.e. berth at the Breakwater Wharf). Consultation with the cruise industry and Port Authority NSW indicates that, while ships in the 220-260 m size range (and smaller) will continue to be used for over 30 years, there will likely be an increasing number of longer vessels (greater than 300 m) within 5-10 years.

In order to accommodate cruise ships of up to and exceeding 300 m in length, DoI – Lands has identified the need to extend the Eden Breakwater Wharf and dredge the approach channel and berth pock. To the spatial area of the proposed dredge footprint, will result in a maximum dredge volume of approximately 231,500 m^3, including an allowance for over-dredging (**Figure 1**).

The Department engaged Australasian Marine Associates (AMA) to support the permitting and approval requirements for the Breakwater Wharf Extension Project. As part of this scope of work, negotiations with State and Federal government regulators has been required. During the course of these meetings the Federal Government communicated their expectation for ecological characterisation at the proposed offshore dredge disposal location. This infauna characterisation work is a requirement for securing any future DoE issued Sea Dumping Permit. On 25 May 2015, a representative for the Commonwealth Department of Environment (Ms Kimberly Shields) clarified their expectations with the following written statement:

> *"The sampling will need to sufficiently inform on the potential impacts for placing the dredged spoil at the nominated disposal site. Refer to section 4.3 of the National Assessment Guidelines for Dredging (NAGD), which outlines a number of aspects that require your consideration when surveying the disposal site. The surveying you undertake will need to be representative of the entire site. It is also recommended that a few samples from outside of the footprint of the disposal site are completed to characterise/set baseline of ambient conditions."*

This infauna survey has been implemented to address the DoE requirement for characterising the offshore disposal site infauna community and has been specifically guided by NADG (Section 4.3) and the need to representatively sample the disposal site (including sampling from outside of the disposal site to characterise/set baseline conditions).

1.1 Ecological importance of Twofold Bay

Twofold Bay is the only ocean embayment in the Twofold Shelf bioregion. The bay comprises four wave dominated barrier estuaries, with extensive coastal and open water marine habitat. The diverse habitats of this region supports a range of migratory (i.e. marine mammals and epipelagic finfish) and residential marine communities (i.e. demersal fish and macroinvertebrates). The full description of the existing environment in the vicinity of the Twofold Bay area is described in the REF (AMA, 2015).

Infauna organisms are a vital component in marine ecosystems, as they provide a functional link between the physical environment and regional fauna. Benthic infauna communities are defined as the invertebrate fauna that are typically larger than 0.5 mm (Inglis, 1995), which predominately live in the sediments (Simpson *et al* 2005).

Commonly recognised as foundation species, benthic infauna comprise a diverse group of taxa that generally live within the top 30 cm of the surface sediment layer (Seitz & Lipcius, 2001). As these organisms are not very mobile they are useful indicators of long-term changes in marine habitat from activities such as dredge material disposal. Dominant groups of infauna species include polychaete worm, amphipod and crustacean. Assemblages of macroinvertebrates also vary across depth gradients where higher species richness, abundance and biomass are typically observed in deeper water assemblages (compared to those in shallow waters) (BAC 2007). This trend is driven by increased wave and current disturbance in shoal or shallow water environments restricting the establishment of these communities (BAC 2007).

The recolonization of soft-sediment communities is an important aspect when considering recovery from natural or anthropogenic disturbance and is known to be governed by three factors; biotic interactions (facilitation, tolerance and predation), environment conditions (temperature, salinity, sediment characteristics, hydrodynamics and food levels) and life history (life span, generation time and reproductive periodicity) (Zajac *et al.,* 1998.) This is no different for macroinvertebrate communities of Twofold Bay, which are of critical importance in the ecosystem, as they play a vital role in nutrient cycling, detrital decomposition and as a food source for higher trophic levels (Reiss *et al.,* 2009), particularly to commercially important fishes.

Eden has a rich history of commercial fishing, which represents one of the major industries on the south coast of NSW the ports of Eden and Bermagui account for approximately 10% of the total NSW catch (Dalton, 2005). The catch is dominated by 20 finfish species, many of which are demersal and rely heavily upon infauna species as a primary food source (Dalton, 2005). A number of these species such as snapper, yellow fin bream, flathead and whiting also represent significant value to the recreational sector, demonstrating the value of infauna not only to the ecosystem, but also local communities on the south coast of NSW.

1.2 Objectives and Scope of the Environmental Assessment

The objective of the infauna survey was to characterise the background conditions (species abundance and diversity) at the disposal location, prior to dredge material disposal activities. To fulfil the project objective, the following scope of work was undertaken:

- Mobilise and undertake a benthic infauna sampling campaign within the proposed offshore disposal area, using a Van Veen grab sampler and commercial vessel;
- Maintain sample integrity and send samples to a suitably qualified taxonomist for identification to family level; and

- Analysis of the infauna and presentation/interpretation of the data within a scientifically robust report.

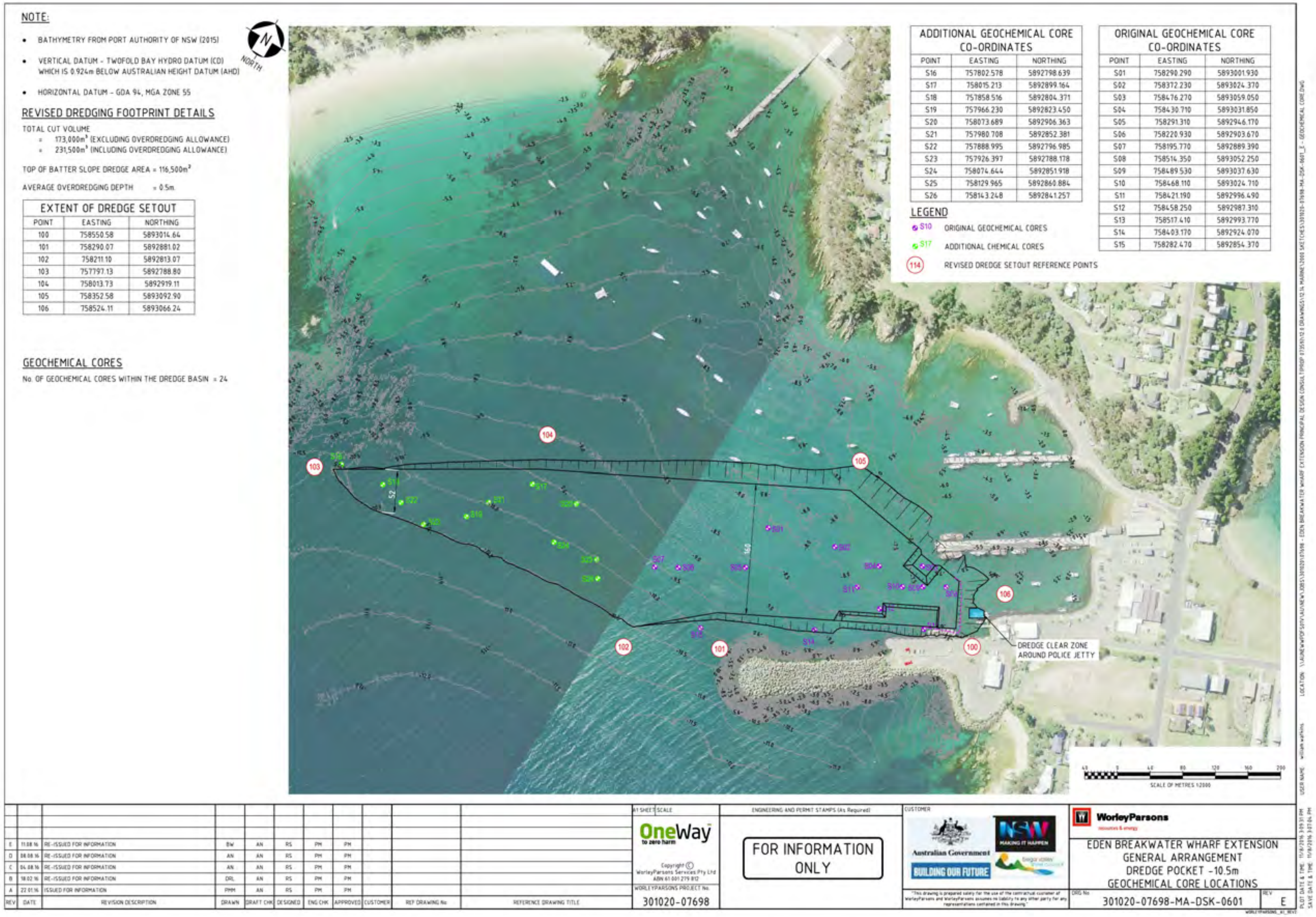


Figure 1 Proposed Dredge Area (N.B. Black area represents the proposed dredge area).

2.0 Methods

AMA collected a total of 24 infauna grab samples within and adjacent to the offshore disposal site, including from reference areas outside of the disposal site (**Figure 2**). A total of three (3) replicate samples were collected at each of eight (8) sampling sites.

The sampling locations for the infauna survey were predetermined according to a reduced version of a gradient-sampling design. Samples were collected at discrete distances radiating from the centre of the dredge material ground. The coordinates for each of the sample sites are provided in **Table 1**.

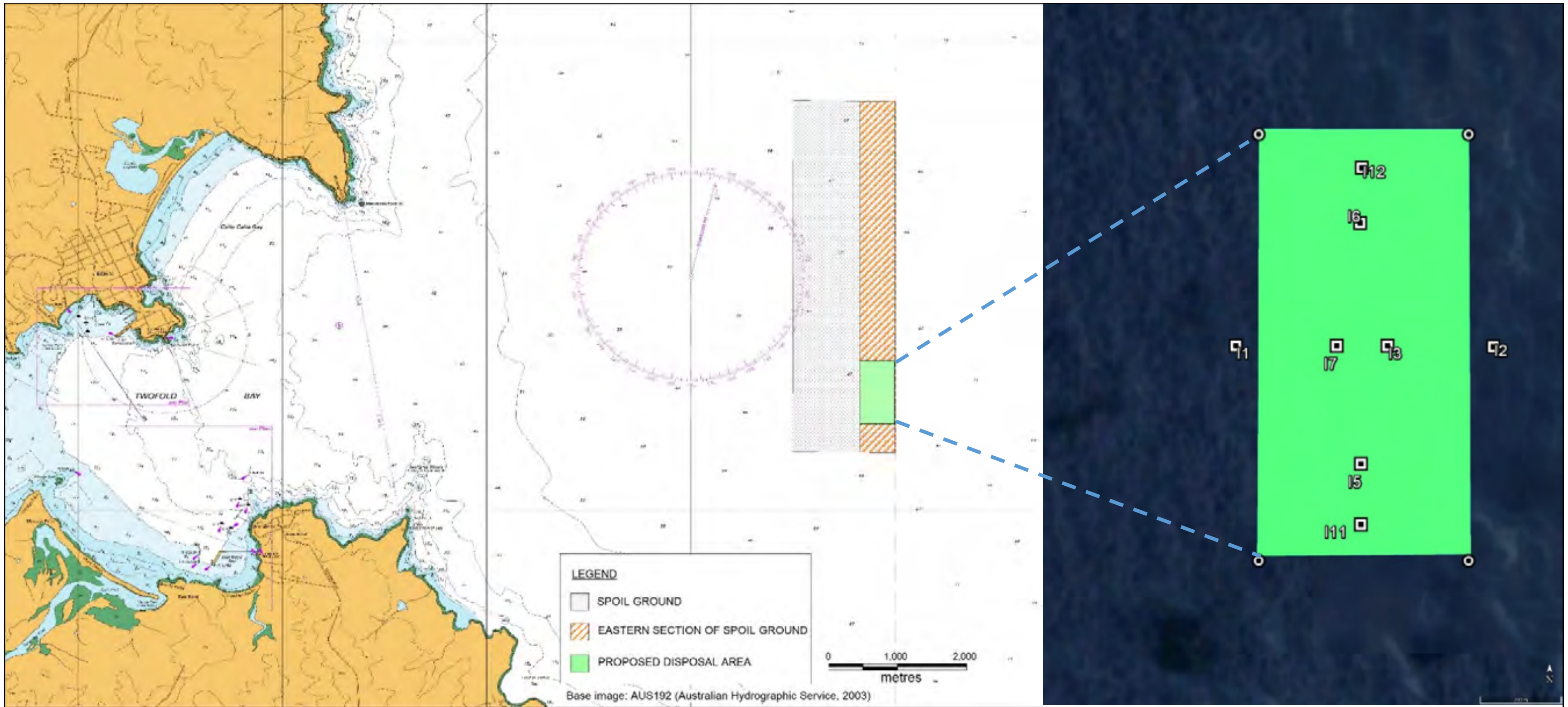
Table 1 Sample site coordinates

Site	South	East
I1	37° 4'59.38"S	150° 1'37.27"E
I2	37° 4'59.45"S	150° 2'2.15"E
I3	37° 4'59.38"S	150° 1'51.93"E
I5	37° 5'8.35"S	150° 1'49.36"E
I6	37° 4'50.05"S	150° 1'49.28"E
I7	37° 4'59.38"S	150° 1'47.02"E
I11	37° 5'12.95"S	150° 1'49.36"E
I12	37° 4'45.87"S	150° 1'49.44"E

A Van Veen grab was used to collect sediment in approximately 68 m water depth (see **Plate 1**). The reference area sites contained similar depths and benthic habitat types. This design enabled the characterisation of baseline infauna communities from within and outside of the proposed offshore disposal ground.

The specific spatial location of the sampling design was guided by the seabed video transect work, performed prior to infauna sampling. After the footage of the seabed was captured, the AMA Principal Marine Scientist assessed the footage and based on the habitat types and bathymetry, the sampling design was then finalised.

The sediment samples were sieved in the field using a 1 mm mesh sieve and then transferred to 5% formaldehyde for preservation and transport to the laboratory (i.e. existing lab used for invertebrate taxonomy). A single grab was also taken at each location and analysed for particle size distribution (8 samples). The samples collected at each location for particle size analysis were sent to ALS laboratories for wet sieving and characterisation of grain size between 60 and 2000µm.



									NSW GOVERNMENT	Australasian Marine Associates
A	1/08/2015	Issued in Draft Report	DS	AC	AC	AD	WGS84	PO124122014		Eden Breakwater Wharf Extension Project – Offshore Infauna Sampling Sites
Rev	**Date**	**Comments**	**Drawn**	**Checked**	**Approved**	**Customer**	**Projection**	**Project No.**	Sample site image produced under licence by AMA using google Earth Pro	Revision A

Figure 2 Infauna sample sites

Plate 1 Van Veen grab sampler

2.1 Data Analysis

For infauna data analysis, Analysis of Variance (ANOVA) was applied using PERMANOVA+, to test for differences and/or similarities between each of the sampling sites.

Bray-Curtis Similarity

Community structure is a multivariate function of both the identity of species present and the relative abundance of each species. The community structure between pairs of samples was compared using the Bray-Curtis similarity coefficient. This index compares the abundance of each species between two samples to give a single value of the similarity between the samples, expressed as a percentage with the range from zero (no similarity at all) to 100 (identical).

Non-metric Multidimensional Scaling (nMDS)

Based on the Bray-Curtis dissimilarity matrix, community differences have been depicted using ordination plots (non-metric multidimensional scaling or nMDS). The purpose of nMDS is to construct a 2-dimensional 'map' or visual configuration of the samples, with the degree of dissimilarity between each sample being represented by the relative distance between each point.

ANOSIM

This analysis provides "Analysis of similarities" hypothesis for differences between predefined groups of community samples, using permutation/randomisation methods on a dissimilarity matrix. It returns a global test statistic (R) and significance levels based on random rearrangements of the observed data but can only be applied to very simple sampling designs.

SIMPER

Based on the Bray-Curtis similarity matrix, SIMPER (similarity percentages) analysis in PRIMER assists with identifying those species responsible for particular aspects of the multivariate picture and provides information about the average similarity (expressed as a percentage) within a group of samples (for example, replicate samples within a site) and also the average dissimilarity between paired groups of samples (for example, the dissimilarity between two sites).

3.0 Results

The benthic infauna communities within and adjacent to the offshore disposal ground were examined to determine any differences in species number and abundance between sites, both within and adjacent to the offshore disposal ground.

3.1 Infauna Data Analyses

nMDS Ordination Plot of Benthic Grabs

The Bray-Curtis Similarity index (see Appendix A) was calculated from 4th-root transformed data (see **Appendix A**) for benthic grab samples. An nMDS ordination plot was produced following transformation of the data (**Figure 3**).

The results for the ordination plot show little similarities between grab samples collected along each of the transect lines. There was also little similarity in species composition reported between replicates within each site, suggesting high variability in species composition throughout the areas sampled.

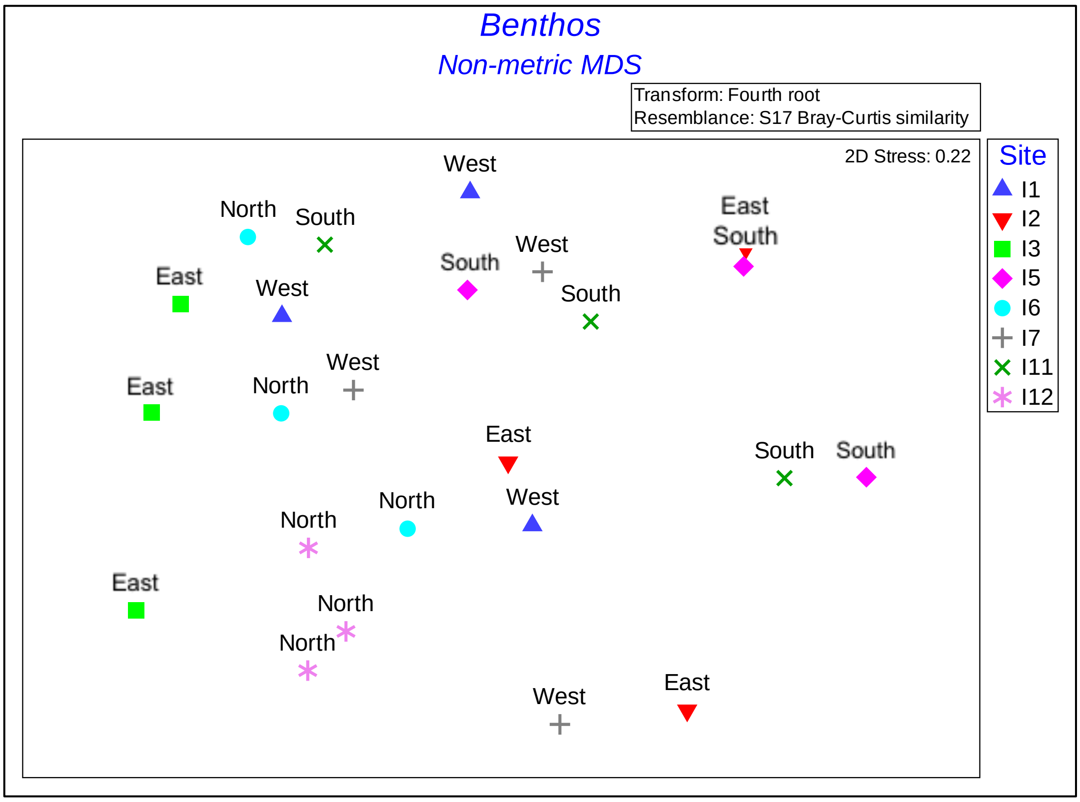


Figure 3 The nMDS ordination plot of Bray-Curtis similarity indices for infauna samples according to position in and directly adjacent to the disposal location at the Port of Eden (Stress = 0.22). There appears to be little resemblance of samples collected along the transect lines.

ANOSIM

The relationship between similarities of grab samples was assessed as a one-way design using ANOSIM, followed by a pair wise test on positions North, South, East and West. The results show that there is some association between the similarities in species composition of grab samples with sampling position (see **Table 2**). The strongest association was in the West-North (0.2) transects.

Tests for differences between unordered Position groups
Global Test
Sample statistic (R): 0.249
Significance level of sample statistic: 0.5%
Number of permutations: 9999 (Random sample from a large number)
Number of permuted statistics greater than or equal to R: 51

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
West, East	0.064	31.8	220	220	70
West, North	0.281	0.2	24310	9999	16
West, South	-0.172	84.1	220	220	185
East, North	0.573	1.4	220	220	3
East, South	-0.148	80	10	10	8
North, South	0.523	0.9	220	220	2

Table 2 ANOSIM test results

SIMPER

The species responsible for the clustering and grouping of grab samples were tested using SIMPER. The results suggest that the northern samples had the highest average similarity (Bray-Curtis = 44.2), compared with other positions on the map of South, East and West. Polychaetes from the Family *Spionidae*, species of *Gammaridean* amphipods, the Tanaids from the Family *Aspeusidae* and the Isopods from the Family *Anthuridae* were responsible for distinguishing the northern samples.

PERMANOVA

The one-way PERMANOVA analysis on sampling position, suggested a significant difference between the similarity of the benthic community and position of grab samples ($P < 0.05$, pseudo-F = 1.7, P= 0.019). Further analysis of the samples included a 2-way design with Position (North, South, East and West) as the factor and a pair-wise test on the groups within position. The results of the PERMANOVA pair-wise test demonstrated significant differences in the similarity of species composition between positions West and North ($P < 0.01$, t= 1.7, P = 0.0013).

Dominant and invasive species

Despite the MDS detecting little similarities among sites, there was consistency among the dominant species. The infauna investigation identified a total of 44 families across the eight sites. The results of this sampling suggested that of the 44 infauna specimens sampled within the disposal location five families (*Spionidae, Orbiniidae, Gammaridea, Apseudida* and *Hydrozoa*) accounted for 63% of the overall biodiversity. Each of these families were consistently observed across the offshore disposal location.

An invasive species was detected in the disposal location during the sampling efforts. The European fan worm, *Sabella spallanzanii* was detected at the northern site (I6) across multiple grab samples. A total of 4 individuals were identified across the replicate samples.

3.2 Particle Size Distribution Analyses

The results of the particle size analyses indicated that the sediments were predominantly sand, containing between 85% and 94% sand (see **Figure 4**). The % clay and % silt was relatively consistent throughout the sites, with the greatest percentage fines (i.e. <60 μm) reported at site I11 and I2.

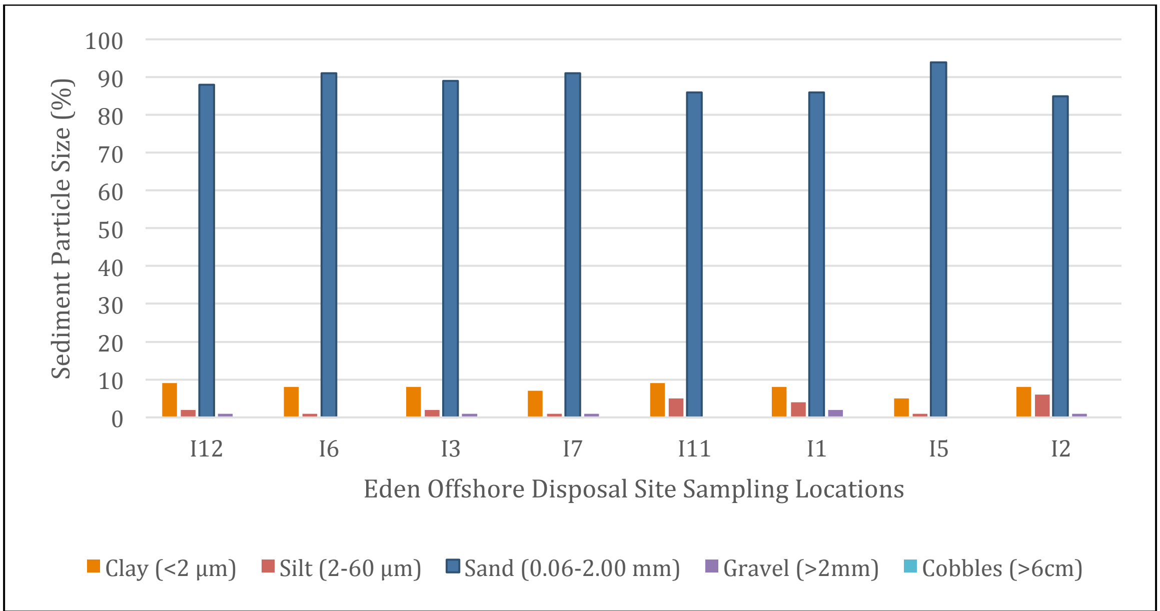


Figure 4 Particle size analyses at infauna sample sites

3.3 Particle Size Comparison with SAP

The overall physical composition of the offshore disposal location was shown to closely reflect the Eden Harbour dredge site (AMA, 2015). The sediment profiles of the disposal location and dredge site were dominated by sand containing 89% and 84% respectively and did not differ significantly ($p < 0.05$) between sites. Similarly, the average concentration of silt and cobble remained consistent between the current results from the dredge disposal site and those samples collected from the dredge footprint.

Variability in sediment composition between the dredge footprint and the disposal location was noted for the percentage clay and gravel. Clay was found in higher concentrations at the disposal location (7.75%), compared to the dredge site (4.75%).

4.0 Discussion

In summary, the infauna communities in the offshore disposal ground were examined to gain an understanding about species composition prior to dredge material disposal. The species composition in samples from sites along each of the transect lines displayed little similarity. There was however, an association reported in species composition between the West-North (0.2) transects, which may suggest some spatial similarities in this part of the dredge material ground.

4.1 Particle Size

The particle size distribution analyses revealed that the composition of the sediment was similar among all disposal location samples. In addition, the analysis also concluded that the overall sediment composition observed is also similar to the proposed dredge area (AMA, 2015). Both sites were found to be dominated by sand, which is considered a relatively course sediment.

The overall composition of the disposal site is largely dominated by sand, which suggests a low probability of expansive and persistent plumes from dredging activity. Compositions dominated by large particle size sediments have also been shown to benefit the recolonization of some benthic macroinvertebrate communities (Brooks and Boulton, 1991). This research demonstrated that rapid recolonizers showed little difference in their ability to recover from natural disturbance across sediment types; however, slow recolonizers favoured gravel substrata (Brooks and Boulton, 1991).

4.2 Infauna composition

Ensuring that dominant species will be able to recolonise in a modified habitat is a primary consideration for evaluating the impact of dredge spoil. When recolonization operates over large spatial scales (such as in the current displacement of dredge spoil), the environment and life history of a species are suggested to be the most influential.

The families observed to be dominant across all sites (*Spionidae, Orbiniidae, Gammaridea, Apseudida* and *Hydrozoa*) are each characterised by similar life history characteristics (i.e high reproductive capacity), which are indicative of opportunistic species (Zajac *et al.* 1991). Such characteristics enable them to dominate other less adaptable species within soft-sediment communities.

Three of the aforementioned dominant families comprise Polycheates, Amphipods and Hydrozoa, which are taxa widely acknowledged to tolerate disturbance events, such as severe environmental conditions, elevated salinity and human degradation of the environment (Stark *et al*. 2014; Grabowski et al 2007). Therefore, given the dominant life history characteristics of these families and tolerance to disturbance, it would suggest that they are likely to compete and maintain dominance within the community structure post-disturbance. It should be noted however that the resilience of polychaetes is seasonally dependent, with reproductive potential increasing through spring and early summer. This suggests the timing of dredge works is imperative to the opportunistic re-colonisation of this species.

It has been suggested that the rate of recolonization of benthic organisms can also be dictated by the depth of overburden at the disposal site (Wilber and Clarke 2007). Given however that benthic species are characterised by planktonic larval stages, infauna communities usually recolonize capped areas rapidly, within months to a few years (Polayes, 1997). Recovery of organisms occupying spoil sites prior to overburden disposal has also been investigated in a number of studies. These investigations had noted that that bivalves and polychaetes have demonstrated the ability to undertake vertical movements up to 32 cm (Maurer *et al*, 1981: 1982). Which is expected considering many burrowing polychaetes, amphipods and molluscs generally occupy the top 30 cm of the surface sediment layer (Seitz & Lipcius 2001).

4.3 Invasive species

The detection of an invasive marine fan worm of the family *Sabellidae* was identified at the northern site of the soil ground. Previous investigations in the area of Snug Cove have reported this species presence in the area. In Port Phillip Bay, Victoria, the European fan worm is considered a major threat to infauna communities, with additional concerns associated with their effect on nutrient cycling processes (Stabilia *et al* 2006). Despite the *Sabellidae* being reported in the region, extensive survey effort (DPI) suggests that it has not been able to out compete native filter-feeding fauna for food and space, resulting in an inability to stabilize in high numbers.

Biannual monitoring and removal of introduced *Sabella* has been recommended as an action to decrease the probability that *Sabella* will be translocated or dispersal occur to neighbouring areas around Twofold Bay (Dalton 2005). Ongoing monitoring of *Sabella* is important to ensure the long term future of Eden's muscle aquaculture industry, due to the ability of Sabellids to grow on mussel ropes, out competing commercially important mussels and oysters, due to their high filtering capacity (Stabilia *et al* 2006).

Future monitoring recommendations

Future sampling should be undertaken approximately 12 months following dredge material disposal, to examine recolonization of the disposal location. A power analysis should be undertaken on the data to determine the level of future sampling effort required. The dominant species reported in the northern transect line included Polychaetes, Amphipods, Tanaids and Isopods. Discussion should be provided on any observed changes in species composition along the predetermined axes, as well as changes in overall numbers of species and overall abundance, following dredge material disposal activities.

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Appendix A Raw Data

Family	Code	I1-1	I1-2	I1-3	I2-1	I2-2	I2-3	I3-1	I3-2	I3-3	I5-1	I5-2	I5-3	I6-1	I6-2	I6-3	I7-1	I7-2	I7-3	I11-1	I11-2	I11-3	I12-1	I12-2	I12-3	Total
Cirratulidae	Cirr	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4
Lumbrineridae	Lumb	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	5
Onuphidae	Onup	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Nephtyidae	Neph	1	0	0	0	2	0	0	3	0	0	0	0	0	1	0	0	1	0	0	0	0	1	1	0	10
Nereididae	Nere	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Sabellidae	Sabe	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	4
Sigalionidae	Siga	1	0	1	0	1	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	6
Syllidae (sf. Sylllinae)	Syll	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Spionidae	Spio	3	2	4	7	4	3	9	16	15	5	3	2	3	4	3	3	10	1	1	6	10	7	1	12	134
Terebellidae	Terr	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4
Trichobranchidae	Trich	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3
Maldanidae	Mald	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Orbiniidae	Orbin	1	1	3	0	0	0	0	2	0	0	0	1	2	1	1	4	2	1	3	0	2	0	0	1	25
Oweniidae	Owen	0	0	0	0	0	0	1	1	0	0	0	1	1	0	1	0	3	0	3	0	0	0	0	0	11
Opheliidae	Ophel	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2
Paraonidae	Para	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Polychaeta sp.	Poly	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Copepoda	Cope	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Seaspider	Pycn	0	0	0	0	0	0	1	3	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	7
Gammaridea spp	Gamm	0	1	2	1	0	0	2	2	2	0	0	1	1	1	4	0	2	0	1	0	0	2	2	1	25
Callianassidae	Call	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2
Shrimp sp.	Shri	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Anthuridae	Anth	0	0	0	1	0	0	0	0	1	0	0	0	1	1	0	0	0	2	0	0	0	1	1	2	10
Cirolanidae	Ciro	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1

Apseudida	Aspe	0	0	2	0	0	0	2	3	0	0	0	0	3	1	3	1	2	0	1	0	0	1	1	1	21
Family	**Code**	**I1-1**	**I1-2**	**I1-3**	**I2-1**	**I2-2**	**I2-3**	**I3-1**	**I3-2**	**I3-3**	**I5-1**	**I5-2**	**I5-3**	**I6-1**	**I6-2**	**I6-3**	**I7-1**	**I7-2**	**I7-3**	**I11-1**	**I11-2**	**I11-3**	**I12-1**	**I12-2**	**I12-3**	**Total**
Blunt rostrum	Tana	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1	0	4
Leptocheliidae	Lepto	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Tanaidacea sp (other)	Tana2	0	0	1	0	0	0	0	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	6
Ostracoda	Ostr	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	6
Hydrozoa sp (branching)	Hydro	2	0	0	1	0	2	2	0	0	0	1	1	6	0	2	3	4	0	1	0	1	0	0	0	26
Mytilidae	Mytil	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Cardiidae	Card	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	4
Chaetodermatidae	Chaet	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	2
Nuculanidae	Nucu	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Nassariidae	Nass	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Dentalidae	Dent	0	0	0	0	0	0	0	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	4
Turritellidae	Turri	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Nematoda	Nema	2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	5
Hoplonemertea spp.	Neme	1	0	1	0	0	0	1	1	1	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	8
Polycladida sp.	Poly	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	3
Hexactinellida sp.	Hexa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Phascolomatidae	Phas	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	4
Sipuncula spp (other)	Sipu	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Eel	Eel	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
	Total	13	5	18	12	9	6	24	45	29	7	5	9	22	12	26	12	28	6	15	7	14	14	8	23	369