



Slope-shelf faunal link and unreported diversity off Nova Scotia: Evidence from polychaete data

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ABSTRACT

Deep-water sedimentary habitats off Nova Scotia have only rarely been explored. The topographically and oceanographically complex shelf of Nova Scotia harbours two interesting topographic features, Emerald Basin, a sedimentary habitat reaching greater depths (max of 270 m) than the surrounding shelf and the Gully, the largest canyon in NW Atlantic. Emerald Basin is exposed to upwellings of slope water and harbours predominantly deep-sea hexactinellid sponges. Such distributional pattern resembles “deep-water emergence”. In this study an abundant benthic group, the polychaetes, were selected to test for such deep-water faunal link. Qualitative boxcores were collected from Emerald Basin (180 m depth, $N = 5$) and the adjacent Gully Canyon (1600 m, $N = 3$). At species level, there was no overlap in distribution between Emerald Basin ($N = 73$, $S = 29$) and Gully Canyon ($N = 351$, $S = 60$) fauna based on morphological assessment of all specimens and molecular analysis (COI and 16S markers) of selected morphotypes. In an alternative approach, Multivariate analysis (nMDS, Cluster Analysis) of incidence data for polychaete genera ($N = 179$) from 24 Atlantic sites (5–1600 m) was carried out. These results showed a greater similarity of Emerald Basin polychaetes to bathyal sites (400–1000 m), particularly the 680 m site off Nova Scotia rather than shelf sites (5–80 m), including those on the Nova Scotia shelf. Thus, at 1600 m, the Gully Canyon samples were likely “too deep” for our comparative purposes and depths of < 1000 m should be targeted in the future.

Our data also provide the first published assessment of polychaete diversity from the Gully Canyon, suggesting the presence of a diverse assemblage ($S = 60$). Unusually for a deep-sea site, the Gully Canyon polychaetes are mostly known taxa with wider distribution across bathyal NW Atlantic. Additionally, our molecular data provide an interesting insights into the distribution of several polychaete species commonly found in deep-sea (e.g. *Auropsio dibranchiata* Maciolek, 1981; *Ophelina abranchiata* Støp-Bowitz, 1948) suggesting wide geographical distribution for some but revealing species complexes for others.

1. Introduction

Soft sediments of the deep-sea represent the largest, and least explored habitat on the planet (e.g. Gage and Tyler, 1991; Snelgrove, 1997; Glover et al., 2010). These soft sediments represent an ideal habitat for polychaete worms, an important component of benthic macrofauna worldwide in terms of numbers of individuals and species, as well as diversity of functional groups (e.g. Grassle and Maciolek, 1992; Giangrande, 1997; Hutchings, 1998; Van Hoey et al., 2008; Herringshaw et al., 2010). Therefore, understanding the diversity and distribution of polychaetes can significantly contribute towards the knowledge of deep-sea ecology. Historically however, there has been an assumed lack of geographic structure of deep-sea polychaetes

assemblages (e.g. Glasby and Alvarez, 1999). This is now considered an artefact of poorly understood taxonomy, and a tendency to “lump” morphologically similar species together, leading to wide geographic and/or bathymetric ranges for some species. In addition, polychaetes are prone to fragmentation when preserved, which often confounds a reliable morphological identification and thus species differentiation. Molecular methods have provided new tools for taxonomists, often revealing species complexes (see Nygren, 2014 for review), but in rare cases the wide distributions of polychaete species have been confirmed (e.g. Ahrens et al., 2013; Georgieva et al., 2015; Paxton et al., 2017).

Majority of polychaete studies from Nova Scotia (and wider Atlantic Canada) have been confined to shelf depths (Hughes et al., 1972; Pocklington, 1979, 1989; Pocklington and Tremblay, 1987; Quijón and

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Snelgrove, 2005), with only few including sites sampled along the slope at 1000 m (Volckaert, 1987) and 680 m (Pocklington, 1991). The major Canada-wide contribution to the knowledge of polychaetes was provided by Carr (2011) who summarised the biodiversity of Canadian polychaetes and subsequently investigated distribution of species throughout the Canadian Pacific, Arctic and Atlantic regions using a molecular approach, and revealed greater diversity than previously reported with high prevalence of “cryptic” or previously overlooked species.

The area of continental shelf off Nova Scotia is large, extending 125–230 km offshore, with complex topography as a result of the past erosional and glacial (see Davis and Browne, 1996 for summary). This diverse topography is mirrored by complex oceanographic conditions, producing distinct temperature and salinity stratification due to the influence of ocean currents (the Gaspé Current in the Northumberland Strait, the Nova Scotia Current along the continental shelf and the Gulf Stream off East Georges Bank), as well as coastal upwellings, estuarine circulation, tidal gyres, shelf-break fronts and frequent upwellings of slope water onto shelf (see Davis and Browne, 1996). These complex environmental conditions are likely to have consequences for the distribution of marine fauna. In this study polychaete diversity and distributional patterns are investigated using samples from two topographic features on the shelf of Nova Scotia – the Gully Canyon and Emerald Basin.

1.1. Gully Canyon

The Gully (Fig. 1A) is the largest submarine canyon of eastern Canada and lies approximately 200 km off Nova Scotia. It is 6–10 km wide and 40 km long at its 500 m isobath, reaching depths of > 2500 m. Submarine canyons are major deep-sea topographic features found on continental margins around the world (Harris et al., 2014). Because of their steep topography and hydrodynamic regimes, canyons play an important role in connecting the continental shelf to the abyssal plain by sediment, nutrient and even pollutant transportation (Harrold et al., 1998; Vetter and Dayton, 1998, 1999; Puig et al., 2003; Palanques et al., 2005, 2008; Arzola et al., 2008). This may result in enhanced food supply inside the canyons compared to the adjacent open slopes and abyssal plains, leading to canyons being labelled as ‘hotspots’ of biomass in the deep-sea (Vetter, 1994; De Leo et al., 2010). Canyons also add to habitat heterogeneity (McClain and Barry, 2010), and may

enhance biodiversity on a regional level, by supporting different assemblages to those found on the adjacent open slopes and abyssal plains (Schlacher et al., 2007; Vetter et al., 2010; De Leo et al., 2014; Gunton et al., 2015a). However, there is no agreement on whether local species diversity is higher inside canyons or on the adjacent slopes (see Gunton et al., 2015a for discussion).

Canyons are also important for pelagic organisms, as they provide fish (Würtz, 2012) and cetacean feeding and breeding grounds (Hooker et al., 1999). Indeed, it was the presence of 11 cetacean species, particularly the resident population of northern bottlenose whales (Hooker et al., 1999), that led to the Gully Canyon being granted Marine Protected Area (MPA) status in 2004 (see e.g. Harrison and Fenton, 1998; Fenton et al., 2002; Gordon and Fenton, 2002). Deep-water corals have also been found in the Gully Canyon in high densities (Mortensen and Buhl-Mortensen, 2005; Buhl-Mortensen et al., 2010; Kenchington, 2014), creating biogenic habitat, thus increasing habitat complexity and providing refugia for diverse faunal communities (e.g. Rogers, 1999; Roberts et al., 2006). Apart from these, there have been few other studies of the canyon on benthic epifauna (Hargrave et al., 2004) and pelagic Crustacea (MacIsaac et al., 2014). However, there are no published studies on the infaunal macrofauna and its dominant component, the polychaete worms. Further afield, there is only one macrofaunal dataset from a canyon in the NW Atlantic, Carson Canyon (Houston and Haedrich, 1984). In contrast, the canyon macrofauna of NE Atlantic have received considerable attention including: Bay of Biscay canyons (Marquiegui and Sorbe, 1999; Sorbe, 1999), Iberian margin canyons (Cunha et al., 2011; Paterson et al., 2011) and Whittard Canyon (Gunton et al., 2015a, 2015b). Our study sets out to provide the first published data on polychaete diversity and species composition from Gully Canyon.

1.2. Emerald Basin

Emerald Basin (Fig. 1A) is one of several deep basins found on the shelf of Nova Scotia, extending to depths of 270 m. The surrounding shelf is at a maximum depth of around 180 m but includes shallower banks at 30–80 m depth (Davis and Browne, 1996). Interestingly, oceanographers have long recognised that waters of Emerald Basin have a different origin and water properties to those of the surrounding shelf (McLellan et al., 1953; McLellan, 1956). Its waters are formed partially by the upwelling of Central Atlantic Water (200–1000 m) and

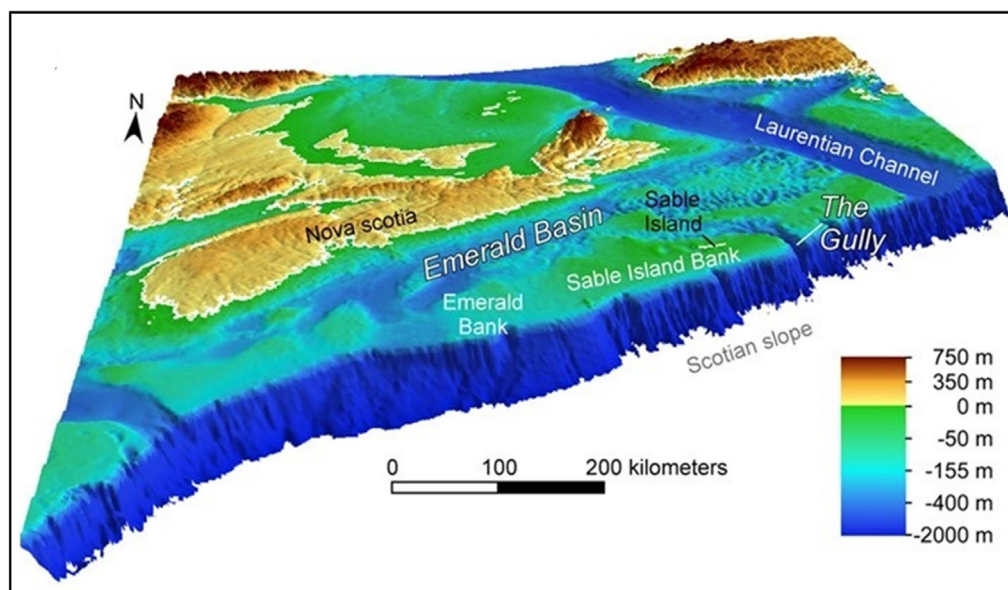


Fig. 1. Map of the Nova Scotia shelf, showing position and depth of Emerald Basin and Gully Canyon. Details of sampling sites are given in Table 1.

Table 1
Sampling information for boxcores collected during this study.

Site	Sampling device	Sampling date	Latitude	Longitude
Emerald Basin	Boxcorer	20/07/2016	44.319275	– 62.604977
Emerald Basin	Boxcorer	21/07/2016	44.319632	– 62.605143
Emerald Basin	Boxcorer	21/07/2016	44.319987	– 62.605332
Emerald Basin	Boxcorer	21/07/2016	44.319208	– 62.604125
Emerald Basin	Boxcorer	14/08/2016	44.320517	– 62.606402
Emerald Basin	ROV biobox	14/08/2016	44.321053	– 62.605472
Emerald Basin	ROV biobox	15/08/2016	44.283172	– 62.600208
Gully Canyon	Boxcorer	10/08/2016	43.82782	– 58.923147
Gully Canyon	Boxcorer	10/08/2016	43.828861	– 58.923226
Gully Canyon	Boxcorer	10/08/2016	43.828842	– 58.923237

its mixing with “slope water” (~ 400 m) as well as coastal surface water, resulting in warmer (up to 9.2 °C) and more saline (32.2–35.0‰) water in comparison to the waters overlaying the shelf (McLellan et al., 1953; McLellan, 1956). The “slope water” was recognised by Iselin (1939) who observed that water found at 400 m off Nova Scotia had similar properties to that of 1000 m in the Sargasso Sea, suggesting upwelling of this water mass under the Gulf Stream. Emerald Basin, as well as other mid-shelf basins, is connected to the edge of the continental shelf through “saddles” of up to 200 m in depth, which enables the ingress of deep-water (Davis and Browne, 1996). Frequent incursions of slope water upon the Scotian shelf have been observed (McLellan et al., 1953) as a result of shoreward transport of the deeper denser water under the surface coastal waters and/or of severe storms forcing the slope water from the shelf edge into the basins.

The documentation of deep-sea basin faunal communities of the Nova Scotia lags behind that of the physical oceanography. Pocklington and Tremblay (1987) showed that Emerald Basin harbours polychaete assemblages distinct from other NW Atlantic shelf sites, although the resolution of their faunal analysis was reduced by the inclusion of samples collected by different sampling devices (e.g. cores and dredges). It has been suggested, that the presence of distinct assemblages were likely due to the influence of deeper slope waters at Emerald Basin (Pocklington and Tremblay, 1987). However, no comparison with polychaete assemblages from deeper waters was undertaken to date. Recently, Emerald Basin became the focus of benthic studies because of the occurrence of the sponge *Vazella pourtalesi* (Schmidt, 1870) (e.g. Fuller, 2011; Kenchington, 2014; Beazley et al., 2016), a representative of the typically deep-sea class Hexactinellida (Tabachnick, 1994). If environmental factors (i.e. supply of larvae through upwelling of deep water) are responsible for the atypical distribution of the sponges in Emerald Basin, other benthic fauna besides *V. pourtalesi* are likely to follow the same pattern. Such distributional pattern would mimic the phenomenon known as “deep-water emergence”, where environmental conditions resemble those of much deeper depths. This has been proposed for habitats such as fjords (Försterra and Häussermann, 2003; Häussermann and Försterra, 2007), submarine caves (e.g. Iliffe et al., 1983, 1984; Hart et al., 1985; Vacelet et al., 1994), shelf environments (Ross et al., 2015) and polar regions (e.g. Kussakin, 1973).

Pocklington (1991) proposed that deep shelf basins and slope fauna of Nova Scotia comprised a single biogeographical province as an extension of an earlier hypothesis formed by Hartman and Fauchald (1971). This hypothesis has so far received little attention, with the exception of Rowe et al. (1975) who commented that macrofauna from 270 m sites in the Gulf of Maine Basins were most similar to that from 350 to 1300 m sites in NW Atlantic, a pattern also suggested for megafauna (Watling and Skinder, 2007). Here we test the hypothesis that fauna of the Emerald Basin is more similar to that of the deep Atlantic rather than other shelf sites, using polychaete worms as model taxa and adopting a morphological and molecular approach.

To summarise, the aims of this study are twofold: (1) provide the

first assessment of polychaete diversity and species composition in Gully Canyon and (2) test the hypothesis of presence of deep-sea polychaete assemblages in Emerald Basin, the deep feature on the shelf of Nova Scotia, using a combined morphological and molecular approach.

2. Methods

2.1. Sample collection and processing

Emerald Basin and Gully Canyon were sampled by USNEL spade box core (Hessler and Jumars, 1974) in July and August 2016 aboard *CCGS Hudson* during Hud-019 cruise. In total eight boxcores were collected. Three boxcores were collected from Gully Canyon at a depth of around 1600 m. Five boxcores were collected from Emerald Basin at a depth of around 180 m. In Emerald Basin, additional specimens were obtained by sieving residual mud amassed in the remotely operated vehicle (ROV) biobox, which was deployed for *Vazella pourtalesi* collection at depths of 180–210 m. Details of all sampling sites are given in Table 1.

All boxcores were disturbed (those from Emerald Basin greatly so as the closing mechanism was obstructed by boulders) and therefore all samples were treated as qualitative. From boxcores collected in Gully Canyon about 5 cm of the top sediment was removed for analysis, while approximately 2 L of sediment was processed from each of the boxcores collected in Emerald Basin. Therefore, while in total approximately 37.5 L of sediment was processed from the Gully Canyon, only about 10 L of sediment was processed from Emerald Basin. In both locations samples were sieved through 1000 µm and 500 µm mesh-sizes, while in Gully Canyon an additional 300 µm mesh-size was also used. When possible a selection of specimens were taken for live sorting and photography, which was followed by fixation and preservation in 80% ethanol and storage at – 20 °C for DNA analysis. The rest of the material was either bulk preserved in 96% ethanol and stored at – 20 °C or fixed in borax buffered 10% formalin and later transferred to 80% ethanol.

2.2. Laboratory sorting and identification

Polychaetes were identified to the lowest possible taxonomic level using Leica MZ6 and DM5000 stereo and compound microscopes. Only head-bearing specimens/fragments were counted and identified. Named species identification (where possible) was carried out using identification keys and original literature, with particular focus on NW Atlantic, deep Atlantic and Arctic regions (e. g. Hartman, 1965; Hartman and Fauchald, 1971; Maciolek, 1981; Jirkov, 2001; Oug, 2010 and Blake, 2016). Where a named species identification could not be obtained (either due to damage of specimens or presence of novel taxa), the specimen was recorded as a morphospecies in a genus (e.g. *Tharyx* sp. A). All specimens have now been accessioned into the Natural History Museum London annelid collection (see Supplementary data).

2.3. Molecular work

DNA was extracted from 18 specimens assigned to seven morphospecies. Six of these morphospecies were targeted as they were considered to be present in both Emerald Basin and Gully Canyon based on morphological examination: *Ophelina abbranchiata* Støp-Bowitz, 1948; *Ceratocephale loveni* Malmgren, 1867 *Galathowenia* cf. *oculata* (Zachs, 1923); *Notomastus* cf. *latericeus* Sars, 1851; *Lumbrineris* sp. 1 and *Lumbrineris* sp. 2. The other targeted species was *Auospio dibranchiata* Maciolek, 1981 from Gully Canyon, a common cosmopolitan deep-sea species with published sequences from the Pacific Ocean morphotypes available for comparison (Mincks et al., 2009). Another specimen, morphologically consistent with *A. dibranchiata*, obtained by L. N. during the Discovery-077 cruise aboard *RRS Discovery* to the Porcupine

Table 2
Environmental characteristics of Atlantic sites included in the multivariate analysis.

Site	Region	Habitat (general)	Depth (m)	Sediment type	Temperature (°C)	Salinity (‰)	Sampler	Sieve (µm)	Source
off Tromso	North Sea (Arctic)	Sounds, fjord	Littoral	Sand, mud	2–6 (winter), 10–15 (summer)	31–34 (25 in parts of fjord, summer)	Spade	1000	Oug (2001) (limited to sedimentary data)
Irish Sea	Irish Sea (NE Atlantic)	Sublittoral	5–14	nr	nr	nr	Grab?	1000	Ferrero et al., unpublished data
NFL fjord	NW Atlantic (subarctic)	Fjord	15–30	Mud	nr	nr	Scuba collected cores	500	Quijón and Snelgrove (2005)
NFL fjord	NW Atlantic (subarctic)	Fjord	15–30	Sand	nr	nr	Scuba collected cores	500	Quijón and Snelgrove (2005)
St. Margaret's Bay	Nova Scotia shelf (NW Atlantic)	Inner shelf	46	Clay, silt	0.02–13.9	30–32.9	Boxcorer	125	Volckaert (1987)
Sable Bank	Nova Scotia shelf (NW Atlantic)	Outer shelf	44–56	Sand, gravel	4.5–5.8	32.4	Video grab	1000	Rincón and Kenchington (2016)
Western Bank	Nova Scotia shelf (NW Atlantic)	Outer shelf	53–59	Sand, gravel	ca 5.5	32.6–33.3	Video grab	1000	Rincón and Kenchington (2016)
Emerald Bank	Nova Scotia shelf (NW Atlantic)	Outer shelf	75–83	Sand, gravel	7.7	34	Video grab	1000	Rincón and Kenchington (2016)
North Sea	North Sea	Shelf	70–72	Fine muddy sand	nr	nr	Grab?	500	Bamber et al., unpublished data
North Sea	North Sea	Shelf	84–86	Fine sand	nr	nr	Grab?	500	Bamber et al., unpublished data
Emerald Basin	Nova Scotia shelf (NW Atlantic)	Shelf (deep-basin)	180	Coarse, gravelly	11	35.2	Boxcorer	500	unpublished data of Yashayaev
Emerald Basin	Nova Scotia shelf (NW Atlantic)	Shelf (deep-basin)	264–272	Silty clay	8.8–9.8	34.6–35	Boxcorer	125	Volckaert (1987)
Rockall Trough	NE Atlantic (Hebridean Slope)	Trough	400	Fine sand	ca 5	ca 35	Boxcorer	420	Paterson and Lambshead (1995); Ellett and Martin (1973); Lambshead et al. (1994)
Rockall Trough	NE Atlantic (Hebridean Slope)	Trough	600	Fine sand	ca 5	ca 35	Boxcorer	420	Paterson and Lambshead (1995); Ellett and Martin (1973); Lambshead et al. (1994)
Rockall Trough	NE Atlantic (Hebridean Slope)	Trough	1061	Fine sand	ca 5	ca 35	Boxcorer	420	Paterson and Lambshead (1995); Ellett and Martin (1973); Lambshead et al. (1994)
Scotian Slope	Nova Scotia slope (NW Atlantic)	Slope	680	nr	nr	nr	Boxcorer	800	Pocklington (1991)
Faroe-Shetland Channel	NE Atlantic	Slope (channel)	932–986	Sand, coarse	nr	nr	Grab?	500	Bamber et al., unpublished data
Scotian Slope	Nova Scotia slope (NW Atlantic)	Slope	1000	Silty sand	ca 4	35	Boxcorer	125	Volckaert (1987)
OS Sines	NE Atlantic	Slope	1000	nr	nr	nr	Cores	500	Paterson et al. (2011)
OS South	NE Atlantic	Slope	1000	nr	nr	nr	Cores	500	Paterson et al. (2011)
Serðiball Canyon	NE Atlantic	Canyon	1000	nr	nr	nr	Megacorer	500	Paterson et al. (2011)
Cascais Canyon	NE Atlantic	Canyon	1000	nr	nr	nr	Megacorer	500	Paterson et al. (2011)
Nazaré Canyon	NE Atlantic	Canyon	1000	Silt, clay	nr	nr	Megacorer	500	Paterson et al. (2011)
Gully Canyon	NW Atlantic	Canyon	1600	Fine mud	3.8	34.9	Boxcorer	300	Unpublished data of Yashayaev

Key: n/r – not reported.

Abyssal Plain (PAP) Observatory (~ 4800 m) (Hartman et al., 2012), was also sequenced and included in this study for comparison.

DNA was extracted from parapodia or the posterior part of the body from ethanol-preserved material with the Tissue and Blood Qiagen extraction kit (Qiagen, www.qiagen.com) following the protocol provided by the manufacturer. Approximately 650 bp of the mitochondrial cytochrome c oxidase I (COI) was amplified using the primers LCO1490 and HCO2198 (Folmer et al., 1994) and polyLCO and polyHCO (Carr et al., 2011). A fragment of ca. 500 bp of the mitochondrial 16S rDNA (16S), which also has the power to discriminate between polychaete species (e.g. Brasier et al., 2016; Álvarez-Campos et al., 2017), was amplified using the primers 16SaRL and 16SbrH (Palumbi, 1996), and ann16SF and ann16SR (Sjölin et al., 2005).

PCR reactions contained 1 µl of each primer (10 µM), 2 µl template DNA and 21 µl Red Taq DNA Polymerase 1.1 × MasterMix (VWR) in a mixture totalling 25 µl. The temperature profile was as follows: 96 °C for 240 s, followed by (94 °C for 30 s, 48 °C for 30 s then 72 °C for 60 s) × 35 cycles, followed by 72 °C for 480 s. PCR purification was performed using a Millipore Multiscreen 96-well PCR Purification System, and sequencing was performed on an ABI 3730XL DNA Analyser (Applied Biosystems) at the Natural History Museum, London Sequencing Facility.

Overlapping sequence fragments were merged into consensus sequences using Geneious vs 8.1.7 (Kearse et al., 2012), edited unambiguously by eye and deposited in Genbank. For COI, the sequences were translated into an amino acid alignment and checked for stop codons to avoid pseudogenes. Obtained sequences were checked against records available in GenBank, using the BLAST tool.

2.4. Data analysis - species richness in Gully Canyon

Local diversity was assessed by the rarefaction approach (Sanders, 1968), which is used to estimate species diversity patterns independent of sample size, although it is influenced by species dominance (Gage and Tyler, 1991; Gage and May, 1993). The individual-based rarefaction was conducted on pooled boxcore samples collected in Gully Canyon and compared with available data from canyons and adjacent open slopes of mid-bathyal depth (~ 1000 m) from NE Atlantic (see Paterson et al., 2011 for details). The raw data of Paterson et al. (2011) were re-analysed here to obtain 95% confidence intervals (CIs) to test for statistical significance. For consistency with other available data, only data collected from 500 µm mesh size in Gully Canyon were included in the comparative biodiversity analysis. The mean values were calculated and their statistical significance was tested by calculating 95% CIs using ESTIMATES S software (Colwell, 2009).

2.5. Data analysis - species delimitation

Both COI and 16S sequences were aligned using MAFFT (Katoh et al., 2002) with default settings, provided as a plug-in in Geneious. The most appropriate evolutionary model for each marker (GTR + I + G for COI in the *Lumbrineris* alignment and GTR + G for 16S for the rest of species) was obtained by running the alignments in jModelTest (Posada, 2008) and evaluated using the Akaike Information Criterion (AIC). A combined analysis was conducted using Maximum Likelihood analyses (ML) with RAxML (Stamatakis, 2006; Stamatakis et al., 2008) and Bayesian Inference analyses (BI) with MrBayes 3.1.2 (Ronquist and Huelsenbeck, 2003). ML was run using two heuristic searches and robustness of the nodes was determined with 10 runs and 500 replicates. BI analyses were run twice for each dataset with four chains for 2 million generations (25% trees discarded as burn-in) sampling a tree every 1000 generations. In both ML and BI analyses partition codons were used for COI and the best evolutionary models previously inferred for every marker were applied. Convergence among chains, mixing within chains (i.e. ESS values) and the number of burn-in generations were monitored with the program TRACER 1.6 (Rambaut et al., 2014).

Results were visualized in FigTree v.1.4.2 (Rambaut, 2006). Trees were constructed to visualise the similarities/differences between species, not to recover their phylogenetic relationships. As a supplementary approach, the distances among sequences were calculated in MEGA v 5.0 (Tamura et al., 2011) and expressed as Kimura 2 parameters (K2P) distances.

2.6. Data analysis - assemblage comparisons

To evaluate the hypothesis of Emerald Basin harbouring a deep-sea community, the distributional data of polychaete taxa from 24 North Atlantic sites, spanning littoral to bathyal depths (5–1600 m), were obtained from original literature (where a list of taxa was provided) and from available unpublished data (see Table 2. for details). Only samples collected by cores or grabs were included, excluding sleds, dredges or trawls, which tend to sample different fauna. Although different mesh sizes are commonly used in shallow and deep-waters (1000 µm versus 300–500 µm), this reflects the difference in faunal body size, which tends to be smaller in deep-sea habitats (e.g. Gage and Tyler, 1991). Given the non-quantitative nature of the data from Emerald Basin and Gully Canyon, only presence-absence data was used in the data analysis. Deep-sea datasets are commonly identified to morphospecies at genus level (due to high prevalence of new species), therefore we carried out data analysis at this taxonomic level.

Presence-absence data matrix of 179 genera from 24 sites was constructed in MS Excel and is available as [Supplementary data \(Table S1.\)](#). Data analyses were conducted using PRIMER v6 (Clarke and Gorley, 2006). Inter-site resemblances were calculated using the Sørensen coefficient (Sørensen, 1948), which is suitable for occurrence-only data. This index also takes the identities of the taxa into account, therefore ignoring null values shared between assemblages. Similarities among the sites were visualized using nonmetric multidimensional scaling (nMDS), which reflects the distribution along the environmental gradient (changing depth) (Clarke, 1993), and Cluster analysis, which reflects similarity. The data were pooled from a variety of sources spanning different North Atlantic regions, depths and environmental conditions (see Table 2.). As a result, there is lack of consistency in coverage of environmental variables other than depth, as well as problem of co-variance of some of these with depth. Therefore, an analysis of similarity (ANOSIM; Clarke, 1990) was used to test the statistical significance of obtained clusters based on depth only. A similarity percentage analysis (SIMPER; Clarke and Warwick, 2001) was used to identify the taxa driving any differentiation of the assemblages.

3. Results

3.1. Sampling efficiency

A total of 424 polychaete specimens were examined from both sites. From Emerald Basin, 73 specimens were collected in total, with majority from the boxcores ($N = 68$), with five additional specimens from the ROV biobox belonging to the representatives of species found in boxcores. Sixty three specimens collected from Emerald Basin were identifiable and yielded 29 morphospecies. In the Gully Canyon 351 specimens (of which 339 were identifiable) led to the recognition of 60 morphospecies. The species lists from both sites, together with known distribution of these species can be found in [Supplementary data \(Tables S2 and S3\)](#). Rarefaction curves were used to assess the sampling efficiency. Both sites are considered to be undersampled, particularly the Emerald Basin where the curve rises more steeply, while for better sampled Gully Canyon the curve begins to level off (Fig. 2). At both sites, the greatest number of both individuals and species was contributed by 500 µm mesh size ($N = 53$ and $S = 25$ for Emerald Basin; $N = 215$ and $S = 48$ for Gully Canyon) (Fig. 2). The 300 µm partition collected in Gully Canyon consisted mostly of smaller-bodied individuals ($N = 88$) of species captured by 500 µm, collecting only three

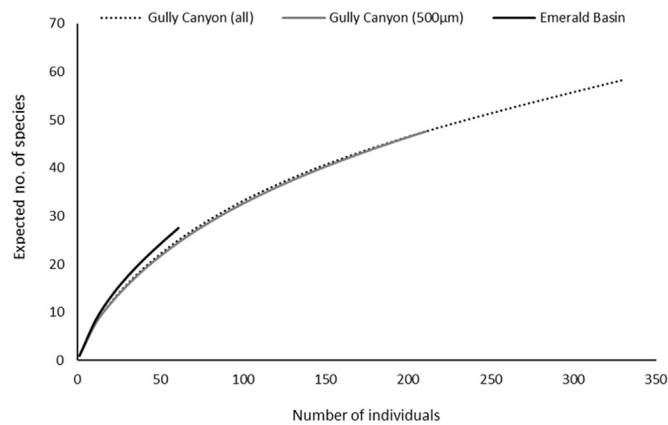


Fig. 2. Rarefaction curves based on number of individuals collected from the Gully Canyon (all mesh sizes and 500 µm only), and Emerald Basin (all mesh sizes).

additional species. The largest mesh size of 1000 µm was the least efficient in capturing specimens ($N = 36$) but led to collection of an additional eight species from the Gully Canyon. The top five most abundant species found in Gully Canyon were: *Aurospio dibranchiata* Maciolek, 1981 ($N = 78$), *Aricidea parva* Hartman, 1971 ($N = 45$), *Ophelina abranchiata* Støp-Bowitz, 1948 ($N = 31$), *Glycera mimica*, Hartman (1965) ($N = 23$) and *Erinaceusyllis* sp. 1 ($N = 11$), while Emerald Basin was dominated by *Ophelina abranchiata* ($N = 7$), *Eclysippe eliasoni* (Day, 1973) and *Notomastus* cf. *latericeus* Sars, 1851, both represented by five individuals.

3.2. Species richness comparison (Gully Canyon vs NE Atlantic Canyons)

Rarefaction revealed that Gully Canyon contains species-rich polychaete assemblages with higher species richness than NE Atlantic open slope sites and Nazare and Cascais canyons, but comparable to Setúbal Canyon at similar bathyal depths (~ 1000 m) as estimated at values of ES ($40, 80, 190$) and their 95% CIs (Table 3).

3.3. Assemblage comparison

As the stress used to assess the goodness of fit of data in 2D nMDS (Fig. 3A) representation was high (Stress 0.2), the 3D nMDS graph (Fig. 3B) is also presented (Stress 0.13). The multivariate analysis, nMDS (Fig. 3A, B) and Cluster analysis (Fig. 3C) recovered groupings related to depth (ANOSIM: factor – depth: global $R = 0.535$, $P = 0.1\%$) labelled as shelf (< 100 m) and bathyal (400–1600 m) with dissimilarity of 76.6% estimated by SIMPER analysis. The Emerald Basin samples from 180 m depth (this study) and 270 m (Volckaert, 1987) were more similar to other bathyal sites (Fig. 3A, B, C) than other shelf locations. More specifically the Emerald Basin samples were most similar to each other and then to samples at 680 m on the slope of Nova Scotia (Fig. 3A, B, C). Genera driving the separation of shelf and bathyal (including Emerald Basin) sites were identified by SIMPER analysis

(factor: depth). The five most frequent genera in shelf waters were *Nephtys*, *Phyllodoce*, *Scoloplos*, *Pholoe* and *Polydora*, while at bathyal depths these were *Glycera*, *Levinsonia*, *Prionospio*, *Aricidea* and *Notomastus*. The similarity estimated by SIMPER analysis of both clusters was relatively low (40% for shelf and 32% for bathyal cluster). The similarity between Emerald Basin sites and Scotian Slope at 680 m site was driven by genera *Aglaophamus*, *Ceratocephale*, *Lumbrineris*, *Ophelina*, and *Terebellides*.

3.4. Molecular data

Amplification of the COI marker had a limited success for live-sorted specimens collected at Emerald Basin, while amplification of 16S produced better results with sequences obtained from both Emerald Basin and Gully Canyon specimens (sequencing success and results summarised in Table 4). Molecular data did not confirm presence of the same species at both Emerald Basin and Gully Canyon (Table 4, Fig. 4).

Two specimens collected from the Emerald Basin identified as *Lumbrineris* were shown to represent different species, with a genetic divergence of 24.6% of the COI sequences (Fig. 4A; Table 4). *Notomastus* cf. *latericeus* from Emerald Basin and Gully Canyon belong to different species based on 16S (K2P 23.6%; Table 4) and these were recovered as sister species in the phylogenetic analysis (Fig. 4B). Phylogenetic results and K2P distances using 16S (Fig. 4C; Table 4) suggested that specimens identified as *Ceratocephale loveni* from the Emerald Basin (this study) and Bohuslän – Sweden, North Sea (Ruta et al., 2007) belong to the same species, while specimens identified as *Ceratocephale* cf. *loveni* from Gully Canyon represented a different species. Two morphotypes of *Ophelina abranchiata* (both from Emerald Basin) appeared as two different taxa in the 16S phylogenetic tree (Fig. 4D), forming a clade with *Opheliidae* sp. 2 from Goban Spur, NE Atlantic, 1000 m depth (Gunton, 2015), with K2P distances ranging 13.2–20.3% (Table 4). As for *Aurospio dibranchiata*, the 16S phylogenetic analysis (Fig. 4E) identified two different species: the specimen collected at Porcupine Abyssal Plain (~ 4800 m) (this study) clustered with sequences from equatorial abyssal Pacific (Mincks et al., 2009); and the specimen from the Gully Canyon clustered with the morphospecies *Spionidae* sp. 2 (Gunton, 2015) from Goban Spur, 992 m depth (Fig. 4E). Between clade K2P distances of *A. dibranchiata* were 14.6%, while within clade variation was 0.6–1.5% (Table 4).

4. Discussion

4.1. Sampling efficiency

Qualitative sampling in Emerald Basin (180 m) and Gully Canyon (1600 m) led to recognition of 28 and 60 morphospecies of polychaetes, respectively. Both sites were undersampled (Fig. 2) and therefore the results presented here should be treated with caution. However to date, they do represent the best coverage of species richness from Emerald Basin and the first published assessment from the Gully (see following sections on Gully Canyon and Emerald Basin for details).

Table 3

Comparison of polychaete species richness of Gully Canyon (this study), and other canyons and open slope (OS) environment of similar depths based on rarefaction at three sample sizes ($N = 40$, $N = 70$ and $N = 190$) (comparative data of Paterson et al., 2011).

Site	Habitat	Depth (m)	S	ES(40)	95% low	95% high	ES(70)	95% low	95% high	ES(190)	95% low	95% high
Nazaré canyon	Canyon	~ 1000	20	13.86	8.92	18.8	18.27	12.28	24.27	n/a	n/a	n/a
Setúbal canyon	Canyon	~ 1000	26	19.01	14.2	23.82	23.82	18.39	29.25	n/a	n/a	n/a
Cascais canyon	Canyon	~ 1000	22	12.7	9.11	16.29	15.8	12.16	19.45	21.78	18.04	25.53
Gully canyon	Canyon	~ 1600	48	18.87	13.91	23.82	26.63	20.59	32.68	45.23	36.71	53.74
OS near Setúbal canyon	Open slope	~ 1000	21	20.73	15.41	26.05	n/a	n/a	n/a	n/a	n/a	n/a
OS near Nazaré canyon	Open slope	~ 1000	17	15.87	11.98	19.76	n/a	n/a	n/a	n/a	n/a	n/a

Key: n/a – not applicable due to low sample sizes.

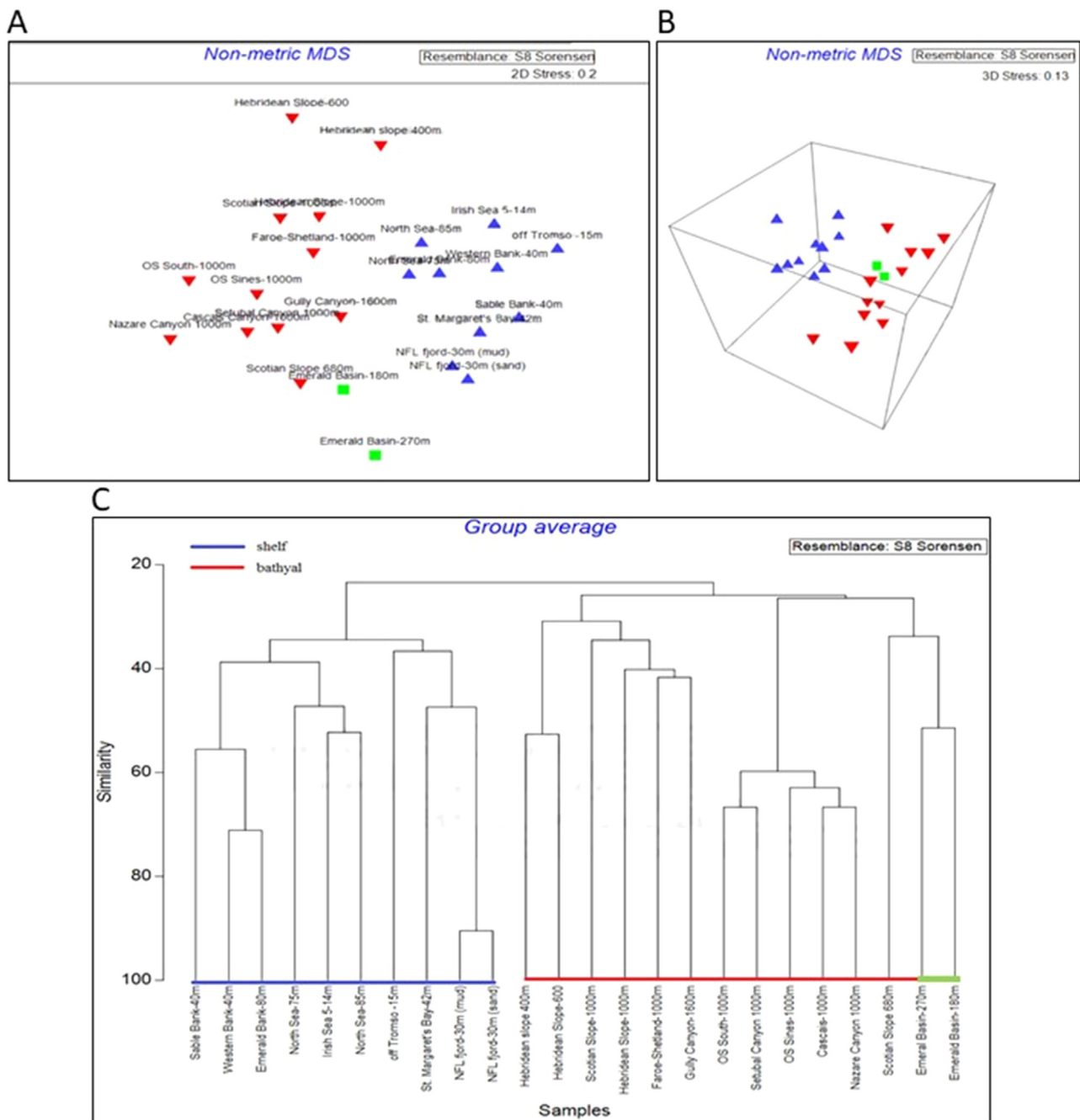


Fig. 3. Multivariate analysis based on presence - absence data at genus level data from Atlantic sites, showing the similarity of Emerald Basin (green) polychaete assemblages with those of shelf (blue) and bathyal (red) sites based on (A) nMDS in 2D (B) nMDS in 3D and (C) Cluster analysis. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

4.2. Species richness and composition of polychaetes at Gully Canyon

With no published data on any infaunal macrofauna from the Gully Canyon, our study represents an important contribution towards the biodiversity knowledge of this canyon. The polychaetes of the Scotian slope have, in general, received little attention. Volckaert (1987) targeted a depth of 1000 m as part of a study on patterns of assemblage patchiness, which yielded 22 species (nine boxcores samples, 125 µm mesh size, *N* not reported). Pocklington (1991) investigated a depth of 680 m (boxcores, 800 µm mesh size) with the collection of 20 species out of 71 specimens. In both cases a much smaller number of species were found compared to the 60 morphospecies collected from Gully Canyon in our study, even with the use of a smaller mesh size and larger

sampling effort by Volckaert (1987). The observed enhanced richness in the Gully Canyon could provide support for the hypothesis that canyons enhance the regional (beta) diversity, by harbouring different species to those occurring in the open slopes. This has also been seen in canyons from the Hawaiian archipelago, where high levels of beta diversity were observed for megafauna (Vetter et al., 2010) and for macrofauna, particularly the polychaetes (De Leo et al., 2014).

In terms of wider comparisons, it is important to state that these are still driven mainly by the availability of published deep-sea data and all such comparisons should be treated with caution. The local (alpha) diversity assessed by rarefaction suggests that, the Gully Canyon harbours species rich polychaete assemblages compared to other North Atlantic canyons and their open slopes of mid-bathyal depths (Table 3).

Table 4
K2P distances between targeted specimens, their location and GenBank Accession Numbers.

Species 1, (Location), Genbank Accession No.	Species 2, (Location), Genbank Accession No.	K2P Distance (%)	Marker	Source
<i>Lumbrineris</i> sp. 1 (Emerald Basin), MH379975	<i>Lumbrineris</i> sp. 2 (Emerald Basin), MH379976	0.246	COI	This study
<i>Notomastus</i> cf. <i>latericeus</i> (Emerald Basin), MH379977	<i>Notomastus</i> cf. <i>latericeus</i> (Gully Canyon), MH379978	0.236	16S	This study
<i>Ceratocephale loveni</i> (Emerald Basin), MH379973	<i>Ceratocephale loveni</i> (Gully Canyon), MH379974	0.234	16S	This study
<i>Ceratocephale loveni</i> (Emerald Basin), MH379973	<i>Ceratocephale loveni</i> (Bohuslän, Sweden), DQ442614	0.007	16S	This study; Ruta et al. (2007)
<i>Ophelina abranchiata</i> 1 (Emerald Basin), MH379980	<i>Ophelina abranchiata</i> 2 (Emerald Basin), MH379979	0.132	16S	This study
<i>Ophelina abranchiata</i> 1 (Emerald Basin), MH379979	Opheliidae sp. 2 (Goban Spur), KT592243	0.203	16S	This study; Gunton (2015)
<i>Ophelina abranchiata</i> 2 (Emerald Basin), MH379980	Opheliidae sp. 2 (Goban Spur), KT592243	0.157	16S	This study
<i>Aurospio dibranchiata</i> (Gully Canyon), MH379972	Spionidae sp. 1 (Goban Spur), KT592247	0.009	16S	This study; Gunton (2015)
<i>Aurospio dibranchiata</i> (Gully Canyon), MH379972	<i>Aurospio dibranchiata</i> (Porcupine Abyssal Plain), MH379971	0.146	16S	This study
<i>Aurospio dibranchiata</i> (Porcupine Abyssal Plain), MH379971	<i>Aurospio dibranchiata</i> (equatorial abyssal Pacific), EU340083–7	0.006–0.015	16S	This study; Mincks et al. (2009)

The species richness of polychaetes in the Gully Canyon is higher than Nazaré and Cascais canyons on the Iberian margin as well as their adjacent open slopes, but it is similar to that of Setúbal Canyon (Table 3). As a general trend, the diversity within the canyons is often thought to be reduced because of a build-up of large populations of opportunistic species (e.g. Paterson et al., 2011) as a result of extreme environmental conditions (e.g. strong currents, high sedimentation rates, resuspension, sediment slumps and high productivity). Such arguments were proposed to explain the reduced diversity observed in Nazaré Canyon across different taxa and time scales (see references in Paterson et al., 2011), Setúbal Canyon (Gage et al., 1995) and Hawaiian canyons (Vetter et al., 2010). However, the highly dynamic environment of canyons can lead to differences in diversity estimates across depth even within the same canyon (e.g. Cunha et al., 2011; Paterson et al., 2011).

It is difficult to explain the observed patterns in the absence of detailed environmental data. It is possible that Gully Canyon's relatively high species richness may be related to its status as a MPA, which should reduce its exposure to anthropogenic disturbance. However, in the absence of baseline studies prior to the establishment of the MPA this cannot be ascertained. More studies covering additional depths and parts of the canyon are needed to test whether the high species richness we observed is a prevailing pattern within the canyon.

Unlike in other deep-sea studies of polychaetes (e.g. Paterson and Lamshead, 1995; Glover et al., 2001, 2002; Paterson et al., 2011), the fauna of Gully Canyon was mostly assigned to known species (see Supplementary data, Table S3), previously reported from the NW Atlantic including its most abundant species: *Aurospio dibranchiata*, *Aricidea parva*, *Ophelina abranchiata* and *Glycera mimica* [considered here a valid species in contrast to Böggemann (2002)]. This knowledge of fauna is a result of an extensive deep-sea transect of NW Atlantic conducted by the Woods Hole Oceanographic Institution's expedition from Gay Head (Massachusetts) to Bermuda in the 1960's, with polychaetes documented in two monographs (Hartman, 1965; Hartman and Fauchald, 1971).

The most abundant species collected from the Gully Canyon was the spionid *Aurospio dibranchiata*. This finding is of importance in terms of both the ecology and biogeography of this species. In ecological terms, species of *Aurospio* and the closely related genus *Prionospio* have been reported in high abundances inside the canyons on the Iberian margin (Cúrdia et al., 2004; Paterson et al., 2011) as well as the Whittard Canyon (Gunton et al., 2015b). In general, Spionidae are common in sedimentary environments (Rouse and Pleijel, 2001), but tend to build up large populations in disturbed environments such as canyons, exploiting new patches of recently disturbed seafloor and organically enriched sediments (e.g. Gerino et al., 1999; Paterson et al., 2011; Gunton et al., 2015b).

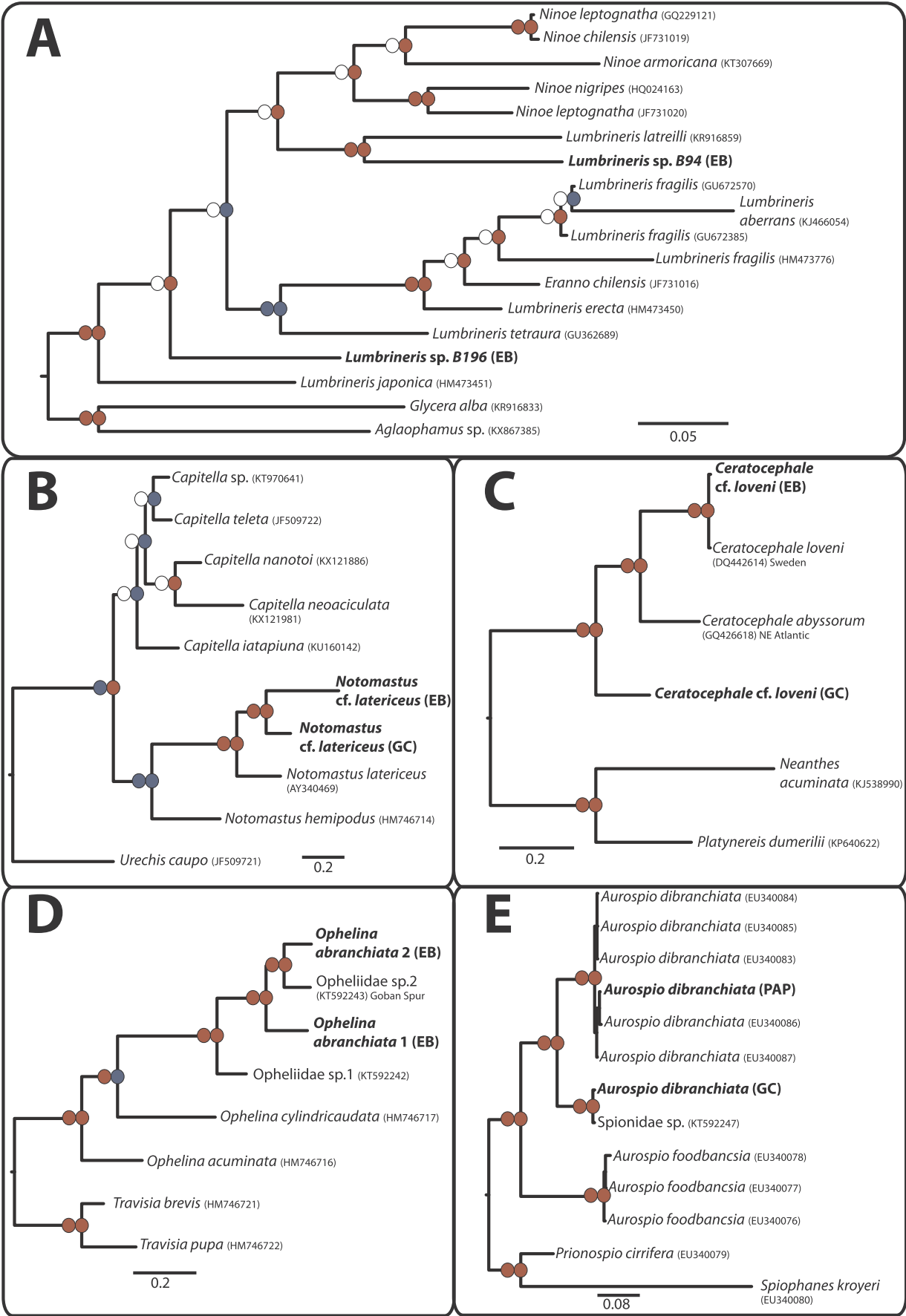
While the holotype of *Aurospio dibranchiata* was selected from deep (2041–2048 m) Argentine Basin (SW Atlantic) material, Maciolek (1981) considered this species to be widespread in the Atlantic with a 300–3600 m bathymetric range. Subsequent studies extended the range

of *A. dibranchiata* to the abyssal Pacific (Mincks et al., 2009) and deep shelf of the Southern Ocean (Neal et al., 2017). Such a wide distribution was, however, established purely on the morphological examination of specimens. Sequencing individuals from the Gully Canyon and Porcupine Abyssal Plain combined with sequences from the abyssal Pacific (Mincks et al., 2009) enabled us, for the first time, to assess the distribution of this species on a molecular basis. We confirmed the presence of two genetically distinct, depth (bathyal vs abyssal) related clades (Fig. 4E), separated by 14.6% (Table 4) with the nearest congener *Aurospio foodbancsia* Mincks et al., 2009 separated by a genetic distance of around 33% (Fig. 4E). Specimens of *A. dibranchiata* from the abyssal Pacific and Atlantic Oceans had highly similar (0.6–1.5%) 16S sequences (Table 4, Fig. 4E), while specimens of the bathyal Atlantic clade from Gully Canyon and Goban Spur showed similar limited separation of 0.9% (Table 4, Fig. 4E); in both cases this is similar to the intraspecific variation seen in congener *A. foodbancsia* (0.3–1.2% in 16S). Amplification of COI was unsuccessful for this species, and this marker may have possibly revealed further genetic differences between geographic areas. Given that depth is likely to exert a much greater control on physiology than geography, our results showing greater affinities between specimens collected from distant sites at a similar depth compared to those from closer, but bathymetrically divergent sites are not surprising. These results are concordant with other studies (e.g. Schüller, 2011; Glazier and Etter, 2014). For example, protobranch bivalves separated by 3 km depth were considerably more genetically divergent than those separated by over 10,000 km at the same isobath (Zardus et al., 2006; Etter et al., 2011). Our data also suggest that deep-sea specimens identified as *A. dibranchiata* are in need of a taxonomic revision, as morphologically similar species may be present, but were previously overlooked. However, such investigation is beyond the scope of this study.

4.3. Emerald Basin – is there a link to deep-sea fauna?

Based on the evidence presented here, we suggest that polychaete assemblages of Emerald Basin are deep-sea in character (Fig. 3a–c). In a large scale biogeographical study, Pocklington and Tremblay (1987) of NW Atlantic shelf polychaetes (from Hudson Strait to Cape Hatteras) suggested the presence of unique polychaete assemblages in Emerald Basin within the Labrador shelf faunal zone, possibly as a result of the influence of deeper slope waters (Pocklington and Tremblay, 1987). However, no comparison with assemblages from deeper waters was undertaken prior to our study.

With access to specimens from 1600 m collected in Gully Canyon during the same sampling cruise, we first compared the species composition in Emerald Basin and the Gully samples. Of 28 species found in Emerald Basin, only eight (~ 30%) were considered to be present in both locations based on morphological assessment. However, when specimens from both locations were sequenced, they were genetically distinct, thus suggesting no overlap in species distribution between two



(caption on next page)

Fig. 4. Phylogenetic trees of taxa targeted in this study. (A) Phylogenetic tree based on a *COI* alignment for the genus *Lumbrineris*; (B) Phylogenetic tree based on a *16S* alignment for the genus *Notomastus*; (C) Phylogenetic tree based on a *16S* alignment for the genus *Ceratocephale*; (D) Phylogenetic tree based on a *16S* alignment for the genus *Ophelina*; (E) Phylogenetic tree based on a *16S* alignment for the genus *Auospio*. Topology of all trees is based on the Bayesian inference analysis (BI). Left circles on the nodes refer to BI while right circles refer to Maximum Likelihood analysis (ML). Red circles indicate posterior probability values (PP) > 0.95 or bootstrap support (BS) > 75. Blue circles indicate PP < 0.95 or BS < 75. White circles indicate that this topology was not recovered in ML. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

sites. However, the molecular data provided insights into distribution of some species outside the Emerald Basin. In the case of *C. loveni*, the sequenced Emerald Basin specimen was identical to those from Bohuslän, Sweden (depth not given) (Ruta et al., 2007) and other North Sea locations from depths of 192–310 m based on comparison with unpublished data (Kongsgrud pers. comm.). Further comparison with unpublished data (Kongsgrud pers. comm., unpublished data of Oug) showed that the *COI* sequence of *Lumbrineris* sp. 1 was identical to specimens from Skagerrak, North Sea (416–513 m), while *Lumbrineris* sp. 2 was recovered as a sister taxon to a putative new species in the poorly defined genus *Augeneria* from the deep-sea (> 1340 m) around Spitzbergen. We have also shown that morphotypes of *Ophelina abbranchiata* from Emerald Basin belong to two genetically distinct species based on *16S*, with a third species in this complex (*Opheliidae* sp. 2) represented by a specimen collected at 1000 m at Goban Spur (Gunton, 2015). The genetic distances for *COI* and *16S* reported here (Table 4) are highly variable and species dependent as shown in other polychaete barcoding studies (Carr et al., 2011; Maturana et al., 2011; Brasier et al., 2016; Álvarez-Campos et al., 2017). Therefore, while no shared species between Emerald Basin and Gully Canyon were confirmed genetically, our results suggest that some species found in Emerald Basin (or their close relatives) have deeper distribution in North Sea and/or NE Atlantic. Complimentary to these observations, in those instances when known, non-cosmopolitan species were identified based on morphology alone, their Emerald Basin occurrence represented an upper limit of their known distribution at least outside the polar regions (see Supplementary data, Table S3). It is likely that at 1600 m Gully Canyon samples were “too deep” to detect such pattern, as the documented upwellings of slope water are from depths of < 1000 m (McLellan et al., 1953).

In another approach to our hypothesis, a suite of Pan-Atlantic sites (see Table 2. for details) were compared using incidence data of polychaete genera. It is important to stress that genera were established using classical taxonomy, with modern phylogenetic approaches revealing that some higher taxonomical groupings (including genera) do not necessarily represent natural groups. Phylogenetic knowledge of polychaetes is still minimal, therefore it is important to bear these caveats in mind when interpreting the results. As a general pattern, the clustering related to depth was revealed (Fig. 3a–c), while the multivariate analysis showed the affinity of Emerald Basin sites with bathyal sites, rather than with shelf sites. This includes those off-Nova Scotia – the outer shelf bank sites and inner-shelf St. Margaret's Bay or Newfoundland sites. Perhaps most surprisingly, the geographically proximal bank sites, including Emerald Bank (depth around 80 m), which are also characterised by coarse gravely sediment, were shown to support polychaete assemblages different from Emerald Basin. The outer shelf Bank sites were more similar to other and then to other shallow, but geographically distant sites (Fig. 3). These shallow banks are likely not conducive to the retention of the upwelled slope water as salinity and temperature profiles of Western and Sable Banks (around 40 m depth) suggest the presence of colder and less saline water, similar to coastal surface water (Table 3). However, the deeper Emerald Bank (80 m) has more saline, warmer water approaching that found in Emerald Basin and on the slope (Table 3), yet their fauna are dissimilar (Fig. 3). We thus propose that physiological adaptation to the increased depth achieved in Emerald Basin (up to 270 m) may play a role in differentiating these assemblages.

The Emerald Basin polychaete assemblages, which belong to the

deep-sea cluster were most similar to a 680 m site on the slope off Nova Scotia – the depth within the range of slope water upwelling. Observations of Rowe et al. (1975), from similarly deep Gulf of Maine Basin sites for macrofauna and of Watling and Skinder (2007) for megafauna, were also consistent with such a pattern. However, this is unlikely an example of true “deep-water emergence”, which would require “historic element” of taxa evolved to live in deep water to move into the shallows. In the case of Emerald Basin we propose that there is present day connectivity with deep-waters via periodical upwellings of slope water, and taxa subsequently settle in the depression on the shelf. However, further molecular work would be necessary to assess this hypothesis. A similar mechanism has been proposed for deep shelf basins in the Amundsen Sea (Southern Ocean) an area with similarly complex topography, where fauna showed a similar pattern in distribution to the one described here (e.g. Kaiser et al., 2009; Linse et al., 2013; Neal et al., 2017) and for northeastern Florida (Ross et al., 2015).

Our analysis also suggests a great level of faunal heterogeneity across the Scotian Shelf and slope (Fig. 3C) in agreement with Rincón and Kenchington (2016) who reported high level of macrofaunal dissimilarity (65.1–75.8%) between Scotian shelf banks. There is clearly a need for greater spatial and bathymetrical sampling coverage within this topographically and oceanographically complex area. Specifically, to our hypothesis, future sampling should target depths of < 1000 m on outer shelf and slope, as well as within the “saddles” connecting these areas with deep basins. Molecular methods should also be used to investigate the occurrence of cryptic species, and to document gene flow should the same species are found in the Emerald Basin and on the slope.

5. Conclusions

Polychaete data from the Gully Canyon and the Emerald Basin off Nova Scotia provide new data on diversity, distribution and species composition of this group using morphological and molecular data. The Gully Canyon harbours a species rich assemblage, largely composed of species previously recorded from bathyal depths of the NW Atlantic. The most abundant species in Gully Canyon, *Auospio dibranchiata* was shown to be a species complex (based on the *16S* marker) with bathyal and abyssal clades. The polychaete assemblages of Emerald Basin showed support for the hypothesis of deep-water faunal link to the shelf, with the affiliation of Emerald Basin polychaetes to other bathyal Atlantic sites, rather than geographically proximate shelf sites. To provide further support for the hypothesis tested here, future studies should target depths of < 1000 m off Nova Scotia, with the use of molecular techniques as species complexes were shown to be present.

Nevertheless, finding deep-water sites in relatively shallow water is not only of scientific interest, but given the immense logistical difficulties of studying deep-sea environment, may represent opportunities for more frequent sampling and in-situ experiments, as already suggested for marine caves (see Glover et al., 2010). Finally, preservation of such sites should be prioritised and conservation measures proposed considering their unique faunal assemblages.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.dsr.2018.07.003.

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