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底棲性有孔蟲群集組成與冷泉生地化環境之關連
– 以臺灣西南海域四方圈合海脊為例

The benthic foraminifera communities in relation to cold seep biogeochemistry
– an example from the Four Way Closure Ridge, offshore southwestern Taiwan

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致謝

這是一篇致謝文。我覺得致謝不該只記下風雨趨於平靜之後的感言，亦該記錄風雨之強勁。

如果說碩士是人生其中一道關卡，那麼我想把它比喻成一場 RPG。說到 RPG，最經點的莫過於一直繞圈卡關，唯有找各路人馬說話、緩慢獲得技能或新武器，才有一束破關的希望。

感謝設下關卡的人、傳授經驗的各路人馬、給我魚吃或教我釣魚的人，讓我終於破了這歷時兩年半的 RPG。

特別感謝林玉詩老師不遺餘力、兩肋插刀得協助，有 OR3-1806 航次成功的採樣、兩次阻止我拿出休學申請單，以及不厭其煩得校對初稿，才有這篇論文。特別感謝黃敦友先生的家人，將先生畢生的藏書贈與臺大，提供我重要的參考文獻。特別感謝沈聖峰老師提供顯微鏡，雖然他很可能不知道有這回事。特別感謝詹仕凡學長與謝志豪老師，提供統計分析方面的協助與諮詢。特別感謝遠在歐亞大陸彼端島國的羅立與俞舜文兩位學長，打拼之餘還要照顧此端島國的學妹。特別感謝郭思廷與余采倫兩位學姐，讓走入死胡同的關卡出現轉機。特別感謝中山海科系研究所的各路同學，有你們好歡樂啊！特別感謝張冕學姐大方讓我在臺北下雪的夜裡住進她的溫馨小窩。其他待感謝的人族繁不及備載，在此就不一一唱名。

最後，我想肯定一下自己：雖然這個學位念了兩年半，其中一年無所事事，但從 2013 年 11 月拿到樣本起，經歷九個月一千小時的蒐集數據以及兩個月的論文寫作，在 15 個月後完成這份論文，我應該沒有浪費太多生命吧！特別感謝林伯聰老師，有你，這道已經超越我心力與能力範圍的關卡才有破關的可能。

摘要

底棲性有孔蟲是深海沈積物碳循環中最重要的真核生物之一，然而，其在冷泉生態系中的地位仍在初期研究階段。本研究以數種多變量統計方法探討臺灣西南海域四方圈合海脊冷泉區的底棲性有孔蟲群集結構，以及造成物種組成差異的主要環境因子，並以具備即時影像系統的採樣器在冷泉、過渡區，以及背景環境各採了一根岩芯為研究材料。在表層 1 公分的沈積物中，體型 >250 μm 的群集有超過 50% 的膠結質殼體底棲性有孔蟲，可能是因上覆水以及孔隙水中碳酸鹽飽和度偏低所致。冷泉底棲有孔蟲群集的生物多樣性指標在三者中數值最低，過渡區群集與背景群集的數值則十分相近。然而，群集分析顯示過渡區群集與冷泉群群集組成上較相似。指標物種分析結果指出，冷泉的優勢指標物種是膠結質有孔蟲 *Haplophramoides bradyi niigataensis*，而鈣質有孔蟲 *Bulimina aculeata* 和 *Cassidulinoides differens* 則是泛冷泉環境的優勢指標物種。典型相關分析結果顯示，影響底棲性有孔蟲物種組成差異的主要環境因素是孔隙水中的硫酸鹽與溶氧濃度。更多冷泉底棲性有孔蟲生態資訊有賴後續定量研究分析。

關鍵字：底棲性有孔蟲、物種組成、冷泉、四方圈合海脊、指標物種分析、典型相關分析

Abstract

Benthic foraminifera are the most abundant eukaryotes and play an important role in the cycling of organic matter in deep sea environments. However, their ecology in cold seep environments, one of the most unusual seafloor habitats, is just beginning to be revealed. This study employed multiple multivariate statistical approaches to investigate the benthic foraminiferal community composition and the controlling environmental factors in the cold seep region on the Four Way Closure Ridge, offshore SW Taiwan. Sediment cores were retrieved from three sites (seep, transition, and reference) using video-guided sampling equipment. Faunal analysis based on the size class >250 μm showed that the three sites shared the same feature of having abundant agglutinated benthic foraminifera (>50%) in the topmost sediment, probably as a result of the low carbonate saturation state in the overlying and pore waters. The cold seep communities had the lowest biodiversity, but cluster analysis indicated substantial similarity in community composition shared between the seep and transition sites. Indicator species analysis suggested *Haplophramoides bradyi niigataensis*, an agglutinated species, to be the dominant indicator of the seepage hotspot, whereas *Bulimina aculeata* and *Cassidulinoides differens* were the dominant indicator species in the broadly defined cold seep region. Canonical correspondence analysis showed that

the concentration of sulfate and dissolved oxygen in the pore water were the most significant biogeochemical factors explaining the community variance. The patterns delineated objectively and quantitatively by these numerical ecology tools offered a basic understanding of the benthic foraminiferal ecology in modern cold seeps developed on accretionary wedges.

Keywords: benthic foraminifera, species composition, cold seeps, Four Way Closure Ridge, indicator species analysis, canonical correspondence analysis.

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1. Introduction

Benthic foraminifera are the most abundant eukaryotes (DeLaca, 1986) and play an important role in the cycling of organic matter in deep sea environments (Altenbach, 1992). The tolerance to different environmental conditions allows them to adjust to a variety of habitats (Gooday and Jorissen, 2012). Gooday (2003) summarized the factors directly affecting living deep-sea benthic foraminiferal communities, including seasonal food supply, dissolved oxygen concentration, carbonate saturation state, sediment types, bottom currents, and biotic interactions. As these factors are inextricably linked, the attempts to explain the distribution or dynamics of benthic foraminiferal communities by few dominating factors were considered too simplistic. The deep sea presents as an exception, in which the spatial and temporal variability of several environmental factors are so small that it is possible to isolate the principal control, i.e., the oxygen and the flux of organic carbon (Murray, 2001).

The TROX model, first proposed by Jorissen et al. (1995), explains the distribution of living benthic foraminifera as the result of the conflict between food (organic carbon) supply and oxygen demand. In oligotrophic environments, food supply was the main reason limiting the distribution of benthic foraminifera, as laboratory experiments showed that the behavior of overfeeding as a strategy to deal with periods of low food supply is

not common in these protists (Altenbach, 1992). In eutrophic environments, the high organic carbon flux causes rapid oxygen depletion and exerts selection pressure for foraminifera tolerating low oxygen regimes. As a consequence, species richness tends to decrease, whereas the dominance increases (Gooday, 2003). Therefore, both oligotrophic and eutrophic environments bear fewer species and lower abundance than mesotrophic environments.

Cold seeps are exceptional deep-sea habitats in that methane gas advectively transported to shallow sediment through passages such as cracks or faults made by tectonics activities. Having wide geographic and bathymetric distribution along continental margins (Sibute and Olu, 1988), cold seeps nurture chemosynthetic ecosystems that are based on the microbial process of anaerobic oxidation of methane (AOM; Boetius et al., 2000; Boetius and Wenzhöfer, 2013). In general, cold seeps have species richness higher than hydrothermal vents and regular seafloor, with the majority of species involved in animal-microbe symbioses endemic to single seep sites or individual cold seep ecosystem (Carney, 1994; Sibuet and Olu, 1998). Because of the sizable biomass and the involvement in symbiotic activities, the meiofauna are receiving increasing attention in cold seep studies. Earlier studies of benthic foraminifera in cold seeps have been focusing on the use of their stable carbon isotopic values to reconstruct seepage history (McCorkle et al., 1990; Sen Gupta and Aharon, 1994). In the past two

decades, authors started to employ ecological approaches with the overarching goals of characterizing the biodiversity, identifying the endemic species, or finding the controlling factors for the seep community (Akimoto et al., 1994; Bernhard et al., 2001; Rathburn et al., 2003; Heinz et al., 2005; Martin et al., 2007; Panieri and Sen Gupta, 2008; Martin et al., 2010; Panieri et al., 2014).

Previous studies on the biodiversity of cold seep communities are inconclusive. Some studies suggested that modern seep areas are generally characterized by lower benthic foraminifera diversity than the regular ocean bottom (Bernhard et al., 2001; Panieri, et al., 2014), while others claimed the diversity to be comparable or even higher (Heinz et al., 2005; Martin et al., 2010). Yet, most studies pointed out that the major type of tests is calcareous; agglutinated benthic foraminifera (ABF) were minor components (Bernhard et al., 2001) and usually neglected due to their low abundance (Akimoto et al., 1994; Bernhard et al., 2001; Rathburn et al., 2003; Martin et al., 2007; Panieri and Sen Gupta, 2008; Panieri et al., 2014).

Equally inconclusive is the search of endemic species of cold seeps. So far, no benthic foraminifera species are reported to be endemic in cold seep environments (Martin et al., 2010; Gooday and Jorissen, 2012); the species found living in cold seep areas could also be found in non-seep regions (Bernhard et al., 2001; Hill et al., 2003). Some species were found to be more abundant or even dominant in cold seeps. In general,

species belonging to the genus of *Bolivina*, *Bulimina*, *Cassidulina*, *Epistominella*, *Nonionella*, *Uvigerina*, to name a few, often showed up in the list of dominant seep species (see Appendix 1 of Chien, 2014, for details). These species have been associated with high organic content, low oxygen, and reducing environments (Hill et al. 2003). However, the dominant seep species seem to exhibit geographical distinction (Cheng et al., 2007). For example, the dominant seep species found in NE and NW Pacific Ocean differed from those found in NW Atlantic Ocean (Akimoto et al., 1994; Bernhard et al., 2001; Rathburn et al., 2003; Panieri et al., 2014).

The major controlling factor proposed to explain the difference in community composition between cold seeps and regular deep-sea environments is the ability of the dominant species to endure the methane-rich and sulfidic condition (Akimoto et al., 1994). The approach employed in previous studies to reach the conclusion is to directly compare the faunal compositions of seep and non-seep (or "reference") sites, and the observed difference in dominant species was directly associated with the difference in measured environmental parameters. This approach overlooks the fact that in a broadly defined cold seep region, there could be substantial variation in the seepage intensity at a local scale. Sampling along geochemical gradients that can be translated to different seepage intensity should allow better definition of seep community. In addition, the implementation of numerical ecology tools, such as indicator species analysis and canonical correspondence

analysis, could avoid arbitrary assignments of species that should be considered seep representative and offers a means to objectively assess the correlation between community composition and environmental factors.

This study investigates the benthic foraminiferal community composition and its environmental controlling factors in a cold seep area offshore SW Taiwan. We used sediment samples retrieved from three stations representing different levels of seepage intensity (cold seep, transition, and regular bathypelagic environments). First, identification down to species level and analysis of environmental factors (together with partner project of Hung (2015) and Guo (2015)) were carried out. Second, the information of community structure of the three sites was explored by numerical approaches including basic statistics, biodiversity indices, hierarchical cluster analysis, and indicator species analysis. Lastly, the association between benthic foraminiferal species compositions and environmental factors was examined by canonical correspondence analysis. Our results provide a basic understanding of the benthic foraminiferal ecology in modern cold seeps developed on accretionary wedges.

2. Material and Methods

2.1 Sampling procedure and classification of benthic foraminifera

The study sites are located at the northern top of on the Four Way Closure Ridge (FWCR), offshore SW Taiwan. This region is characterized by massive authigenic carbonate slabs along with prosperous cold seep communities and wide spread bottom simulating reflector (Liu et al., 2006), implying the presence potential reservoir of gas hydrate. All the sediment cores were collected by a video-guided coring system consisting of the Abyss Twisted-pair Imaging System (ATIS; Underwater Mechantronics Lab, Institute of Undersea Technology, National Sun Yat-Sen University) and a multicorer during the cruise OR3-1806 (October 27 to 31, 2014) by *R/V Ocean Researcher III*. The cold seep site C5-2 (22.060 °N, 119.800 °E, water depth 1351 m) was about 9 m away from a massive mussel bed, whereas the transition site C5-1 (22.059 °N, 119.800 °E, water depth 1351m) and reference site C10 (22.050 °N, 119.801 °E, water depth 1328m) with regular bathypelagic sediment were ~150 and 2200 m, respectively, away from site C5-2 (Figure 1). Deep seawater ~10 m above seafloor was taken in the nearby stations (site C5_CTD: 22.060 °N, 119.803 °E, maximum water depth 1337 m; site C10_CTD: 22.049 °N, 119.801 °E, maximum water depth 1315 m) with a conductivity, temperature and depth (CTD) instrument (Sea-Bird Electronics, Bellevue, USA) equipped with a

Rosette sampler. Details of sampling have been described in Guo (2015).

The pretreatment process followed the protocol established by FOraminiferal BIo-MOnitoring (FOBIMO) expert workshop (Schönfeld et al, 2012), including (1) sampling the upper most 5 cm sediment with one centimeter interval, (2) washing the sediment on a 63 μm screen after more than 14 days of staining by ethanol-rose Bengal solution (rose Bengal at a concentration of 2 g per liter 95% ethanol) right after sampling on broad, (3) drying picking, counting and analyzing both the living and dead benthic foraminiferal specimens of the >250 μm, 150-250 μm, and 125-150 μm fractions in a bulk of ~30 cm^3 sediment, (4) storing all counted specimens in micropaleontological slides, and (5) cataloguing the faunal data (see Appendix 1).

The classification of benthic foraminifera was mainly based on the characteristics of the test, including the wall material and structure, chamber arrangement, location of the aperture, etc. Severe synonyms and homonyms problems made proper name assignments to some of the specimens difficult. This study basically followed the classification described in Loebich and Tappan (1988) and Zeng and Fu (2001). Moreover, only the names and synonymies accepted by World Register of Marine Species (WoRMS, www.marinespecies.org), an online database providing authoritative and comprehensive lists of names of marine organisms, were consulted.

2.2 Biogeochemical analysis

The parameters essential for carbonate chemistry, i.e., the pH value, total alkalinity (TA), and dissolve inorganic carbon (DIC) were determined for the seawater samples overlying sediment in the cores (cf. Guo, 2015). For biogeochemical characterization of the sediment, dissolve oxygen (DO), DIC, stable carbon isotopic value of dissolve inorganic carbon ($\delta^{13}C_{DIC}$), and sulfate concentration have been determined using the pore water, whereas ^{210}Pb activity, total organic carbon (TOC) content, carbon isotopic value of total organic carbon ($\delta^{13}C_{TOC}$), and C/N ratio of the sedimentary organic matter have been determined for the solid phase (cf. Guo, 2015). To complete the geochemical characterization of the sediment, the following additional parameters were analyzed in the present study: dissolved sulfide, total sulfur (TS), and grain size.

Dissolved sulfide concentration was measured by the methylene blue-spectrophotometry method (Cline, 1969; protocol available at (http://www.niea.gov.tw/analysis/method/m_n_1.asp?m_niea=W433.52A). Dissolved sulfide was fixed onboard by mixing 500 μL of pore water with 250 μL of 5% zinc acetate solution. Diluted pore water, amine-sulfuric acid solution, ferric chloride hexahydrate ($FeCl_3 \cdot 6H_2O$) solution, and di-ammonium hydrogen phosphate ($(NH_4)_2HPO_4$) solution were added sequentially in a volume ratio of 750:50:15:160. The analytes were transferred into cuvettes with the absorbance measured at the wave length of 665 nm by

a spectrophotometer (V-550, Jasco, Easton, USA).

To measure TS, sediment powder was mixed with tungsten trioxide in a weight ratio 1:2 in a tin foil boat, which was tightly packed and measured by an elementary analyzer (Vario MICRO cube; Elementar, Hanau, Germany).

For grain size analysis, sediment (~0.3 g) with salts, organic matter, and carbonate sequentially removed was mixed with 1% sodium hexametaphosphate solution and measured in a laser diffraction particle analyzer (Beckman Coulter LS13 320, Brea, USA)

2.3 Statistical analysis

Biodiversity and multivariate analysis were performed using the free statistics software **R** (R Core Team, 2015) available on the CRAN webpage (http://www.R-project.org). The operation codes used in the study for R basically followed the instruction of Borcard et al. (2011). Except for the rarefaction curves in section 2.3.2, which compared the results of three size fractions in samples 0-1 cm, the rest considered specimens in size fraction >250 μm of samples 0-5 cm.

2.3.1. Descriptive statistics

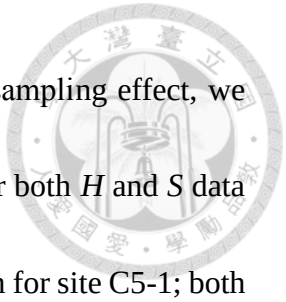
The raw counting data were transformed into relative abundance (in percentage) by dividing the number of one species by the sum of the total individuals found in one sample,

and standardized to absolute abundance in the unit of number of individuals per 50 cm^3 wet sediment. Basic descriptive statistics include benthic foraminifera faunal density, percentage of calcareous or agglutinated benthic foraminifera (CBF or ABF), and the living/total ratio (L/T ratio), calculated by dividing the number of living individuals by the sum of the total individuals.

2.3.2. Biodiversity index

There are several biodiversity indices available to quantitatively evaluate the variability of natural communities (Heip et al., 1998). In this study, we chose the Shannon diversity (*H*), species richness (S), and Pielou's evenness (*J*). Detailed description of these three indices is provided in Appendix 2. In short, the Shannon diversity is a measure of the variance of community composition by species relative abundance. Richness defines the maximum number of species found in a community. Evenness measures how equal a community is by calculating the ratio of *H* to the maximum *H*. These three indices were used to show the changes and tendency of faunal composition through depth and between sites.

Since both *H* and *J* depend on sample size, which in turn affected by *S*, biodiversity indices should be discussed under a uniform sample size. A unified sampling framework predicted by rarefying or extrapolating the data could be attained by the **R** package



"iNEXT" (Chao et al., 2014; Hsieh et al., 2014). To overcome the sampling effect, we first drew the rarefaction and extrapolation (R/E) sampling curves for both *H* and *S* data of the uppermost 1 cm (>125 μm for sites C5-2 and C10, and >150 μm for site C5-1; both living and total assemblages) with 95% confidence intervals generated from 100 bootstrap replications. The models allowed us to compute the species richness and Shannon diversity in a specific sample size from the R/E curves. The simulated *S* and *H* data were further used to calculate the *J* values. We chose to normalize our sample size to 120 individuals, the average sample size of the raw counting data of the 15 samples. We were aware of the threshold of 250 individuals suggested by Bouchet et al. (2012) to be the lower limit for calculating diversity. In fact, only one of the fifteen samples met this criterion (see Appendix 1). As material limitation made each of the 15 sediment samples valuable and indispensable, we chose to normalize the biodiversity index values to a small sample size in order to include all of them in the analysis.

2.3.3 Hierarchical cluster analysis

Hierarchical cluster analysis using the ward linkage was employed to evaluate the degree of dissimilarity among sites based on the species composition of benthic foraminifera using the R packages "stats" (R Core Team, 2015) and "cluster" (Maechler et al., 2015).The raw counting data were pre-transformation into Hellinger distance

matrix. Objects with the minimum within-group sum of squares were defined as a cluster. The optimum number of clusters was tested by the silhouette width, which measures the degree of membership of an object to the cluster that it belongs to.

2.3.4 Canonical correspondence analysis

Canonical correspondence analysis (CCA) was carried out using R package "vegan"(Oksanen et al., 2015)to seek for the crucial abiotic factors explaining the benthic foraminiferal community compositions between different samples. The responsible variables were the raw counting data without any pre-transformation to preserved chi-square distance among sites. The explanatory variables were the unscaled biogeochemical environmental factors, including DO, DIC, δ^{13}C-DIC, sulfate and sulfide concentration TOC, δ^{13}C-TOC, C/N ratio, and TS. The linear correlations among the environmental factors were tested to avoid synonymous parameters. Forward selection and permutation test were carried out to achieve parsimonious explanatory variables and the number of axes worth displaying. As all environmental measurements contained errors, we used weighted averages scores instead of linear combination scores as site scores in the CCA biplots.

2.3.5 Indicator species analysis

The indicator value (IndVal) index, first designed by Duferne and Legender (1997), was a measure of the association between a species and an environment, reaching maximum when a species was found in all sites of a single environment (see Appendix 3 for details). Prior to analysis, the 15 samples were divided into groups according to the result of the cluster analysis. Permutation of 999 times and p-value <0.05 were used in order to find a better representative of an environment with a higher IndVal and a smaller p-value.

De Càceres et al. (2010, 2012) advanced indicator species analysis by introducing the algorithm allowing for (i) the combination of pairs of and even triplets of groups, and (ii) species combinations instead of merely single species to be "indicative". Indicator species analysis was performed using the **R** package "indicspecies" (De Caceres and Legendre, 2009). In this study, the advanced approach was implemented, with the species combinations construed as valid when the following criteria were all met: (1) the species combinations should yield higher association value than single indicator species, (2) the species combinations should be the most parsimonious one that yielded the highest association value, and (3) no ubiquitous species, i.e., species that appear in all groups, should be present in the species combinations.

3. Results

3.1 Environmental factors

The biogeochemistry and ^{210}Pb-derived sedimentation rate (Fig. 2) of the whole sediment column (up to 25 cm) has been described in detail in Guo (2015). In this section, we will briefly summarize the environmental data of the upper-most 5 cm sediments.

The three sites showed distinct patterns in DO depletion (Fig. 2A). DO was ~0.15 mM at the sediment-water interface and remained ~0.09 mM at 2 cm below the seafloor (cmbsf) at site C10. In contract, DO was only ~0.10 mM at the sediment-water interface in the cold seep area, dropped to ~0.03 mM at 2 cmbsf at site C5-1, and even approached zero at the same depth of site C5-2, clearly defining the boundary of oxic (0-2 cmbsf) and anoxic (2-5 cmbsf) zones. As for the other environmental factors, neither a clear pattern in the downcore distribution nor distinction among the three sites could be observed, probably because seawater still exchanges with pore water of the shallow sediment or the seep activity is not intense enough to cause substantial diagenetic difference in recently deposited sediment.

Sulfide concentrations were generally low (0.5 to 2 μM) in surface sediment and increased mildly with depth, with site C5-2 (1.5 to 1.7 μM) reaching two to three times the values of the other two sites (0.5 to 0.9 μM) in the upper 2 cmbsf (Fig. 2I). The TS

content also showed an increasing trend with depth, with site C5-2 (~1.3%wt) reaching twice the value of the other two sites (~0.6%wt) at 4-5 cmbsf (Fig. 2J).

Physical property analysis showed that the sediment on the Four Way Closure Ridge was mainly consisted of well-sorted silt with a median grain size of ~7ϕ (Figs. 2K to 2O). Compare to sites C5-1 and C10, site C5-2 had sediment that was a slightly less sorted (sorting value = 1.24 to 1.33; Fig. 2L) and more sandy (% sand = 1.1 to 2.2; Fig. 2O).

3.2 Faunal composition

The absolute abundance in the two cold seep sites ranged widely from ~100 to 550 individuals per 50 cm^3 wet sediment, whereas site C10 had a relatively constant abundance of ~300 to 400 individuals per 50 cm^3 wet sediments (Fig. 3A1). The abundance of living individuals was in general <50 individuals per 50 cm^3 wet sediment, accounting for <15% of the total assemblage (Figs. 3A2 and 3B). The exception is the top 0-1cm sediment of the three sites. At the cold seep sites, the percentage of the living individuals was ~60% at site C5-2 and ~45% at site C5-1, whereas at the reference site the percentage was only ~20%. It should be noted that only site C5-2 had considerable absolute abundance (~300 living individuals per 50 cm^3 wet sediment), whereas site C5-1 had absolute abundance comparable to that of site C10 (~70 living individuals per 50 cm^3 wet sediments).

In general, CBF with carbonate tests were 30% to 60% more abundant than ABF with agglutinated tests (Fig. 3C1). Again, the top 0-1 cm of sediment is the exception: ABF constituted ~65% and 55% of the total assemblages at the seep and reference sites, respectively, and 65% to 86% of the respective living assemblages (Fig. 3C). The zig zag profiles shown beneath 1 cmbsf in the ABF% of living assemblages (Fig. 3C2) were resulted from sparse specimens and were considered unreliable.

3.3 Biodiversity indices and difference among size classes

The numbers of specimens of the size class >250μm was in most case inadequate (<250 individuals) to allow for proper calculation of the diversity indices (Bouchet, 2012). Our model results showed that on the one hand, even with adequate sample sizes of 250 individuals, neither the total nor the living assemblages in the size classes >150 μm and >125 μm reached the asymptotic species richness values (Figs. 4A and 4C). That is, the benthic foraminifera were so diverse that no practicable sample size can reach the equilibrium. Moreover, the difference in biodiversity index values among the sites, particularly between the seep site C5-2 and reference site C10, could be resolved with this sample size of 120 individuals, as manifested by the non-overlapping 95% confidence intervals. This result supports the choice of using 120 individuals, which should be sufficient for our purpose of identifying the biodiversity difference between the seep and

reference sites.

In general, the normalized values of biodiversity indices for both total and living assemblages decreased in the order of site C10 ≈ C5-1 >> C5-2 (Figs. 4 and 5).

The Shannon diversity values of site C10 (H = 37.6 to 46.2; Fig. 5A) were slightly higher those of site C5-1 (H = 43.2 to 36.8). Both sites did not show clear downcore variation. The 95% confidence intervals of site C10 and site C5-1 strongly overlapped and were significantly higher than that of site C5-2. The top 1 cm of site C5-2 had a Shannon diversity value close that of C5-1 (H = 29.1), whereas the deeper sediment had the lowest values of all samples (H = 20.4; Fig. 5A). In terms of species richness, sites C10 and C5-1 showed comparable S values of 53 to 67, significantly higher than those of site C5-2 according to the 95% confidence intervals (35 to 44; Fig. 5B). The Pielou's evenness also decreased in the order of C10>C5-1>C5-2 (Fig. 5C), with site C10 (J = 0.92 to 0.93) slightly higher than site C5-1 (J = 0.90 to 0.92), and distinct from site C5-2 (J = 0.82 to 0.90). The broad 95% confidence intervals for the J values of three sites were resulted from the errors propagated from H' and S values.

3.4 Degree of dissimilarity among samples

Results from the clustering analysis suggested that the 15 samples were grouped following the nature of geographic and biogeochemical differences, i.e., they were

divided according to their site, indicating distinct species composition among sites (Fig. 6). Of notion was that although the transition site C5-1 had biodiversity index values closer to those of the reference site C10 (Fig. 5), its community composition was closer to that of the cold seep. This result reinforces the representativeness of the indicator species and species combinations (see below).

Both the cold seep (cluster 2) and regular bathypelagic (cluster 3) environments had samples in the oxic layer (0-1 cmbsf and 1-2 cmbsf; fig. 2A) linked together (Fig. 6), suggesting a higher degree of similarity in species compositions. In the transition site (cluster 1), the five samples, particularly the upper two sediment layers, were linked at higher nodes compared to the other two clusters, implying a lower degree of downcore similarity and different faunal composition in the oxic layer.

3.5 Indicator species and species combinations

An indicator species is not equal to a dominate species, which has the simple definition of having high relative abundance in the community. A good indicator species can only be found in a particular environment (A = 1, cf. Appendix 3) and wide spread over the environment (B = 1). Hence, species or species combinations with higher IndVal or "stat", the square root of IndVal, can be better indicators of their habitats (Tables 1 to 3).

The indicator species analysis showed that the combinations among *Haplophragmoides bradyi niigataensis*, *Trochammina vesicularis*, *Recurvoides laevigata*, *Bolivinita quadrilatera*, *Bulimina aculeata*, and *Plectina nanissima* can best indicate the cold seep environment (site C5-2), whereas the combinations among *Rutherfordoides rotundiformis*, *Uvigerina auberiana*, *C. differens* and *Osangularia bengalensis* were the best representatives for transition site C5-1 (Table 1). The shared indicator species in the cold seep and transition environment were *B. aculeata* and *C. differens* (Table 1). Among these 10 indicator species, *H. bradyi niigataensis*, *T. vesicularis*, *R. laevigata*, and *P. nanissima* are ABF, and the rest CBF.

Indicators found in the regular bathypelagic sediment in the northern South China Sea (SCS) were more diverse, including *Karreriella bradyi*, *Uvigerina proboscidea*, *Uvigerina hollick*, *Bathysiphon macilentus*, *Globocassidulina elegans*, *Karreriella parkerae*, *P. nanissima*, *O. bengalensis*, *Uvigerina auberiana*, *Cibicides pachyderma*, *Cibicides wuellerstorfi*, *Cibicidoides* sp. D and their combinations (Table 2). Although *P. nanissima* showed up in the indicator species combinations of both cold seep and regular bathypelagic environments, it is not a significant single-species indicator in either environment (p-value = 0.064). Note that the fragile nature resulting from the stick-liked appearance of *B. macilentus* test tends to mask its true abundance, making the species an indicator only when the preservation status is ideal. The shared indicator species in the

regular bathypelagic and transition environment were *U. auberiana*, *O. bengalensis*, and *C. pachyderma* (Table 2). Among these 12 indicator species, *K. bradyi, B. macilentus*, *K.parkerae,* and *P. nanissima* are ABF, and the rest CBF.

There are several species showing good tolerance to all three environments. These ubiquitous species have no particular preference of living habitats and therefore were inappropriate to be used as indicator species. These include *Gyroidinoides soldanii*, *Heterolepa broeckhiana, Karrerotextularia philippinensis*, *Pullenia bulloides*, *Globocassidulina subglobosa, Sphaeroidina bulloides*, *Sigmoilopsis schlumbergeri*, *Lenticulina inornata*, *Melonis barleeanus, Arenogaudryina* sp. C, *Saccammina sphaerica*, *Reophax scorpiurus, Discammina compressa*, *Oridorsalis umbonatus*, Unknown sp. A, *Chilostomella oolina, Rhabdammina discrete, R. scabra, Gyroidina* sp. D, *Lagenammina cushmani*, and *Uvigerina pygmaea* (Table 3). Sharing the same problem of *B. macilentus*, *Rhabdammina* spp. might have overestimated abundance. Among these 21 species, *K. philippinensis*, *S. schlumbergeri*, *R. scorpiurus, D. compressa, C. oolina*, *R. discrete*, *R. scabra,* and *L. cushmani* are ABF, and the rest CBF.

There are uncertainties in assigning names to some of the indicator or ubiquitous species. The specimens identified as *H. bradyi niigataensis* are very likely called *Cribrostomoides subglosa* in other published work. The species *K. philippinensis* might have been lumped into *Karrerotextularia flintii* (also called *Siphontextularia flintii* by

some authors) in some cases. *Arenogaudryina* was originally considered as a fossil genus (Loeblich and Tappan, 1988), but the idea was later rejected by Zeng and Fu (2001). Being a "Lazarus" genus, *Arenogaudryina* has very little information from field studies. Further studies on specimens or published photos are necessary to clarify their taxonomy.

3.6 Correlation with environmental Factors

In the first CCA, all environmental variances could explain 69.6 % of the community variance, with CCA 1 and CCA 2 accounting for 42.2 % and 36.7 % of the community variance, respectively (Fig. 7). There was a tendency that site C10 samples were more related to environment with higher DO and TOC content, site C5-1 samples were more related to higher sulfate and lower TOC, and those from cold seep site C5-2 favored environments with higher dissolved sulfide and TS.

In the second CCA, only the biogeochemical parameters with p-value <0.1 were plotted (Fig. 8). The two main factors that significantly (p-value <0.05) explained the variance of benthic foraminiferal community structures were the sulfate and DO concentrations, which explained 11.4% and 9.9%, respectively, of the variance of communities and were almost perpendicular to each other on the CCA biplot (Fig. 8). The explanatory power of TS was lower (9.1%), with the p-value between 0.05 and 0.1. CCA1, which explained 11.7% of the community variance, was greatly contributed by DO

concentration and TS, whereas CCA 2, which explained 11.2% of the community variance, was mostly contributed by sulfate concentration.

DO concentration separated the reference site from the others, while sulfate concentration separated the cold seep site from the others (Fig. 8A). For the reference site, the 1-2 cm was discriminated from the others along the factor of sulfate concentration, whereas the samples below 2 cmbsf were arranged in parallel to the factor of sulfate concentration, reflecting the dominance of sulfate concentration in discriminating these depths. The five samples of the transition site (C5-1) had orientation more or less similar to those of the reference site but with displacement towards the third quadrant, implying comparable discriminating environmental factors but at a lower DO regime. The samples from the cold seep (C5-2) were separate from those of transition site by sulfate concentration, arranged parallel to none of the parameters, reflecting the combination of downcore increasing sulfate concentration and TS, as well as decreasing DO concentration (Fig. 2A, 2G, and 2J).

In agreement with the result of cluster analysis (Fig. 6), the sediment layer of 1-2 cm of site C5-1 seems to be distant from all the other C5-1 samples, which generally dotted the statistical space between reference and cold seep samples. The remote position of this sample was attributed to the presence of abundant CBF, particularly the species *R. rotundiformis*. The CCA biplot with this sample excluded (data not shown) did not differ

significantly from Fig. 8, implying that this sample should not be taken as an outlier.

Figures 7B and 8B are CCA biplots with species scores. The cold seep indicators, *H. bradyi niigataensis*, *T. vesicularis*, *R. laevigata*, and *B. quadrilatera* (marked in red; Table 1), favored a low DO, low sulfate, high TS and sulfidic environment, while the transition indicators *R. rotundiformis* (marked in yellow) favored a low DO but sulfate-rich environment. The diverse regular bathypelagic sediment indicators (marked in blue; Table 2) preferred an environment with high DO and sulfate concentration, and sufficient supply of TOC. The indicator species of site combinations tend to occupy the statistical space between the single-site end indicators.

4. Discussion

With the assistance of video-guided sampling, we were able to associate benthic foraminiferal faunal assemblage to seafloor features, which are the primordial indicators of cold seep activity. Sites C5-1 and C5-2, geographically only 150 m apart, would have been easily considered equally representatives of cold seep environments. The fact that site C5-2 was taken from a location about 9 m away from a massive mussel bed with the seafloor having dark gray patches (presumably iron sulfide precipitates) substantiates the use of C5-2 sediment as a cold-seep end member. The biogeochemical study of the same suite of sediment cores also confirmed at site C5-2, there was extensive and pronounced influence of methane-derived carbon to the major carbon pools in pore water and sediment (Guo, 2015), a typical characteristic of all methane seep sediment. However, the main drawback of this sampling tool, i.e., the low recovery of cores compared to conventional coring methods, poses substantial limitation on biodiversity research. The present work is based on only three cores with five sediment depths from each instead of 15 surface sediments from different stations, which would be the more ideal sample set. Hence, before discussing the results, we would like to elaborate the underlying constraints, limitations, and assumptions.

4.1 Constraints, limitations, and assumptions

4.1.1 Validity of Rose Bengal staining in living individuals

Rose Bengal staining, a protein stain, is the easiest technique that allows for quick shipboard identification of living benthic foraminifera individuals from dead ones (Bernhard, 2000) and has been extensively employed in the study of benthic foraminifera ever since its introduction by Walton (1952). Earlier studies claimed that the "accuracy" of distinguishing living from dead specimens can be as high as 92% (Lutze and Altenbach, 1991). However, several articles argue that this method could lead to overestimating the actual abundance of the living individuals by staining the organic remains of organisms that have been dead months to years (Bernhard, 1988; Corliss and Emerson, 1990; Hannah and Rogerson, 1997; Bernhard et al., 2006). The use of more critical vitality assays was strongly recommended by Schönfeld et al. (2012) to deal with samples collected from low oxygen environments such as site C5-2, where the decay of the dead organisms is even lower.

According to the ^{210}Pb dating results (Fig. 2H), the sedimentation rates in the upper 5 cm are 0.029 to 0.060 cm/yr at site C10, 0.066 cm/yr at site C5-1, and 0.046cm/yr at site C5-2 (for details see Guo, 2015). Therefore, accumulation of 5 cm thick sediment would maximally require 119 yrs at site C10, 76 yrs at site C5-1, and 109 yrs at site C5-2. If the preservation condition investigated in Hannah and Rogerson (1997) and Corliss

and Emerson (1990) also applies in our study area, the error (months to years) of the staining technique in identifying living individuals is much smaller than the age of the sediment, validating the interpretation of stained specimens as endogenically active fauna, even in depths up to 5 cmbsf.

Site C5-2 was considered to represent the environmental condition with active seepage (Guo, 2015). As seepage could be an ephemeral event, the next question would be if the stained samples found at this site can represent communities affected by methane seepage. A recent study on cold seep mussels provides a means to gauge the age of modern seepage activities offshore SW Taiwan. Gaining energy via symbiosis with methanotrophic or thioautotrophic prokaryotes (Sibuet and Olu, 1998; Duperron et al., 2007), these mussels can thrive only when there is seep activity. Investigations of the cold seep mussels *Bathymodiolus platifrons* found in the cold seep areas of the northern South China Sea revealed that a 99.21 mm *B. platifrons* was at least 245 years old according to the growth lines counted under a scanning electron microscope (Chao, 2015; Li-Lian Liu, personal communication). This estimation was in agreement with the study of the growth equations (Nix et al., 1995) and the encroachment rate (Smith et al., 2000) of the cold seep mussel *Bathymodiolus childressi* in the Gulf of Mexico, as well as the ^{228}Ra dating and the sclerochronology results of deep sea clams (Turekian et al., 1975). Massive mussel beds of *B. platifrons* were also observed during the video survey of the Four Way

Closure Ridge (Guo, 2015). According to the video images, the average shell length of the mussels was estimated to be 85 mm, suggesting that the methane seepage has been active for at least 210 years.

As the inferred error of Rose Bengal technique is much smaller than the age of the sediment and the time span of the seepage, we concluded that the stained specimens represent benthic foraminifera that were being affected by the special environments created by seepage activity.

4.1.2 Environmental conditions of the recent past

Debris of shells was frequently observed during the survey with V-corer (Yu-Shih Lin, personal communication). This raises the question of whether the environmental conditions, particularly the seep activity, have been relatively constant over tens of years when the first 5 cm sediment of our study sites was deposited. With the assumption that the seep activity decreases with distance from the massive mussel bed, we can estimate the change in distance as a proxy of seep activity based on the encroachment rate of the mussel bed. No direct measurement on the encroachment rate is available for the *B. platifrons* community on the FWCR. Smith et al. (2000) studied the mussel bed of *B. childressi*, a close relative of *B. platifrons*, and obtained a rate of 1.0 cm/yr which, according to the authors, was an overestimate. Were this encroachment rate applicable to

the *B. platifrons* community in our study area, the maximum expansion distance of the mussel bed was estimated to be 75 to 170 cm. This change in distance to the mussel bed was insignificant considering the systematic sampling error from the multicorer (the maximum horizontal distance between the corers was close to 100 cm). Therefore, we concluded that the environmental conditions of our study sites have been constant over the past decades.

4.1.3 Validity to associate the total assemblages to pore-water geochemistry

In CCA, we tried to explain the variance of the total assemblages by environmental factors (Figs. 7 and 8). It turned out that DO and sulfate concentrations, two dissolved constituents, were the most significant explanatory parameters. A question arises as to why the total assemblage, which is composed mainly of the dead assemblage accumulated above this depth over time plus a minor living assemblage now thriving at this depth, can be explained by pore-water geochemistry, which largely reflects recent biogeochemical processes. We argue that since the environmental conditions are considered to stay relatively constant during the past decades, the dead assemblage of sediment in 1 to 5 cmbsf should be mostly originated from the past living assemblage when the sediment was at the top (Figs. 2A2 and 9). Therefore, the different depths from one site share the same bulk of assemblage that formed when the sediment layer was on the surface of

seafloor, but vary from each other in terms of the living assemblage, which is affected by pore-water geochemistry. As the purpose of CCA is to explain the variance in species composition among samples by environmental factors, our observation of DO and sulfate concentrations being explanatory parameters is considered reasonable.

4.2 Benthic foraminiferal community composition and indicator species

4.2.1 Community structure of the cold seep

The cold seep benthic foraminiferal community on the FWCR had higher absolute abundance but lower diversity compared to the transition and reference sites, implying monotonous faunal composition dominated by a few species (Figs. 3 and 5). The species richness in the size class >150 μm was around 100 to 150 species (Fig. 4A). The values of both absolute abundance and biodiversity indices are comparable to the samples collected from the continental shelf offshore SW Taiwan (Hsieh, 2005) of from locations of similar water depth in the southern SCS basin (Miao and Thunell, 1993).

While the absolute abundance of benthic foraminifera in cold seeps varies widely (up to 4000 individuals/cm^3 in the Blake Ridge; Panieri et al., 2014), the biodiversity, as also demonstrated in this study, was in general lower than the respective reference site. A direct comparison of the species richness values reported from different cold seep environments is difficult, though. This is because species richness is proportional to the

sample size, but there is no convention as to which sample size the species richness values should be normalized if the asymptotic value is not reached. Yet, there are some extreme cases of low biodiversity in cold seeps. With a sample size of hundreds to thousands of individuals, the richness was only ~40 species on the Hikurangi margin, New Zealand (Martin et al., 2010). In the cold seeps in the Gulf of Mexico, the biodiversity was so low that a sample size of less than 200 individuals sufficed to obtain an asymptotic richness value of ~20 species (Robinson et al., 2004). As pore-water geochemistry was not always well characterized in these biodiversity studies, it is unclear whether the biodiversity of cold seep sediment is related to the intensity of AOM activity.

4.2.2 Ecological meaning of the indicator species

The indicator species with relative abundance ≧2 % were considered as dominant ones and plotted in Figure 10. Some of the ubiquitous species with relative abundance higher than 2% in only two sites, such as *G. subglobosa* and *K. philippinensis* (Table 3),were also plotted for comparison.

All the species present in Fig. 10, except for *Arenogaudryina* sp. C, *H. bradyi niigataensis*, and *K. philippinensis*, were CBF and cosmopolitan deep sea foraminifera. The cold seep of the FWCR seems to share indicator species with the dominant species identified in the cold seeps in the Sagami Bay, Miura Peninsula, and Kakegawa area,

Japan. *H. bradyi niigataensis* was the only dominant indicator species found at the cold seep. It is the first time that this species is associated with cold seep environments. *H. bradyi niigataensis* was an ABF first described and named by Uchio (1962), who collected the holotype in the estuary of River Shinano at a water depth 80 m. The finding of *H. bradyi niigataensis* to be indicative of the cold seep is surprising given the fact that ABF were minor components (Bernhard et al., 2001) and usually neglected in cold seep studies (Akimoto et al., 1994; Bernhard et al., 2001; Rathburn et al., 2003; Martin et al., 2007; Panieri and Sen Gupta, 2008; Panieri et al., 2014). The ecological meaning of this species will be discussed (see Chapter 4.3.2). *B. aculeate* has been reported having high abundance in sediment with elevated methane concentration (Akimoto et al., 1994, 1966a), as well as in regular bathypelagic sediments with high organic carbon content (Mial and Thuncll, 1999). Other *Bulimina* spp. were also claimed to be linked with high methane concentration and could tolerance sulfidic environments (Akimoto et al., 1994, 1996a, 1996b).

While some *Rutherfordoides* spp. have been associated with seep environments (Akimoto et al., 1994, 1996a, 1996b), *R. rotundiformis* was found to be representative of the transition site rather than the seep site (Table 1). The species *C. differens* was indicative of the site combination of C5-1 and C5-2, i.e., the broadly defined cold seep region. It is also the first time that both species are associated with seep-related

environments.

Some of the abundant ubiquitous species had higher abundance in the broadly defined cold seep region: *K. philippinensis*, was more abundant in site C5-1 whereas *S. bulloides* and *P. bullodies* were more abundant in site C5-2. *G. subglobosa* was found along with *Uvigerina* spp, *Melonis affinus*, *Bolivina robusta*, and *Heoglundina elegans*, as the dominant species in the SCS basin at water depth of 900 to 1500 m (Miao and Thunell, 1993). While *G. subglobosa* and *Uvigerina* spp. were abundant (≧2 %) and could reach up to ~15 % in the reference site C10, the other three were sparse (<2 %) or even absent in our samples. It should be noted that *G. subglobosa* was reported as a dominant cold seep species in the Blake Ridge diaper (Panieri et al., 2014).

4.2.3 Nature of the transition site assemblages

As gas seepage is a highly spatiotemporally heterogeneous phenomenon, it is very challenging to acquire material from "hotspots", such as the cores from site C5-2, even with the use of a towed coring system guided with video. The majority of cores taken via the conventional coring device from broadly defined "seepage regions" (e.g., Chuang et al., 2010) have geochemical characteristics close to that of site C5-1, that is, a diffusion-controlled setting with methane flux just slightly higher than the reference site. The next questions are: what is the nature of the transition site assemblage? To which extent do

samples took from locations like the transition site approximate cold seeps in terms of benthic foraminiferal composition?

We formulated two conceptual models that might apply to the relationship of community composition among the cold seep hotspot, the transition, and the background environment (Fig. 10). In the first model, the transition site as an intermediate along the geochemical gradient hosts species from either of the two end-member environments. These species are probably those with tolerance to a broader spectrum of environmental conditions. In the alternative model, the transition site should be viewed as a unique combination of environmental parameters and is propitious to the development of its own characteristic community, which bears little resemblance to those in the other two environments. We further posited that the extraction of cold seep signals from transitional environments is feasible for both models while the first model is a more common case.

The first model applied better to our case because (i) the transition site samples were grouped together with the cold seep samples in the cluster analysis (Fig. 6), and (ii) in the indicator species analysis, the transition site alone had fewer indicator species than the site combinations containing site C5-1 (Table 1). Species such as *B. aculeata* and *C. differens*, were successfully identified as the indicators of the site combination C5-1 plus C5-2, while the dominance of the ABF species *H. bradyi niigataensis* were absent in site C5-1 (Table 1, Fig. 10). Furthermore, low biodiversity index values were also missing in

the transition site that was only 150 m away from the seepage “hotspot”. We concluded that materials from transition environments may offer partial information of cold seep assemblages but should not be used to substitute hotspot samples.

4.3 Associations between faunal composition and environmental factors

4.3.1 Dominance of agglutinants in the near-surface sediment

That ABF exceeded 50% of the total assemblage in the uppermost centimeter (Fig. 3C1) of our seep site is in strong contract to other cold seep studies, in which ABF were often neglected due to their low abundance (Akimoto et al., 1994; Bernhard et al., 2001; Rathburn et al., 2003; Martin et al., 2007; Panieri and Sen Gupta, 2008; Panieri et al., 2014). However, higher proportions of ABF (up to 45 %) have been reported in the reference sites of some studies (Panieri and San Gupta., 2008; Martin et al., 2010). This observation led to the posterior presumption that ABF have poor tolerance to seep gases and low oxygen conditions compared to CBF (Gooday et al., 2000; Panieri and Sen Gupta, 2008; Panieri et al., 2014), although early physiological studies suggests that the presence of tectin, an organic inner layer of the test should make ABF more tolerant to the low oxygen, carbonate deficient, and low pH conditions (Hedley, 1963 and 1964).

Wu and Wang (1989) argued that the abundance of ABF in the marginal seas of

China was associated with seawater pH, which governs the carbonate saturation state, a key constraint of CBF. To test if low carbonate saturation states could be the reason for the abundant ABF in our study area, we calculated the degree of calcite saturation (Ω_{ca} = $[Ca^{2+}] \times [CO_3^{2-}]/K_{sp}$; K_{sp} is the solubility product of calcite) using the fluid chemistry data presented in Hung (2015) and Guo (2015). We assumed that (i) the salinity and temperature measured in the deepest depth (~10 m above seafloor) of the CTD casts were applicable to the bottom waters overlying the sediment and the uppermost 1 cm sediment, and (ii) the TA and pH values of overlying waters apply to pore waters of the uppermost 1 cm sediment because of interfacial fluid exchange. We then computed the Ω_{ca} values of overlying and pore waters using the program developed by Pierrot et al. (2006).

We obtained generally low Ω_{ca} values of 1.13 to 1.46 for the overlying waters and 1.43 to 1.63 for the pore waters (Table 4). The result is in agreement with Chou et al. (2007), who showed that the saturation depth of calcite in the northern SCS (SEATS site) is at water depth ~2500 m. As our study area is still above the lysocline, carbonate does not readily dissolve. However, Feely et al. (2004) reported lowered biogenic calcification rate of both planktons and benthos when the Ω_{ca} higher than but approaching 1. Furthermore, dissolution might happen well above calcite lysocline (Feely et al., 2002), probably in microenvironments. For instance, in the uppermost sediment, intensified respiration, particularly in the seep environment, should theoretically enhance the level

of CO_2, which is converted to HCO_3^- after interacting with carbonates (Milliman et al., 1999; Chen, 2002). Given that the calcite saturation state is close to equilibrium in our study area, perturbation of CO_2, even at a small dosage, is likely to trigger carbonate dissolution in microenvironments and making the condition unfavorable to CBF. This argument is also supported by the study of fossil assemblages in the Yenshuikeng Shale containing ancient cold seeps in SW Taiwan (Chien, 2014): Samples collected within 50 to 60 cm from the paleo-seepage "hotspots" had CBD <30 %, probably due to pore water acidification resulting from the generation of bicarbonate during AOM.

The alternative explanations for elevated proportions of ABF include high proportions of sands (mainly consist of median to fine sand; Wang et al., 1988) or the low salinity of water mass (Murray, 1973), neither of which were supported by our data (Fig. 2O and Table 4). Therefore, we conclude that the most possible explanation for the high abundance of ABF in the top 1 cm sediment in all three sites is the generally low Ω_{ca} in the overlaying and pore waters, although the exact physiological response of benthic foraminifera to lowered carbonate saturation state remains unknown (Feely et al., 2004).

4.3.2 Controlling factors of the community composition

CCA analysis accompanied by forward selection and permutation tests showed that sulfate and DO concentration were the most important environmental factors explaining

the variance of species compositions among sites (Fig. 8), followed by TS as the third significant factor. No parameters related to organic carbon were found to be significant.

The TROX model suggests organic matter to be one of the two most important factors controlling the distribution of deep-sea benthic foraminifera, although results from field studies, including the present work, do not always conform to this "paradigm". Miao and Thunell (1993) concluded that only TOC content and oxygen penetration depth, among other parameters including salinity, temperature, grain size, water depth, and bottom water DO concentration, correlated well with the benthic foraminiferal distributions in the SCS. However, no correlation between the abundance of benthic foraminifera and TOC content could be found on the continental slope along Gao-Ping Canyon, offshore SW Taiwan (Hsieh, 2005). One explanation for the disparity is that most published work used TOC content as the proxy for the quality and quantity of organic matter. This is inappropriate due to the fact that the majority of sedimentary organic matter is consisted of refractory to semi-refractory components (Killops and Killops, 2005). Endeavors to characterize the degradability of sedimentary organic matter, such as the use of amino acid-based degradation index (Dauwe, 1999) should be made in the future to better understand the influence of food quality to benthic foraminifera.

The importance of the other primary controlling factor in the TROX model, DO concentration, is generally acknowledged in field studies. As oxygen consumption rates

of cold seeps are orders of magnitude of higher than those of non-seep environments (Boetius and Wenzhöfer, 2013), availability of oxygen becomes a crucial limiting factors for eukaryotes living in sediment, including benthic foraminifera. In the TROX model, the DO concentration of 1 or 2 mL/L (equivalent to 0.031 or 0.063 mM) was proposed to be the threshold below which no benthic foraminifera can thrive (Murray, 2001). With the use of CCA, we advanced the knowledge of this controlling factor by showing the preference of the indicator species to different DO regimes (Fig. 12B). For example, *U. proboscidea*, occyping the region where the DO arrow points to, would prefer more oxygen environments than *H. bradyi niigataensis*, which dotted the regin in the opposite direction. CCA results not only provided an illustration that DO concentration was not merely an environmental threshold, but proved that the correlation between oxygen and fauna abundance at species level did exist.

Sulfate is a significant explanatory parameter in our CCA result. As benthic foraminifera do no respire sulfate, the rationale for having sulfate as the controlling factor is most likely due to (AOM), with the net reaction (Barnes and Goldberg, 1976) expressed as

$$CH_4 + SO_4^{2-} \rightarrow HCO_3^- + HS^- + H_2O$$

with the reference sediment providing constraints on organotrophic sulfate reduction, the lower sulfate concentration of seep sites can be attributed to methane oxidation, the

intensity of which is related to the upward methane flux (Niewöhner et al., 1998). Therefore, the parameter of sulfate can be viewed as the inverse proxy of seep intensity and becomes the controlling factor discriminating transition samples from cold seep ones (Fig. 14A) and their respective dominant indicator species (Fig. 14B), such as *H. bradyi niigataensis* (cold seep) and *R. rotundiformis* (transition).

TS, instead of dissolved sulfide, was found to be the last significant explanatory parameter. This is surprising, as dissolved sulfide has been considered as one of the major environmental constraints on the distribution of benthic foraminifera because of its toxicity to eukaryotic life in low oxygen environments (Bernhand, 1992; Moodley et al., 1998). Adaptation mechanisms such as dormancy (Bernhard, 1992) and peroxisome proliferation (Bernhard et al. 2001; Bernhard and Bowser, 2008) have been reported in a few cold seep foraminiferal species. We noted that the C5-2 sulfide concentrations determined months after the cruise were orders of magnitude lower than those reported from in situ analysis with a microsensor (up to ~ 0.2 mM; Rathburn et al., 2003, Boetius and Wenzhöfer, 2013). This is contradictory to the shipboard observation of strong sulfidic smell when the cores of site C5-2 were retrieved. Therefore, we cannot preclude the possibility that prolonged sample storage has compromised the quality of the dissolved sulfide data. Unlike dissolved sulfide, TS is less prone to storage effects. Furthermore, this parameter should reflect the long-term accumulation of reduced sulfur

and should be proportional to AOM activity. The CCA result met our anticipation that samples from site C5-2 dotted the region explained by high TS (Fig. 8A), with cold seep dominant indicator species *H. bradyi niigataensis* occupying the high TS end (Fig. 8B). Therefore, it is likely that this species proliferated in the cold seep because of its tolerance to sulfidic conditions.

Taken together, while the explanatory parameters diagnosed by CCA have been all proposed as the controlling factors in previous studies, CCA offers a means of quantitative assessment from a multivariate perspective, and evaluation of the explanatory power of the significant parameters, both of which are missing in the existing methodology used to study benthic foraminifera.

5. Conclusions

This is the first ecological study of cold seep benthic foraminifera in the SCS based on materials retrieved by video-guided sampling. In addition, this study also utilized multiple multivariate statistical approaches including hierarchical cluster analysis, indicator species analysis, and canonical correspondence analysis. Such a methodology has not been employed in published studies on similar topics. The main conclusions are:

(1) At the three study sites, most of the living individuals were found in the top 1 cm sediment. Agglutinated benthic foraminifera were exceptionally abundance, probably as a result of the generally low carbonate saturation state in the overlying and pore waters.

(2) The biodiversity index values including species richness, Shannon diversity and Pielou's evenness decreased in the order of site C10 ≈ C5-1 > C5-2 for both total and living assemblages.

(3) Although having biodiversity index values closer to those of the reference site, the transition site had community composition more similar to the seep site according to the cluster analysis.

(4) The dominant indicator species with relative abundance ≧ 2 % were *Haplophragmoides bradyi niigataensis*, *Rutherfordoides rotundiformis*, and *Uvigerina proboscidea* for the cold seep, transition, and regular bathypelagic site, respectively.

Bulimina aculeata and *Cassidulinoides differens* are the most dominant indicator species in the site combination of cold seep + transition area, while *Uvigerina auberiana* represent the site combination of reference + transition area.

(5) Canonical correspondence analysis showed that the main controlling factors of the benthic foraminiferal community structure were sulfate and DO concentrations, which explained 11.4% and 9.9%, respectively, of the community variance. Total sulfur is considered as the third essential controlling factor explaining 9.1% of the community variance, but with lower significance.

More surface sediment samples from the cold seep region of the FWCR should be collected and analyzed to confirm the pattern observed in the present study. Furthermore, our strategy of focusing on the size class of >250 μm needs to be examined and discussed. A compromise between workable size fraction, sufficient sample size and affordable workload needs to be reached in order to make benthic foraminifera more facile indicators of seafloor environments.

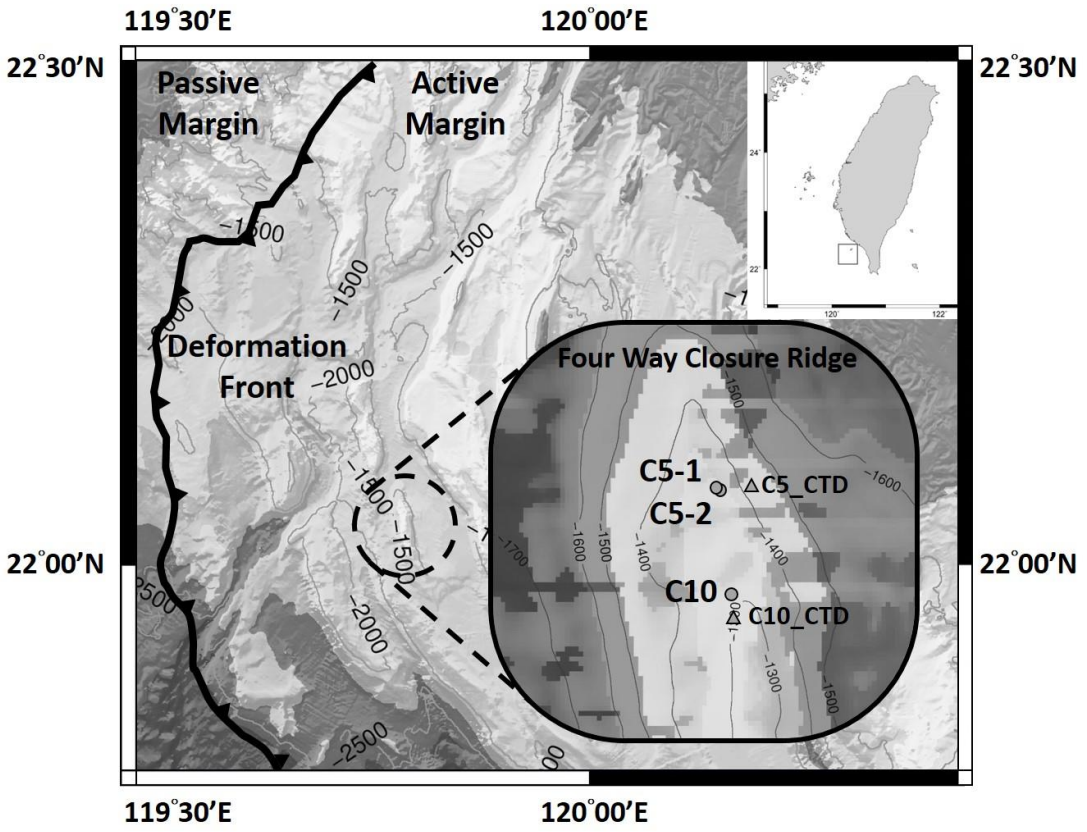


Figure 1. The study sites of the Four Way Closure Ridge, offshore SW Taiwan. The dots and triangles denote the location where sediment and deep seawater were taken, respectively.

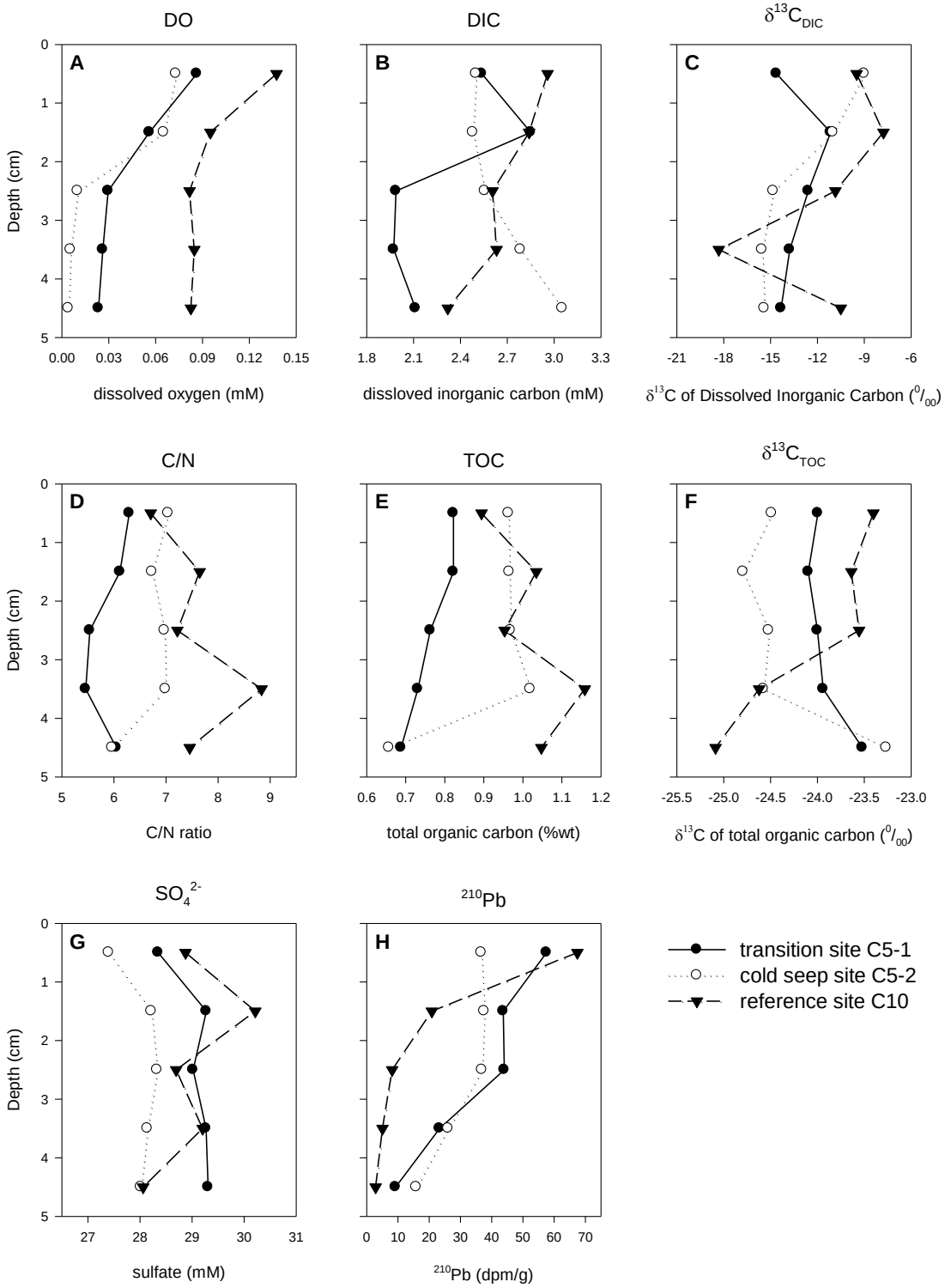


Figure 2. The environmental factors of the study sites. Abbreviations: DO, dissolve oxygen; DIC, dissolve inorganic carbon; $\delta^{13}C_{DIC}$, stable carbon isotopic value of dissolve inorganic carbon; C/N, C/N ratio; TOC, total organic carbon; $\delta^{13}C_{TOC}$, carbon isotopic value of total organic carbon.

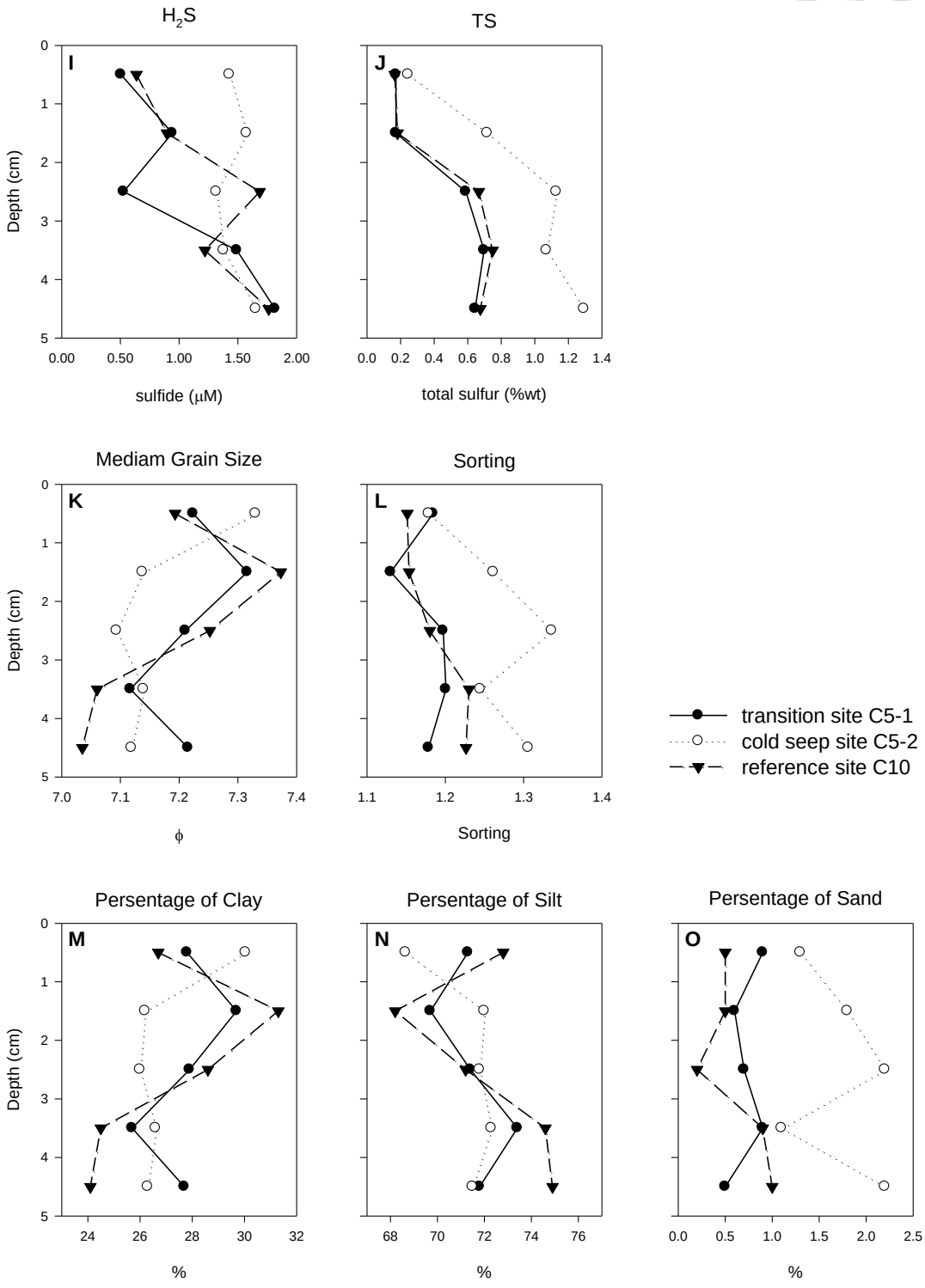


Figure 2 (Cont.). The environmental factors of the study sites. TS is the abbreviation of total sulfur.

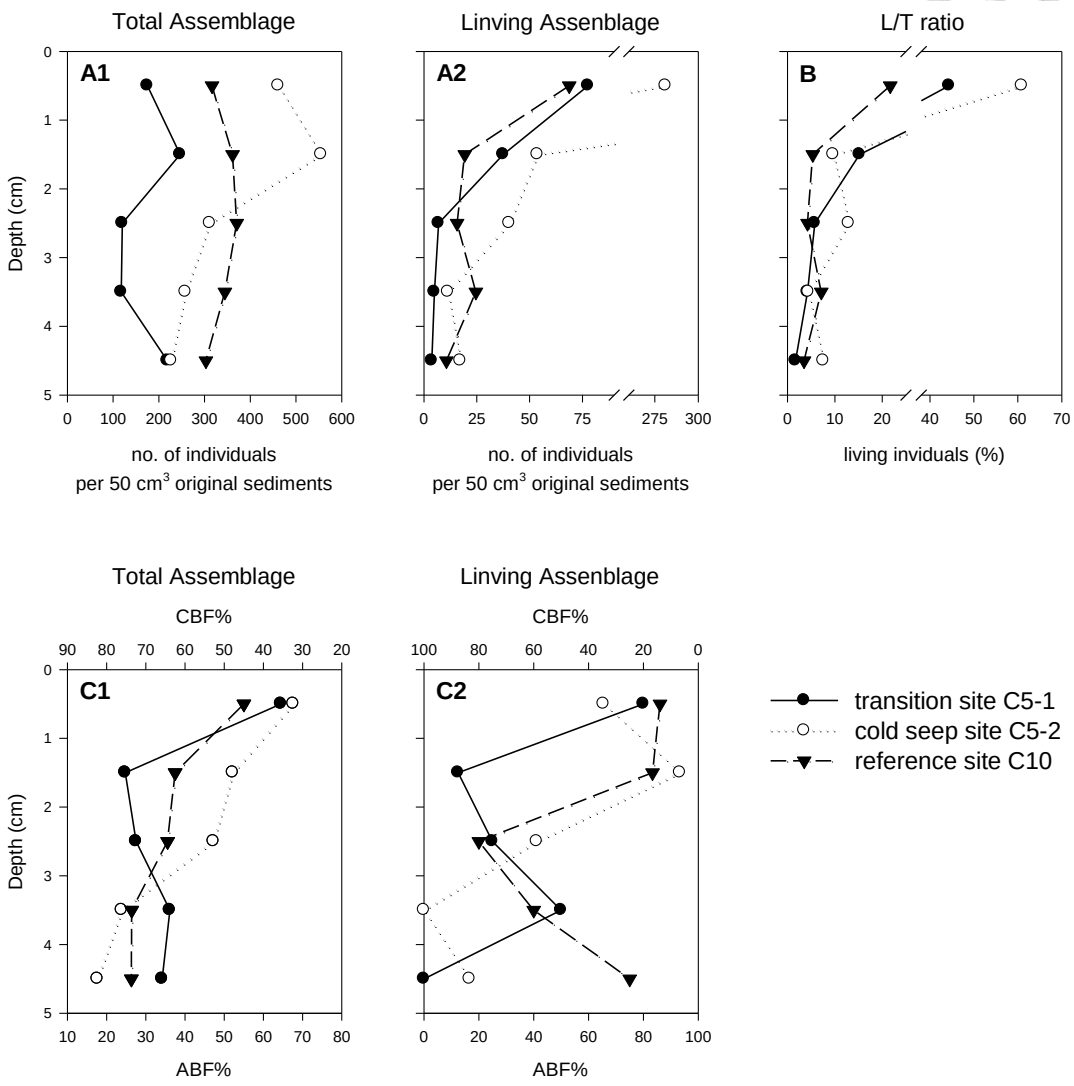


Figure 3. Benthic foraminiferal fauna structure of the size class >250 μm. Abbreviations: L/T ratio, living/total ratio; ABF, agglutinated benthic foraminifera; CBF, calcareous benthic foraminifera.

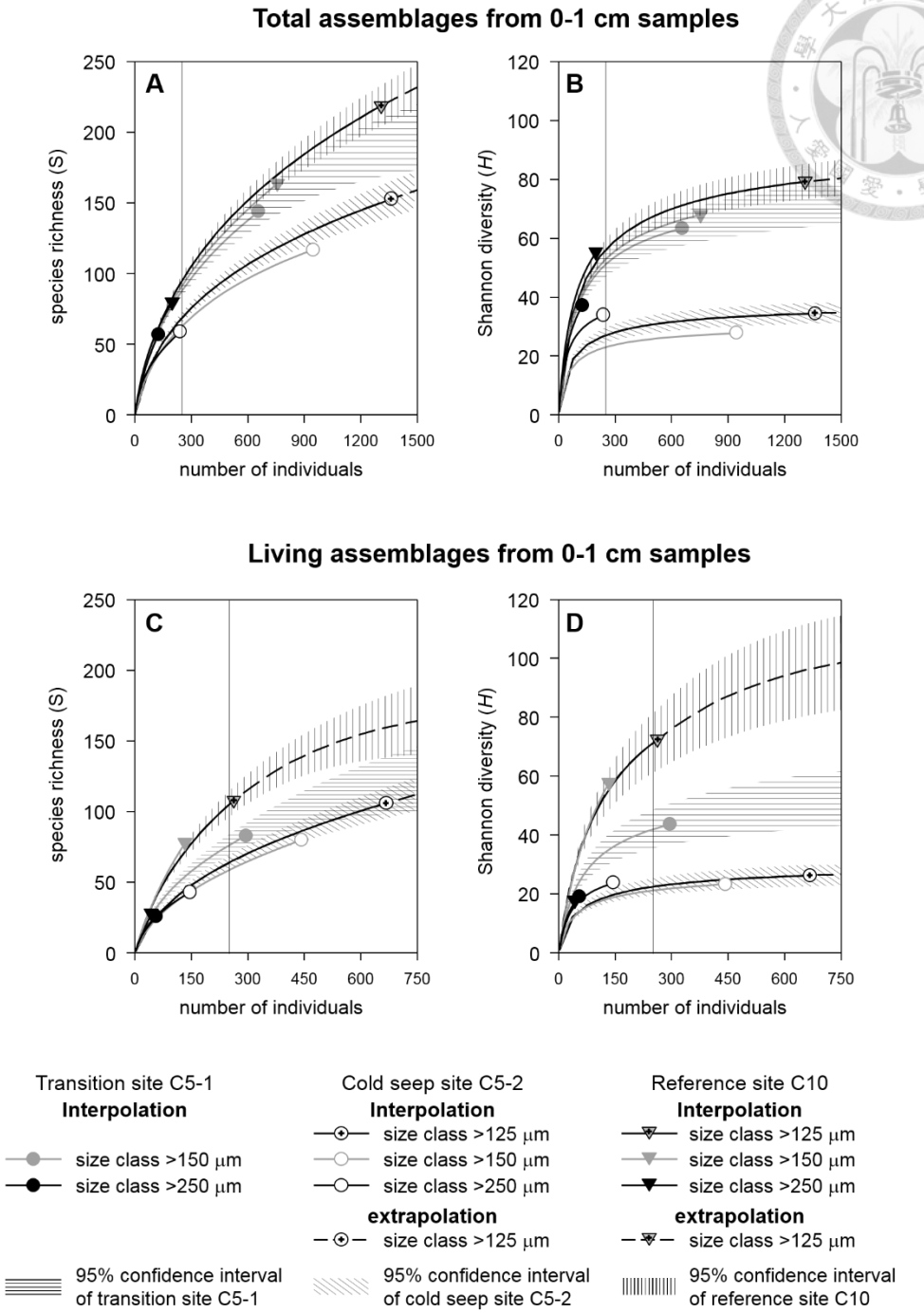


Figure 4. Mathematical models for predicting diversity index values-sample size relationships of different size fractions in the total (A and B) and living (C and D) assemblages. Shaded areas denote the 95% confidence intervals predicted from the size class >125 μm. Due to the lack of the data of size fraction 125-150 μm in site C5-1, the confidence interval was predicted from size class >150 μm. The vertical line mark the sample size of 250 individuals.

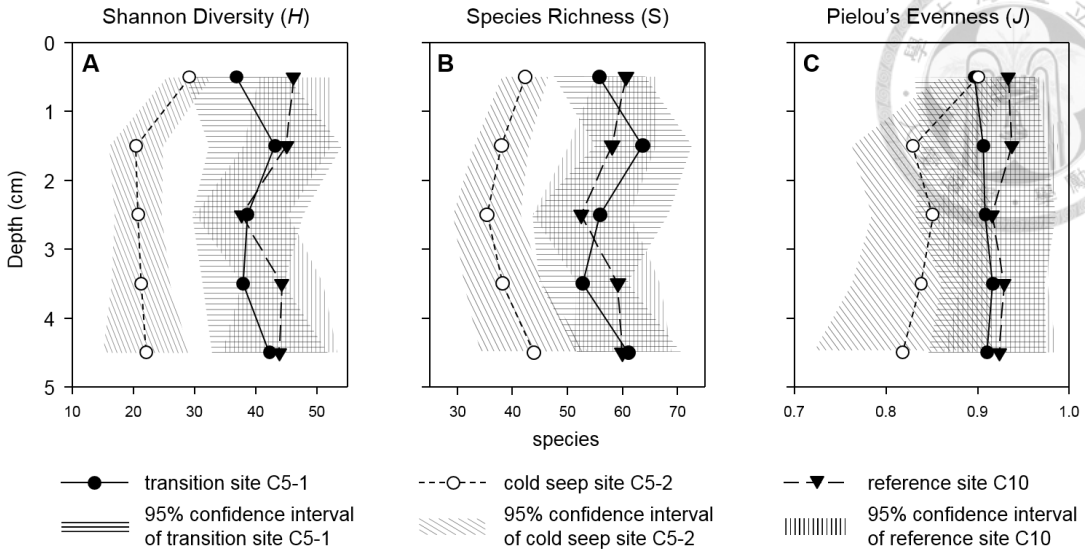


Figure 5. Diversity index values of the total assemblages in the size class >250 μm with the sample size of 120 individuals. Shaded areas denote 95% confidence intervals. The broad confidence intervals of evenness were resulted from the propagation of errors.

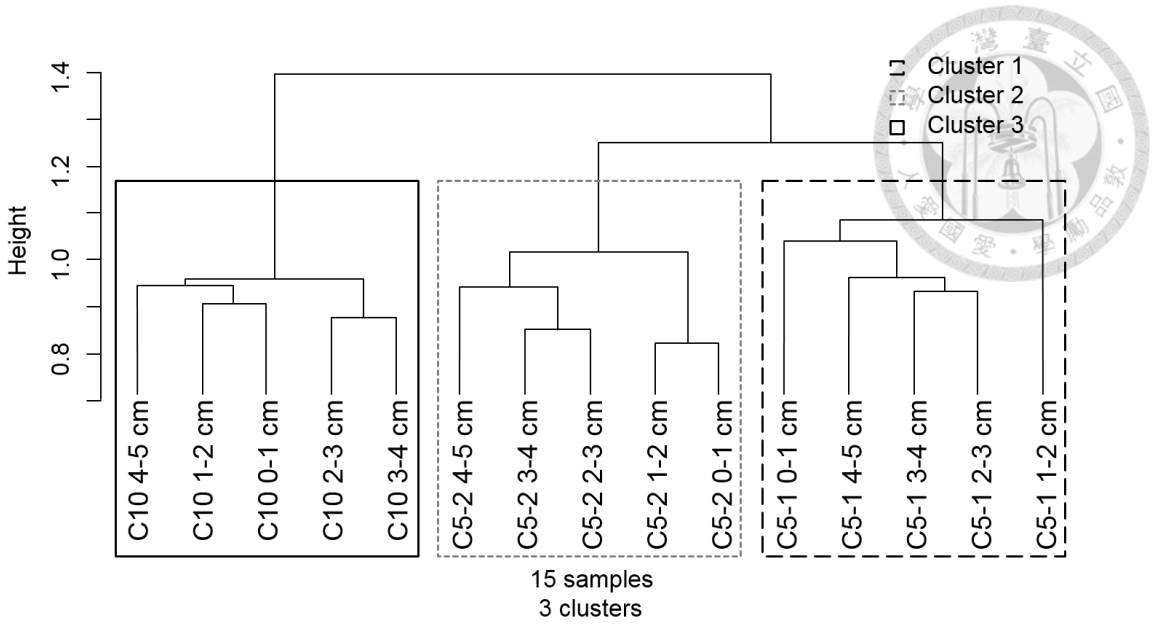


Figure 6. Cluster analysis partitioned 15 samples into 3 groups, which conformed to the sites. Yellow square: transition site C5-1; red square: cold seep site C5-2; blue square: reference site C10.

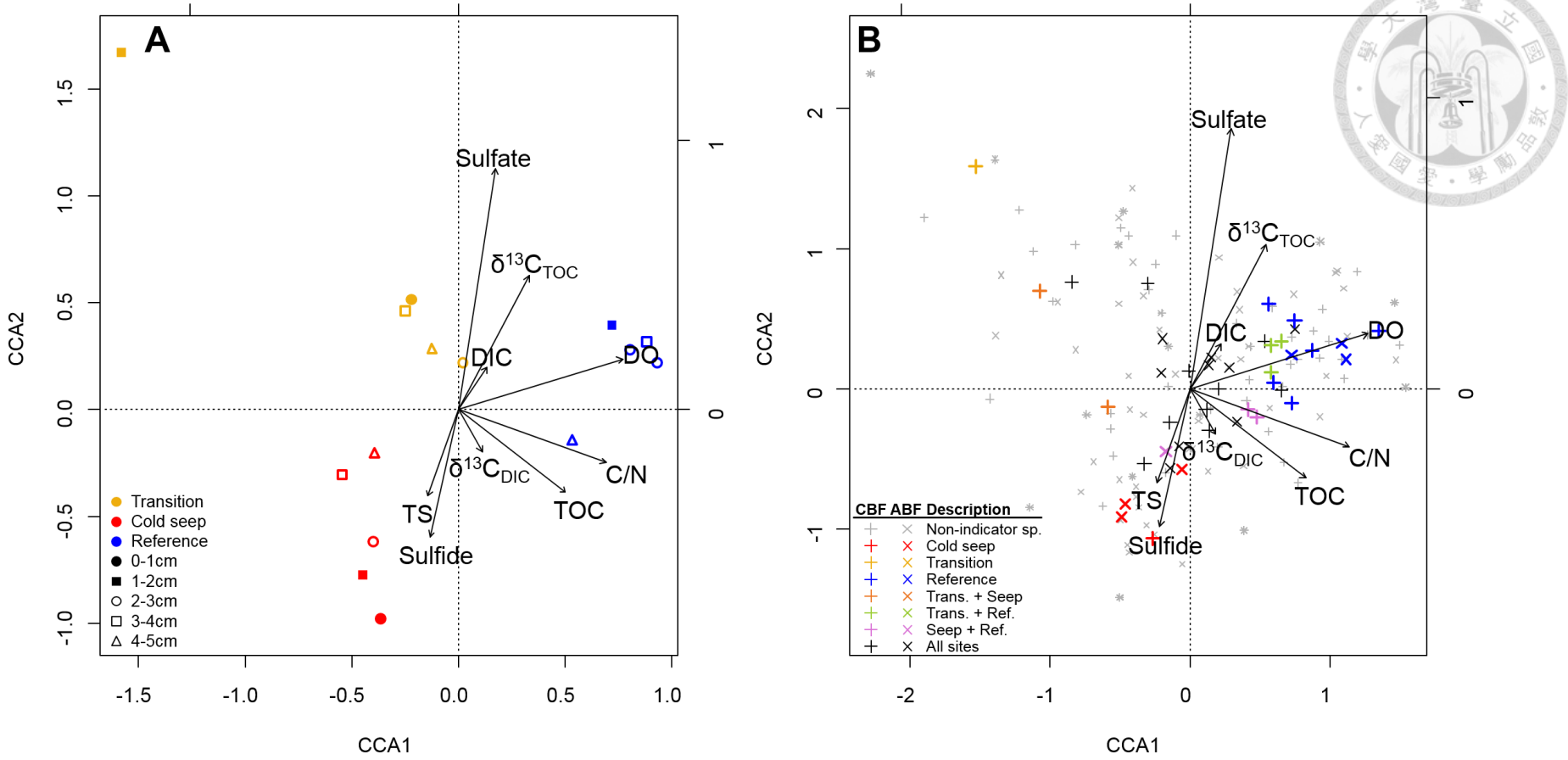


Figure 7. CCA biplots of all environmental variables. **A.** CCA biplots of scaling 1. The symbols are color-coded based on the site. **B.** CCA biplots of scaling 2. The symbol of calcareous benthic foraminifera (CBF) is the cross, while that of agglutinated benthic foraminifera (ABF) is the X. Indicator species are color-coded based on the site or site groups that they indicate.

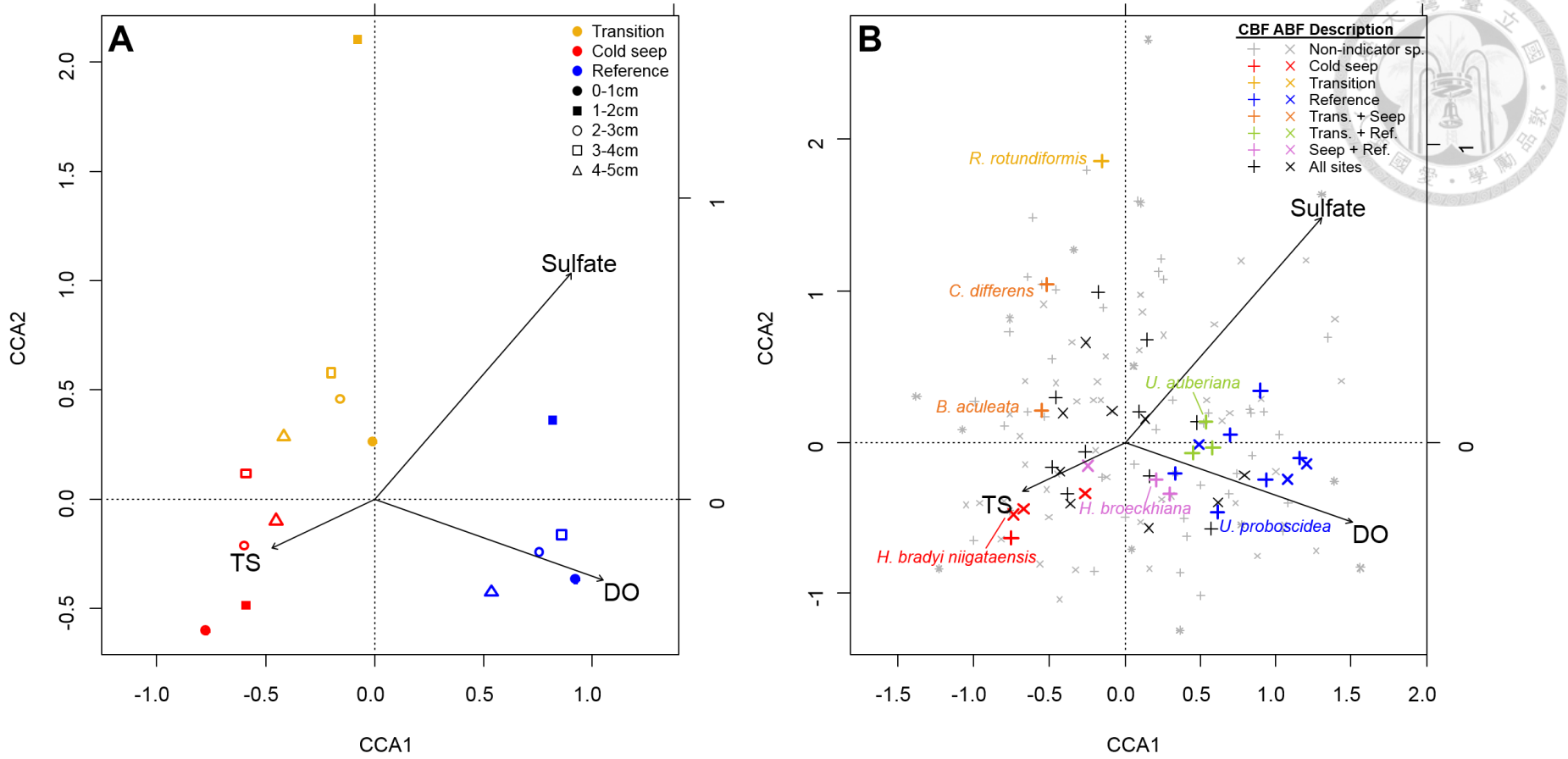


Figure 8. CCA biplots showing the three main explanatory factors (DO, sulfate, and TS) controlling the species compositions of the sites (A, scaling 1) and the distribution of the species (B, scaling 2). Percentage of community variance explained: DO, 11.3%; sulfate, 10.9%; TS, 9.1%. CCA1 and CCA2 represent 11.7% and 11.2% of the total inertia, respectively.

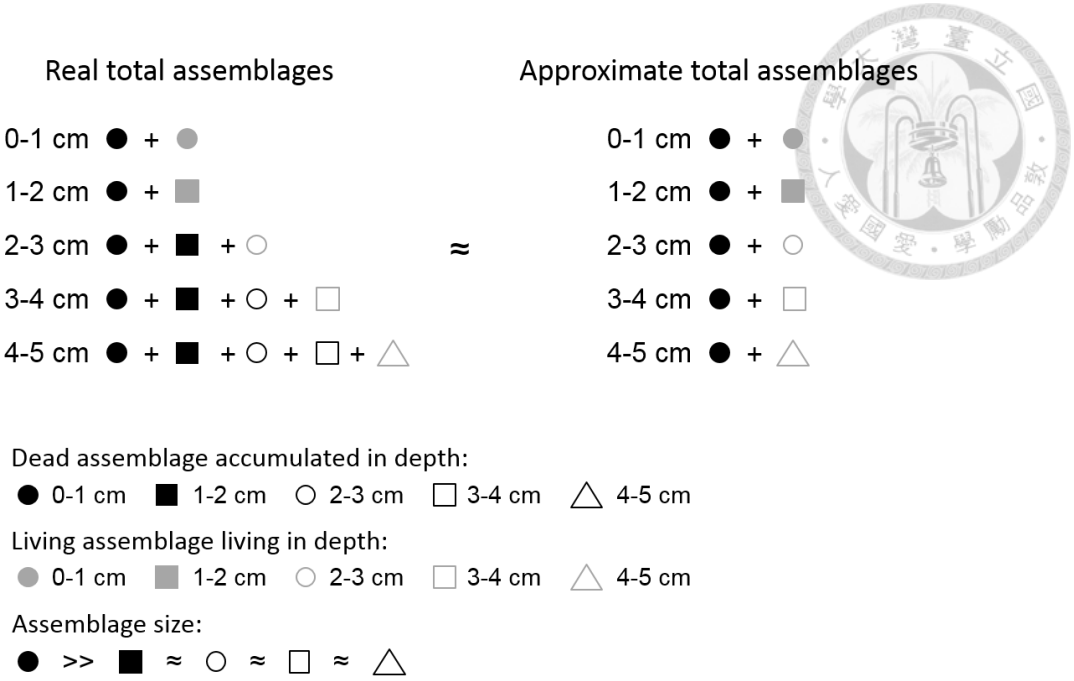


Figure 9. Schematic diagram explaining the contribution of living and accumulated dead assemblages to total assemblage in samples at different depths.

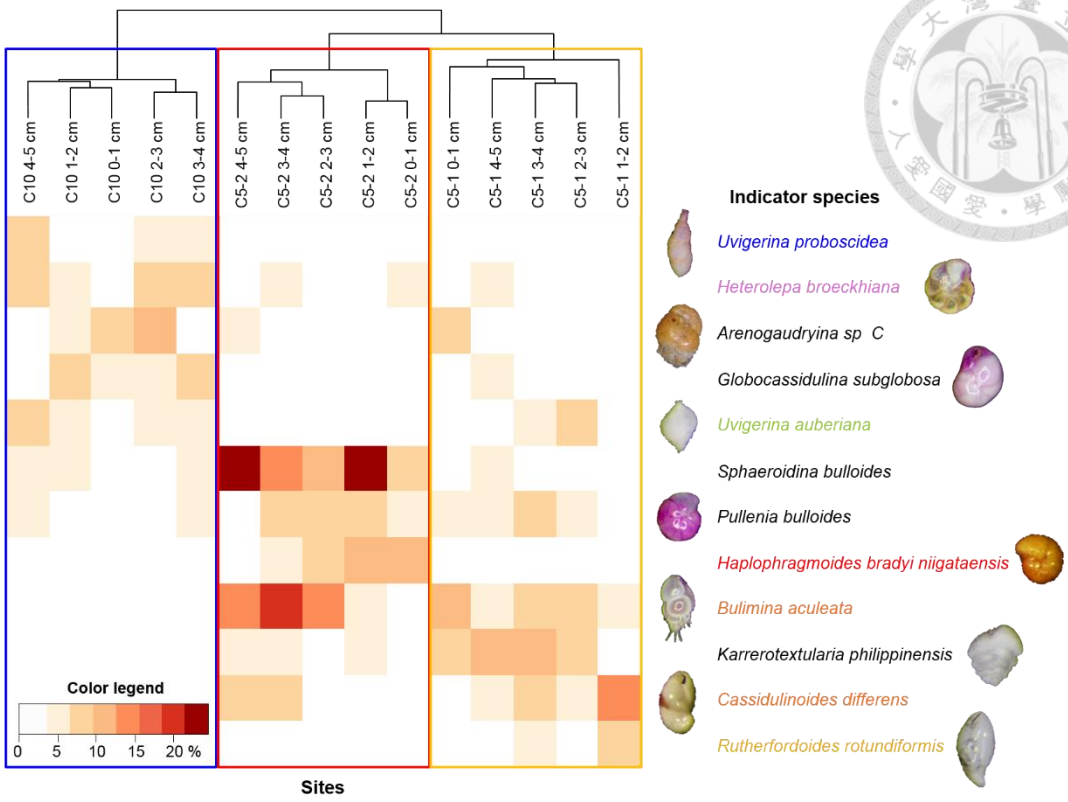


Figure 10. Heat map of the relative abundance of the dominant (≧2 %) indicator species. The darker the color, the more abundant the indicator species is in the samples. Noted that the percentage of 2-3 % is also marked in white color. The species names are color-coded based on the site or site groups (cf. Tables 1 to 3) that they indicate.

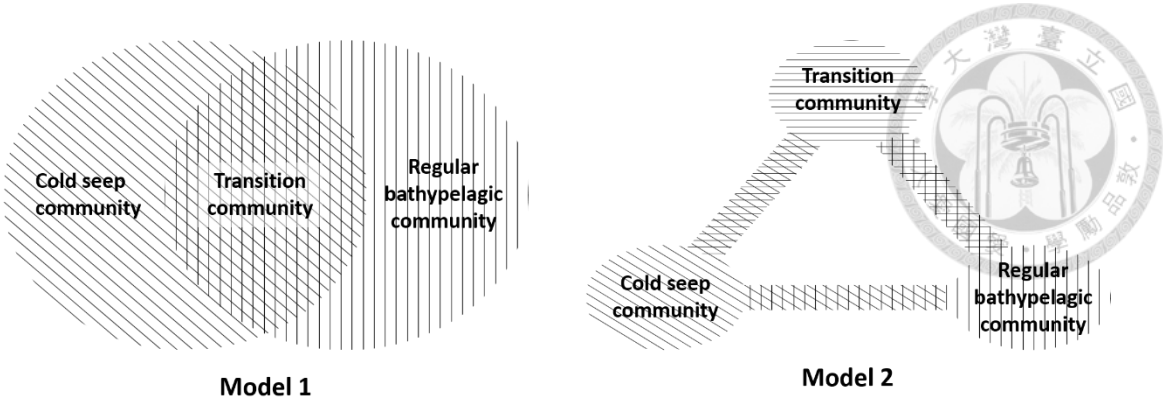


Figure 11. Two conceptual models explaining the relationship of community composition between the cold seep, transition, and regular bathypelagic environments.

Table 1. Indicator species (p-value smaller than 0.05) of the cold seep and transition environments. Association statistic (stat) is the square root of indicator value (IndVal), which is the product of *A* (specificity) and *B* (filelity).

Transition site C5-1	*A*	*B*	IndVal	stat	p-value
Rutherfordoides rotundiformis + Uvigerina auberiana	1.00	0.80	0.80	0.89	0.009
Cassidulinoides differens + Osangularia bengalensis + U. auberiana	1.00	0.80	0.80	0.89	0.015
R. rotundiformis	0.93	0.80	0.74	0.86	0.032

Cold seep site C5-2	*A*	*B*	IndVal	stat	p-value
**Haplophragmoides bradyi niigataensis + *Recurvoides laevigata + *Trochammina vesicularis*	1.00	1.00	1.00	1.00	0.002
**H.bradyi niigataensis + *T. vesicularis*	0.95	1.00	0.95	0.97	0.003
**H. bradyi niigataensis + *R. laevigata*	0.94	1.00	0.94	0.97	0.007
**R. laevigata + *T. vesicularis*	0.92	1.00	0.92	0.96	0.003
**H. bradyi niigataensis*	0.92	1.00	0.92	0.96	0.007
**T. vesicularis*	0.91	1.00	0.91	0.95	0.002
Bolivinita quadrilatera + Bulimina aculeata	1.00	0.80	0.80	0.89	0.012
*B. aculeata + *R. laevigata*	0.80	1.00	0.80	0.89	0.017
*C. differens + *R. laevigata*	1.00	0.80	0.80	0.89	0.015
*B. quadrilatera + *Plectina nanissima*	0.91	0.80	0.73	0.85	0.045
*B. quadrilatera + *R. laevigata*	0.91	0.80	0.73	0.85	0.045
**R. laevigata*	0.71	1.00	0.71	0.84	0.040
B. quadrilatera	0.87	0.80	0.69	0.83	0.045

Transition site C5-1 and cold seep site C5-2	*A*	*B*	IndVal	stat	p-value
B. aculeata	0.95	1.00	0.95	0.98	0.002
C. differens	1.00	0.80	0.80	0.89	0.032

* agglutinated benthic foraminifera

Table 2. Indicator species (p-value smaller than 0.05) of the transition and regular bathypelagic sedimentary environment.

Reference site C10	*A*	*B*	IndVal	stat	p-value
Globocassidulina elegans + **Karreriella parkerae* + **P. nanissima*	1.00	1.00	1.00	1.00	0.001
G. elegans + *O. bengalensis* + **P. nanissima*	1.00	1.00	1.00	1.00	0.001
G. elegans + *U. auberiana* + **P. nanissima*	1.00	1.00	1.00	1.00	0.001
**Karreriella bradyi*	1.00	1.00	1.00	1.00	0.001
O. bengalensis + *Uvigerina proboscidea* + **P. nanissima*	1.00	1.00	1.00	1.00	0.001
U. auberiana + *U. proboscidea* + **P. nanissima*	1.00	1.00	1.00	1.00	0.001
U. proboscidea + **K. parkerae* + **P. nanissima*	1.00	1.00	1.00	1.00	0.001
U. auberiana + *U. proboscidea*	0.92	1.00	0.92	0.96	0.001
Cibicides pachyderma + *U. proboscidea* + **K. parkerae*	0.89	1.00	0.89	0.95	0.001
C. pachyderma + **K. parkerae* + **P. nanissima*	0.89	1.00	0.89	0.94	0.008
G. elegans + *U. proboscidea* + **K. parkerae*	0.88	1.00	0.88	0.94	0.003
G. elegans + *O. bengalensis*	0.88	1.00	0.88	0.94	0.003
G. elegans + *U. auberiana*	0.88	1.00	0.88	0.94	0.003
U. proboscidea + **K. parkerae*	0.86	1.00	0.86	0.93	0.001
C. pachyderma + *O. bengalensis* + **P. nanissima*	0.86	1.00	0.86	0.93	0.008
O. bengalensis + **K. parkerae* + **P. nanissima*	0.86	1.00	0.86	0.93	0.008
C. pachyderma + *O. bengalensis* + *U. proboscidea*	0.85	1.00	0.85	0.92	0.002
G. elegans + **P. nanissima*	0.83	1.00	0.83	0.91	0.006
C. pachyderma + **K. parkerae*	0.83	1.00	0.83	0.91	0.001
C. pachyderma + *U. proboscidea*	0.82	1.00	0.82	0.90	0.001
U. proboscidea	0.81	1.00	0.81	0.90	0.001
Cibicides wuellerstorfi + *G. elegans*	1.00	0.80	0.80	0.89	0.007
Cibicidoides sp. D + *G. elegans*	1.00	0.80	0.80	0.89	0.007
G. elegans + *Lenticulina limbosa*	1.00	0.80	0.80	0.89	0.006
Uvigerina hollick	1.00	0.80	0.80	0.89	0.013
**Bathysiphon macilentus*	1.00	0.80	0.80	0.89	0.014
C. pachyderma + *U. auberiana*	0.80	1.00	0.80	0.89	0.001
C. wuellerstorfi + **P. nanissima*	1.00	0.80	0.80	0.89	0.013
Cibicidoides sp. D + **P. nanissima*	1.00	0.80	0.80	0.89	0.013
**K. parkerae* + **P. nanissima*	0.80	1.00	0.80	0.89	0.025
Transition site C5-1 and reference site C10	*A*	*B*	IndVal	stat	p-value
U. auberiana	0.98	1.00	0.98	0.99	0.004
O. bengalensis	0.94	0.90	0.85	0.92	0.027
C. pachyderma	0.90	0.90	0.81	0.90	0.046

* agglutinated benthic foraminifera

Table 3. Ubiquitous species that cannot act as indicator species.

Cold seep site C5-2 and reference site C10	*A*	*B*	IndVal	stat	p-value
Gyroidinoides soldanii	0.94	0.90	0.85	0.92	0.034
Heterolepa broeckhiana	0.89	1.00	0.89	0.94	0.029

Appearance in all sites	*A*	*B*	IndVal	stat	p-value
**Karrerotextularia philippinensis*	1.00	1.00	1.00	1.00	NA
Pullenia bulloides	1.00	1.00	1.00	1.00	NA
Globocassidulina subglobosa	1.00	0.93	0.93	0.97	NA
Sphaeroidina bulloides	1.00	0.93	0.93	0.97	NA
**Sigmoilopsis schlumbergeri*	1.00	0.67	0.87	0.93	NA
Lenticulina inornata	1.00	0.80	0.80	0.89	NA
Melonis barleeanus	1.00	0.73	0.73	0.86	NA
**Arenogaudryina* sp. C	1.00	0.67	0.67	0.82	NA
**Saccammina sphaerica*	1.00	0.67	0.67	0.82	NA
**Reophax scorpiurus*	1.00	0.60	0.60	0.77	NA
**Discammina compressa*	1.00	0.53	0.53	0.73	NA
Oridorsalis umbonatus	1.00	0.53	0.53	0.73	NA
Unknown sp. A	1.00	0.53	0.53	0.73	NA
Chilostomella oolina	1.00	0.47	0.47	0.68	NA
**Rhabdammina discreta*	1.00	0.47	0.47	0.68	NA
**Rhabdammina scabra*	1.00	0.27	0.27	0.52	NA
Gyroidina sp. D	1.00	0.20	0.20	0.45	NA
Lagenammina cushmani	1.00	0.20	0.20	0.45	NA
Uvigerina pygmaea	1.00	0.20	0.2 0	0.45	NA

* agglutinated benthic foraminifera

Table 4. The computed calcite saturation state in the overlaying water at the depth of 0-1 cm.

Station	Type[a]	Depth[b]	*in situ* salinity[c]	*in situ* temperature[c] (˚C)	TA[d] (μmol/kgSW)	25˚C pH[d]	DIC (μmol/kgSW)	*In situ* Ω_{Ca}
C5-1	OWL	1351 m	34.56	3.16	2400	7.60	2287	1.46
C5-2	OWL	1351 m	34.56	3.16	2393	7.55	2311	1.33
C10	OWL	1328 m	34.57	3.00	2365	7.49	2279	1.13
C5-1	PW	0.5 cm	34.56	3.16	2400	7.60	2538	1.63
C5-2	PW	1.0 cm	34.56	3.16	2393	7.55	2491	1.43
C10	pW	0.5 cm	34.57	3.00	2365	7.49	2958	1.46

[a] OWL=over laying water; PW=pore water

[b] Water depth for overlying waters and subseafloor depth for pore waters.

[c] Salinity and temperature data are from the measurements at the deepest depth (~10 m above seafloor) of the CTD casts at site C5 and C10.

[d] Measured TA and pH values of the overlying waters were used to compute the Ω_{Ca} value of the respective pore waters.

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Appendix

Appendix 1

Site	OR3-1806-C5-1										OR3-1806-C5-2										OR3-1806-C10-1									
Depth (cm)	0-1		1-2		2-3		3-4		4-5		0-1		1-2		2-3		3-4		4-5		0-1		1-2		2-3		3-4		4-5	
Size (μm)	>250		>250		>250		>250		>250		>250		>250		>250		>250		>250		>250		>250		>250		>250		>250	
Original sediment volume (cm^3)	35.39		21.29		28.72		39.82		26.72		25.78		13.96		21.02		21.87		17.39		31.28		15.50		15.92		20.32		18.81	
Calcareous Benthic Foraminifera	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D
***Anomalinoides* spp.**																														
**Anomalinoides* sp. A	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Astacolus* spp.**																														
Astacolus crepidulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Bolivina* spp.**																														
Bolivina alata	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bolivina earlandi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Bolivina pacifica	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bolivina pusilla	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Bolivina* sp. D	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Bolivinita* spp.**																														
Bolivinita quadrilatera	0	0	0	0	0	0	0	0	0	0	9	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	2	0	0
***Bulimina* spp.**																														

Bulimina aculeata	7	7	0	4	0	6	0	7	0	4	1	5	0	6	0	17	1	22	0	12	0	2	0	2	0	1	0	0	0	0
Bulimina marginata	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
Bulimina striata	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	1	0	4	0	2	0	2	0	0	0	0
Bulimina truncana	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Cassidulina* spp.**																														
Cassidulina carinata	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Cassidulina moluccensis	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	1
Cassidulina obtusa	0	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	0	0	0	0
**Cassidulina* sp. B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
***Cassidulinoides* spp.**																														
Cassidulinoides differens	0	0	0	14	2	2	1	5	0	6	0	0	0	2	0	1	0	7	0	5	0	0	0	0	0	0	0	0	0	0
***Ceratobulimina* spp.**																														
Ceratobulimina contraria	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1
***Chilostomella* spp.**																														
Chilostomella oolina	0	0	0	4	0	0	0	3	0	1	0	0	0	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	1
***Cibicides* spp.**																														
[2]*Cibicides bradyi* (*Heterolepa bradyi*)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0
Cibicides pachyderma	1	0	0	0	0	1	0	2	0	2	1	0	0	0	0	0	0	2	0	0	1	3	0	4	0	4	1	2	0	5
Cibicides wuellerstorfi	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4	0	2	0	0	0	6	0	3
**Cibicides wuellerstorfi* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1
***Cibicidoides* spp.**																														
Cibicidoides mundula	0	0	0	0	0	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
Cibicidoides globulosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2

Cibicidoides sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
**Cibicidoides* sp. D	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	1	0	1
***Cornuloculina* spp.**																															
Cornuloculina inconstans	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Cornuspira* spp.**																															
Cornuspira foliacea	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cornuspira selseyensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
***Epistominella* spp.**																															
Epistominella exigua	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	
***Euloxostomum* spp.**																															
Euloxostomum bradyi	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
***Fissurina* spp.**																															
Fissurina bispinata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Fissurina fimbriata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Fissurina formosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Fissurina laevigata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Fissurina marginata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	
Fissurina orbignyana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	
**Fissurina* sp. E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
**Fissurina* sp. F	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Fissurina* sp. G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
***Fursenkoina* spp.**																															
Fursenkoina bradyi	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Gavelinopsis* spp.**																															

Gavelinopsis praegeri	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Glandulina* spp.**																															
Glandulina ovula	0	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	0	0	0	0	0
***Globobulimina* spp.**																															
[1]*Globobulimina ovata*	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3
Globobulimina pacifica	0	1	0	0	0	1	0	0	0	1	0	0	0	0	2	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0
Globobulimina pyrula	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0
***Globocassidulina* spp.**																															
Globocassidulina elegans	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	1	0	2	0	2	
Globocassidulina subglobosa	0	1	0	3	0	1	0	2	0	7	3	0	0	0	0	3	0	1	0	2	1	10	0	10	0	7	0	9	0	3	
Globocassidulina sp. 1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	2	
***Gyroidina* spp.**																															
**Gyroidina* sp. B	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
**Gyroidina* C020	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
**Gyroidina* sp .D	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	
**Gyroidina* sp .E	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	
**Gyroidina* sp .F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
***Gyroidinoides* spp.**																															
[2]*Gyroidinoides soldanii* (*Hansenisca soldanii*)	0	0	0	0	0	1	0	0	0	0	1	2	0	2	0	1	0	0	0	1	0	1	0	1	0	1	2	3	0	1	
Gyroidinoides nipponica	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Hansenisca* spp.**																															
Hansenisca soldanii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	

***Heterolepa* spp.**																															
Heterolepa bradyi	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	2	0	1	0	0
Heterolepa broeckhiana	2	0	0	1	0	0	0	0	2	2	7	1	0	1	4	0	0	4	0	2	0	4	0	5	0	9	0	10	0	8
***Hoeglundina* spp.**																															
Hoeglundina elegans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0
***Hyalinonetrion* spp.**																															
Hyalinonetrion elongata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Hyalinonetrion gracillima	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Ioanella* spp.**																															
Ioanella tumidula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Islandiella* spp.**																															
**Islandiella* sp. A	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Laevidentalina* spp.**																															
Laevidentalina aphelis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Laevidentalina filiformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Laevidentalina haueri	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Laevidentalina subemaciata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Laevidentalina subsoluta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
***Lagena* spp.**																															
[2]*Lagena laevis* (*Reussoolina laevis*)	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lagena sp. nov. (1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Laticarinina* spp.**																															
Laticarinina pauperata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0

***Lenticulina* spp.**																															
Lenticulina gibba	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lenticulina inornata	0	1	0	0	0	1	0	2	0	1	0	1	1	3	1	3	0	2	0	3	0	7	0	3	0	0	0	0	0	0	5
Lenticulina limbosa	0	3	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	0	4	0	1	
**Lenticulina* sp. A	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	
**Lenticulina* sp. B	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Lernella* spp.**																															
**Lernella* sp. A	0	0	0	0	0	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	
***Melonis* spp.**																															
Melonis barleeanus	0	0	0	2	1	1	0	1	0	0	3	0	0	2	0	1	0	0	1	1	1	1	1	1	0	1	0	2	0	0	
Melonis sphaeroides	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
***Miliolinella* spp.**																															
Miliolinella subrotunda	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
Miliolinella vigilax	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Mucronina* spp.**																															
Mucronina compressa	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	2	0	2	0	1	
***Neolenticulina* spp.**																															
**Neolenticulina* sp. A	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
**Neolenticulina* sp. B	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Nonion* spp.**																															
Nonion pacificum	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Nonionella* spp.**																															
**Nonionella* sp. A	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
***Oolina* spp.**																															

Oolina apiopleura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Oolina globosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
***Oridorsalis* spp.**																															
Oridorsalis tenerus	0	0	0	1	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Oridorsalis umbonatus	0	1	0	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	5	0	0	0	1	0	2	0	1	
Oridorsalis westi	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Osangularia* spp.**																															
Osangularia bengalensis	0	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	2	0	1	2	1	0	4	1	1	
***Parafissurina* spp.**																															
Parafissurina curvitubulosa	0	0	0	0	0	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	
Parafissurina lateralis	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	
***Praeglobobulimina* spp.**																															
Praeglobobulimina spinescens	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Procerolagena* spp.**																															
Procerolagena gracilis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
***Pseudoeponides* spp.**																															
Pseudoeponides japonicus	0	0	0	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
***Pseudosolenina* spp.**																															
Pseudosolenina wiesneri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	
***Pullenia* spp.**																															
Pullenia bulloides	0	4	0	2	0	4	0	6	0	6	4	8	0	11	0	12	0	8	0	2	0	4	0	3	0	3	0	6	0	5	
Pullenia quinqueloba	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	
***Pyrulina* spp.**																															

Pyrulina cylindroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Quinqueloculina* spp.**																														
Quinqueloculina akneriana	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Quinqueloculina akneriana* aff.	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Quinqueloculina granulosa	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Quinqueloculina neosigmoilinoides	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Rutherfordoides* spp.**																														
Rutherfordoides rotundata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rutherfordoides rotundiformis	0	1	5	3	0	0	1	2	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Rutherfordoides virga	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0
**Rutherfordoides* sp. A	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Saracenaria* spp.**																														
Saracenaria angularis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0
***Sphaeroidina* spp.**																														
Sphaeroidina bulloides	0	1	0	0	0	1	0	1	0	6	12	5	0	38	2	14	2	13	3	16	0	1	0	5	0	3	0	5	0	5
***Spiroloculina* spp.**																														
Spiroloculina robusta	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Triloculina* spp.**																														
Triloculina subcylindrica	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Triloculinella* spp.**																														

**Triloculinella hornibrooki* aff.	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Uvigerna* spp.**																															
Uvigerina ampullaceal (*Siphouvigerina ampullacea*)	0	0	1	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	2	0	2	1	3	0	0	0	2	
Uvigerina auberiana	0	3	0	1	0	6	0	4	0	1	0	0	0	1	0	0	0	0	0	0	0	5	0	6	0	5	1	6	0	7	
Uvigerina hispida (*Siphouvigerina hispida*)	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	1	0	2	
Uvigerina hollick	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	2	0	1	0	0	
Uvigerina peregrina	1	1	0	0	0	4	0	2	0	3	0	2	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	
Uvigerina proboscidea (*Siphouvigerina proboscidea*)	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	3	0	1	0	6	0	2	0	5	1	4	0	8	
Uvigerina pygmaea	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	
**Uvigerina* sp. A	0	0	0	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	0	0	
*Unknown sp. A	0	1	0	4	0	0	0	0	0	2	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	2	0	2	0	0	
**Unknown sp. E	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
**Unknown sp. H	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
*Unknown sp. P	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
*Unknown sp. S	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
*Unknown sp. X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	

Agglutinated Benthic Foraminifera	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D	L	D
***Ammobaculites* spp.**																												
Ammobaculites crassaformis	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Ammodiscus* spp.**																												
Ammodiscus hoeglundi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Ammodiscus intermedius	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Ammoglobigerina* spp.**																												
Ammoglobigerina globigeriniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Ammoglobigerina latestoma	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Ammogloborotalia* spp.**																												
**Ammogloborotalia stellaris* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
***Ammolagena* spp.**																												
Ammolagena clavata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
***Ammoscalaria* spp.**																												
Ammoscalaria tenuissima	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Ammoscalaria* sp.A	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Ammospaeroidina* spp.**																												
Ammosphaeroidina sphaeroidiniforme	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Ammotium* spp.**																												

Ammotium minutum	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ammotium zhanjiangense	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Ammotium* sp. A	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Arenogaudryina* spp.**																																
**Arenogaudryina* sp. A	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Arenogaudryina* sp. C	9	1	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0	3	13	5	0	4	0	11	0	4	0	0		
***Aschemonella* spp.**																																
Aschemonella scabra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1		
**Aschemonella* sp. A	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		
***Astrammina* spp.**																																
[2]*Astrammina sphaerica* (*Saccammina sphaerica*)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0		
***Astrorhiza* spp.**																																
[2]*Astrorhiza crassatina* (*Bathysiphon crassatina*)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	1	0	0	0	0		
**Astrorhiza* sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		
***Astrorhizoides* spp.**																																
Astrorhizoides cornuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	0	1	0	0		
***Bathysiphon* spp.**																																
Bathysiphon macilentus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0	1	0	0	0	1		
Bathysiphon rusticum	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0		
***Cribrostomoides* spp.**																																
Cribrostomoides subglobosa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0		

******Cribrostomoides weddellensis* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
***Cystamminoides* spp.**																														
Cystamminoides quadrilocula	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Discammina* spp.**																														
Discammina compressa	3	4	0	0	0	0	0	1	0	1	2	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1
***Eggerella* spp.**																														
Eggerella bradyi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0
******Eggerella bradyi* aff.	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
******Eggerella nitens* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
***Glomospira* spp.**																														
Glomospira hoeglundi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Haplophragmoides* spp.**																														
[2]*Haplophragmoides bradyi* (*Recurvoidella bradyi*)	0	0	0	0	0	0	0	0	0	0	2	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Haplophragmoides neobradyi	0	0	0	0	0	0	0	0	0	1	17	2	4	5	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
[3]*Haplophragmoides bradyi niigataensis* (*Haplophragmoides bradyi nigataensis*)	2	1	0	0	0	0	0	0	0	2	25	1	3	13	5	7	0	4	0	1	0	0	0	0	0	0	0	0	0	0

Haplophragmoides membranacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Haplophragmoides sphaerilocula	2	0	0	0	0	0	0	0	0	0	4	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
**Haplophragmoides* sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Hormosina* spp.**																																
Hormosina pilulifera	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Hormosina* sp. B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
***Hormosinella* spp.**																																
Hormosinella guttifera	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hormosinella ovicula	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Hyperammina* spp.**																																
Hyperammina clavellata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Hyperammina distorta	0	1	0	0	0	0	0	0	0	0	0	1	0	3	0	2	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1
Hyperammina cf. *maxima*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
**Hyperammina* sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
***Jaculella* spp.**																																
Jaculella acuta	4	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Karreriella* spp.**																																
Karreriella bradyi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	1	0	1	0	1
Karreriella novangliae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Karreriella parkerae	0	0	0	0	0	2	0	1	0	5	0	0	0	1	0	0	0	0	0	1	1	3	0	5	0	4	0	6	1	3		
***Karrerotextularia* spp.**																																

Karrerotextularia crassisepta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Karrerotextularia flintii	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Karrerotextularia philippinensis	4	6	0	1	0	6	0	10	0	13	3	4	2	3	0	3	0	5	1	2	0	3	0	2	0	2	1	1	0	3		
***Labrospira* spp.**																																
[2]*Labrospira scitula* (*Veleroninoides scitula*)	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0		
**Labrospira scitula* aff.	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
***Lagenammina* spp.**																																
Lagenammina arenulata	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	0	1		
Lagenammina asymmetrica	0	0	0	0	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0		
Lagenammina atlantica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0		
Lagenammina bulbosa	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Lagenammina cushmani	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0		
Lagenammina difflugiformis	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
[2]*Lagenammina longicollis* (*Reophax longicollis*)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		
**Lagenammina longicollis* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1		
Lagenammina pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
[2]*Lagenammina testacea* (*Saccammina testacea*)	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1		
Lagenammina tabulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0		

***Lituola* spp.**																														
Lituola hispid	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Lituola robusta	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Martinottiella* spp.**																														
[2]*Martinottiella bradyana* (*Dorothia bradyana*)	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Martinottiella communis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Martinottiella minuta	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	2	0	1	0	5	0	1	0	1
***Paratrochammina* spp.**																														
Paratrochammina tricamerata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
***Placopsilina* spp.**																														
Placopsilina bradyi	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Plectina* spp.**																														
Plectina nanissima	0	0	0	1	0	0	0	3	0	0	2	5	0	4	0	13	0	5	0	0	0	6	0	1	0	1	0	1	0	1
Portatrochammina spp.																														
Portatrochammina antarctica antarctica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Portatrochammina murrayi	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Psammosphaera* spp.**																														
Psammosphaera fusca	2	4	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	4	0	1	0	0	0	2	0	0
**Psammosphaera fusca* aff.	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Psammosphaera fusca* aff.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

***Pseudotrochammina* spp.**																																
Pseudotrochammina dehiscens	0	0	0	2	0	0	0	2	0	0	5	4	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudotrochammina triloba	1	2	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
**Pseudotrochammina* sp. B	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Recurvoides* spp.**																																
**Recurvoides crassa* aff.	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
[2]*Recurvoides laevigata* (*Veleroninoides scitula*)	0	1	0	0	0	0	0	0	0	0	1	6	0	1	0	7	0	1	0	1	3	1	0	1	0	0	0	1	0	0		
Recurvoides gigas	0	0	0	0	0	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		
Recurvoides turbinata	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
**Recurvoides* sp. A	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
**Recurvoides* sp. B	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
***Reophax* spp.**																																
Reophax agglutinatus	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		
Reophax fusiformis	1	0	0	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	0	0		
**Reophax fusiformis* aff.	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Reophax pesciculus	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Reophax platycollaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0		
Reophax pseudoaduncus	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
**Reophax pseudopaucus* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0		
Reophax pyrifera	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Reophax scorpiurus	0	0	0	0	0	0	1	3	0	1	9	1	0	1	1	1	0	0	0	0	2	0	0	1	1	0	1	0	0	0		

Reophax spiculifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Reophax subcapitatus	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
[2]*Reophax dentaliniformis* (*Nodulina dentaliniformis*)	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reophax tenuis	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Reophax* sp. B	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Reophax* sp. H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Reticulophragmium* spp.**																														
Reticulophragmium alveolus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Rhabdammina* spp.**																														
Rhabdammina abyssorum	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhabdammina discreta	1	1	0	0	0	0	0	0	0	1	2	4	0	1	0	0	0	0	0	0	0	6	0	0	0	1	0	1	0	0
Rhabdammina linearis	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhabdammina pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Rhabdammina scabra	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
***Rhizammina* spp.**																														
Rhizammina algaeformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
[2]*Rhizammina indivisa* (*Testulosiphon indivisus*)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0
**Rhizammina* sp. A	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
**Rhizammina* sp. B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
***Saccammina* spp.**																														
Saccammina sphaerica	0	1	0	0	0	1	0	2	0	1	0	13	0	5	0	1	0	1	0	0	0	5	0	1	0	0	0	0	0	0
***Saccorhiza* spp.**																														

Saccorhiza ramosa	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1	1	1	0	0	0	0	0	1
**Saccorhiza* sp. A	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Sigmoilopsis* spp.**																														
Sigmoilopsis schlumbergeri	1	1	1	2	0	2	0	2	0	4	3	0	1	1	0	0	0	1	0	0	0	4	0	3	0	5	0	1	0	3
**Sigmoilopsis* sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
**Sigmoilopsis* sp. B	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Spiroplectammina* spp.**																														
Spiroplectammina biformis	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Subreophax* spp.**																														
Subreophax aduncus	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0
***Technitella* spp.**																														
Technitella spiculosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Textularia* spp.**																														
[2]*Textularia conica* (*Sahulia conica*)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Textularia crassaformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
**Textularia* cf. *earlandi*	0	3	0	2	0	0	0	0	0	1	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Textularia porrecta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Textularia* sp. B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
***Trochammina* spp.**																														
Trochammina boltovskoyi	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trochammina vesicularis	0	0	0	0	0	0	0	0	0	1	5	3	0	6	0	2	0	2	0	2	0	0	0	1	0	0	0	0	0	0
**Trochammina* sp. A	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Trochammina* sp. B	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

***Veleroninoides* spp.**																														
Veleroninoides wiesneri	0	0	0	0	0	0	0	0	0	0	2	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Verneuilinulla* spp.**																														
**Verneuilinulla* sp. A	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Unknown sp. C	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Unknown sp. D	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**Unknown sp. E	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. J	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

Note: the scientific names in brackets are scientific names registered in WoRMS. * represent species with undefined species name. ** represent samples that cannot be classified due to the lack of identifiable characteristics. [1] represent scientific names no registered in WoRMS. [2] represent controversial names. [3] represent scientific names is mispelled in WoRMS

Appendix 1 (Continue)

Site	C5-1		C5-2		C5-2		C10		C5-2		C5-2		C10	
Depth (cm)	0-1		0-1		2-3		0-1		0-1		2-3		0-1	
Size (μm)	150-250		150-250		150-250		150-250		125-150		125-150		125-150	
Calcareous Benthic Foraminifera	L	D	L	D	L	D	L	D	L	D	L	D	L	D
***Anomalinoides* spp.**														
Anomalinoides globulosa	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Anomalinoides* sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	1
**Anomalinoides* sp. B	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Anomalinulla* spp.**														
**Anomalinulla* sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Bolivina* spp.**														
Bolivina alata	0	0	0	0	0	3	0	0	0	0	0	0	0	1
Bolivina earlandi	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Bolivina robusta	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Bolivina striatula	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Bolivina vadescens	0	0	0	0	0	0	0	0	0	0	0	0	0	1
**Bolivina* sp. A	0	0	0	0	0	0	0	0	0	0	0	1	0	0
**Bolivina* sp. D	0	0	0	0	0	0	0	0	1	0	0	0	0	0
***Bolivinita* spp.**														
Bolivinita quadrilatera	1	1	13	5	0	0	1	0	2	0	0	0	0	0
***Bolivinellina* spp.**														
Bolivinellina pescicula	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Bulimina* spp.**														
Bulimina aculeata	25	41	100	82	5	188	1	11	11	4	1	7	0	6

Bulimina elongata	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Bulimina marginata	0	0	1	0	0	0	0	0	0	1	0	0	0	0
Bulimina striata	1	1	0	2	0	0	2	2	1	0	0	1	0	5
Bulimina truncana	1	1	2	1	0	1	0	3	3	0	0	0	6	23
***Cassidulina* spp.**														
Cassidulina carinata	0	6	0	0	0	0	0	3	0	1	0	1	7	6
Cassidulina laevigata	0	0	0	0	0	4	0	1	0	0	0	0	0	0
Cassidulina obtusa	0	0	0	0	0	0	0	0	0	0	0	1	0	7
***Cassidulinoides* spp.**														
Cassidulinoides differens	1	7	0	3	3	11	0	0	0	1	0	4	0	0
***Chilostomella* spp.**														
Chilostomella oolina	1	0	0	0	0	0	0	2	0	0	0	0	1	2
***Cibicides* spp.**														
Cibicides pachyderma	0	0	0	0	0	0	0	2	0	0	0	0	0	1
***Cibicidoides* spp.**														
Cibicidoides mundula	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Cibicidoides globulosus	0	0	0	0	0	0	0	1	0	0	0	0	0	1
**Cibicidoides* sp. A	0	1	0	0	0	0	0	1	0	1	0	1	1	4
**Cibicidoides* sp. B	0	0	0	1	0	0	0	0	0	0	0	0	0	0
**Cibicidoides* sp. D	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Cibicidoides sp. E	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Cibicidoides* sp. F	0	0	0	0	0	0	0	3	0	0	0	0	0	0
***Cornuspira* spp.**														
Cornuspira crassisepta	0	0	0	0	0	0	0	0	0	0	0	0	2	0

Cornuspira involvens	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Cushmanina spp.														
Cushmanina feildeniana	0	0	0	0	0	0	0	0	0	0	0	0	1	0
***Epistominella* spp.**														
Epistominella exigua	0	0	0	0	0	0	0	1	0	0	0	0	0	6
***Euloxostomum* spp.**														
Euloxostomum bradyi	0	1	0	0	0	0	0	0	0	1	0	0	0	0
***Fissurina* spp.**														
Fissurina alveolata	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Fissurina bispinata	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Fissurina claricurta	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Fissurina laevigata	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Fissurina marginata	0	2	0	0	0	1	0	2	0	0	0	4	0	1
**Fissurina marginata* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Fissurina orbignyana	0	0	0	0	0	0	1	0	0	0	0	0	0	0
[2]*Fissurina staphyllearia (Lagena staphyllearia)*	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Fissurina sp. 7	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Fissurina* sp. A	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Fursenkoina* spp.**														
Fursenkoina bradyi	0	2	0	0	0	0	0	0	0	0	0	0	0	0
[1]*Fursenkoina nodosa*	0	1	0	0	0	0	0	0	0	0	0	2	0	0
***Gavelinopsis* spp.**														
Gavelinopsis praegeri	3	1	1	1	0	1	1	2	0	0	1	0	2	10

***Gemellides* spp.**														
Gemellides orcinus	0	0	0	0	0	0	1	0	0	0	0	0	1	0
***Globocassidulina* spp.**														
Globocassidulina bisecta	0	0	0	0	0	0	0	0	0	0	0	0	1	4
Globocassidulina crassa	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Globocassidulina subglobosa	1	2	2	1	0	1	3	10	1	0	0	1	6	11
***Gyroidina* spp.**														
Gyroidina neosoldanii	0	0	0	0	0	0	0	0	1	0	0	0	0	0
**Gyroidina* sp. A	0	0	0	0	0	0	0	0	0	0	0	1	0	0
**Gyroidina* sp. B	0	0	1	1	0	0	1	0	4	1	0	0	0	0
**Gyroidina* sp .D	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Gyroidina* sp .E	0	1	0	0	0	0	0	0	0	0	0	0	0	0
**Gyroidina* sp. G	0	0	0	0	0	0	0	0	0	0	0	0	0	2
**Gyroidina* sp. H	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Gyroidinoides* spp.**														
[2]*Gyroidinoides soldanii* (*Hansenisca soldanii*)	4	1	0	0	0	0	1	3	0	0	0	0	0	0
Gyroidinoides nipponica	2	0	0	0	0	0	1	0	1	1	0	3	0	3
**Gyroidinoides* sp .C	0	1	3	0	0	0	0	0	0	0	0	0	0	0
***Heterolepa* spp.**														
Heterolepa bradyi	0	1	0	0	0	0	2	8	0	0	0	0	0	0
Heterolepa broeckhiana	0	0	7	3	0	0	2	2	2	0	1	0	0	0
***Hoeglundina* spp.**														
Hoeglundina elegans	0	0	0	0	0	0	1	0	0	0	0	0	0	0

***Hyalinonetrion* spp.**														
Hyalinonetrion gracillima	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Ioanella* spp.**														
Ioanella tumidula	0	0	0	0	0	0	0	0	0	0	0	0	2	2
***Islandiella* spp.**														
Islandiella californica	0	0	0	0	0	0	0	0	0	0	1	0	0	0
***Laevidentalina* spp.**														
Laevidentalina advena	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Laevidentalina aphelis	0	0	0	0	0	0	0	0	0	1	0	0	0	1
Laevidentalina baggi	0	0	0	0	0	1	0	0	0	0	0	0	0	0
**Laevidentalina* sp. B	0	1	0	0	0	0	0	0	0	0	0	0	0	0
***Lagena* spp.**														
Lagena nebulosa	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Lagena striata	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Lagena* sp. A	1	0	0	0	0	0	0	0	0	0	0	0	0	0
***Lagenosolenia* spp.**														
Lagenosolenia physamorphina	0	0	0	0	0	0	0	0	1	0	0	0	0	0
***Laterostomella* spp.**														
**Laterostomella* sp. A	1	0	0	0	0	0	0	0	1	1	0	0	0	0
***Lenticulina* spp.**														
Lenticulina gibba	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Lenticulina inornata	1	0	1	1	0	1	0	4	1	0	0	0	0	0
Lenticulina limbosa	0	1	0	0	0	0	0	3	0	0	0	0	0	0
**Lenticulina* sp. B	0	1	0	0	0	0	0	0	0	0	0	0	0	0

***Lernella* spp.**														
Lernella inflata	1	0	0	0	0	0	0	0	0	0	0	0	0	0
**Lernella* sp. A	0	0	0	0	1	0	0	0	0	0	0	0	0	0
***Lotostomoides* spp.**														
Lotostomoides calomorpha	0	1	0	0	0	0	0	1	0	0	0	0	0	1
***Melonis* spp.**														
Melonis barleeanus	1	4	1	3	2	2	1	10	0	0	0	1	0	8
**Melonis barleeanus* aff.	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Melonis sphaeroides	1	0	3	1	0	2	0	3	3	2	0	0	1	0
***Miliolinella* spp.**														
Miliolinella subrotunda	2	2	0	3	0	0	0	0	0	0	0	0	0	0
***Mucronina* spp.**														
Mucronina compressa	0	0	1	0	0	0	0	2	1	0	0	1	0	1
***Nonion* spp.**														
Nonion pacificum	0	0	0	0	0	0	0	0	0	0	0	0	0	2
***Nonionella* spp.**														
Nonionella auris	0	0	0	0	0	0	0	0	0	0	0	0	1	1
**Nonionella* sp. A	0	1	0	0	0	0	0	1	0	0	0	1	0	1
**Nonionella* sp. B	0	0	0	0	0	0	0	1	0	0	0	0	1	1
***Oolina* spp.**														
Oolina baukalionilla	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Oolina globosa	0	1	0	0	0	0	0	0	0	2	0	0	0	2
Oolina lineata	0	0	0	0	0	0	0	0	0	0	0	0	0	1
**Oolina* sp. A	0	0	0	0	0	0	0	0	1	0	0	0	0	0

**Oolina* sp. B	0	0	0	1	0	0	0	0	0	0	0	0	0	0
**Oolina* sp. C	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Oridorsalis* spp.**														
Oridorsalis tenerus	0	1	0	0	0	1	1	0	0	0	0	0	1	1
Oridorsalis umbonatus	1	0	0	1	0	1	1	5	0	0	0	1	0	2
**Oridorsalis umbonatus* aff.	0	0	0	0	0	0	0	3	0	0	0	0	0	1
Oridorsalis westi	0	1	0	0	0	2	0	0	0	1	0	0	0	2
***Osangularia* spp.**														
Osangularia bengalensis	2	0	1	1	1	0	5	14	0	2	0	0	4	24
***Osangulariella* spp.**														
Osangulariella bradyi	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Osangularielloides* spp.**														
Osangularielloides rugosa	0	0	0	0	0	0	1	1	0	0	0	0	0	0
***Palliolatella* spp.**														
Palliolatella sp. 3	0	0	0	0	0	0	0	0	0	0	0	0	0	4
***Parafissurina* spp.**														
Parafissurina himatiostoma	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Parafissurina lateralis	0	1	0	0	0	0	0	0	0	0	0	1	0	2
Parafissurina subventricosa	0	0	0	0	0	0	0	0	0	0	0	1	0	0
**Parafissurina* sp. A	0	1	0	0	0	0	0	0	0	0	0	0	0	0
***Planulina* spp.**														
Planulina ariminensis	0	0	0	0	0	0	0	1	0	0	0	0	1	1
***Procerolagena* spp.**														
Procerolagena cylindrocostata	0	1	0	0	0	0	0	1	0	0	0	0	0	0

Procerolagena meridionalis	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Pseudoeponides* spp.**														
Pseudoeponides japonicus	0	0	0	1	0	0	2	5	0	0	0	2	2	24
***Pseudofissurina* spp.**														
Pseudofissurina metaconica	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Pseudoolina* spp.**														
Pseudoolina fissurinea	0	0	0	0	0	0	0	0	0	0	0	1	0	2
***Pseudosolenina* spp.**														
Pseudosolenina wiesneri	0	0	0	0	0	0	0	2	0	0	0	0	0	1
**Pseudosolenina wiesneri* aff.	0	0	0	0	0	0	1	1	0	0	0	0	0	0
***Pullenia* spp.**														
Pullenia bulloides	1	5	8	17	4	21	0	2	4	0	0	2	0	2
Pullenia quinqueloba	0	0	0	0	0	0	0	2	0	0	0	0	0	0
***Pyrulina* spp.**														
Pyrulina cylindroides	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Pytine* spp.**														
Pytine paradoxa	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Quadrimorphina* spp.**														
Quadrimorphina laevigata	1	0	0	0	0	0	0	0	0	0	0	0	0	0
**Quadrimorphina* sp. A	0	0	0	0	0	1	0	0	0	0	0	1	0	0
***Quinqueloculina* spp.**														
Quinqueloculina neosigmoilinoides	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Quinqueloculina* sp. B	2	2	0	0	0	0	0	0	0	0	0	0	0	0
**Quinqueloculina* sp. C	0	1	0	0	0	0	0	0	0	0	0	0	0	0

***Rutherfordoides* spp.**														
Rutherfordoides rotundata	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Rutherfordoides rotundiformis	2	2	0	1	0	0	0	0	4	1	1	1	0	1
Rutherfordoides virga	0	1	1	0	1	3	0	0	0	0	0	0	0	0
***Sphaeroidina* spp.**														
Sphaeroidina bulloides	4	1	0	2	3	3	0	4	3	0	0	1	0	8
***Spirosigmoilina* spp.**														
Spirosigmoilina pusilla	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Triloculina* spp.**														
[2]*Triloculina consobrina* (*Pseudotriloculina consobrina*)	0	0	1	0	0	0	0	0	0	0	0	0	0	0
**Triloculina* sp.A	0	1	0	0	0	0	0	0	0	0	0	0	0	0
***Triloculinella* spp.**														
Triloculinella hornibrooki	0	0	0	0	0	0	0	0	0	0	0	0	2	0
**Triloculinella hornibrooki* aff.	0	1	0	0	0	0	0	0	0	0	0	0	0	0
***Uvigerna* spp.**														
Uvigerina ampullacea (*Siphouvigerina ampullacea*)	2	2	1	1	3	2	1	17	0	0	0	0	0	0
Uvigerina auberiana	1	15	1	5	0	24	2	75	3	1	0	1	4	19
Uvigerina hispida (*Siphouvigerina hispida*)	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Uvigerina peregrina	5	3	0	2	0	2	0	2	0	0	0	0	0	2
Uvigerina proboscidea (*Siphouvigerina proboscidea*)	2	4	0	0	1	5	2	43	0	0	0	0	0	0

*Unknown sp. A	0	31	0	13	0	15	1	48	0	2	0	9	8	46
**Unknown sp. E	0	4	0	0	0	1	0	0	1	1	0	0	0	0
**Unknown sp. F	0	0	0	0	0	0	0	0	0	0	0	1	0	1
**Unknown sp. G	0	0	0	0	0	0	0	0	0	0	0	1	0	0
**Unknown sp. H	0	0	0	2	0	0	0	0	1	0	0	0	1	0
**Unknown sp. I	0	0	0	0	0	0	0	0	0	0	0	1	0	0
*Unknown sp. J	0	0	0	1	0	0	0	0	0	0	0	0	0	0
*Unknown sp. R	0	0	0	0	0	0	0	1	0	0	0	0	0	0
*Unknown sp. S	0	1	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. T	1	0	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. U	0	2	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. V	0	2	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. W	0	1	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. Z	0	0	0	0	0	0	0	1	0	0	0	0	0	0
*Unknown sp. AA	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Aggultinated Brnthic Foraminifera	**L**	**D**	**L**	**D**	**L**	**D**	**L**	**D**	**L**	**D**	**L**	**D**	**L**	**D**
***Adercotryma* spp.**														
Adercotryma glomerata	3	3	1	2	0	1	0	0	8	16	1	3	1	5
***Ammobaculites* spp.**														
**Ammobaculites crassaformis* aff.	0	0	0	0	0	0	0	0	2	0	0	0	0	0
***Ammodiscus* spp.**														
Ammodiscus hoeglundi	1	0	1	1	0	0	1	1	1	0	0	0	0	0
***Ammoglobigerina* spp.**														
Ammoglobigerina globigeriniformis	0	0	1	3	0	1	0	0	0	0	0	0	0	0

Ammoglobigerina latestoma	6	3	6	6	0	3	0	4	6	11	1	12	0	0
**Ammoglobigerina pygmaea* aff.	0	0	1	2	0	0	0	0	1	1	0	0	0	0
***Ammogloborotalia* spp.**														
Ammogloborotalia stellaris	2	2	1	0	0	0	0	0	10	2	0	0	0	1
**Ammogloborotalia stellaris* aff.	5	1	7	2	0	0	0	0	4	2	0	0	0	0
**Ammogloborotalia* sp.A	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Ammolagena* spp.**														
Ammolagena clavata	1	1	0	0	0	0	0	1	0	0	0	0	0	0
***Ammomarginulina* spp.**														
**Ammomarginulina* sp. A	0	0	0	0	0	0	2	0	0	0	0	0	0	0
***Ammospaeroidina* spp.**														
Ammosphaeroidina sphaeroidiniforme	0	0	1	0	0	0	1	6	1	0	0	0	0	0
***Ammotium* spp.**														
Ammotium minutum	1	1	1	0	0	0	0	0	0	4	1	0	0	0
**Ammotium* sp. A	0	0	0	0	0	1	0	1	0	1	0	0	2	2
***Ammovertellina* spp.**														
Ammovertellina prima	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Arenogaudryina* spp.**														
**Arenogaudryina* sp. A	3	2	1	0	0	0	0	2	2	2	0	0	5	11
**Arenogaudryina* sp. B	0	2	0	0	0	0	0	0	0	1	0	0	0	0
**Arenogaudryina* sp. C	1	0	0	0	0	0	2	4	0	0	0	1	0	0
***Aschemonella* spp.**														
Aschemonella scabra	1	0	0	0	0	0	0	0	0	0	0	0	0	0
***Astrammina* spp.**														

Astrammina rara	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Astrorhiza* spp.**														
**Astrorhiza* sp. B	0	0	0	0	0	0	1	0	0	0	0	0	0	0
***Bathysiphon* spp.**														
Bathysiphon macilentus	0	1	0	0	0	0	0	1	0	1	0	1	0	0
Bathysiphon rufum	0	1	0	0	0	1	0	1	0	0	0	0	0	1
Bathysiphon rusticum	0	0	0	0	0	0	1	1	0	0	0	0	0	0
***Cribrostomoides* spp.**														
Cribrostomoides subglobosa	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Cystamminoides* spp.**														
Cystamminoides quadrilocula	0	1	0	0	0	0	0	0	0	0	0	0	0	0
**Cystamminoides trilocula* aff.	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Dendrophyra* spp.**														
Dendrophyra sp. A	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Discammina* spp.**														
Discammina compressa	5	0	0	0	0	0	1	2	0	0	0	0	0	0
**Discammina compressa* aff.	1	0	4	0	0	0	0	0	0	0	0	0	0	0
***Duquepsammia* spp.**														
Duquepsammia bulbosa	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Eggerella* spp.**														
Eggerella bradyi	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Eggerella nitens* aff.	0	0	1	0	0	0	1	0	0	0	0	0	0	3
***Glomospira* spp.**														
Glomospira fijiensis	0	2	1	2	0	0	0	0	0	1	0	0	1	0

Glomospira gordialis	0	0	2	2	0	0	1	4	0	1	0	0	3	2
**Glomospira gordialis* aff.	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Glomospira hoeglundi	0	0	0	0	0	0	0	0	0	0	0	0	0	1
***Haplophragmoides* spp.**														
[2]*Haplophragmoides bradyi* (*Recurvoidella bradyi*)	1	2	0	0	0	0	0	0	4	6	0	1	0	0
Haplophragmoides neobradyi	9	5	6	21	0	2	2	3	4	3	0	1	7	4
[3]*Haplophragmoides bradyi niigataensis* (*Haplophragmoides bradyi nigataensis*)	9	20	62	122	1	31	1	4	93	10	0	16	4	1
Haplophragmoides membranacea	0	0	0	0	0	0	0	1	0	0	0	0	1	1
Haplophragmoides minima	0	1	0	0	0	1	0	0	0	1	0	0	0	0
Haplophragmoides sphaerilocula	0	0	4	1	0	0	1	0	0	0	0	0	0	0
**Haplophragmoides* sp. B	0	0	0	0	0	1	0	0	0	0	0	0	0	0
**Haplophragmoides* sp. C	0	0	0	0	0	0	0	0	0	0	0	1	0	0
**Haplophragmoides* sp. D	0	0	0	1	0	0	0	0	0	0	0	0	0	0
***Hormosinella* spp.**														
Hormosinella distans	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Hormosinella guttifera	7	6	0	0	0	0	0	0	4	9	0	2	0	1
**Hormosinella guttifera* aff.	1	0	3	0	0	0	1	0	0	0	0	0	0	0
Hormosinella ovicula	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Hyperammina spp.														
Hyperammina distorta	1	3	1	0	3	2	1	0	0	0	0	0	1	1
Hyperammina elongata	0	0	0	0	0	0	0	0	0	0	0	0	0	2
***Jaculella* spp.**														

Jaculella obtusa	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Karreriella* spp.**														
Karreriella parkerae	0	1	0	0	0	0	2	8	0	0	0	0	2	5
***Karrerotextularia* spp.**														
Karrerotextularia flintii	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Karrerotextularia philippinensis	0	2	0	0	0	2	0	3	0	0	0	0	0	0
***Labrospira* spp.**														
**Labrospira quadrilocula* aff.	0	0	0	0	0	0	1	0	0	0	0	0	0	0
[2]*Labrospira scitula* (*Veleroninoides scitula*)	0	0	0	0	1	0	0	0	0	0	0	0	0	0
***Lagenammina* spp.**														
Lagenammina arenulata	5	5	3	6	0	2	5	20	0	0	0	0	3	9
Lagenammina asymmetrica	1	2	1	1	0	2	0	2	0	0	0	0	2	3
Lagenammina atlantica	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Lagenammina bulbosa	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Lagenammina difflugiformis	0	0	0	1	0	0	0	0	0	16	0	2	0	0
[2]*Lagenammina longicollis* (*Reophax longicollis*)	0	0	0	2	0	0	0	0	0	0	0	0	0	0
***Laterostomella* spp.**														
**Laterostomella* sp. A	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Lituola* spp.**														
Lituola hispid	34	5	0	0	0	0	0	0	0	0	0	0	0	0
***Marsipella* spp.**														
Marsipella elongata	0	0	0	0	0	0	0	1	0	0	0	0	0	0

***Martinottiella* spp.**														
[2]*Martinottiella bradyana* (*Dorothia bradyana*)	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Martinottiella communis	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Martinottiella minuta	0	0	0	0	0	0	0	1	0	0	0	0	0	0
***Paratrochammina* spp.**														
Paratrochammina scotiaensis	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Paratrochammina tricamerata	2	1	0	1	0	0	0	0	2	1	0	0	0	0
Paratrochammina zhongshaensis	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Plectina* spp.**														
Plectina nanissima	3	6	1	6	2	36	2	15	6	54	0	172	13	50
Portatrochammina spp.														
Portatrochammina murrayi	14	6	0	5	0	3	0	1	0	4	1	4	0	3
Portatrochammina antarctica weisneri	0	0	0	0	0	0	0	0	0	0	0	0	2	0
**Portatrochammina sp. A*	2	0	0	0	0	1	0	0	0	0	0	0	0	0
**Portatrochammina sp. B*	0	1	0	0	0	0	0	0	0	0	0	0	0	0
***Psammosphaera* spp.**														
Psammosphaera fusca	3	3	0	1	0	0	0	10	0	1	0	0	4	8
**Psammosphaera fusca* aff.	2	0	0	1	0	0	0	8	0	0	0	0	2	0
Psammosphaera parva	0	0	0	2	0	0	0	0	0	0	0	0	0	0
**Psammosphaera parva* aff.	0	0	0	0	0	0	0	0	0	0	0	0	0	2
***Pseudotrochammina* spp.**														
Pseudotrochammina dehiscens	0	0	2	2	0	0	1	0	0	0	0	0	0	0
Pseudotrochammina triloba	9	1	0	0	0	0	1	5	3	0	0	0	0	1

***Recurvoides* spp.**														
[2]*Recurvoides laevigata* (*Veleroninoides scitula*)	0	1	6	4	1	0	0	1	0	0	0	0	0	0
Recurvoides turbinata	1	3	1	1	0	3	1	1	0	1	0	3	2	1
***Reophax* spp.**														
Reophax advena	0	0	0	0	0	0	0	0	0	0	0	0	1	0
**Reophax bilocularis* aff.	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Reophax catenulatus* aff.	0	0	0	0	0	0	1	1	0	0	0	0	0	0
Reophax fusiformis	0	0	2	0	0	0	0	0	0	0	0	0	0	0
**Reophax fusiformis* aff.	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Reophax gibberus	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Reophax littoralis	0	0	0	0	0	0	1	1	0	0	0	0	0	1
Reophax magnicapitatus	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Reophax orientalis	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Reophax paucus	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Reophax pesciculus	1	0	0	0	0	0	0	0	0	0	0	0	0	0
**Reophax pseudopaucus* aff.	0	0	0	0	0	0	4	2	0	0	0	0	0	0
Reophax pulchrus	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Reophax pyrifera	0	0	0	0	0	1	0	0	0	0	0	0	1	1
Reophax scorpiurus	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Reophax spiculifer	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Reophax tenuis	1	2	0	2	0	0	0	0	0	2	0	0	0	0
Reophax tortilis	0	0	0	0	0	0	2	1	0	0	0	0	3	3
**Reophax* sp. A	0	0	0	0	1	1	0	0	0	0	0	0	0	0

**Reophax* sp. E	0	0	1	0	0	0	0	0	0	0	0	0	0	0
***Rhabdammina* spp.**														
Rhabdammina abyssorum	0	0	0	0	0	1	0	0	0	0	1	1	0	0
Rhabdammina discreta	0	1	0	0	0	0	0	1	1	1	0	0	1	0
Rhabdammina fusiformis	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Rhabdammina linearis	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Rhabdammina neglecta	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rhabdammina pacifica	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Rhabdammina scabra	0	0	0	1	0	0	2	2	1	1	0	1	1	1
***Rhizammina* spp.**														
Rhizammina algaeformis	0	0	0	0	0	0	0	0	0	0	0	0	1	0
[2]*Rhizammina indivisa* (*Testulosiphon indivisus*)	0	0	0	0	0	0	0	1	0	0	0	0	1	1
***Saccammina* spp.**														
Saccammina sphaerica	0	0	0	3	0	0	0	1	0	0	0	0	0	0
***Saccorhiza* spp.**														
Saccorhiza ramosa	1	1	0	1	1	1	3	1	1	0	0	1	1	1
**Saccorhiza glabrilocula* aff.	0	0	0	0	0	0	0	0	0	1	0	0	0	0
***Sigmoilopsis* spp.**														
Sigmoilopsis herzensteini	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Sigmoilopsis moyi	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Sigmoilopsis schlumbergeri	4	0	9	0	1	0	1	2	0	0	1	0	1	1
***Siphotextularia* spp.**														
Siphotextularia rolshauseni	0	0	0	0	0	1	0	0	0	0	0	0	0	1

***Spiroplectammina* spp.**														
Spiroplectammina biformis	1	1	0	6	0	0	0	2	0	3	0	0	1	3
Spiroplectammina typica	0	0	0	2	0	0	0	0	0	6	0	0	0	1
***Subreophax* spp.**														
Subreophax aduncus	0	0	0	0	0	0	2	0	0	0	0	0	1	0
***Technitella* spp.**														
Technitella richardi	0	0	0	0	0	0	1	0	0	0	0	0	0	0
***Textularia* spp.**														
[2]*Textularia conica* (*Sahulia conica*)	0	0	0	0	0	0	1	0	0	0	0	0	1	2
**Textularia* cf. *earlandi*	6	12	0	3	0	0	0	0	0	1	0	0	0	0
Textularia porrecta	0	0	0	0	0	0	0	0	1	0	0	0	0	0
**Textularia* sp. A	0	0	0	0	0	1	0	0	0	0	0	0	0	0
***Tritaxis* spp.**														
Tritaxis fusca	0	0	0	0	0	0	0	0	0	0	0	1	0	0
***Trochammina* spp.**														
Trochammina boltovskoyi	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Trochammina inflata	0	1	3	10	0	4	0	0	1	2	0	0	0	0
**Trochammina inflata* aff.	1	0	0	0	0	0	0	0	3	0	0	0	0	0
Trochammina nana	0	0	1	0	0	0	0	0	0	0	0	0	0	0
**Trochammina pintoi* aff.	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Trochammina pseudoinflata	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Trochammina subconica	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Trochammina triloba	0	0	0	0	0	0	0	0	0	1	0	0	0	0
**Trochammina triloba* aff.	0	0	0	1	0	0	0	0	0	0	0	0	0	0

Trochammina vesicularis	2	0	2	14	0	1	1	0	3	4	0	1	1	0
**Trochammina* sp. A	7	3	1	3	0	2	0	0	3	3	1	4	0	1
**Trochammina* sp. B	7	1	0	0	0	0	0	0	1	0	0	0	0	0
***Trochamminoides* spp.**														
Trochamminoides challengeri	0	0	0	0	0	0	0	0	1	0	0	0	0	0
***Usbekistania* spp.**														
Usbekistania charoides	0	0	0	0	0	0	0	0	1	0	0	0	0	0
***Veleroninoides* spp.**														
[2]*Veleroninoides jeffreysii* (*Cribrostomoides jeffreysii*)	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Veleroninoides wiesneri	0	0	2	4	0	0	0	5	1	1	0	0	0	3
***Verneuilinulla* spp.**														
Verneuilinulla compacta	0	0	0	0	0	0	0	1	0	0	0	0	0	0
**Verneuilinulla* sp. A	0	0	0	0	0	0	0	2	0	0	0	0	0	0
**Unknown sp. B	0	0	0	0	0	0	0	0	0	0	0	0	1	1
**Unknown sp. F	0	1	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. G	0	2	0	0	0	0	0	0	0	0	0	0	0	0
*Unknown sp. H	0	0	0	0	0	0	0	4	0	0	0	0	0	0
*Unknown sp. I	0	0	0	0	0	0	0	1	0	0	0	0	0	0
*Unknown sp. K	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Note: the scientific names in brackets are scientific names registered in WoRMS. * represent species with undefined species name. ** represent samples that cannot be classified due to the lack of identifiable characteristics. [1] represent scientific names no registered in WoRMS. [2] represent controversial names. [3] represent scientific names is mispelled in WoRMS

Appendix 2

Biodiversity Indices

Biodiversity index is a way to measure the variability of a given community or a sample collected from it (Shannon and Weaver, 1949; Simpson, 1949). It is calculated from the information of the species richness, the counting of how many different species in a community, and the evenness, the numerical uniformity of every species in this community. It can be calculated in different taxonomic levels, and the species level is the most commonly used. The biodiversity indices used in this study stay in the species level.

The easiest way to measure biodiversity can be simply counting the number of species containing in the given community, i.e. the species richness (S).

S = the number of species contains in a community

The Shannon diversity (*H*) originally proposed by Shannon and Weaver (1949) takes account of the weighted relative quantities of species richness and is defined as the following equations:

$$H = \exp(H')$$

$$H' = -\sum_{i=1}^{S} p_i \ln pi$$

where *H'* is Shannon entropy, p_i represent the proportion of species *i* , and *S* is the number of the species in the community. Because the relative abundance is always smaller than

one, unless there is only one species in the community, the natural log of p_i is a negative value. The negative sign is added to keep *H'* positive. *H'* reaches maximum value when the community is completed even, that is, all species have equal amount, and $p_i = 1/S$ for all i. When evenness stays the same, a community with larger *S* receives higher *H'*.

Evenness indices are not independent of species richness, they are either relative to the minimum or maximum observed richness, and therefore consider as "relative evenness" (Jost, 2010). Introduced by Pielou (1966), Pielou's evenness (*J*) is the most widely used evenness indices (Heip et al.), calculated by the following equation:

$$J = H' / \ln S$$

where ln *S* is the maximum value of *H'*. *J* is a positive value not greater than 1.

Two communities, with one having many species but strong dominance and with the other having few species but high evenness, may eventually yield the same value of the Shannon index. Hence, the Shannon index alone is insufficient to distinguish these different community structures; the species richness and evenness should be displayed in parallel to offer a more balanced view of biodiversity.

Appendix 3

Indicator species analysis (Duferne and Legender, 1997)

Indicator species as an alternative to sample the entire community, can reflect the environment conditions, identify the change of the environment, or predict the diversity of other species, taxa or communities within the environment (De Càceres, 2013).

Duferne and Legender (1997) introduced indicator species analysis with the first step divide the sites into groups. Clustering the sites on the basis of independent data (for instance, environmental variables) is better than clustering on the basis of species data (Borcard et al., 2011). Nonhierarchical clustering procedure such as the *k* means is often used. In this study, as each site was considered to represent different biogeochemical conditions, the 15 samples were divided into three "clusters", containing 5 "sites."

The second step is to identify indicator species. The indicator value of species *i* in site cluster *j* is defined as following equations:

$$A_{ij} = \frac{\text{Nindividuals}_{ij}}{\text{Nindividuals}_{i}}$$

$$B_{ij} = \frac{\text{Nsites}_{ij}}{\text{Nsites}_{j}}$$

$$INDVAL_{ij} = A_{ij} \times B_{ij} \times 100$$

where A_{ij}, the measure of specificity (the relative abundance), is the quotient of the mean of individuals of species *i* in site groups *j* (Nindividual_{ij}) divided by the sum of the mean of species *i* across all sites in formula for measuring (Nindividual_{j}), while B_{ij}, the measure

of fidelity (the relative frequency), is the quotient of the number of sites in cluster *j* with the present of species *i* ($Nsite_{ij}$) divided by the total number of sites in the cluster ($Nsites_j$). IndVal index has maximum value 100% when the species *i* occurs only in sites belonging to site groups *j* (environment *j*) and appears in all sites over environment *j*.

The last step is to test the significance of the IndVal value, via a random reallocation procedure of sites among site groups. Permutation with 999 times.

De Càceres et al. (2010, 2012) expend the function of this method by creating combinations of groups and combinations of species. The former allow more flexible definition of groups to better fit the complexity of real environments, whereas the latter considers the possibility that the concomitant presence of a few species (to a maximum of 5) bears more ecological information than individual species. They also noted that the species consisting of the indicator combination are not necessarily significant single-species indicators at the same time. Instead of the IndVal value, it is the square root of the IndVal value, the association statistic (stat), counted in the new methods.

Appendix 4

Raw data present in this study

Table A1. Pore-water and solid-phase data of site C5-1

Depth (cm)	H_2S (μm)	TS (wt%)	Grain size (ϕ)	Sorting	Clay (%)	Silt (%)	Sand (%)
0-1	0.51	0.17	7.22	1.18	27.8	71.3	0.9
1-2	0.94	0.18	7.32	1.13	29.7	69.7	0.6
2-3	0.53	0.67	7.21	1.20	27.9	71.4	0.7
3-4	1.49	0.75	7.12	1.20	25.7	73.4	0.9
4-5	1.82	0.68	7.22	1.18	27.7	71.8	0.5

Table A2. Pore-water and solid-phase data of site C5-2

Depth (cm)	H_2S (μm)	TS (wt%)	Grain size (ϕ)	Sorting	Clay (%)	Silt (%)	Sand (%)
0-1	1.43	0.25	7.33*	1.18*	30.1*	68.7*	1.30*
1-2	1.58	0.72	7.14	1.26	26.2	72.0	1.80
2-3	1.32	1.13	7.09	1.34	26.0	71.8	2.20
3-4	1.38	1.07	7.14	1.24	26.6	72.3	1.10
4-5	1.65	1.29	7.12	1.31	26.3	71.5	2.20

* Due to the insufficient of the sediment sample, the data are the average of original sediment without pretreatment, which would be larger than those with pretreatment, and the sediment <63 μm with pretreatment, which would be smaller than those in whole size fraction.

Table A3. Pore-water and solid-phase data of site C10.

Depth (cm)	H_2S (μm)	TS (wt%)	Grain size (ϕ)	Sorting	Clay (%)	Silt (%)	Sand (%)
0-1	0.64	0.17	7.19	1.15	26.7	72.8	0.50
1-2	0.90	0.18	7.37	1.15	31.3	68.2	0.50
2-3	1.69	0.67	7.25	1.18	28.6	71.2	0.20
3-4	1.22	0.75	7.06	1.23	24.5	74.6	0.90
4-5	1.76	0.68	7.04	1.23	24.1	74.9	1.00