**Result**

**Environment data**

**CTD**

　　The temperature profile was presented in Fig. 3. There’s no evident difference in bottom water temperature between the two sites. The average bottom water temperature in GC1 was 13.54°C, as a result, the calculated *Tlim* equaled 1.05.

While *Tlim* was 1.09 resulting from the average bottom water temperature of 13.90°C in GS1 (Table 6). *Tlim* value was an important correction factor that controlled the biomass-specific maintenance respiration in the LIM model. On the other hand, although the characteristics (i.e. density, salinity, temperature;) of bottom water masses were not drastically different, the profile data of light transmission showed a notable distinction (Fig.4). Little to no light transmission was observed in GC1 throughout the sampling cruises, indicating a benthic nepheloid layer (BNL) presented consistently over a long period. This result coincided with the observation in Liu et al. (2010) in which they suggested the BNL be 100 m thick with high suspended sediment concentration (SSC) in GPSC measured with moored devices.

Carbon budget of non-living component of OC

Detrital organic carbon

Considering the seasonal variation in sediment fluxes caused by hydrodynamic changes (e.g. turbulent mixing, Lee et al., 2009) under the effect of monsoon, the seasonality (if present) between cruises in different seasons was first examined. Results from PERMDISP showed no significant difference in dispersion between habitat groups nor between season groups (Table 7, Habitat, P=0.1051; Season, P=0.2263). The statistical analysis of sediment organic carbon was presented in Table 7. The seasonal variation was not significantly different (Table 7, PERMANOVA, p=0.8816), whereas the difference between the two habitats was significant (Table 7, PERMANOVA,, p=0.0003). The sediment OC content in each cruise was shown in Fig. 5, indicating that OC in the sediment of GS1 was higher as a general trend. The average OC was taken for the input of the LIM model due to non-significant seasonality, average detritus OC in GC1 was 350270104003.4 mg C/ m2 , whereas this value was 524425.7 34800.15 mg C/ m2 in GS1.

Carbon budget of living component of OC

Prokaryote biomass

Prokaryotes were only sampled during the cruise OR1\_1190. Fig. 6 showed each count for 10 times replicates. In addition, the statistical difference between the two habitats was significant (Table 8, t-test, p<0.001). For the model input, the average bacteria biomass was 65.3112.74 mg C/ m2 and 42.806.75 mg C/ m2, respectively in GC1 and GS1.

Meiofauna biomass

Among meiofauna, Nematodes were always the most abundant metazoan in sediments, accounting for more than 90% of abundance (Giere, 2009; Danovaro, 2012). The meiofauna abundance with Nematodes and without Nematodes in GC1 and GS1 was presented in Fig. 7. Total meiofaunal abundance in GS1 was about two times higher than in GC1; besides, the composition differed between the two sites. From Fig. 7 showing meiofaunal abundance without Nematodes, Copepods were the second most abundant group in the faunal composition in GC1; however, multiple groups comprised the remaining part in GS1, including Copepods, Polychaeta, Kinorhyncha, and Turbellaria.

Fig. 8 showed the consolidated biomass from all taxa groups. Table 9 was the PERMDISP results, indicating significant dispersion both between habitat groups and between season groups (Table 9, Habitat, P=0.0001; Season, P=0.0001). For the PEMANOVA test, only habitat difference was tested. The biomass difference was significant between canyon and slope (Table 9, PEMANOVA, p=0.0002). Regardless of the habitat or seasonal effect, it should be noted that there were only three samples for each sites, and only one sampling cruise for each season; therefore, given the limited sample size, I decided to ignore this difference temporarily and take the average of meiofaunal biomass, which was, 1.491.53 mg C/ m2 in GC1, and 33.3926.48 mg C/ m2 in GS1.

Macrofauna biomass

Macrofauna sampling was conducted in a total of eight cruises for the two habitats respectively. In general, Polychaetes accounted for half of the total abundance and around one-third to half of the total species richness among macrofauna (Gage and Tyler, 1991). In our sampling, Polychaetes dominated the macrofauna assemblages in all cruises (Fig. 9), while the composition on the slope was relatively many and various.

Macrofaunal biomass in two sites was calculated and presented in Fig. 10. Note the difference in the scale of the y-axis. Biomass in GC1 was about an order of magnitude lower than in GS1, while the abundance in the canyon was five times lower than on the slope. For the statistical analysis, Table 10 showed that there was a significant difference in dispersion between habitat groups but not between season groups (Table 10, PERMDISP, Habitat, P=0.0001; Season, P=0.298). In addition, there was significant biomass difference between the two sites but not between different seasons(Table 10, PERMANOVA, Habitat, p<0.0001; Season, P=0.1906). As a consequence, the biomass average of all cruises was taken with the value of 3.657.70 mg C/ m2 in GC1, and 80.20 mg C/ m2 in GS1.

The standing stocks of all compartments in the model were presented in the Table 5, while only the mean values were used for the LIM model input. Generally, the OC contents in standing stocks of GS1 were higher except for the bacteria, which was higher in GC1. The stock of non-living components constituted the largest part of OC in both sites, which was fourth-order of magnitude higher than that of living components. In the canyon, the biomass and richness of meiofauna and macrofauna were remarkably depressed as a result of the canyon effect (Liao et al., 2017; 2020). In contrast, the larger size group macrofauna had greater biomass than that of meiofauna on the slope.

Oxygen utilization

The TOUs resulting from the incubation experiment on shipboard were converted to carbon units (Fig.11), indicating that the means and standard deviations were 72.5916.60 mg C/ m2/ d and 53.384.06 mg C/ m2/ d in GC1 and GS1, respectively (Table 11). Moreover, the measured DOUs which represented aerobic respiration of bacteria showed little difference between the two sites, with values of 19.8122.73 mg C/ m2/ d in the canyon head and 11.688.15 mg C/ m2/ d on the slope (Table 11). Note that the standard deviations were greater than or closer to the mean value in both sites, suggesting wide variations between each cruise. Surprisingly, TOUs showed no significant difference between GC1 and GS1 (Table 12, PERMANOVA, Habitat, P=0.2867). Though GC1 had higher bacterial biomass, however, DOU was not significantly lower in GS1 (Table 13). The other partition of oxygen utilization was BMU, which was calculated as the difference between TOU and DOU. It was presumed that BMU was lower in GC1 because of lower biomass and thus lack of benthos-mediated oxygen utilization. Nevertheless, the calculated mean and standard deviation values of BMU were respectively 62.3445.87 mg C/ m2/ d in GC1, and 62.0140.56 mg C/ m2/ d in GS1 (Table 11), showing no difference between the two habitats (Table 14). Note that the calculation of BMUs was only conducted when both the TOUs and DOUs were measured in the same cruise; in addition, this mean value was first derived from the difference between TOU and DOU and then taken for the average. These oxygen utilizations were combined into LIM model input as the constraints of respiration. TOUs were assigned to be the total respiration (i.e. sum of all the respiration flow), and DOUs were set as the flow of bacterial respiration (the grey flow of Bacteria→DIC in Fig. 2), finally, BMUs were specified as the combination of flow of Meiofauna→DIC and Macrofauna→DIC in Fig. 2).

**Model results**

The first attempt to solve the model which combined the OC stocks and default setting was unsuccessful, indicating that some of the data included in LIM conflicted with each other. The main problem had arisen from the contradiction between little biomass and relatively high oxygen utilization. For example, the sum of maintenance respiration meiofauna and macrofauna in GC1 would be = 0.05397 mg C/ m2/ d, which was far less than the constraint of BMU (c.a. 62.3445.87 mg C/ m2/ d). Because BMU comprised not only benthos’ respiration, but included the mediated utilization through their bioturbation by definition (Glud, 2008), here I decided to remove BMU as the constraints of meiofaunal and macrofaunal respiration. The *in situ* measurements of oxygen consumptions were still important site-specific field data, so I decided to retain the constraints on bacterial respiration (Bacteria→DIC) but modify it as 30% of TOUs (Mahaut et al., 1995) instead of directly using the measured DOUs. Finally, the respirations of benthos (Meiofauna→DIC and Macrofauna→DIC in Fig. 2) were left to be determined by the models.

The other problem awaited to be handled was the rain of POC. Firstly, I directly used 53.85 mg C/ m2/ d as the POC input flux and 24% of POC input as the minimal burial rates (Hsu et al., 2014) to run the model, resulting in a conflicted situation. This infeasible problem resulted from insufficient POC input to support the system. To solve this disagreement, another idea was introduced. The sedimentation rates reported in Huh et al. (2009) and Hsu et al. (2014) were converted to carbon units after timing TOC contents, with the outcome values 106.9230.994 mg C/ m2/ d in GC1, and 61.994.81 mg C/ m2/ d in GS1. These values were set as constraints for the minimum and maximum for the flow Sediment→Burial (Fig. 2). Meanwhile, 24% of POC input as the minimal burial rates was retained to back-calculate the POC input (POC→Sediment in Fig. 2) . Henceforward, LIM would not only solve the unknown values of flows between the compartments but give us a more comprehensive view of carbon demands in two modeling systems respectively.

**LIM result in GC1**

Fig. 12 showed the results solved by LIM modeling with different algorithms. The black dots in Fig. 12 marked the values solved by the most parsimonious method, whereas the pink dots labeled the mean values from MCMC algorithms with 10,000 iterations. Except for the interaction flow between meiofauna and macrofauna (MEI→MAC), all of the solutions solved by the most parsimonious method underestimated the flow quantity. Note that the x-scale was expressed in exponential form with base 10.

MCMC-solved flows in GC1 model could be generally separated into three parts according to the order of magnitude of the mean values (Fig. 13). First, the mean value for POC flux was 131.08 mg C/ m2/ d, and the burial export occupied about 88% of the OC input (115.77 mg C/ m2/ d), both fluxes were directly related to the detritus stock. The second-largest flow values were those related to bacteria and the interactions between bacteria and the environment, including SED→BAC (24.65 mg C/ m2/ d), BAC→SED (9.33 mg C/ m2/ d), and BAC→DIC\_W(15.13 mg C/ m2/ d). Although the remaining flows were all less than 1 mg C/ m2/ d, we could still differentiate the flows related to meiofauna and macrofauna stocks by the mean values, which were an order of magnitude higher in meiofauna-related flows.

**LIM result in GS1**

Similar trends were found in the Fig. 14, most of the solutions by the most parsimonious method were lower than that solved by MCMC algorithm, except for MEI→MAC and the burial flux (SED→EXP\_S), the latter was with similar results by two different methods. The POC flux was estimated 78.95 mg C/ m2/ d in GS1 by MCMC method, while about 80% of which flowed out of the system (SED→EXP\_S, 63.23 mg C/ m2/ d). On the other hand, the interaction flows between bacteria and the environment in GS1 were not that strong in comparison with those in GC1, instead, the importance of larger size groups increased according to overall higher mean values of flows between the compartments of meiofauna and macrofauna. Likewise, in GS1, the meiofauna-related flows were an order of magnitude higher than those related to macrofauna.

Because of the same structure of the two food webs, LIM results could be compared directly. To begin with, the values of the internal flows (black flows in Fig. 14) which represented biological interactions in GS1 were higher, corresponding to the higher biomass of meiofauna and macrofauna on the slope site. Although the bacteria stock accounted for a large proportion of the biomass in the canyon in comparison to the slope, the energy flows between bacteria and sediment stock however were not distinctly different between the two habitats. On the other hand, the flow values of biotic outputs (i.e. energy loss through predation and respiration) were reasonably consistent with the standing stocks. Finally, the ratio of the burial flux to input flux, representing the fraction of unused OC which flowed out of the system to reach the balanced steady-state, was about 8% higher in the canyon head.

**Turnover rates**

The turnover rate was calculated through dividing the carbon stock by directly measured oxygen consumption and model estimated flows, respectively (Table 15). For example, the turnover rate of total carbon was calculated as the sum of detrital and biotic carbon divided by *in situ* TOU and the sum of flows BAC→DIC, MEI→DIC, and MAC→DIC, which corresponds to the definition of TOU.

Overall, both the *in situ* measurement and modeling results showed that organic carbon turned over much more slowly at the slope sites. For the detrital carbon, it turned over about 1.5 times more slowly in GS1 with direct TOU estimation. The calculated turnover rate through model results revealed a 5 times slower turnover rate compared to direct TOU measurement for both sites. Bacteria turnover rates in two habitats calculated by different methods were almost consistent, with 3.3 to 4.3 days in GC1 and 3.7 days in GS1. However, the turnover time for meiofauna and macrofauna estimated by the two methods were distinctly different. In GC1, the turnover time estimated by *in situ* BMU was 550 times more than which calculated by the model. Though the time difference between the two estimated methods in GS1 was not as vast as in GC1, it was 40 times slower by model estimation. The turnover time was much shorter in GC1 with the calculation of BMU (GC1: 0.08 day; GS1:1.83 day), in contrast, the time estimated by models was slightly longer in GC1 (GC1: 44.64 day; GS1:42.06 day).

**Network indices results**

In addition to directly comparing the flow values, network indices were calculated to examine the food web functioning. Selected indices were calculated for the complete set of LIM solutions (10,000 solutions for each sites) and compared between canyon and slope. The distributions of calculated network indices values in the two habitats were plotted in Fig. 15, showing that the median value of the and were apparently higher in the food web of GC1 (: 295.13 mg C/ m2/ d; : 164.62 mg C/ m2/ d) than in that of GS1(: 203.92 mg C/ m2/ d; : 125.24 mg C/ m2/ d). , and were relatively lower in the canyon. Median values of were 0.070 and 0.134 for the canyon and the slope, respectively. Median values were not distinctly different between the two sites, with median values of 1.157 and 1.191 for GC1 and GS1, respectively.

Another way to determine if the indices differed between the two sites was to calculate the fraction of which the randomized set of indices of GC1 was larger than GS1. For instance, when this fraction was 0.90, implying that 90% of the values of indices of GC1 were larger than those of GS1. As defined in van Oevelen et al. (2011), the difference was considered highly significant when the fraction larger than 10% (i.e. fraction <0.10 or >0.90); when the distinction was more than 5% (i.e. fraction <0.05 or >0.95), the difference was considered highly significant. The comparison result was presented in Table 16. Only and were significantly higher in the canyon head, while of GC1 was marginally significantly lower (fraction=0.1043)