CONGO RIVER CANYON CROSSING PROJECT, BENTHIC ANALYSES

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INTRODUCTION

The purpose of this project is to provide analyses of benthic communities from samples taken off the Northwestern coast of Angola to provide a baseline assessment for Chevron for the Congo River Canyon Crossing Pipeline Project.

METHODS

A total of 78 samples were collected between 10 and 16 March 2006. The samples were taken with two different size boxcores: 30 cm x 30 cm (900 cm^2) and 50 cm x 50 cm (2500 cm^2). The samples were sieved on board, preserved, and shipped to the laboratory in Texas.

The locations of the samples were in the Congo River Canyon region off the west coast of equatorial Africa (Table 1). The samples were taken in five areas along two different types of environments (Figure 1). Samples were taken along the shallow south shelf averaging 48.9 m, north shelf averaging 68.1 m, and area C1 averaging 87.3 m. Canyon samples were taken in two areas: B2A averaging 433.9 m, and B4 averaging 534.2 m.

Laboratory Methods

Macrofauna are extracted using 0.5 mm sieves. Individuals are sorted to major taxa, and then identified to the lowest taxonomic level possible, which is normally to the family level. Because samples were taken using boxcores of different sizes, abundances were converted to number per meter square (n m^{-2}) prior to analysis.

Level of Taxonomic Effort

Analysis of benthic infaunal communities has been widely used in environmental assessment and monitoring studies. The use of species level data is powerful, but expensive because of the level of expertise and labor intensive effort required. This has inspired efforts to determine if species level data are really necessary. At the GEEP workshop, all levels of biological organization were studied from the molecular to the community, and all biological components from bacteria to macrofauna were included in both mesocosm and field experiments (Bayne *et al*. 1988). In the field study, diversity indices did not detect the pollution gradient, but community structure differences were distinct and species level data gave no more information for discrimination than did nematode suborder or harpacticoid family groupings (Heip *et al*. 1988). Macrofauna family groupings also were just as good for distinguishing the pollution gradient as was species level data (Warwick 1988). Higher level identifications were found to be just as good as species identifications to detect pollution gradients in the Southern California Bight (Ferraro and Cole 1990). These and many other studies have shown that identification at the family level detects environmental change as well as the species level.

Community indices, i.e., diversity and evenness, were calculated for each station using the average number of individuals/m^2 for all replicates. Diversity was calculated using Hill's diversity number one (N1) (Hill 1973). It indicates the number of abundant species in a sample, and is a measure of the effective number of species (Ludwig and Reynolds 1988). The effective number of species is a measure of the degree to which proportional abundances are distributed among species (Hill 1973). It is calculated as the exponentiated form of the Shannon diversity index:

$$N1 = e^{H'}.$$

As diversity decreases N1 will tend toward 1. The Shannon index (H') is the average uncertainty per species in an infinite community made up of species with known proportional abundances (Shannon and Weaver 1949). Hill's N1 is used because the unit, numbers of species, is easier to interpret than most other diversity indices. In addition, richness, the total number of species in a sample was tallied.

Evenness is an index that expresses that all species in a sample are equally abundant. Evenness is a component of diversity. The evenness index used here is probably the most common, it is the familiar J' of Pielou (1975). It expresses H' relative to the maximum value of H'.

Statistical Analyses

Statistical analyses to test for differences among treatment means (i.e., stations) are performed using parametric, general linear models. Prior to analysis data are transformed, generally by natural logarithm, to achieve homogeneity of error variance, normality of residual errors, and additivity of effects. A data set of residual errors is created for each model and tested for normality. Both untransformed and transformed residuals are computed, and the data set that are normally distributed with means of zero are used for analyses.

Multivariate analysis was used to test for changes in community composition among stations. Ordination of samples was performed using the non-metric multidimensional scaling (MDS) procedure described by Clarke and Warwick (2001) and implemented in Primer-e software (Clarke and Gorley 2001). The MDS is a non-parametric multivariate technique for examining similarity or dissimilarity between stations, replicates, or other dependent variables in the experimental design. First, a similarity or dissimilarity index is computed for elements of the design (e.g., stations) then a plot of the distance among points is created. The plot enables us to identify unknown variables that affect the similarity or dissimilarity between stations. Because the MDS procedure is based on non-parametric (Kruskal-Wallis like) models, it is most useful to summarize biotic data (e.g., community structure). Cluster analysis on the similarity matrices was performed to determine the degree of relatedness of stations that were grouped near one another in the MDS plot. The relatedness of different MDS plots is computed by comparing the similarity matrices using the RELATE procedure. An analysis of similarity to determine if there were treatment differences was performed on the similarity matrix using the ANOSIM procedure.

Linking the biotic response to the environment was accomplished by reducing the environmental data using principal components analysis (PCA) to two principal factors and then correlating these new factors with the biotic variables. The SAS programs and PCA approach to characterize environmental data and link it to biotic responses is described in detail in Long et al. (2003). Environmental chemistry and geological data was obtained from TDI-Brooks International (TDI Brooks International, Inc. and Maxon Consulting, Inc. 2006).

RESULTS

A total of 246 species were found among the 78 samples (Table 2). Phyletic diversity was high. The 246 species were distributed among 210 genera, 65 families, 41 orders, and 10 phyla. The total average abundance was 286.15 individuals m^{-2}. Three fish species were found, but they were rare, altogether averaging only 0.58 individuals m^{-2}.

Annelids, primarily polychaetes, were the most commonly found phylum making up about 51% of all individuals (Table 3). Annelids, Crustacea (about 26%) and Mollusca (about 15%) together comprised were about 92% of all organisms found.

Even though annelids were the most common organisms, the dominant species found were an *Amplisca* amphipod species (about 9 %) and small unidentified bivalves (about 5 %) (Table 4). The dominant polychaete was the third most dominant species and it contributed about 4 % of all organisms found. Altogether the top 15 dominant species accounted form 50 % of all organisms found. There were 1 sipunculid species, 2 bivalve species, 3 crustaceans, and 9 polychaete species in the top 15 species.

Abundance and diversity were quite variable among the samples (Table 5). Eleven samples (31, 36, 38, 47, 55, 64, 65, 68, 69, 70, 76, and 80) had no animals at all. One sample (37) had only one animal, and two samples (56 and 66) had two individuals. The highest abundance of organisms found in a sample was 1,733 individuals m^{-2} in sample 13A, but the highest diversity of 46 species was found in sample 3.

In general, there were more individuals (Figure 3) and more species diversity (Figure 4) in the shelf samples. In particular, the South Shelf area had the highest densities followed by the North Shelf. There was also moderate abundance in the B2A region, but the deeper Canyon regions of B4 and C1 had the lowest abundances. Diversity was much higher in the South Shelf region than any other region. The North Shelf had the next highest diversity. Although area B2A had one sample (23) with high diversity and abundance, the area had many samples with no individuals present.

There was little similarity among samples at the species level (Figure 5). One station, 67, had no species in common with any of the other stations. Most stations, except for 78 and 66 had only 10% of species in common. There were 12 groups of samples that shared 20% similarity of species. For the most part areas fell within these groupings.

One group was composed solely of samples (39, 35, 50, 32A, 34, and 30) from the C1 area, although four samples (29, 45, 24, and 77) did not fall within that group. All the North Shelf samples also grouped together except for two (10 and 6). The North Shelf and South Shelf samples also shared one similarity group at the 20% level. Although the samples from area B4 generally fell within the lower part of the graph, the samples did not group together and shared similarity with four different groups. Samples from the area B2A were the most heterogeneous falling in nearly all parts of the graph, and within nine different groups.

The data set was aggregated at the genus level, which reduced the number of taxa from 246 to 210 (Figure 6). The pattern for genera was exactly the same as for species, i.e., 67 had nothing in common with other samples and except for 78, 77, 56, and 66 had only 10% of species in common. There were 11 groups of samples that shared 20% similarity of genera. Whereas the areas grouped more closely to one another on the MDS plot, all areas shared genera in common with other areas. Again, only the area B2A was heterogeneous with samples falling in all parts of the graph.

The data set was aggregated again at the family level, which reduced the number of taxa to 65 families (Figure 7). The pattern for families was still similar to that for the species, i.e., sample 67 had nothing in common with other samples. However, at the family level, more similarity began to emerge. There were only 7 groups of samples that shared 20% similarity of families. One large group included all samples from the North and South Shelf and some C1 and B4 samples. Again, area B2A samples are spread throughout the MDS plot and are represented in all but one group.

The data set was aggregated again at the order level, which reduced the number of taxa to 41 orders (Figure 8). The pattern for families was still similar to that for the species, however, at the order level, more similarity began to emerge. There were only 2 groups of samples that shared 20% similarity of families. Also there were five groups of samples that shared 30% similarity of orders. Sample 67 appears on the MDS chart for the first time because the two orders do appear in other groups.

The spatial representation of the samples was similar at all levels of biological organization (Table 7). There was no statistically significant evidence that the patterns were different from one another due to chance alone. Based on the Rho statistic, the strongest association was at the species, genus, and family level.

Diversity was also calculated on the aggregated data sets. Although diversity can be calculated in many different ways, two approaches were used in the current study. Species richness, S, is the total number of species; or genera, families, or orders for the aggregated data sets. However, S is a function of total number of individuals, so the number of dominant species, Hill's N1, was also calculated. N1 is the exponential form of the Shannon H′ index, but is easier to interpret because it is in units of number of species; or genera, families, or orders for the aggregated data sets.

Another way to compare diversity among the areas is to examine species accumulation curves in samples (Figure 8). The samples were arranged in order from shallow to deep and from northeast to southwest. The samples divide into two patterns: one for the South and North Shelves, and one for the Canyon samples from areas B2A, B4, and C1. The shelf samples were much more diverse than the Canyon samples, which is indicated by the steeper rise is finding new species and the larger number of species. None of the areas are saturated, meaning none of the curves have leveled off, which indicates that there are many more species in this region than have been found in the current set of samples.

The environmental data was comprised of 27 variables: 4 for sediment size, 5 summary variables for hydrocarbons, and 18 metals. Because the number of variables can influence the PCA, an initial PCA was run on just metals to pick 8 that represented most of the variance in that data set. The top 8 metals (Ba, Cd, Cr, Fe, Hg, Ni, Se, and Zn) represented 99% of the variance in the metals data set, so just those were used in the environmental PCA. There were two main principal components comprising a cumulative 77% of the variance in the data; where the first contained 67% and the second contained 10 % of the variance. The first component (PC1) represented a gradient of sandy sediments to muddy sediments because the highest negative load was for sand and the highest positive loads were for moisture, clay and silt (Figure 10). The organic chemicals were also associated with high, positive values of PC1. The second component (PC2) represented metals concentrations, in particular iron (Fe) and zinc (Zn).

The sample and area PC1 scores demonstrate that the South Shelf is the principal sandy area and the canyon samples, particularly area B2A are muddy (Figure 11). The second factor, PC2, is useful only in separating some of the South Shelf samples that have high (15 – 21) and low (11 - 14) iron and zinc content.

There were strong, significant, inverse correlations between PC1 and all biotic responses (Table 8). Thus, as mud content decreased and sand content increased the abundance and diversity increased. There was also a strong, significant, inverse correlation between PC1 and depth indicated more mud in deeper water and more sand in shallower water. Thus the changes in the biotic community was related to both depth and sediment composition. There was only a weak correlation between PC2 and abundance and N1 diversity, but no correlation between PC2 and depth or species number. As metals (Fe and Zn) content increased, abundance decreased, but N1 diversity increased. There was no correlation between PC1 and evenness (J′), but there was a positive correlation between evenness and PC2.

DISCUSSION

Overall, the there was quite a bit of heterogeneity among the samples. Some samples appeared similar in terms of abundance, diversity and community composition. In particular, 11 samples had no animals at all: 31, 36, 38, 47, 55, 64, 65, 68, 69, 70, 76, and 80 (Figure 3, Table 5). All of these samples came from canyon areas where there was

greater variability in relief (i.e., water depth was variable), for example samples 31, 36, and 38 came from area C1; samples 47, 55, 64, 65, 68, 69, 70 came from area B2A; and sample 80 came from area B4. In contrast, the shelf samples typically had the highest abundances. The south shelf area (especially stations 11 – 16) was especially rich in abundance and diversity. The north shelf had somewhat lower abundances and diversity than the south shelf. The South Shelf also had the highest sand content (Figure 11).

The samples with the fewest number of individuals had a tendency to be more different from the others (compare Figure 3 and Figure 5). In fact, sample 67from the center of area B2A had just 4 individuals, and had no species in common with any other sample. Except for stations 71 – 75, area B4 had no or very few organisms. One interesting note is that sample 67 also had the highest PC1 environmental score (Figure 11) indicating it was environmentally different from all other samples as well.

In general, those samples with a high number of species typically had no more than 20% in common (compare Figure 3 and Figure 5). There was more similarity among shelf stations than the canyon stations, because the shelf stations typically fell in the lower half of the MDS in Figure 6, and in contrast the canyon stations in areas C1 and B2A were found in the top half of the MDS plot. Area B4 was the most heterogeneous in terms of community composition. The stations in area C1 were typically found in the right hand part of the MDS plot.

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Table 1. Sample descriptions. Depth in meters.

Area	Sample	Date-Time	Latitude	Longitude	Depth	Description
North Shelf	1	12-Mar-2006	S05 29.6760	E011 42.4527	99.5	clay and black sand
North Shelf	2	12-Mar-2006	S05 34.2863	E011 45.3181	83.8	clay + big worm tube in jaws of box core and black sand
North Shelf	3	11-Mar-2006	S05 38.9303	E011 48.1084	71.0	good boxcore, all samples were taken from clay
North Shelf	4	11-Mar-2006	S05 40.2339	E011 48.4778	69.5	clay with "black sand"
North Shelf	5	11-Mar-2006	S05 45.6655	E011 48.4976	68.8	clay with "black sand"
North Shelf	6	11-Mar-2006	S05 51.0954	E011 48.4291	69.5	clay with "black sand"
North Shelf	7	12-Mar-2006	S05 40.0461	E011 49.1343	66.7	clay, found an empty shell of a Heart Urchin
North Shelf	8	12-Mar-2006	S05 43.7450	E011 53.0932	55.3	EEL caught in box core jaws, clay
North Shelf	9	12-Mar-2006	S05 45.9849	E011 55.2921	48.1	Clay
North Shelf	10	12-Mar-2006	S05 49.8447	E011 59.1039	38.1	clay sediment with very high water content
South Shelf	11	13-Mar-2006	S06 05.4645	E012 12.6620	18.1	Sand
South Shelf	12	13-Mar-2006	S06 13.4142	E012 15.4152	13.9	Sand
South Shelf	13	10-Mar-2006	S06 10.8032	E012 12.4918	13.4	6inch of fine sand. Using 50cm x 50cm box core
South Shelf	13A	13-Mar-2006	S06 10.6977	E012 12.4904	14.2	Sand
South Shelf	14	13-Mar-2006	S06 15.9705	E012 12.2981	20.0	chemical sample
South Shelf	15	13-Mar-2006	S06 14.7753	E012 03.6726	48.7	sand
South Shelf	16	13-Mar-2006	S06 13.5714	E011 58.8669	58.4	sandy clay, chemical sample
South Shelf	17	13-Mar-2006	S06 10.8959	E011 54.0509	74.9	Clay and black sand ,chemical
South Shelf	18	13-Mar-2006	S06 08.5420	E011 50.1211	84.9	Clay and black sand ,chemical
B2A	19	11-Mar-2006	S06 04.7941	E011 47.9905	98.4	sandy clay processed for chemical samples
South Shelf	20	11-Mar-2006	S06 04.9713	E011 46.9679	95.7	clay and black sand (pellets or ooids)?
South Shelf	21	11-Mar-2006	S06 05.2870	E011 46.0454	95.7	clay and black sand (pellets or ooids)?
B2A	22	11-Mar-2006	S06 04.0512	E011 47.4335	197.0	clay and black sand, processed for chemistry
B2A	23	11-Mar-2006	S06 03.3328	E011 45.8227	195.7	clay and black sand (pellets or ooids)?
B4	24	11-Mar-2006	S06 02.4481	E011 42.6387	195.7	clay and black sand (pellets or ooids)?
C1	25	12-Mar-2006	S06 03.2803	E012 12.7543	47.4	good core (photo as EBS025)
C1	26	13-Mar-2006	S06 03.9446	E012 13.7057	49.5	good core
C1	28	13-Mar-2006	S06 03.8531	E012 13.8429	91.7	good core, silty clay

Area	Sample	Date-Time	Latitude	Longitude	Depth	Description
C1	29	12-Mar-2006	S06 03.0199	E012 12.6976	96.7	good
C1	30	12-Mar-2006	S06 02.7288	E012 10.9927	97.4	clay silt
C1	31	12-Mar-2006	S06 03.7680	E012 13.8992	143.8	good core
C1	32	12-Mar-2006	S06 02.8625	E012 12.6556	136.0	small amount of firm clayey silt, one bag for grainsize
C1	32	12-Mar-2006	S06 02.8636	E012 12.6282	109.5	Site move 50m west, good box
C1	34	12-Mar-2006	S06 01.1674	E012 12.2202	41.0	clay, full
C1	35	12-Mar-2006	S06 01.7817	E012 13.9906	41.0	clay
C1	36	12-Mar-2006	S06 01.2206	E012 12.1585	96.7	Black anoxic sediment, H2S
C1	37	12-Mar-2006	S06 01.8434	E012 13.9414	89.5	clay with black sand
C1	38	12-Mar-2006	S06 01.2556	E012 12.1147	146.0	very dark silt, H2S
C1	39	12-Mar-2006	S06 01.9079	E012 13.9091	147.4	dark gray clay with H2S
B2A	40	11-Mar-2006	S05 57.8069	E011 47.4594	95.7	mud good boxcore,.clay with "black sand"
B2A	41	11-Mar-2006	S05 58.1761	E011 48.2402	92.4	good boxcore
North Shelf	42	11-Mar-2006	S05 45.0561	E011 47.9604	71.0	clay with "black sand"
North Shelf	43	11-Mar-2006	S05 50.2800	E011 46.0827	81.0	clay with "black sand"
North Shelf	44	11-Mar-2006	S05 55.2825	E011 44.2666	98.1	clay with "black sand"
B2A	45	11-Mar-2006	S05 56.8823	E011 44.2153	149.1	25cm mud good boxcore
B2A	46	11-Mar-2006	S05 58.1210	E011 47.2385	145.7	Full, will do all but trace metals
B2A	47	11-Mar-2006	S05 58.5356	E011 48.2214	145.7	Full, will do all but trace metals
North Shelf	48	12-Mar-2006	S05 53.7944	E012 02.9776	28.1	clay sediment with very high water content
North Shelf	49	12-Mar-2006	S05 57.6206	E012 06.7486	25.3	clay
C1	50	12-Mar-2006	S05 58.8932	E012 10.0231	22.4	clay, + fish
North Shelf	51	12-Mar-2006	S05 25.5277	E011 39.8833	115.3	clay
B2A	52	15-Mar-2006	S06 02.0755	E011 43.5453	396.8	clay
B2A	53	15-Mar-2006	S06 01.6230	E011 43.6150	596.8	clay silt, very soft
B2A	54	15-Mar-2006	S06 01.2064	E011 43.6770	199.6	clay silt, very soft
B2A	55	16-Mar-2006	S06 00.8884	E011 43.7482	982.4	Clay, Silt. All samples taken
B2A	56	15-Mar-2006	S06 03.0729	E011 44.7716	380.2	cast touched lid, all samples taken
B2A	57	15-Mar-2006	S06 02.5140	E011 44.9282	602.4	clay
B2A	58	15-Mar-2006	S06 01.7229	E011 45.1631	802.4	clay

Area	Sample	Date-Time	Latitude	Longitude	Depth	Description
B2A	59	15-Mar-2006	S06 01.2053	E011 45.3713	880.0	clay
B2A	60	14-Mar-2006	S06 03.7197	E011 47.5840	393.4	clay, full but processed
B2A	61	14-Mar-2006	S06 02.9952	E011 47.4470	591.3	clay, full but processed
B2A	62	14-Mar-2006	S06 01.6248	E011 47.4748	791.3	clay
B2A	64	14-Mar-2006	S05 59.1176	E011 47.7663	591.3	silty clay
B2A	65	14-Mar-2006	S05 58.7148	E011 47.9366	382.9	silty clay
B2A	66	14-Mar-2006	S05 58.4150	E011 46.7160	388.5	silty clay
B2A	67	14-Mar-2006	S05 59.2353	E011 46.2911	594.0	clay silt
B2A	68	14-Mar-2006	S05 57.9049	E011 44.7284	563.5	clay silt with very high organic content
B2A	69	15-Mar-2006	S05 57.3457	E011 44.5613	385.7	clay with very high organic content
B2A	70	14-Mar-2006	S05 58.9806	E011 45.4247	591.3	clay silt with very high organic content
B4	71	15-Mar-2006	S06 02.3247	E011 41.1897	402.4	clay, sea urchins caught
B4	72	15-Mar-2006	S06 01.5860	E011 41.0858	602.4	clay silt with 2cm red layer over soft gray
B4	73	15-Mar-2006	S06 02.8293	E011 39.4088	403.4	very soft clay
B4	74	15-Mar-2006	S06 02.1872	E011 39.3660	599.1	clay silt
B4	75	15-Mar-2006	S06 01.7733	E011 39.2506	783.6	clay silt, very soft
B4	76	16-Mar-2006	S05 58.1719	E011 40.5376	766.7	clay ,cast touched lid, all samples taken
B4	77	16-Mar-2006	S05 57.2908	E011 40.7453	573.8	clay and black sand, cast touched lid, all samples taken
B4	78	16-Mar-2006	S05 56.6606	E011 40.8471	386.3	clay cast touched lid, all samples taken
B4	79	16-Mar-2006	S05 56.2086	E011 40.9238	194.9	clay cast touched lid, all samples taken
B4	80	16-Mar-2006	S05 58.9818	E011 41.2488	967.4	clay and black sand.cast touched lid, all samples taken

Table 2. Taxonomic list of all species found, and average density over all samples. Abbreviations: PH = Phylum, CL = Class, OR = Order, and FA= Family.

PH	CL	OR	FA	Genus Species	Mean n m^{-2}
Cnidaria					
	Anthozoa				
				Anthozoa (unidentified)	0.10
		Pennatulacea			
				Pennatulacea (unidentified)	0.15
Nemertinea					
				Nemertinea (unidentified)	4.42
Phoronida					
				Phoronis sp.	0.14
Mollusca					
	Aplacophora				
				Aplacophora (unidentified)	1.49
	Gastropoda				
				Gastropoda (unidentified)	2.45
		Heterostropha			
			Pyramidellidae		
				Odostomia sp.	0.34
				Turbonilla sp.	0.05
		Neotaeniogloassa			
			Naticidae		
				Polinices sp.	0.47
		Cephalaspidea			
			Ringiculidae		
				Ringicula sp.	0.14
			Haminoeidae		
				Haminoea sp.	0.05
		Neogastropoda			
			Buccinidae		
				Colus sp.	0.33
			Nassariidae		
				Nassarius sp.	0.24
			Columbellidae		
				Columbellidae (unidentified)	0.05
			Olividae		
				Oliva sp.	0.05
	Bivalvia				
				Bivalvia (unidentified)	14.68
		Pholadomyoida			
			Cuspidariidae		
				Cardiomya sp.	0.30
				Cuspidaria sp.	0.10
		Veneroida			

Cardiidae	
Cardiidae (unidentified)	0.19
Carditidae	
Cyclocardia sp.	0.05
Lasaeidae	
Erycina sp.	1.83
Neaeromya sp.	0.14
Lasaeidae (unidentified)	0.15
Lucinidae	
Lucinidae (unidentified)	0.10
Mactridae	
Mactra nitida	0.14
Mactridae (unidentified)	0.62
Pharidae	
Ensis sp.	0.05
Solecurtidae	
Tagelus sp.	0.14
Tellinidae	
Macoma sp.	0.05
Tellina sp.	1.70
Tellidora sp.	0.15
Thyasiridae	
Thyasiridae (unidentified)	6.57
Ungulinidae	
Diplodonta sp.	1.32
Veneridae	
Chione sp.	1.06
Pitar sp.	0.05
Veneridae (unidentified)	0.56
Nuculoida	
Nuculidae	
Nucula sp.	3.76
Nuculanidae	
Nuculana sp.	0.95
Arcoida	
Noetiidae	
Arcopsis sp.	0.05
Ostreoida	
Pectinidae	
Pectin sp.	0.05
Scaphopoda	
Dentaliida	
Dentaliidae	
Dentalium sp.	0.96
Gadilida	
Gadilidae	

Cadulus sp.	0.86
Annelida	
Polychaeta	
Polychaetea (unidentified)	0.52
Errantia	
Polynoidae	
Malmgreniella sp	0.48
Perolepis sp.	0.14
Polynoidae (unidentified)	0.28
Eulepethidae	
Grubeulepis sp.	0.19
Sigalionidae	
Pholoe sp.	1.06
Sthenelanella sp.	0.14
Leanira sp.	0.05
Ehlersileanira sp.	0.20
Fimbriosthenelais sp.	0.05
Amphinomidae	
Chloeia viridis	0.05
Paramphinome pulchelle	0.14
Paramphinome sp.	0.34
Amphinome sp.	0.05
Amphinomidae (unidentified)	0.05
Phyllodocidae	
Anaitides sp.	0.43
Pilargiidae	
Pilargis sp.	0.10
Sigambra tentaculata	3.12
Litocorsa sp.	2.42
Ancistrosyllis papillosa	0.24
Sigambra sp.	0.05
Ancistrosyllis sp.	0.71
Parandalia sp.	0.05
Hesionidae	
Gyptis sp.	0.68
Hesionidae (unidentified)	0.05
Syllidae	
Syllis sp.	0.47
Exogone sp.	0.05
Odontosyllis sp.	0.14
Sphaerosyllis sp.	0.39
Nereidae	
Nereis sp.	0.46
Micronereis sp.	0.05
Nereidae (unidentified)	0.05
Paralacydoniidae	

Paralacydonia paradoxa	0.66
Paralacydonia sp.	0.05
Nephtyidae	
Aglaophamus verrilli	0.05
Aglaophamus sp.	5.99
Glyceridae	
Glycera sp.	0.14
Glycera longipinnis	0.52
Glycera prashadi	0.10
Goniadidae	
Goniada sp.	0.96
Glycinde sp.	0.24
Goniadopsis sp.	0.34
Goniadides sp.	0.10
Goniadidae (unidentified)	0.05
Eunicidae	
Marphysa sanguinea	0.14
Eunice indica	0.14
Eunicidae (unidentified)	0.14
Onuphidae	
Diopatra cuprea	5.55
Diopatra papillata	0.05
Diopatra sp.	0.20
Onuphis eremita	0.15
Lumbrineridae	
Lumbrineris sp.	6.01
Lumbrineris hartmani	0.15
Arabellidae	
Drilonereis sp.	0.57
Acoetidae	
Eupanthalis sp.	0.05
Polyodontes sp.	0.10
Sedentaria	
Spionidae	
Dispio sp.	0.51
Laonice cirrata	1.69
Paraprionospio sp.	2.31
Prionospio sp.	6.28
Prionospio cirrobranchiata	0.05
Prionospio cristata	0.28
Prionospio saldanha	0.05
Prionospio malmgreni	6.17
Prionospio sexoculata	0.14
Prionospio steenstrupi	0.66
Prionospio cirrifera	0.70
Prionospio ehlersi	0.39

Prionospio pygmaea	0.14
Spiophanes bombyx	0.80
Spiophanes sp.	0.71
Magelonidae	
Magelona sp.	1.81
Magelona papillicurnis	0.28
Magelona capensis	0.92
Magelona cincta	0.14
Poecilochaetidae	
Poecilochaetus johnsoni	0.14
Poecilochaetus sp.	0.05
Chaetopteridae	
Spiochaetopterus sp.	0.10
Cirratulidae	
Tharyx sp.	11.38
Dodecaceria sp.	0.20
Cirratulideae (unidentfied)	0.19
Cossuridae	
Cossura delta	5.91
Orbiniidae	
Scoloplos sp.	10.61
Phyllo capensis	0.05
Paraonidae	
Aricidea sp.	12.34
Cirrophorus sp.	0.69
Tauberia sp.	0.35
Paraonis gracilis	0.15
Paraonis sp.	5.62
Paraonides sp.	0.05
Opheliidae	
Opheliidae (unidentified)	0.05
Capitellidae	
Capitella sp.	0.35
Heteromastus sp.	0.30
Mediomastus sp.	1.17
Barantolla sp.	0.53
Notomastus aberans	0.14
Notomastus sp.	1.64
Capitellidae (unidentified)	0.62
Maldanidae	
Maldane sarsi	0.64
Euclymene sp.	0.05
Asychis capensis	0.14
Axiothella sp.	0.15
Clymenella sp.	0.05
Maldanidae (unidentified)	0.75

	Oweniidae	
	Myriochele sp.	0.19
	Myriochele oculata	7.02
	Owenia sp.	0.10
	Sternaspidae	
	Sternapis sp.	0.85
	Flabelligeridae	
	Pherusa sp.	0.05
	Piromis sp.	0.15
	Flabelligeridae (unidentified)	0.20
	Pectinariidae	
	Pectinaria sp.	0.05
	Ampharetidae	
	Ampharete sp.	0.71
	Amphicteis sp.	3.86
	Isolda pulchella	0.47
	Isolda sp.	0.10
	Lysippe sp.	0.52
	Melinna cristata	0.14
	Melinna sp.	0.28
	Ampharetidae (unidentified)	7.92
	Terebellidae	
	Pista cristata	0.56
	Pista sp.	0.70
	Terebellides stroemi	1.23
	Polycirrus sp.	0.25
	Sabellidae	
	Sabella sp.	0.28
	Bogueidae	
	Boguella sp.	0.30
	Longosomatidae	
	Heterospio sp.	0.89
Oligochaeta		
	Oligochaeta (unidentified)	3.95
Sipuncula		
	Sipunculida (unidentified)	0.14
	Aspidosiphonidae	
	Aspidosiphon sp.	2.84
	Aspidosiphon brocki	0.05
	Golfingiidae	
	Golfingia sp.	0.05
	Golfingia (unidentified)	1.72
	Phascolionidae	
	Onchnesoma sp.	6.13
	Onchnesoma stenstrupii	0.42
Crustacea		

Ostracoda	
Ostracoda (unidentified)	0.15
Myodocopa	
Cylindroleberididae	
Cycloleberis sp.	1.06
Prionotoleberis sp.	0.51
Philomedidae	
Philomedes sp.	4.71
Pseudophilomedes sp.	0.05
Asteropteron sp.	0.10
Alternochelata sp.	0.66
Rutidermatidae	
Sarsiella sp.	1.59
Podocopa	
Podocopa (unidentified)	0.10
Malacostraca	
Nebaliacea	
Nebalia sp.	0.064
Stomatopoda	
Squillidae	
Squillidae (unidentified)	0.25
Natantia	
Pasiphaeidae	
Pasiphaeidae (unidentified)	0.14
Alpheidae	
Alpheidae (unidentified)	0.56
Ogyrididae	
Ogyrides sp.	0.66
Crangonidae	
Metacrangon sp.	0.14
Reptantia	
Callianassidae	
Callianassa sp.	0.53
Paguridae	
Paguridae (unidentified)	0.29
Dromiidae	
Dromiidae (unidentified)	0.05
Leucosiidae	
Persephona sp.	0.10
Leucosidae (unidentified)	0.10
Brachyuran Larvae	
Brachyuran (unidentified)	0.19
Cumacea	
Leuconidae	
Hemileucon sp.	0.10
Paraleucon sp.	1.77

Leucon sp.	1.02
Bodotriidae	
Pomacuma sp.	0.94
Cyclaspis sp.	1.64
Amphipoda	
Amphipoda (unidentified)	0.38
Ampeliscidae	
Ampelisca sp.	25.68
Gammaridae	
Gammaridae (unidentified)	0.47
Oedicerotidae	
Monoculodes sp.	1.56
Oedicerotidae (unidentified)	0.10
Corophiidae	
Photis sp.	0.15
Corophiidae (unidentified)	0.56
Lysianassidae	
Orchomenella sp.	0.33
Lysianassidae (unidentified)	0.15
Liljeborgiidae	
Listriella sp.	0.15
Phoxocephalidae	
Harpinia sp.	0.05
Phoxocephalidae (unidentified)	5.44
Haustoriidae	
Haustoriidae (unidentified)	6.71
Stenothoidae	
Stenothoe sp.	0.10
Argissidae	
Argissa sp.	0.14
Melitidae	
Eriopisa sp.	0.38
Melitidae (unidentified)	0.10
Ischyroceridae	
Erichthonius brasiliensis	0.24
Erichthonius sp.	0.14
Dexaminidae	
Dexamine sp.	0.14
Dexaminidae (unidentified)	0.20
Isopoda	
Anthuridae	
Cyathura sp.	1.82
Apanthura africana	0.15
Apanthura sp.	0.10
Anthuridae (unidentidied)	0.28
Gnathiidae	

	Gnathia sp.	0.35
	Gnathia africana	0.05
Cirolanidae		
	Eurydice sp.	0.14
Idoteidae		
	Edotea sp.	0.14
Bopyridae		
	Bopyridae (unidentified)	0.05
Ischnomesidae		
	Ischnomesus sp.	0.28
Nannoniscidae		
	Nannonisconeus sp.	0.05
	Nannoniscidae (unidentified)	0.05
Tanaidacea		
	Tanaidacea (unidentified)	8.66
Apseudidae		
	Apseudidae (unidentified)	2.28
Pseudotanaidae		
	Pseudotanaidae (unidentified)	0.30
Pycnogonida		
	Pycnogonida (unidentified)	0.05
Echinodermata		
Ophiuroidea		
	Ophiuroidea (unidentified)	5.12
Echinoidea		
Spatangoida		
Brissidae		
	Meoma sp.	0.10
Holothuroidea		
	Holothuroidea (unidentified)	1.48
Chordata		
Actinopterygii		
Anguilliformes		
Ophichthidae		
	Dalophis boulengeri	0.19
Ophidiiformes		
Ophidiidae		
	Ophidiidae (unidentified)	0.29
Synbranchiformes		
Synbranchidae		
	Ophisternon afrum	0.10

Table 3. Dominant higher taxa. Occurrences and number of species within each higher taxa (phylum, subphylum, or class level) encountered, and the percent contribution to each higher taxa based on the average number of individuals found among all samples.

Taxa	Species (n)	Abundance (n m^{-2})	Contribution (%)
Annelida	128	145.01	50.63%
Crustacea	62	75.62	26.40%
Mollusca	38	42.27	14.76%
Sipuncula	7	11.36	3.97%
Echinodermata	3	6.70	2.34%
Nemertinea	1	4.42	1.54%
Chordata	3	0.59	0.20%
Cnidaria	2	0.25	0.09%
Phoronida	1	0.14	0.05%
Pycnogonida	1	0.05	0.02%
Total	246	286.41	100.00%

Table 4. Dominant Species. Species abundance and percent contribution of the 15 dominant species. Abbreviations: N = mean abundance per sample, % = percent contribution to the total mean abundance, and Cum% = cumulative percent abundance.

Species Name	**N (n m^{-2})**	**%**	**Cum%**
Ampelisca sp.	25.68	8.97%	8.97%
Bivalvia (unidentified)	14.68	5.13%	14.09%
Aricidea sp.	12.34	4.31%	18.40%
Tharyx sp.	11.38	3.97%	22.38%
Scoloplos sp.	10.61	3.70%	26.08%
Tanaidacea (unidentified)	8.66	3.02%	29.10%
Ampharetidae (unidentified)	7.92	2.77%	31.87%
*Myriochele oculat*a	7.02	2.45%	34.32%
Haustoriidae (unidentified)	6.71	2.34%	36.66%
Thyasiridae (unidentified)	6.57	2.29%	38.95%
Prionospio sp.	6.28	2.19%	41.15%
Prionospio malmgreni	6.17	2.15%	43.30%
Onchnesoma sp.	6.13	2.14%	45.44%
Lumbrineris sp.	6.01	2.10%	47.54%
Aglaophamus sp.	5.99	2.09%	49.63%
231 other species	142.15	50.37%	100.00%
Total	286.41	100.00%	

Table 5. Diversity values for each sample. Abbreviations: S=number of species, N=number of individuals m^{-2}, J'=Pielou evenness index, and H'=Shannon diversity index based on log e.

Area	Sample	S	N	J'	H'	N1
B2A	19	23	400	0.96	3.00	20.1
B2A	22	8	111	0.97	2.03	7.6
B2A	23	31	900	0.89	3.06	21.4
B2A	40	20	188	0.88	2.64	14.0
B2A	41	27	276	0.91	2.99	19.9
B2A	45	25	152	0.97	3.11	22.4
B2A	46	5	28	0.96	1.55	4.7
B2A	46	5	28	0.96	1.55	4.7
B2A	47	0	0		0	1
B2A	52	10	164	0.58	1.34	3.8
B2A	53	14	384	0.66	1.73	5.6
B2A	54	4	28	0.83	1.15	3.2
B2A	55	0	0		0	1
B2A	56	2	8	1	0.69	2.0
B2A	57	14	164	0.83	2.18	8.9
B2A	58	6	36	0.97	1.74	5.7
B2A	59	3	16	0.95	1.04	2.8
B2A	60	6	56	0.86	1.54	4.6
B2A	61	5	24	0.97	1.56	4.8
B2A	62	7	32	0.98	1.91	6.7
B2A	64	0	0		0	1
B2A	65	0	0		0	1
B2A	66	2	8	1	0.69	2.0
B2A	67	3	16	0.95	1.04	2.8
B2A	68	0	0		0	1
B2A	69	0	0		0	1
B2A	70	0	0		0	1
B4	24	30	967	0.88	3.00	20.1
B4	71	18	260	0.81	2.33	10.3
B4	72	11	116	0.80	1.93	6.9
B4	73	14	168	0.78	2.06	7.9
B4	74	18	516	0.73	2.11	8.3
B4	75	12	180	0.83	2.07	7.9
B4	76	0	0		0	1
B4	77	5	20	1	1.61	5.0
B4	78	3	12	1	1.10	3.0
B4	79	5	20	1	1.61	5.0
B4	80	0	0		0	1
C1	25A	38	660	0.83	3.02	20.4
C1	26B	27	584	0.75	2.46	11.7
C1	27	0	0		0	1

Area	Sample	S	N	J'	H'	N1
C1	28	3	152	0.30	0.33	1.39
C1	29	7	56	0.75	1.45	4.27
C1	30	13	96	0.94	2.41	11.08
C1	31	0	0		0	1
C1	32A	13	68	0.97	2.48	11.9
C1	34	12	152	0.85	2.12	8.3
C1	34	12	152	0.85	2.12	8.3
C1	35	12	200	0.75	1.87	6.5
C1	36	0	0		0	1
C1	37	1	4		0	1
C1	38	0	0		0	1
C1	39	3	20	0.87	0.95	2.6
C1	50	12	144	0.74	1.84	6.3
North	1	26	208	0.95	3.09	22.0
North	2	24	140	0.96	3.04	20.9
North	3	46	472	0.92	3.53	34.1
North	4	20	340	0.73	2.20	9.0
North	5	36	392	0.90	3.24	25.5
North	6	14	112	0.90	2.36	10.6
North	7	36	344	0.92	3.30	27.0
North	8	23	176	0.86	2.69	14.7
North	9	16	124	0.92	2.54	12.7
North	10	14	108	0.94	2.47	11.8
North	42	44	496	0.92	3.47	32.3
North	43	35	396	0.90	3.21	24.7
North	44	37	492	0.82	2.98	19.6
North	48	14	124	0.81	2.14	8.5
North	49	16	140	0.92	2.55	12.8
North	51	13	92	0.89	2.28	9.8
South	11	36	424	0.86	3.07	21.5
South	12	28	1900	0.75	2.50	12.2
South	13	46	1116	0.71	2.73	15.3
South	13A	26	1733	0.77	2.50	12.2
South	14	41	1578	0.87	3.21	24.9
South	15	27	889	0.84	2.77	16.0
South	16	43	1156	0.92	3.45	31.5
South	17	25	644	0.92	2.95	19.1
South	18	23	456	0.95	2.99	19.9
South	20	25	622	0.90	2.91	18.4
South	21	26	567	0.95	3.11	22.4

Table 6. Average diversity values by area. Abbreviations: S=number of species, N=number of individuals m^{-2}, J'=Pielou evenness index, and H'=Shannon diversity index based on log e.

Area	Depth	Samples	S	N	J'	H'	N1
B2A	434	28	8.1	112	0.90	1.35	6.5
B4	534	11	10.5	205	0.87	1.62	6.9
C1	87	18	9.6	143	0.78	1.31	6.1
North	68	16	25.9	260	0.89	2.82	18.5
South	49	11	31.5	1008	0.86	2.93	19.4

Table 7. Results of RELATE procedure to determine if patterns in MDS plots could be the same due to chance alone.

Test	Sample statistic (Rho)	Significance level
Species v. Genus	0.98	0.001
Species v. Family	0.92	0.001
Genus v. Family	0.94	0.001
Species v. Order	0.77	0.001
Genus v. Order	0.80	0.001
Family v. Order	0.86	0.001

Table 8. Relationship between environmental variables and biotic responses. Abbreviations: S = number of species, N1 = Hill's N1 index, J′ = Pielou's evenness index, r = Pearson Correlation Coefficient, P = Probability, n = number of samples.

Response	Parameter	Factor1	Factor2	Factor3
Depth	r	0.717	0.003	-0.328
	P	<0.0001	0.9818	0.0030
	n	80	80	80
Abundance	r	-0.719	-0.270	-0.167
	P	<.0001	0.0153	0.1386
	n	80	80	80
Diversity (S)	r	-0.649	0.016	0.154
	P	<0.0001	0.8908	0.1731
	n	80	80	80
Diversity (N1)	r	-0.582	0.239	0.192
	P	<0.0001	0.0327	0.0883
	n	80	80	80
Evenness (J′)	r	0.093	0.386	-0.097
	P	0.454	0.0012	0.437
	n	67	67	67

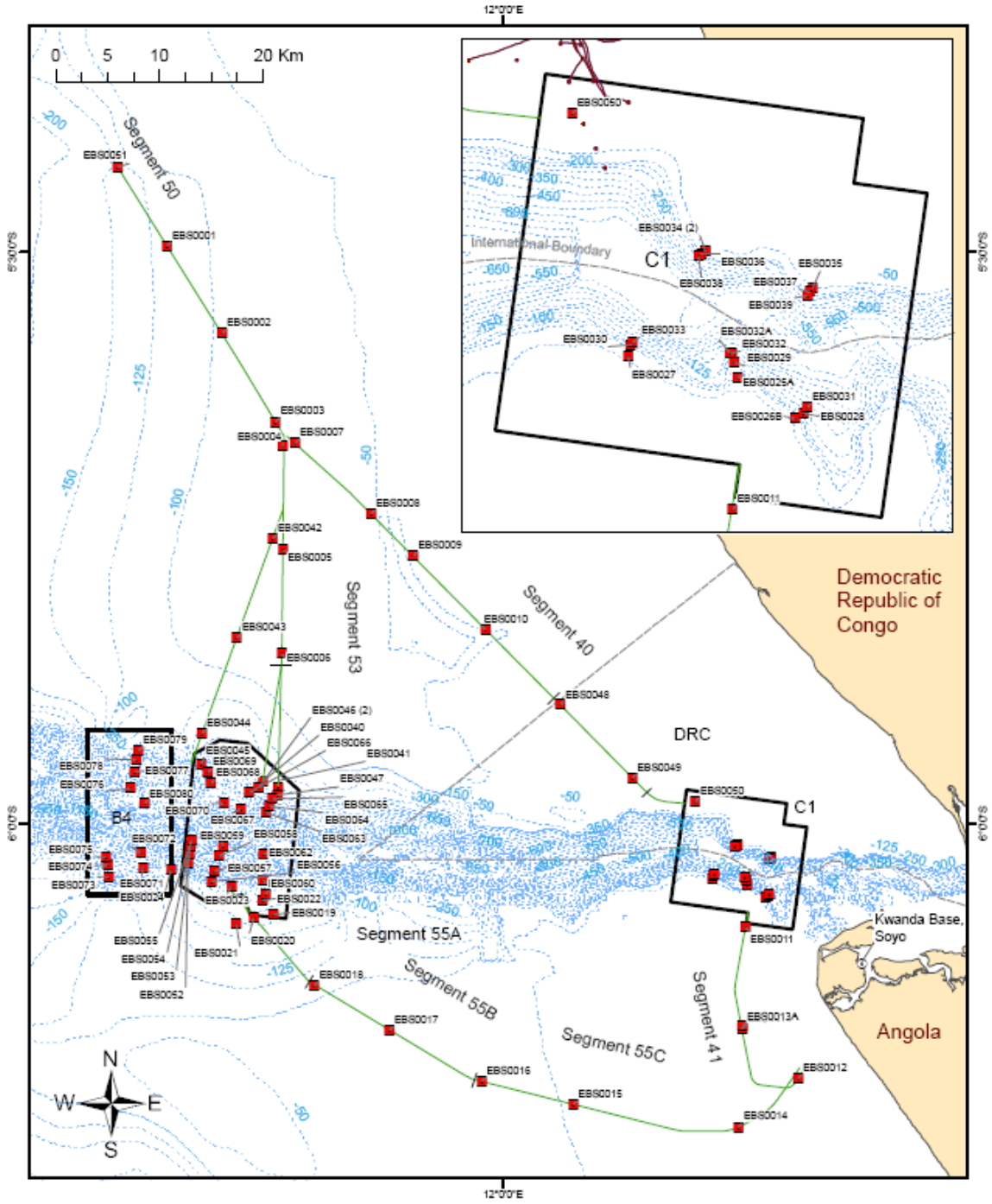

Figure 1. Map of Congo River Canyon study area. Map shows piplines and core locations (with prefix EBS).

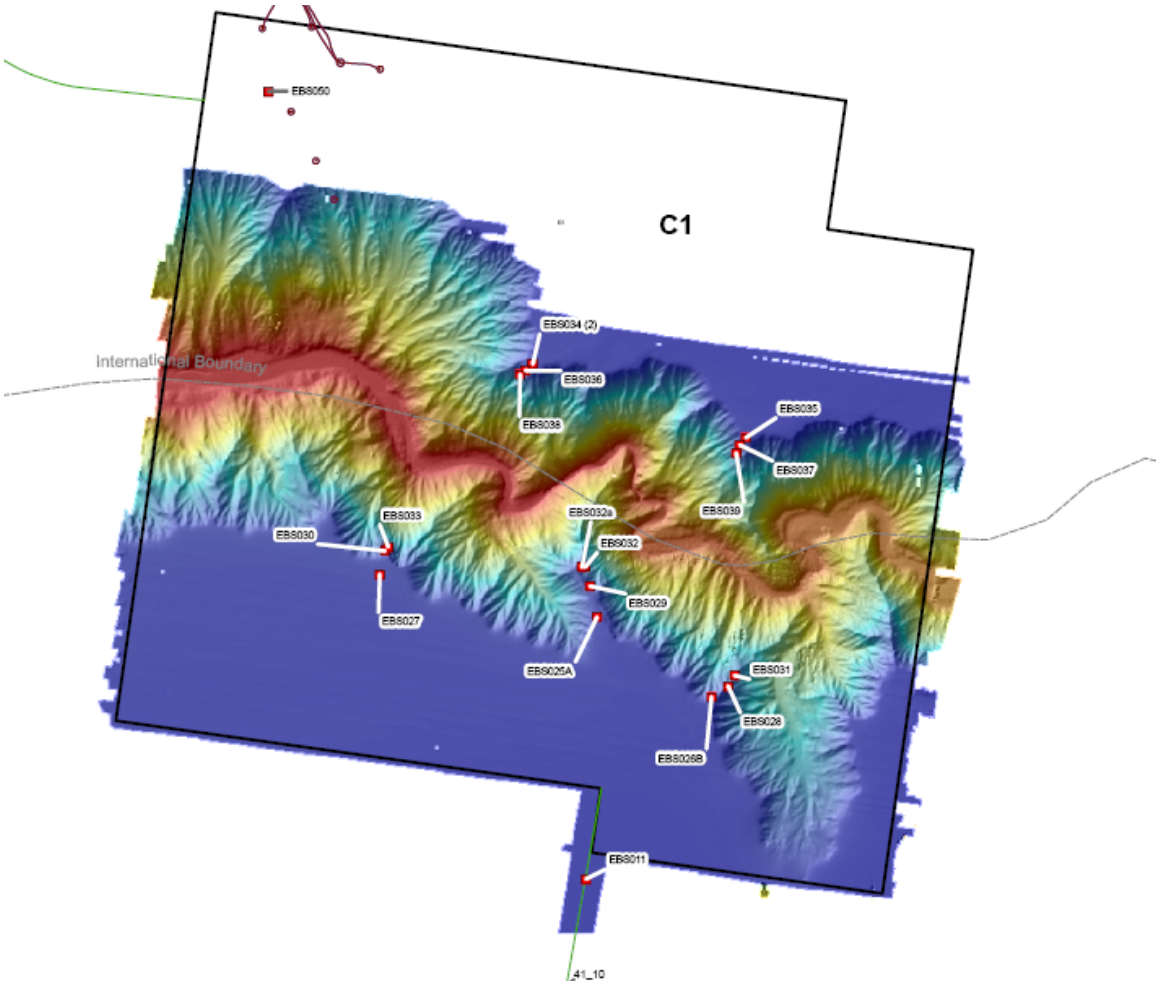

Figure 2. Detailed map of the area named C1 in the Congo River Canyon.

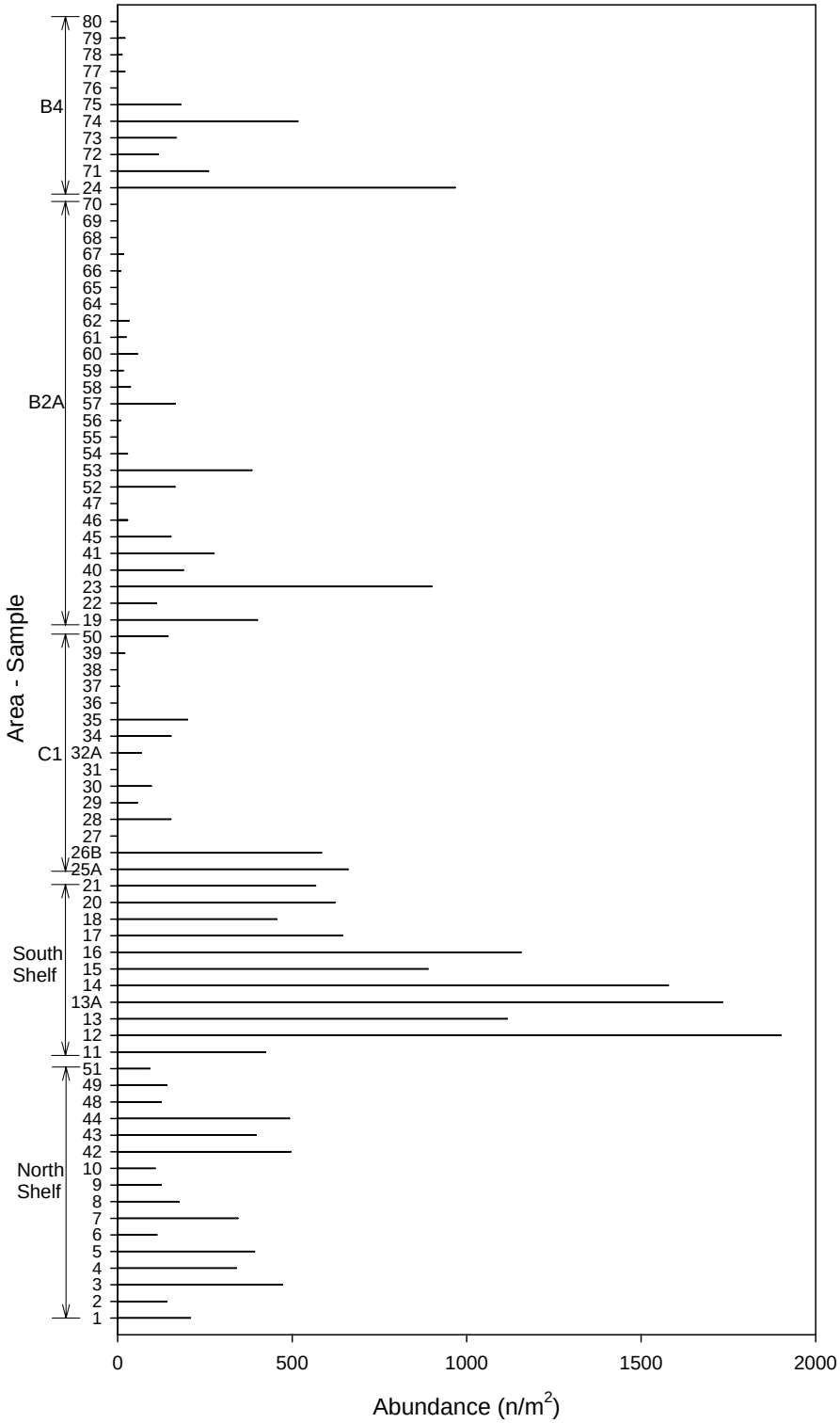

Figure 3. Total abundance as number per sample.

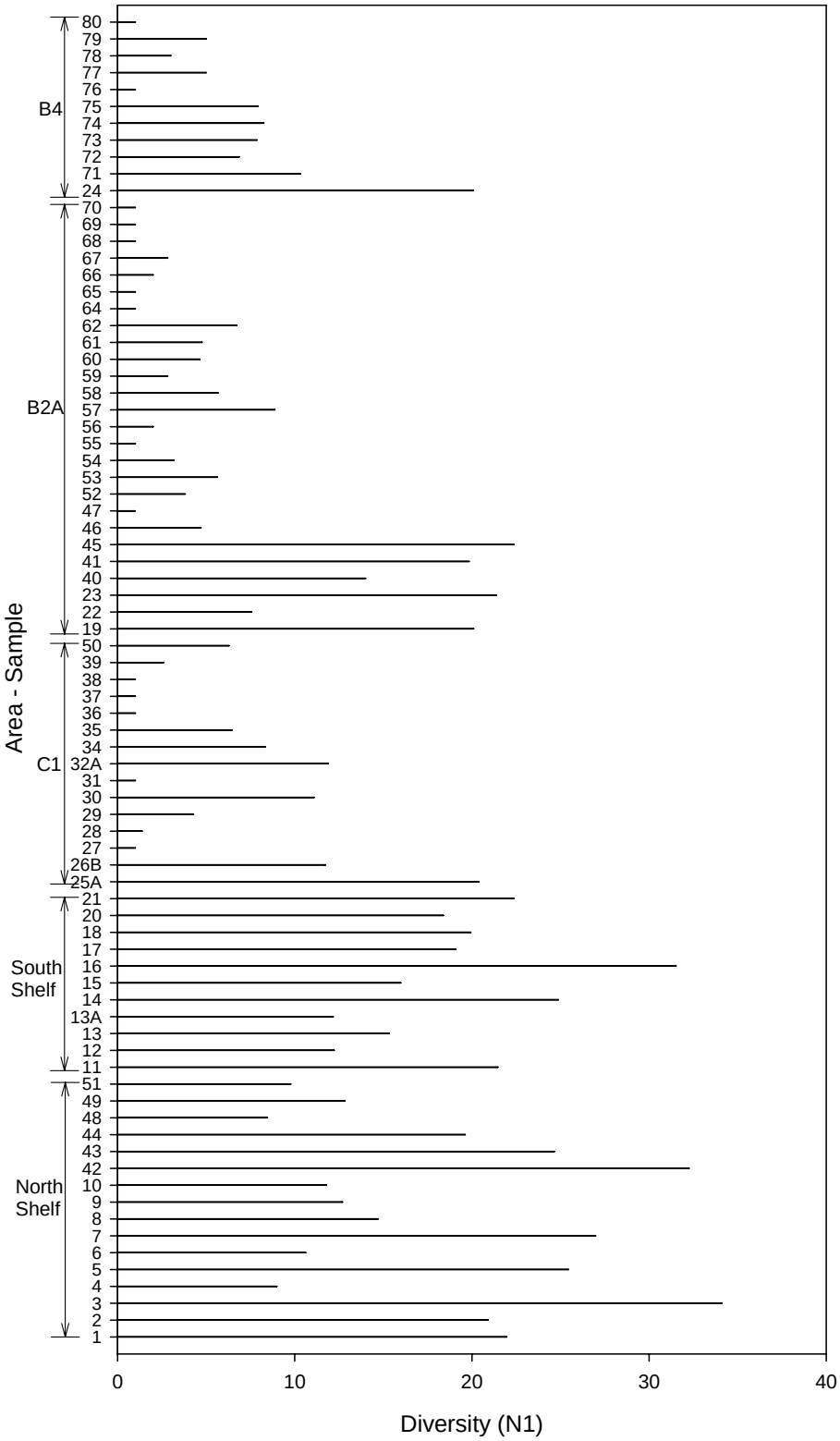

Figure 4. Number of dominant species (N1) among samples. Note 1 = 0 species.

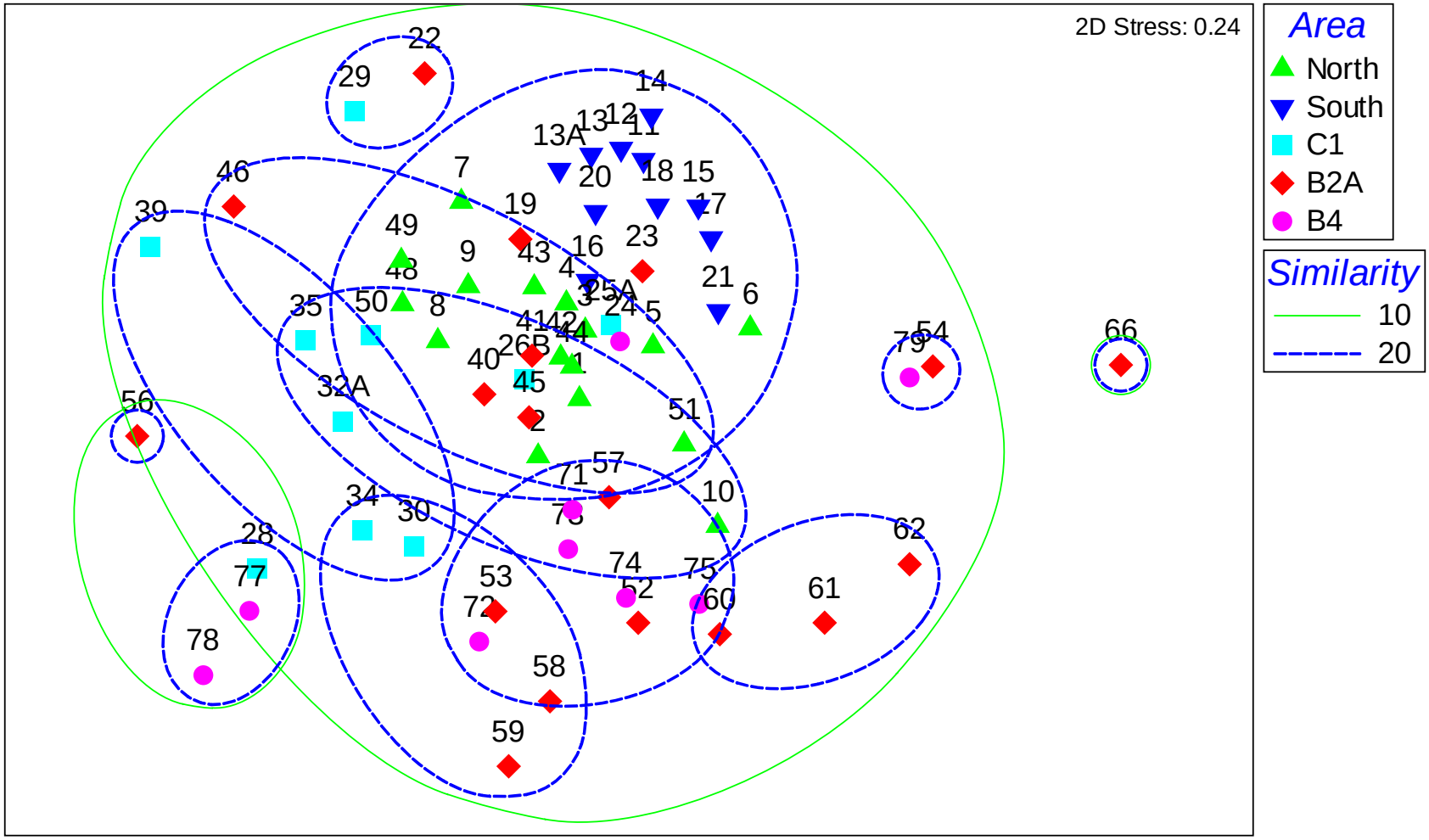

Figure 5. Multidimensional scaling of stations based on species abundance in samples. Stations with no organisms deleted from analysis. Station 67 deleted from analysis because it had no species in common with other stations. Stations groups based on a cluster analysis at community similarity levels of 10% and 20%.

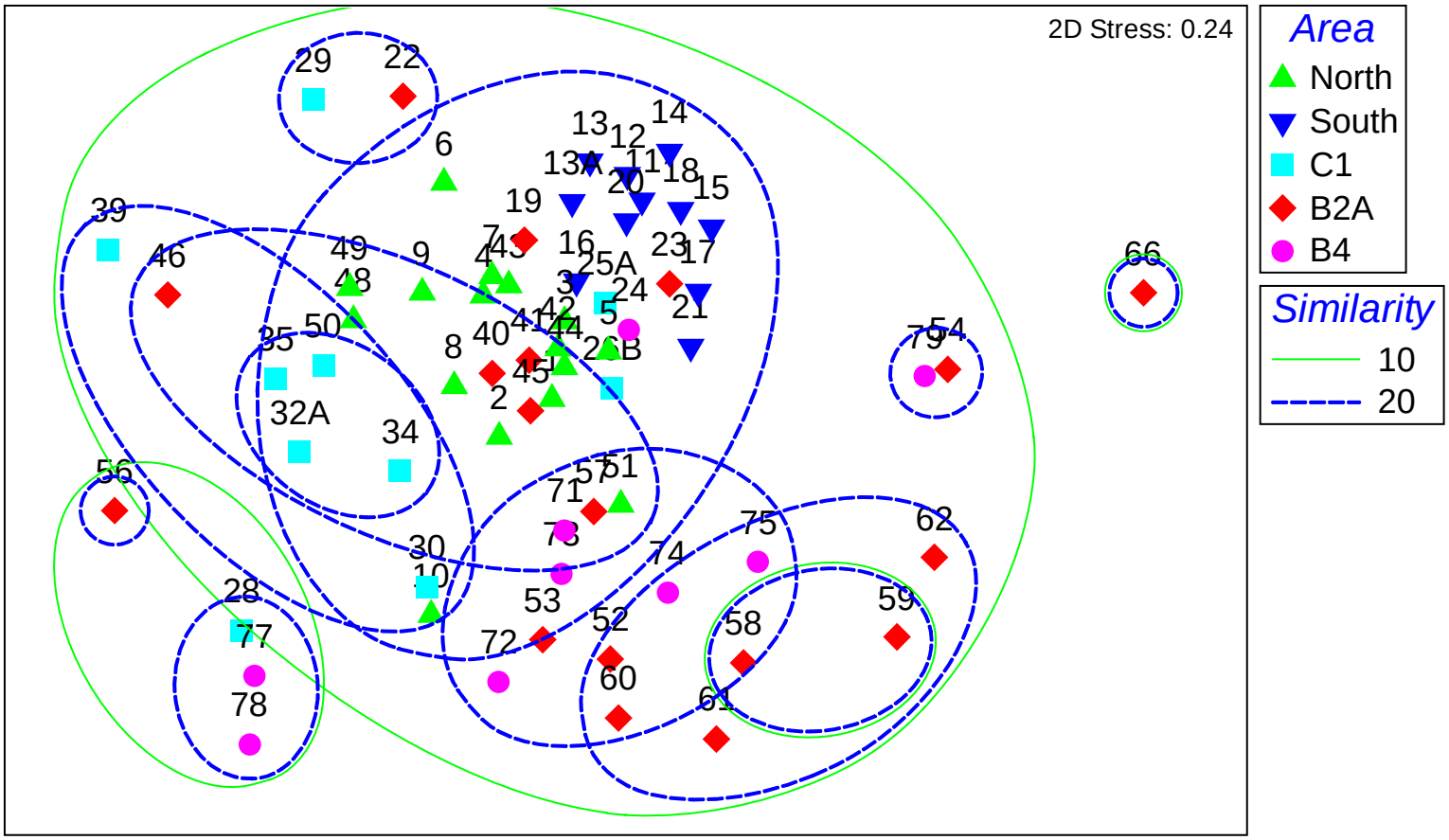

Figure 6. Multidimensional scaling of stations based on abundance aggregated at the genera level in samples. Stations with no organisms deleted from analysis, and station 67 deleted from analysis because it had no species in common with other stations. Stations groups based on a cluster analysis at community similarity levels of 10% and 20%.

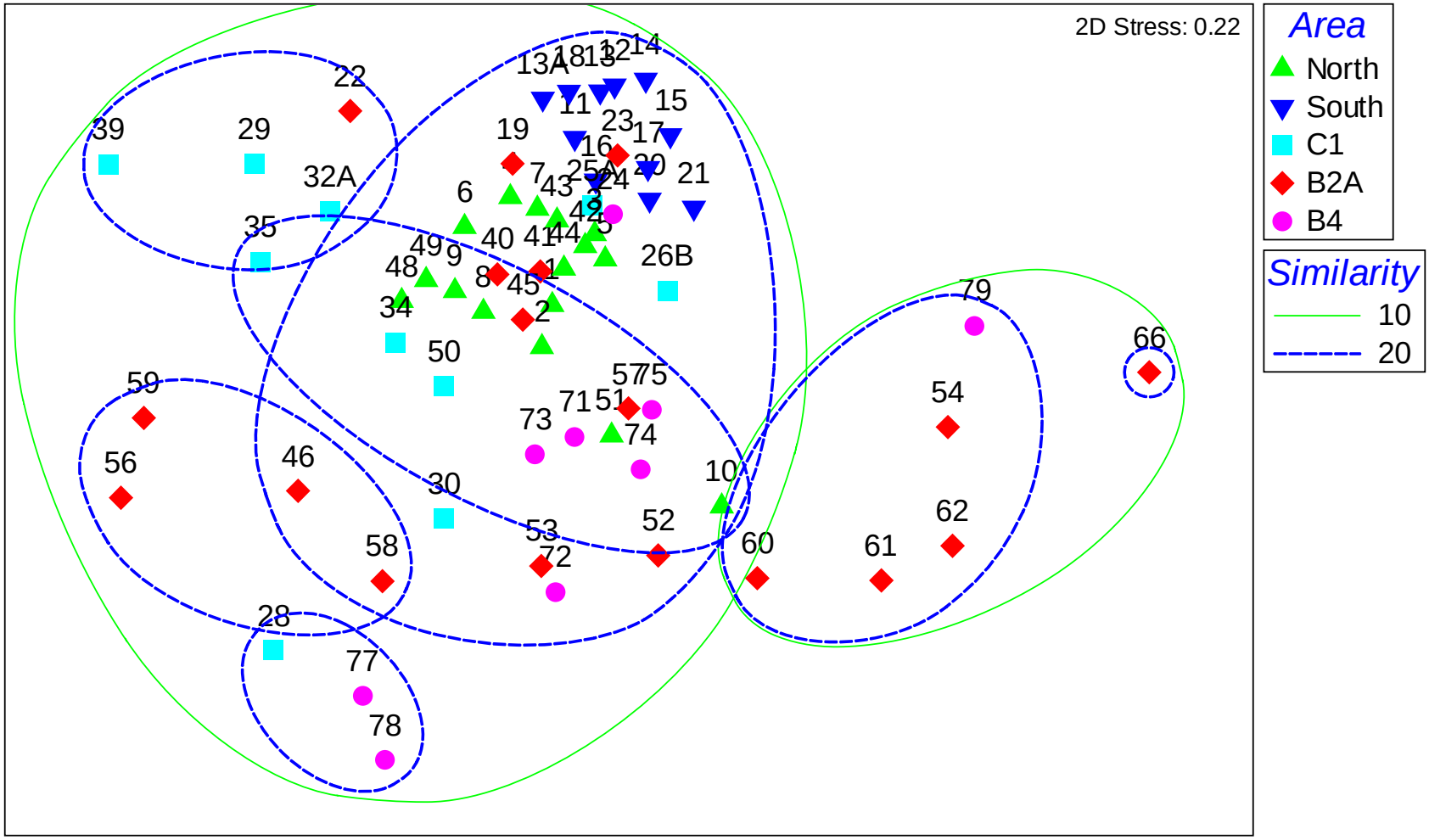

Figure 7. Multidimensional scaling of stations based on abundance aggregated at the family level in samples. Stations with no organisms deleted from analysis, and station 67 deleted from analysis because it had no species in common with other stations. Stations groups based on a cluster analysis at community similarity levels of 10% and 20%.

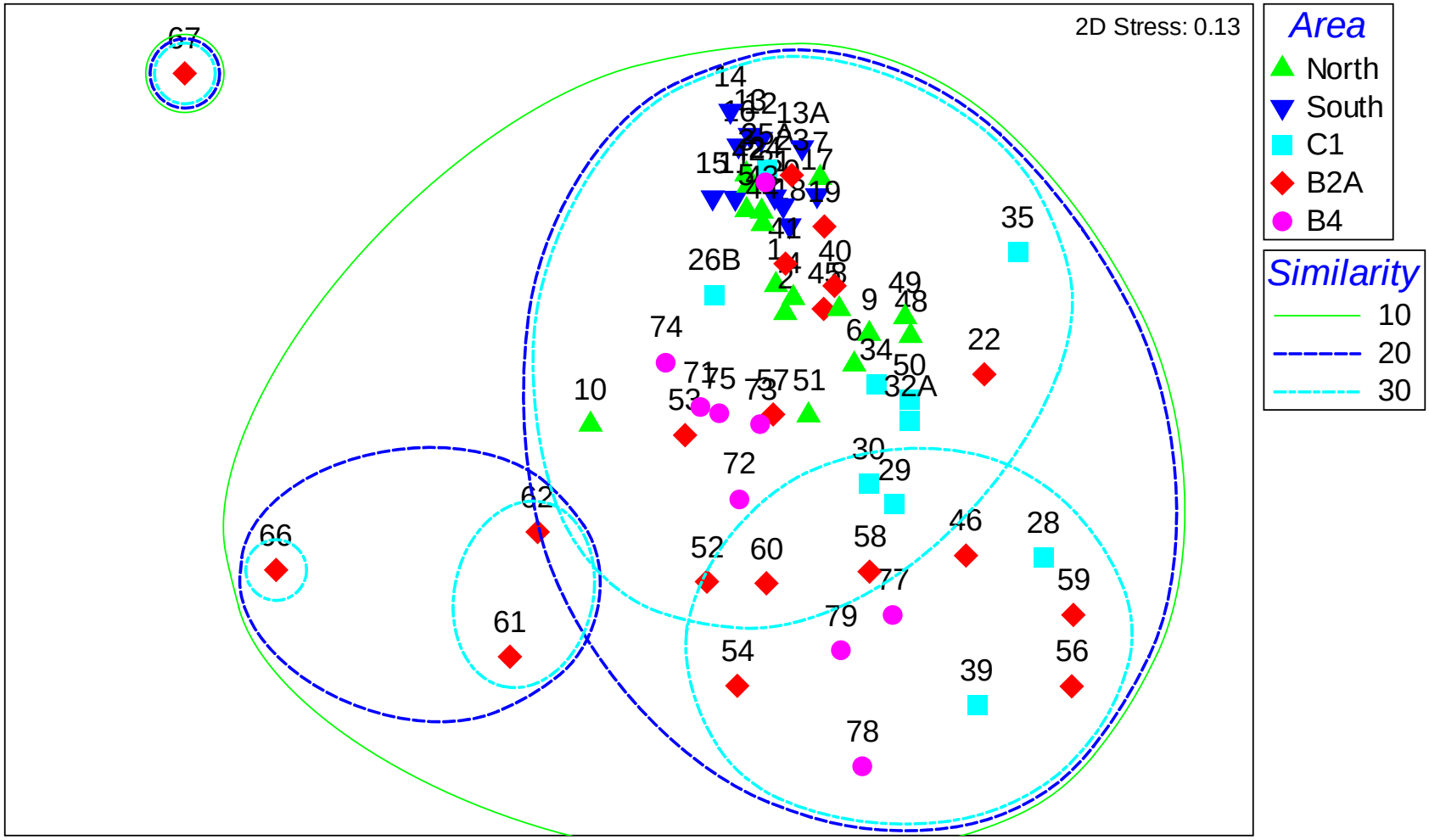

Figure 8. Multidimensional scaling of stations based on abundance aggregated at the order level in samples. Stations with no organisms deleted from analysis. Stations groups based on a cluster analysis at community similarity levels of 10%, 20%, and 30%.

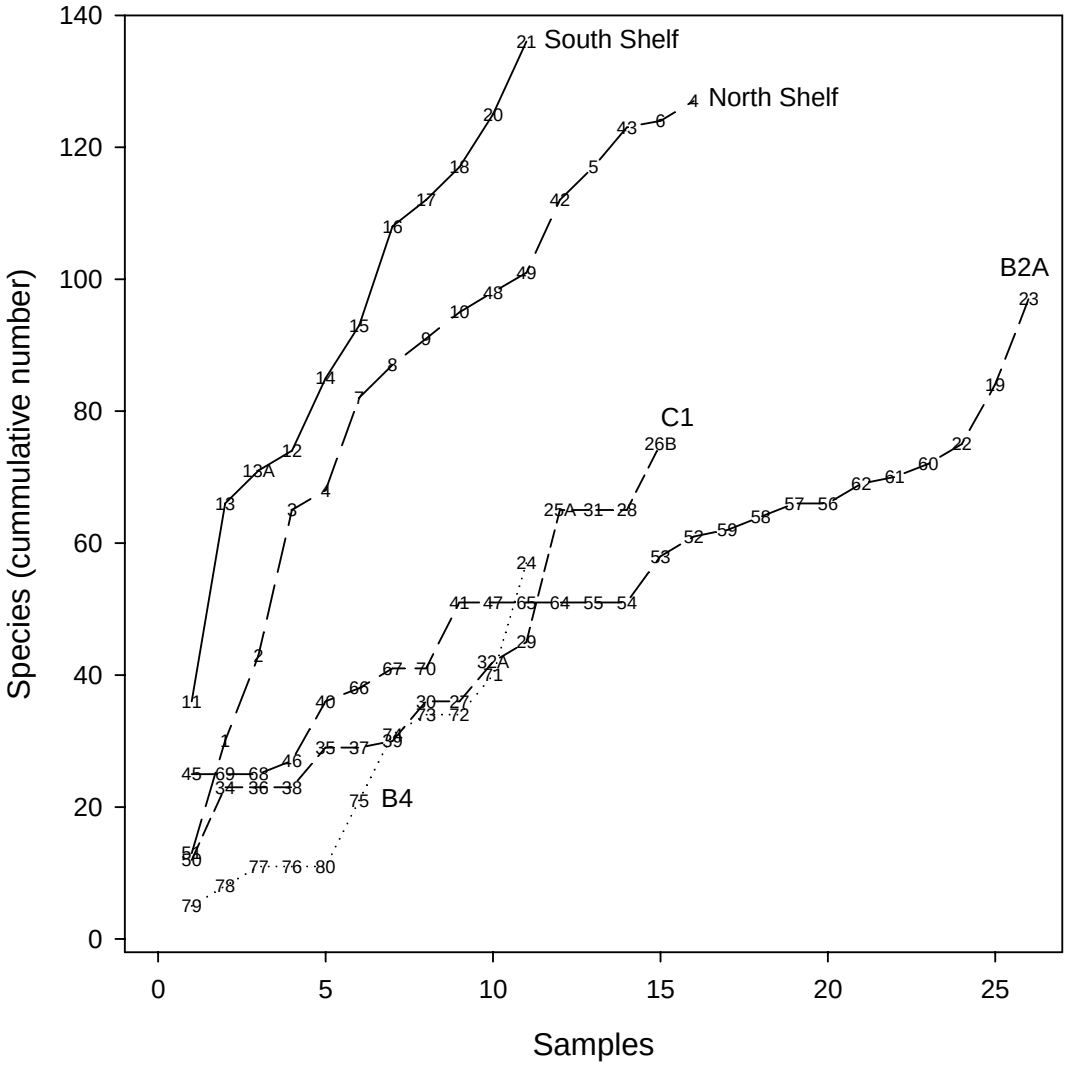

Figure 9. Species accumulation curves for all samples within areas. Symbols are sample numbers, which are ordered left-to-right geographically from northwest to southwest and from shallow to deep.

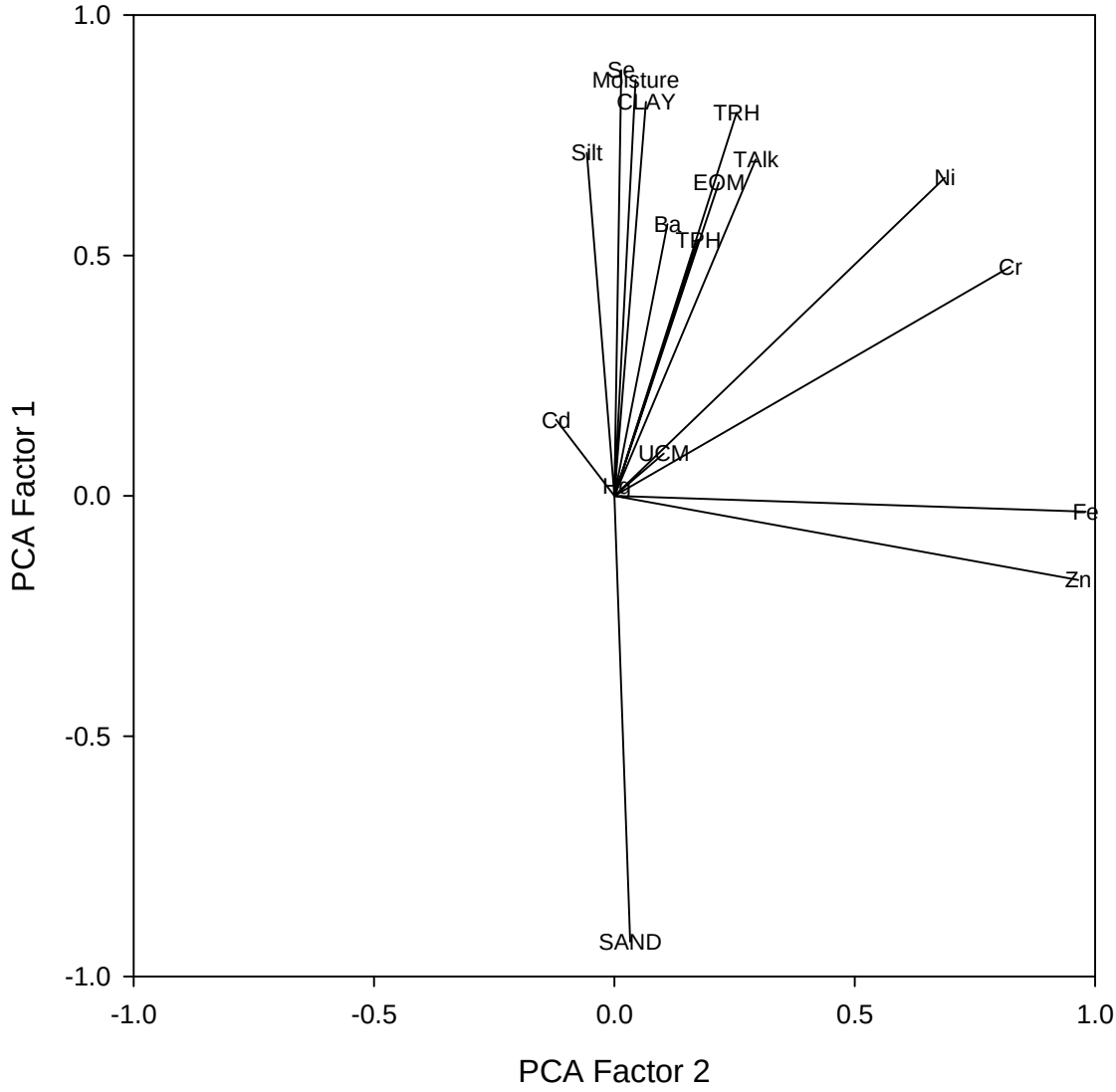

Figure 10. Principal components analysis (PCA) of environmental data. Vector loads of each environmental variable. Abbreviations: Ba=barium, Cd=cadmium, Cr=chromium, Fe=iron, Hg=mercury, Ni=nickel, Se=selenium,Zn=zinc, EOM=Extractable Organic Matter (ug/dry g), Talk=Total Alkanes, TPH=Total Petroleum Hydrocarbons, TRH=Total Resolved Hydrocarbons, and UCM=Unresolved Complex Mixture

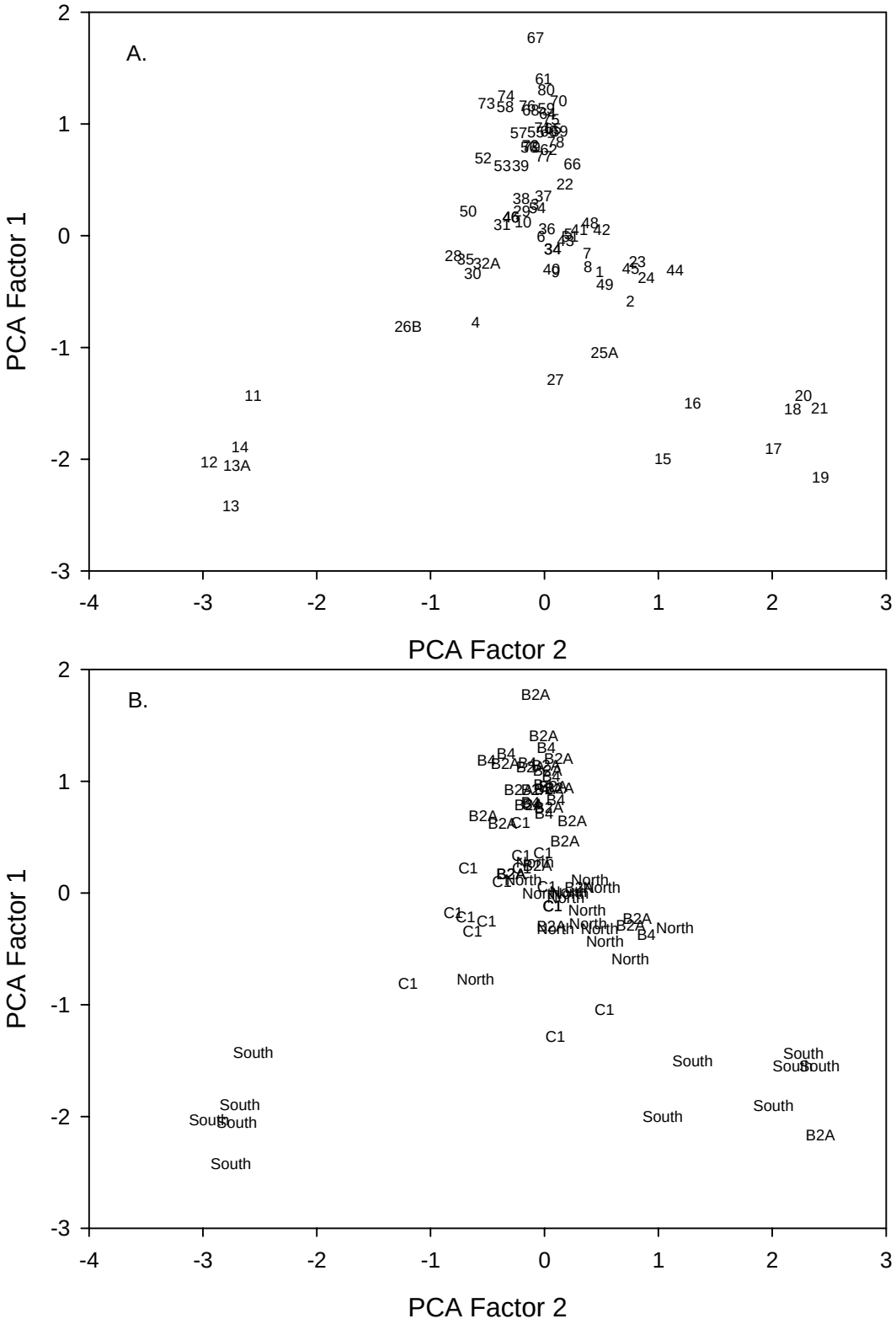

Figure 11. Principal components scores. A. Samples as labels. B. Areas as labels.