

Nitrogen and phosphorus recycling mediated by copepods and response of bacterioplankton community from three contrasting areas in the Western Tropical South Pacific (20°S)

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Supplementary information

Table S1: Epipelagic copepod composition used at each experiment.

Specie	LD A	LD B	LD C
<i>Haloptilus longicornis</i>	X		
<i>Pleuromamma sp</i>	X	X	X
<i>Acartia sp</i>	X		
<i>Saphirina sp</i>	X		
<i>Temora sp</i>		X	
<i>Miracia efferata</i>		X	
<i>Microsetella sp</i>	X	X	
<i>Copilia sp</i>		X	X
<i>Clausocalanus sp</i>	X	X	X
<i>Lucicutia sp</i>			X

Table S2: ANOVA followed by the Tukey's Honest Significant Difference (HSD), statistical comparison was performed on nutrients concentration in treatment with copepods and control. The mean of HSD is recorded at 95% confidence level with its associated P value for this comparison. Significant P values are bolded. NA indicates that no significant difference was found between treatments. No HSD test was performed for 'T0' (15 min observation), because of too few data.

LD A	T0	T1	T2	T3	T4
NH₄⁺					
Copepod-Control	HSD=0.1 p<0.0001	HSD=0.08 p=0.001	HSD=0.06 p=0.02	HSD=0.08 p<0.0001	HSD=0.003 p=0.9
NO₂⁻					
Copepod-Control	HSD=-0.01 p=0.99	HSD=0.006 p=0.98	HSD=-0.001 p=1	HSD=0.013 p=0.4	HSD=-0.008 p=0.93
NO₃⁻					
Copepod-Control	NA	NA	NA	NA	NA
PO₄³⁻					
Copepod-Control	HSD=0.003 p=1	HSD=0.05 p=0.72	HSD=0.09 p=0.1	HSD=0.006 p=0.99	HSD=-0.01 p=0.99
DON					
Copepod-Control	HSD=0.03 p=0.99	HSD=0.28 p=0.01	HSD=0.1 p=0.87	HSD=0.04 p=0.99	HSD=0.001 p=1
DOP					
Copepod-Control	NA	NA	NA	NA	NA
Bacterioplankton					
Copepod-Control	HSD=2.64 p=1	HSD=8.63 p=0.99	HSD=6.92 p=0.99	HSD=-33.6 p=0.55	HSD=17.82 p=0.97
LD B					
NH₄⁺					
Copepod-Control	HSD=0.07 p=0.1	HSD=0.02 p=0.99	HSD=0.01 p=0.99	HSD=0.16 P<0.001	HSD=0.09 p=0.006
NO₂⁻					
Copepod-Control	NA	NA	NA	NA	NA
NO₃⁻					
Copepod-Control	HSD=-0.05 p=0.99	HSD=0.003 p=0.99	HSD=0.37 p=0.02	HSD=-0.002 p=1	HSD=0.13 p=0.89
PO₄³⁻					
Copepod-Control	NA	NA	NA	NA	NA
DON					
Copepod-Control	NA	NA	NA	NA	NA
DOP					
Copepod-Control	NA	NA	NA	NA	NA
Bacterioplankton					
Copepod-Control	HSD=42.7	HSD=57.9	HSD=-307	HSD=-16.8	HSD=-61.4

	p=0.99	p=0.97	p=0.001	p=0.99	p=0.96
LD C					
NH₄⁺					
Copepod-Control	HSD=0.06 p=0.76	HSD=0.09 p=0.22	HSD=0.14 p=0.02	HSD=0.20 p<0.0001	HSD=0.29 p<0.0001
NO₂⁻					
Copepod-Control	NA	NA	NA	NA	NA
NO₃⁻					
Copepod-Control	HSD=0.21 p=0.66	HSD=0.09 p=0.99	HSD=0.004 p=1	HSD=0.35 p=0.10	HSD=0.48 p=0.009
PO₄³⁻					
Copepod-Control	NA	NA	NA	NA	NA
DON					
Copepod-Control	HSD=0.21 p=0.006	HSD=0.07 p=0.82	HSD=0.10 p=0.50	HSD=0.15 p=0.07	HSD=0.02 p=0.99
DOP					
Copepod-Control	NA	NA	NA	NA	NA
Bacterioplankton					
Copepod-Control	HSD=-25.2 p=0.99	HSD=-101 p=0.56	HSD=5.96 p=1	HSD=-80.1 p=0.81	HSD=-71.4 p=0.89

Table S3: Similarity percentage analysis (SIMPER) showing the contribution and taxonomic affiliation of OTUs explaining 60% of the dissimilarity between treatments through time for present and active bacterial community in both sampling date.

LD A				
Factors	Av. Diss	Phyla/Class	Diss/SD	Contribution (%)
Copepods & Control	15.84	Alteromonadales	0.69	7.15
		Rhodobacterales	1.49	5.62
		SAR11 clade	1.59	4.15
		Vibrionales	1.27	3.65
		Derived from SAR202 clade	1.13	3.23
		SubsectionIII	1.32	3.01
		SAR324 clade (Marine group B)	1.54	2.84
		Flavobacteriales	0.61	2.63
		SubsectionI	1.31	2.61
		Oceanospirillales	0.80	2.28
		Planctomycetales	0.62	1.95
		Derived from PAUC34f	1.18	1.57
		Rhodospirillales	1.33	1.56
		Cellvibrionales	0.75	1.49
		Derived from Subgroup 6	1.23	1.43
		Caulobacterales	1.30	1.32
		Derived from Marinimicrobia (SAR406 clade)	0.14	1.26
		Phycisphaerales	0.72	1.22
		Derived from Arctic97B-4 marine	1.15	1.14
		Rhizobiales	1.39	1.09
		Derived from Poribacteria	1.16	1.09
		Derived from Chloroplast	0.81	0.98
		Pseudomonadales	0.84	0.97
		Sphingobacteriales	1.47	0.94
		Myxococcales	0.87	0.89
		E01-9C-26 marine group	1.35	0.86
		Puniceicoccales	1.35	0.86
		Nitrospinales	0.95	0.82
		Nitrospirales	1.62	0.81
		Cytophagales	0.92	0.78
LD B				
Copepods & Control	9.50	Alteromonadales	1.16	6.53
		Caulobacterales	0.58	5.47
		SAR11 clade	1.77	5.18
		Rhodobacterales	0.78	3.69
		SubsectionI	1.88	3.32
		Vibrionales	0.91	2.98
		Pseudomonadales	1.05	1.83
		Oceanospirillales	1.28	1.60
		Cellvibrionales	0.78	1.45

Derived from Poribacteria	4.13	1.44
Derived from ARKICE-90	1.62	1.36
SAR324 clade(Marine group B)	1.26	1.34
Sphingomonadales	0.25	1.30
Desulfobacterales	1.74	1.19
Hydrogenophilales	9.87	1.15
Acidimicrobiales	1.74	1.14
Chlorobiales	1.37	1.14
Campylobacterales	1.44	1.13
UnknownOrder	1.19	1.13
Acanthopleuribacterales	1.67	1.05
Chromatiales	1.38	1.03
MB11C04 marine group	3.00	1.02
Derived from Marinimicrobia (SAR406 clade)	0.82	1.01
Rhodospirillales	0.96	0.94
Phycisphaerales	1.41	0.93
Kordiimonadales	0.94	0.91
NB1-j	4.36	0.90
Bacillales	1.35	0.89
A714019	1.84	0.88
Derived from Chloroplast	1.09	0.88
Derived from OPB35 soil group	1.21	0.86
Rhizobiales	1.86	0.85
Chlamydiales	1.40	0.85
Derived from TK10	1.02	0.83
Puniceococcales	1.22	0.83
Bdellovibrionales	1.56	0.79
Aeromonadales	1.09	0.79

LD C				
Copepods & Control	18.37	Alteromonadales	1.75	8.94
		Vibrionales	1.24	8.66
		Oceanospirillales	1.46	7.92
		SAR11 clade	1.20	7.61
		SubsectionI	1.77	4.12
		Derived from Marinimicrobia (SAR406 clade)	1.59	2.89
		Caulobacterales	1.11	2.87
		Acidimicrobiales	2.16	2.37
		Rhodospirillales	3.65	2.17
		Rhodobacterales	0.82	2.16
		SAR324 clade (Marine group B)	1.54	1.77
		Rhizobiales	2.05	1.70
		Sphingomonadales	1.97	1.16
		Derived from ML635J-21	1.45	1.13
		Rickettsiales	1.21	1.10

Pseudomonadales	1.68	1.04
Rhizobiales	1.50	1.03
Burkholderiales	0.95	0.99
Micrococcales	0.57	0.97

Table S4: Consumption and production rates obtained in the treatment incubated with copepods. The turnover rates were obtained for each compound studied between incubation times and were estimated using an end-point approach. A positive value indicates a net accumulation and negative values indicates a net consumption of nutrient.

Period of incubation	NH ₄ ⁺ (μmol L ⁻¹ h ⁻¹)	NO ₃ ⁻ (μmol L ⁻¹ h ⁻¹)	NO ₂ (μmol L ⁻¹ h ⁻¹)	PO ₄ ³⁻ (μmol L ⁻¹ h ⁻¹)	DON (μmol L ⁻¹ h ⁻¹)	DOP (μmol L ⁻¹ h ⁻¹)	
LD A	T ₀ -T ₁	0.004 ± 0.117	0.016 ± 0.031	0.013 ± 0.015	0.035 ± 0.049	4.03 ± 5.02	0.68 ± 0.84
	T ₁ -T ₂	-0.003 ± 0.045	0.005 ± 0.077	-0.013 ± 0.014	-0.063 ± 0.129	-3.62 ± 4.82	-0.28 ± 0.54
	T ₂ -T ₃	0.028 ± 0.027	0.015 ± 0.027	-0.007 ± 0.008	-0.142 ± 0.035	0.20 ± 0.04	0.03 ± 0.20
	T ₃ -T ₄	-0.053 ± 0.008	-0.036 ± 0.045	-0.008 ± 0.005	0.001 ± 0.001	0.11 ± 0.12	0.01 ± 0.01
LDB	T ₀ -T _{0.25}	0.331 ± 0.132	0.067 ± 0.050	-0.002 ± 0.006	-0.005 ± 0.017	-0.005 ± 0.37	0.01 ± 0.04
	T _{0.25} -T _{0.5}	-0.015 ± 0.045					
	T _{0.5} -T ₁	-0.095 ± 0.055	1.171 ± 0.910	0.001 ± 0.006	0.002 ± 0.029	-1.157 ± 1.429	0.02 ± 0.03
	T ₁ -T ₂	0.027 ± 0.027	-0.612 ± 0.460	-0.001 ± 0.006	0.003 ± 0.014	0.557 ± 0.206	-0.02 ± 0.04
	T ₃ -T ₄	0.031 ± 0.021	0.110 ± 0.162	-0.011 ± 0.016	0.034 ± 0.054	-0.010 ± 0.117	0.02 ± 0.02
LD C	T ₀ -T _{0.25}	0.056 ± 0.202	0.019 ± 0.318	0.011 ± 0.026	0.067 ± 0.067	-1.85 ± 1.18	0.001 ± 0.18
	T _{0.25} -T _{0.5}	0.043 ± 0.398					
	T _{0.5} -T ₁	0.117 ± 0.193	-0.143 ± 0.210	-0.009 ± 0.025	-0.042 ± 0.075	0.13 ± 0.84	-0.09 ± 0.16
	T ₁ -T ₂	0.061 ± 0.050	0.040 ± 0.079	-0.003 ± 0.004	0.013 ± 0.012	-0.19 ± 0.29	-0.01 ± 0.02
	T ₃ -T ₄	0.036 ± 0.041	0.256 ± 0.081	-0.001 ± 0.003	0.000 ± 0.005	0.02 ± 0.13	-0.001 ± 0.004

Table S5: Consumption and production rates obtained in the control (without copepods). The turnover rates were obtained for each compound studied between incubation times and were estimated using an end-point approach. A positive value indicates a net accumulation and negative values indicates a net consumption of nutrient.

Period of incubation	NH ₄ ⁺ (μmol L ⁻¹ h ⁻¹)	NO ₃ ⁻ (μmol L ⁻¹ h ⁻¹)	NO ₂ (μmol L ⁻¹ h ⁻¹)	PO ₄ ³⁻ (μmol L ⁻¹ h ⁻¹)	DON (μmol L ⁻¹ h ⁻¹)	DOP (μmol L ⁻¹ h ⁻¹)	
LD A	T ₀ -T ₁	0.040 ± 0.004	-0.054 ± 0.114	-0.004 ± 0.002	-0.061 ± 0.114	-0.01 ± 0.88	0.073 ± 0.123
	T ₁ -T ₂	0.041 ± 0.027	0.143 ± 0.036	0.005 ± 0.001	-0.140 ± 0.095	-0.60 ± 1.26	0.142 ± 0.089
	T ₂ -T ₃	-0.046 ± 0.009	-0.111 ± 0.111	-0.022 ± 0.001	-0.023 ± 0.019	0.55 ± 0.39	0.036 ± 0.034
	T ₃ -T ₄	-0.014 ± 0.003	-0.016 ± 0.038	0.001 ± 0.009	0.008 ± 0.008	0.32 ± 0.04	-0.009 ± 0.009
LDB	T ₀ -T _{0.5}	0.143 ± 0.011	-0.094 ± 0.076	0.009 ± 0.016	0.027 ± 0.038	0.323 ± 0.207	-0.02 ± 0.08
	T _{0.5} -T ₁	0.086 ± 0.032					
	T ₁ -T ₂	-0.121 ± 0.098	0.129 ± 0.004	0.005 ± 0.035	0.016 ± 0.136	-0.519 ± 1.322	0.02 ± 0.06
	T ₃ -T ₄	-0.109 ± 0.018	-0.062 ± 0.025	-0.003 ± 0.004	-0.028 ± 0.040	-0.316 ± 0.593	-0.001 ± 0.09
	T ₄ -T ₅	0.103 ± 0.081	0.017 ± 0.024	0.001 ± 0.001	0.003 ± 0.004	0.244 ± 0.267	0.04 ± 0.01
LD C	T ₀ -T _{0.5}	-0.012 ± 0.057	-0.581 ± 0.344	-0.001 ± 0.005	0.047 ± 0.098	-0.03 ± 1.01	-0.04 ± 0.08
	T _{0.5} -T ₁	-0.025 ± 0.061					
	T ₁ -T ₂	0.029 ± 0.021	0.027 ± 0.086	-0.009 ± 0.005	-0.025 ± 0.072	-0.18 ± 0.72	0.03 ± 0.06
	T ₃ -T ₄	-0.005 ± 0.016	0.394 ± 0.261	0.005 ± 0.012	-0.007 ± 0.027	-0.46 ± 0.09	0.0003 ± 0.03
	T ₄ -T ₅	-0.009 ± 0.004	-0.159 ± 0.048	-0.006 ± 0.002	-0.002 ± 0.003	0.40 ± 0.15	0.004 ± 0.01

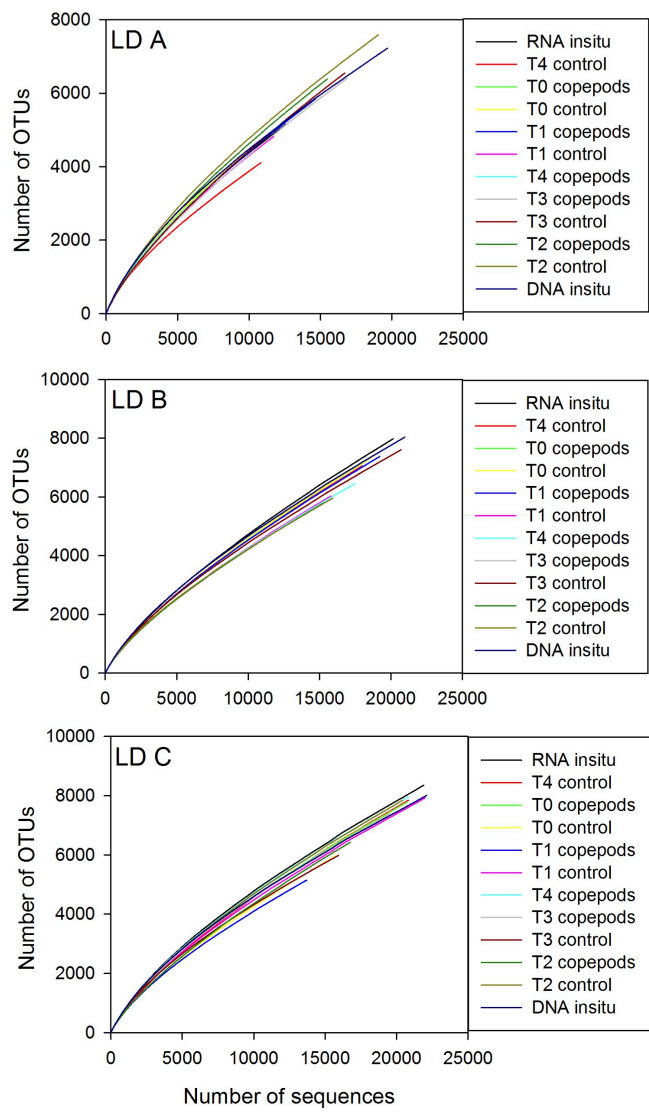


Figure S1: Rarefaction curves derived from classified total and active bacteria OTUs detected from the 16S rDNA and rRNA libraries generated from samples collected *in situ* and the following experimental incubation treatment and control.

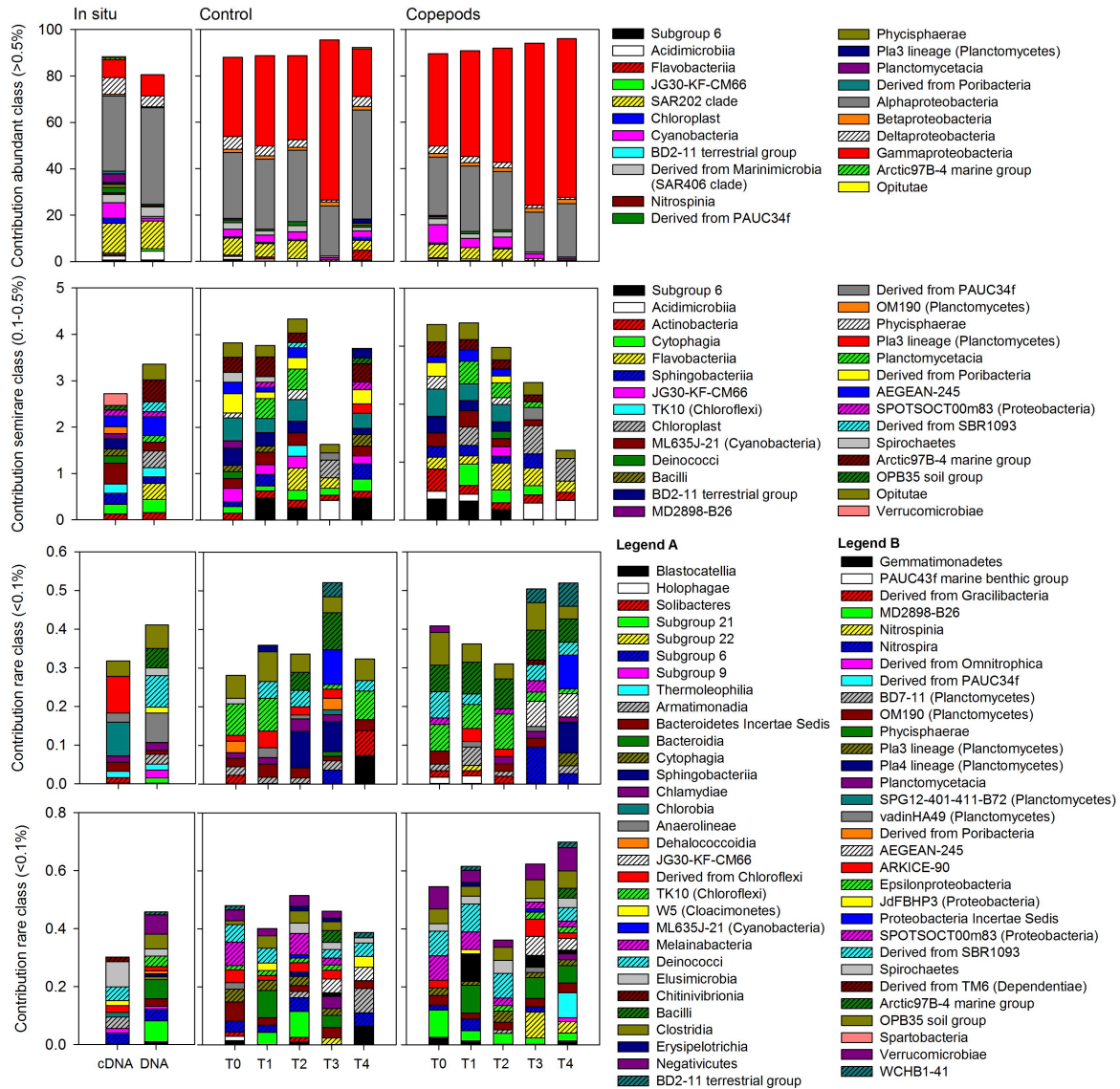


Figure S2: Contribution of total and active Classes classified according to their initial *in situ* contribution as abundant, semi-rare and rare in percentages (>0.5%, 0.1–0.5% and <0.1% of libraries, respectively), and their changes through the time of the experiment with copepods and control in LD A station experiment.

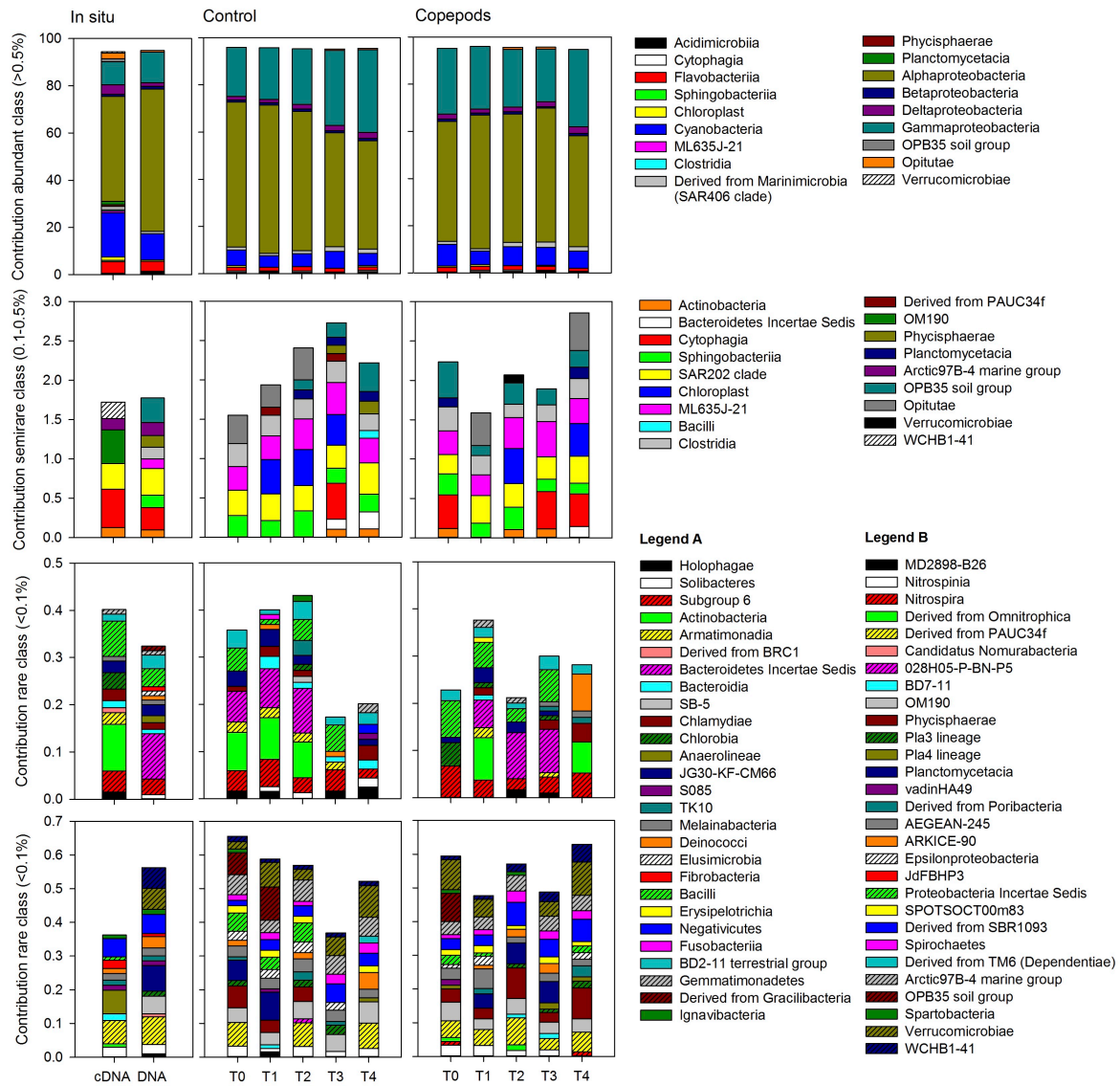


Figure S3: Contribution of total and active Classes classified according to their initial *in situ* contribution as abundant, semi-rare and rare in percentages (>0.5%, 0.1–0.5% and <0.1% of libraries, respectively), and their changes through the time of the experiment at the treatment with copepods and control in LD B station experiment.

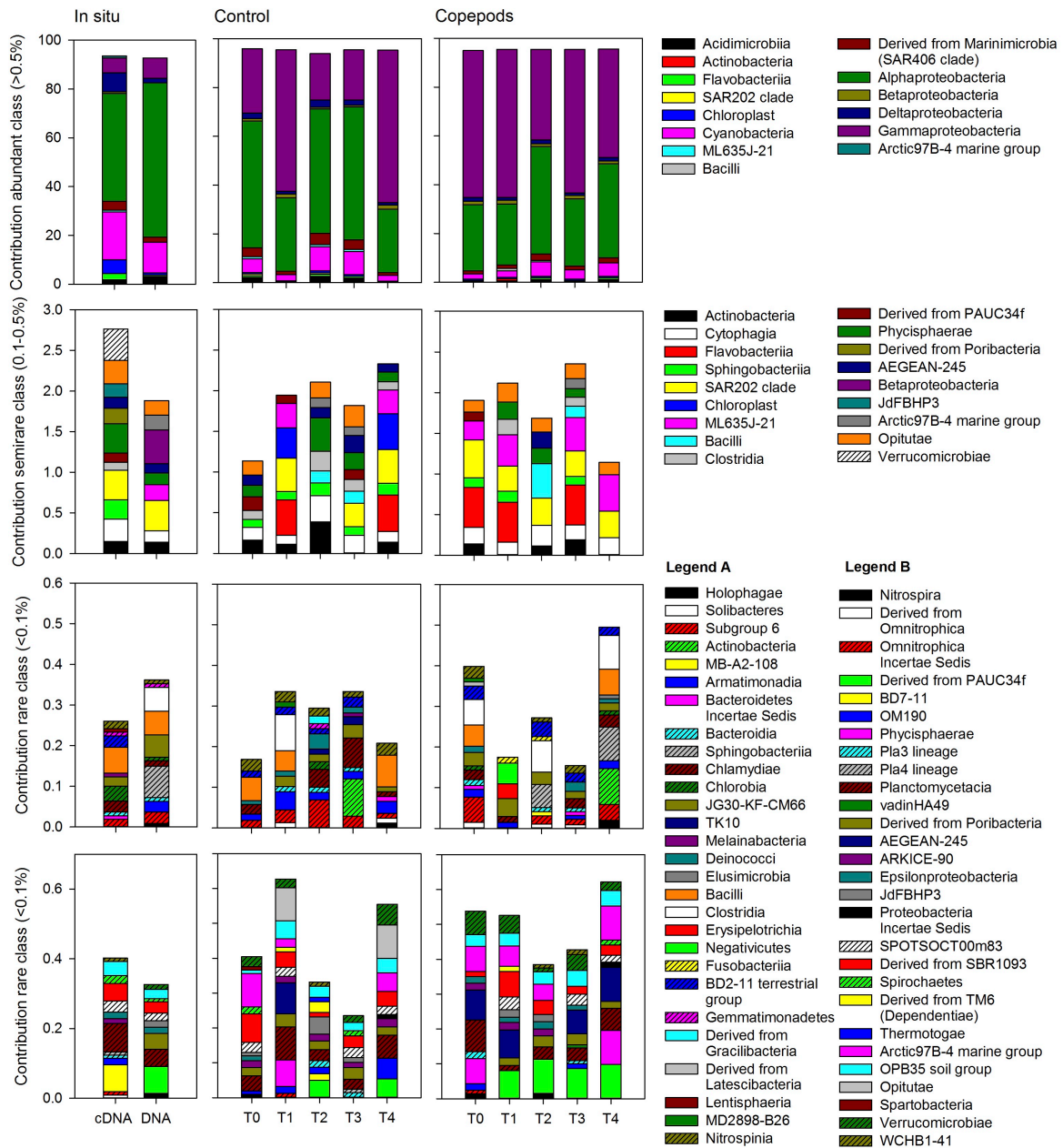


Figure S4: Contribution of total and active Classes classified according to their initial *in situ* contribution as abundant, semi-rare and rare in percentages (>0.5%, 0.1–0.5% and <0.1% of libraries, respectively), and their changes through the time of the experiment at the treatment with copepods and control in LD C station experiment.