

Ecological coherence of diversity patterns derived from classical fingerprinting and Next Generation Sequencing techniques

Angélique Gobet, Antje Boetius, Alban Ramette

Supplementary tables

Table S1. Contribution of environmental parameters to the variation in data sets at different levels of resolution (different techniques, taxonomic assignation, PyroNoise correction, removal of rarer OTU).

Table S1. Contribution of environmental parameters to the variation in data sets at different levels of resolution (different techniques, taxonomic assignment, PyroNoise correction, removal of rarer OTU).

Resolution levels ^a	Total number of sequences or phylotypes ^b	R ² ^c	Individual factor contribution ^c													Cell abundance	
			Salinity	Pigments	Nutrients					Enzymes							
					SiO ₂	PO ₄	NO ₂	NO ₃	NH ₄	Chit	α-glu	β-glu	Lip	Amin	Phos		
ARISA	306	51%***		-0.8	0.2	-0.4	0.2	-0.6	0.4							-0.6	-0.8
Phylum	40,660	75%**	0.2	1	-0.6	0.2	-0.4	0.4	-0.6	0.6	0.8		0.2		0.8		0.9
Class	40,660	75%***	-0.2	-1	0.5	-0.2	0.4	-0.5	0.6	-0.6	-0.8		-0.2		-0.8		-0.9
Order	40,660	64%**	-0.1	-1	0.4	-0.3	0.4	-0.5	0.5	-0.6	-0.8		-0.2		-0.8		-0.9
Family	40,660	57%***	-0.1	-1	0.4	-0.3	0.3	-0.5	0.6	-0.6	-0.8		-0.2		-0.8		-0.9
Genus	40,660	51%***	-0.1	-1	0.4	-0.3	0.3	-0.5	0.6		-0.8		-0.1		-0.8		-0.9
OTU _{annotated}	40,660	14%***		-1												-0.8	-0.9
OTU _{Resident}	60,021	55%***	-0.1	-0.9	0.3	-0.3	0.3	-0.5	0.4	-0.6	-0.7		-0.1		-0.8		-0.9
OTU _{all}	197,684	17%***		-1												-0.8	-0.9
1%	195,707	18%***		-1												-0.8	-0.9
5%	187,799	20%***		-1												-0.8	-0.9
10%	177,915	27%***		-1	0.4	-0.3		-0.5								-0.8	-0.9
15%	168,029	36%***		-1	0.4	-0.3		-0.5			-0.7		-0.1		-0.8	-0.8	-0.9
20%	158,143	41%***		-1	0.4	-0.3		-0.5			-0.7		-0.1		-0.8	-0.8	-0.9
25%	148,258	46%***		-1	0.4	-0.3		-0.5			-0.7		-0.1		-0.8	-0.8	-0.9
30%	138,377	55%***	-0.1	-1	0.4	-0.3	0.3	-0.5	0.5		-0.7		-0.1		-0.8	-0.8	-0.9
35%	128,459	60%*	-0.1	-1	0.4	-0.3	0.3	-0.5	0.5	-0.6	-0.7	-0.6	-0.1	-0.8	-0.8	-0.8	-0.9
40%	118,590	63%*	-0.1	-1	0.4	-0.3	0.3	-0.5	0.5	-0.6	-0.7	-0.6	-0.1	-0.8	-0.8	-0.8	-0.9
45%	108,709	62%***	-0.1	-1	0.4	-0.3	0.3	-0.5	0.5	-0.6	-0.7	-0.6	-0.1	-0.8	-0.8	-0.8	-0.9
50%	98,762	63%*	-0.1	-1	0.4	-0.3	0.3	-0.5	0.5	-0.6	-0.7	-0.6	-0.2	-0.8	-0.8	-0.8	-0.9
55%	88,871	NS															
60%	78,951	NS															
65%	68,789	60%*		-0.9	0.3	-0.3	0.3	-0.5	0.4	-0.6	-0.7		-0.2		-0.7		-0.9
70%	58,637	55%*		0.9	-0.2	0.4	-0.2	0.5	-0.4	0.6	0.7		0.1		0.7		0.9
75%	49,110	52%*	0.3	0.8	-0.4	0.1	-0.4	0.3	-0.3	0.7	0.6		0.2		0.8		0.7
80%	38,299	39%***						0.5	-0.5	-0.7	-0.1						
85%	25,961	47%***			-0.4				-0.7	0.6					-0.1		

90%	16,852
95%	6,550
99%	0

PyroNoise _{3%}	123,431	20% ***	-1	-0.8	-0.9
PyroNoise _{0%}	123,431	19% ***	-1	-0.8	-0.9

^aData sets at several level of resolution: technical (ARISA vs. 454 MPTS), taxonomic assignation of 454 data set, several subsets of the OTU_{all} table (Cutoff levels defined based on the whole data set strategy (see Supplementary Fig. 1) and applied until samples were lost due to lack of sequences), and PyroNoise correction (at 3% and 0% sequence difference).

^bTotal number of sequences for 454 MPTS data sets and phylotypes for the ARISA data set.

^cAdjusted R² indicates the amount of variation explained by environmental parameters (salinity, pigments, nutrients, enzymes and cell abundance), their significance is indicated as NS (non significant), * (P ≤ 0.05), ** (P ≤ 0.01), and *** (P ≤ 0.001). Values were rounded to the first decimal.

^dOnly significant, standardized correlation coefficients to the first redundancy analysis (RDA) axis are indicated for each parameter.

Chl a, chlorophyll a; Pheo, Pheophytin; SiO₂, silicate; PO₄, phosphate; NO₂, nitrite; NO₃, nitrate; NH₄, ammonium; Chit, chitinase; α-glu, α-glucosidase; β-glu, β-glucosidase; Lip, lipase; Amin, aminopeptidase; Phos, phosphatase.