

Supplementary Material

Title:

Temporal succession of bacterial and archaeal communities in a Mediterranean high-mountain lake over the last 430 years using sedimentary DNA

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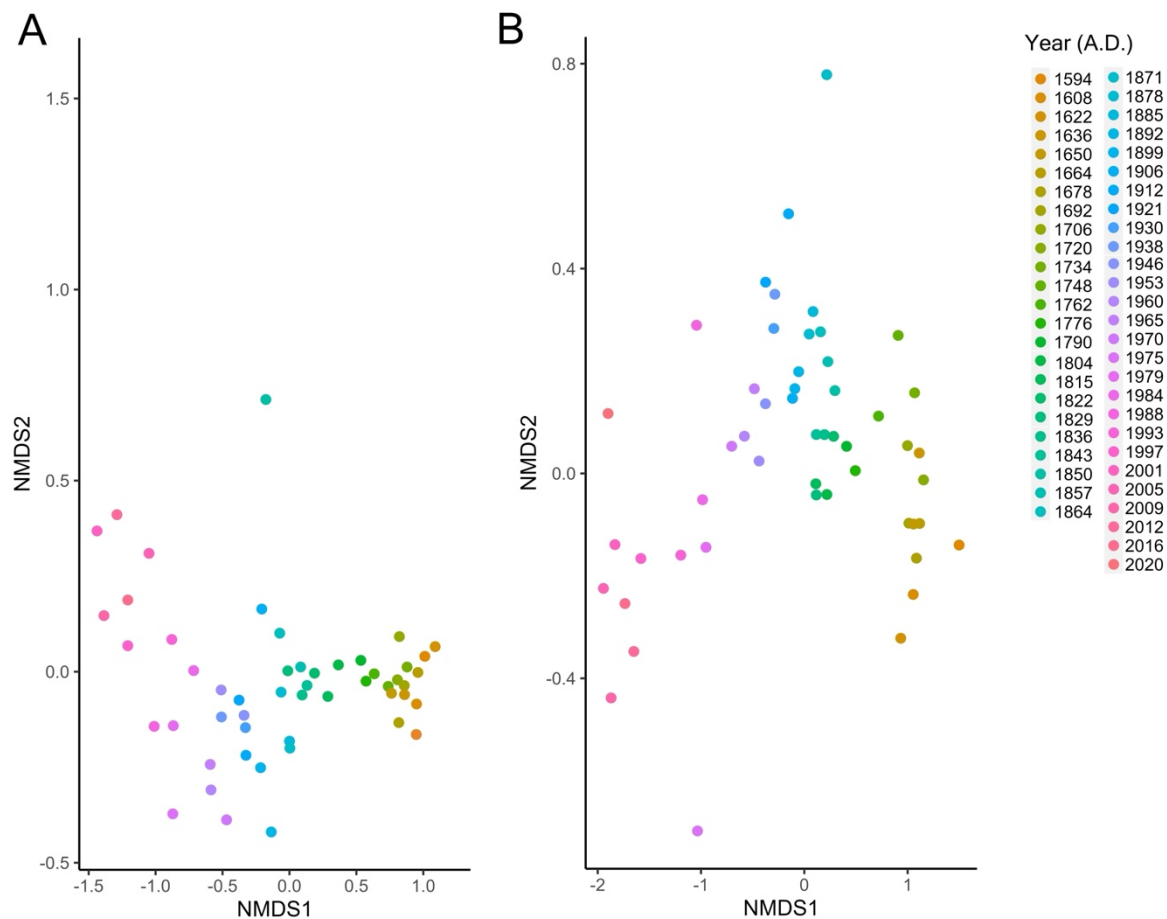
Supplementary Table S1. Primers used for quantification of total abundance of bacteria and archaea (16SB and 16SA, respectively) by qPCR (a). Bacterial and archaeal strains used for generation of qPCR standards are also included. qPCR conditions for the quantification of each of the target genes (b).

a.

Primer	Primer sequence (5'-3')	Target gene	Strains	Reference
341F	CCTACGGGAGGCAGCAG	16S rRNA Bacteria	<i>Pseudomonas putida</i> NCB957	Muyzer et al. (1993)
534R	ATTACCGCGGCTGCTGG			
Arch519F	CAGCCGCCGCGGTAA	16S rRNA Archaea	Genomic clone 29i4	Herfort et al. (2009)
Arch915R	GTGCTCCCCCGCCAATTCCT			

b.

	16SB	16SA
Stage 1: 1 cycle	3 min at 95 °C	7 min at 95 °C
Stage 2: 40 cycles	15s at 95 °C	30s at 95 °C
	30s at 60°C	30s at 65 °C
	30s at 72 °C	30s at 72 °C
Stage 3: 1 cycle	10 min at 72 °C	10 min at 72 °C



Supplementary Fig. S1. Non-metric Multidimensional Scaling (NMDS) ordination plots of archaeal (A) and bacterial (B) communities based on Bray–Curtis dissimilarity matrices. Each point represents a sediment layer, colored by sampling year. The NMDS illustrates temporal turnover in microbial community composition throughout the sediment core of Borreguil Lake.

Supplementary Table S2. Performance metrics (R^2 and RMSE) of the Random Forest (RF) models shown in Figures 7 and 8, used to predict microbial parameters based on paleo-environmental and climate variables. The table reports the coefficient of determination (R^2), which indicates the proportion of variance in the response variable explained by the model, and the root mean square error (RMSE), which measures the average magnitude of prediction errors (i.e., the standard deviation of the residuals). Lower RMSE values and higher R^2 values indicate better model performance.

Metric	Period	Domain	R^2	RMSE
Abundance	1594–1905	Archaea	0.68	0.14
Abundance	1594–1905	Bacteria	0.76	0.11
ASV richness	1594–1905	Archaea	0.64	0.18
ASV richness	1594–1905	Bacteria	0.71	0.13
Shannon index	1594–1905	Archaea	0.58	0.19
Shannon index	1594–1905	Bacteria	0.66	0.17
Beta diversity (DCA1)	1594–1905	Archaea	0.74	0.12
Beta diversity (DCA1)	1594–1905	Bacteria	0.81	0.09
Abundance	1906–2020	Archaea	0.69	0.13
Abundance	1906–2020	Bacteria	0.79	0.10
ASV richness	1906–2020	Archaea	0.62	0.16
ASV richness	1906–2020	Bacteria	0.72	0.12
Shannon index	1906–2020	Archaea	0.55	0.20
Shannon index	1906–2020	Bacteria	0.67	0.15
Beta diversity (DCA1)	1906–2020	Archaea	0.73	0.11
Beta diversity (DCA1)	1906–2020	Bacteria	0.84	0.08

References

- Herfort L, Kim JH, Coolen MJL, Abbas B, Schouten S, Herndl G, Damsté JSS (2009) Diversity of archaea and detection of crenarchaeotal amoA genes in the rivers Rhine and Têt. *Aquat Microb Ecol* 55:189–201
- Muyzer, G., De Waal, E.C., Uitterlinden, A.G., 1993. Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction amplified genes coding for 16S rRNA. *Appl. Environ. Microbiol.* 59, 695-700. <https://doi.org/10.1128%2Faem.59.3.695-700.1993>