SUPPLEMENTARY MATERIAL

Figure S1

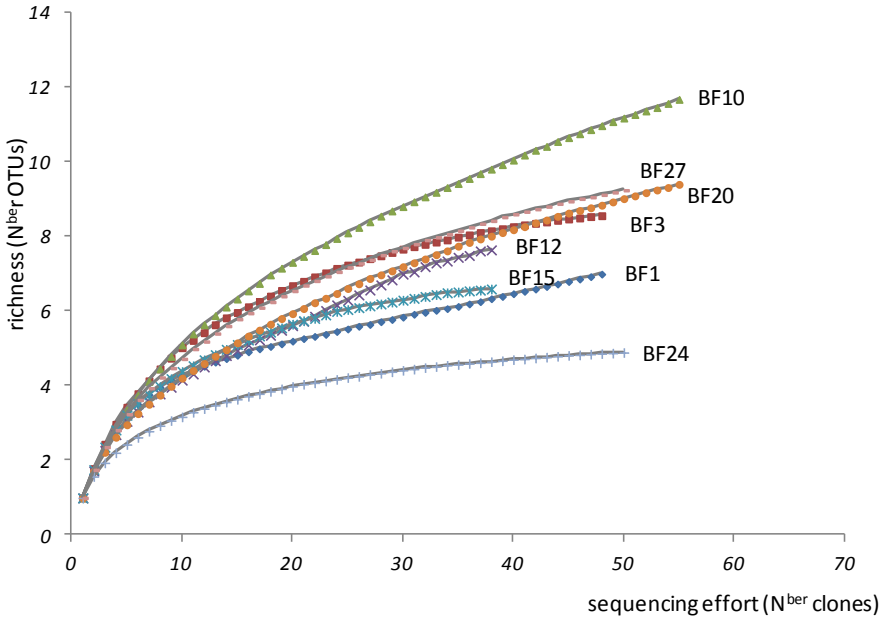


Figure S1. Rarefaction curves obtained for *Synechococcus* sequences (16S) from the 8 genetic libraries (BF1: 2008-2009, BF3: 2000-2001, BF10: 1991-1993, BF12: 1987-1988, BF15: 1981-1983, BF20: 1972-1973, BF24: 1956-1960, BF27: 1951-1952).

Table S1.

Table S1. UNIFRAC results: The grey area (left panel) corresponds to the distance matrix obtained from the comparison of each pair of samples. Bold underlined text denotes values in the upper quartile (i.e. most distant samples).
The white area (right panel) corresponds to the P-values obtained by comparing each sample to each other sample. All P-values have been corrected for multiple comparisons by multiplying the calculated P-value by the number of comparisons made (Bonferroni correction). Bold text denotes significant P values (see level of significance below the table).

	BF1 *2008-2009*	**BF3** *2000-2001*	**BF10** *1991-1993*	**BF12** *1987-1988*	**BF15** *1981-1983*	**BF20** *1972-1973*	**BF24** *1956-1960*	**BF27** *1951-1952*
BF1		0.67	0.24	0.49	0.30	**0.05**	0.17	0.15
BF3	0.545		0.69	**0.07**	0.56	0.58	0.70	0.70
BF10	**<u>0.600</u>**	0.428		0.67	0.67	1.00	0.62	0.64
BF12	0.500	**<u>0.628</u>**	**<u>0.600</u>**		0.75	0.95	0.57	0.54
BF15	0.562	0.514	**<u>0.605</u>**	0.413		0.75	0.55	0.59
BF20	**<u>0.684</u>**	0.526	0.459	0.529	0.418		0.56	0.65
BF24	**<u>0.606</u>**	0.424	0.393	0.466	0.529	0.312		0.55
BF27	**<u>0.611</u>**	0.303	0.575	0.571	0.578	0.424	0,303	

P value significance (white right panel)
(< 0.001) Highly significant
(0.001-0.01) Significant
(0.01-0.05) Marginally significant
(0.05-0.1) Suggestive

Table S2:

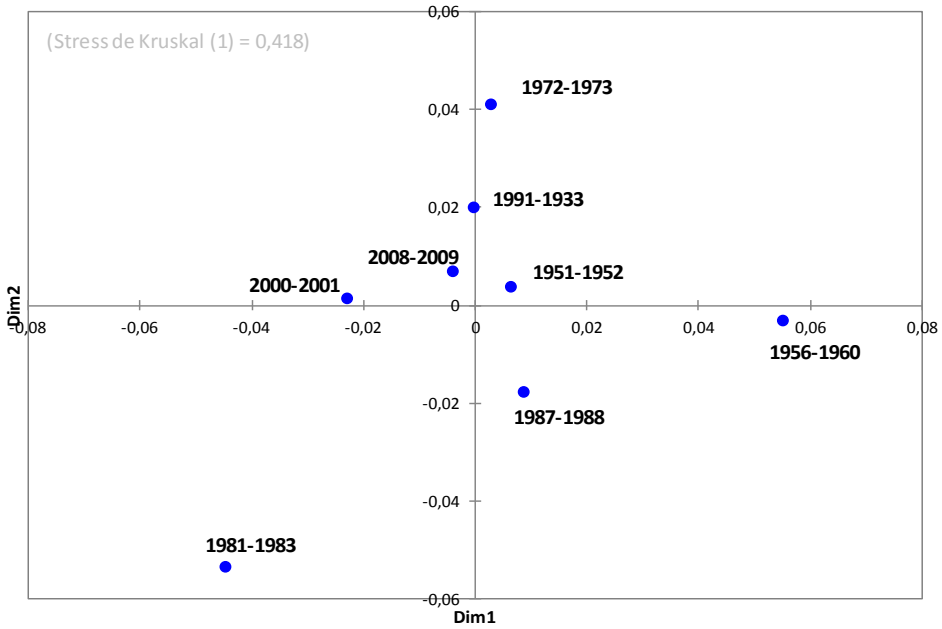
Comparison of cyanobacterial assemblage' pictures obtained from sequencing of different amplicons that varied in length (from ~100bp, to ~1500bp from 16s gene+ITS1 region). Results are expressed as proportion of sequences affiliated to the main genera (identified from sedimentary DNA originating from 4 sediment layers (BF1, BF3, BF10, BF24), by assignation by BLASTN with identity >95%)

		Chrooccocales				Nostocales		Oscillatoriales	
Sediment layer	*origin of amplicons*	Synechococcus	Microcystis	Chroococcus	others	Anabaena	Nostoc	Planktothrix	Leptolyngbia
BF1	16S ITS (< 100bp)	50	6	6	13			19	6
	16S ITS (~1500 bp)	72	10	4	1			10	1
		Chrooccocales				Nostocales		Oscillatoriales	
Sediment layer	*origin of amplicons*	Synechococcus	Microcystis	Chroococcus	others	Anabaena	Nostoc	Planktothrix	Leptolyngbia
BF10	16S ITS (< 100bp)	65	6		6	12	6		6
	16S ITS (~1500 bp)	83	7	4	3	3			
		Chrooccocales				Nostocales		Oscillatoriales	
Sediment layer	*origin of amplicons*	Synechococcus	Microcystis	Chroococcus	others	Anabaena	Nostoc/Aphanizomenon	Planktothrix	others
BF24	16S ITS (< 100bp)	73	7				13		7
	16S ITS (~1500 bp)	93	2	2	1		1		2

Figure S2.

Multidimensional scaling (MDS) plot of genetic differentiation estimates for the 8 sediment layers obtained from 16SrRNA sequences and from ITS region sequences.

16SrRNA



ITS region

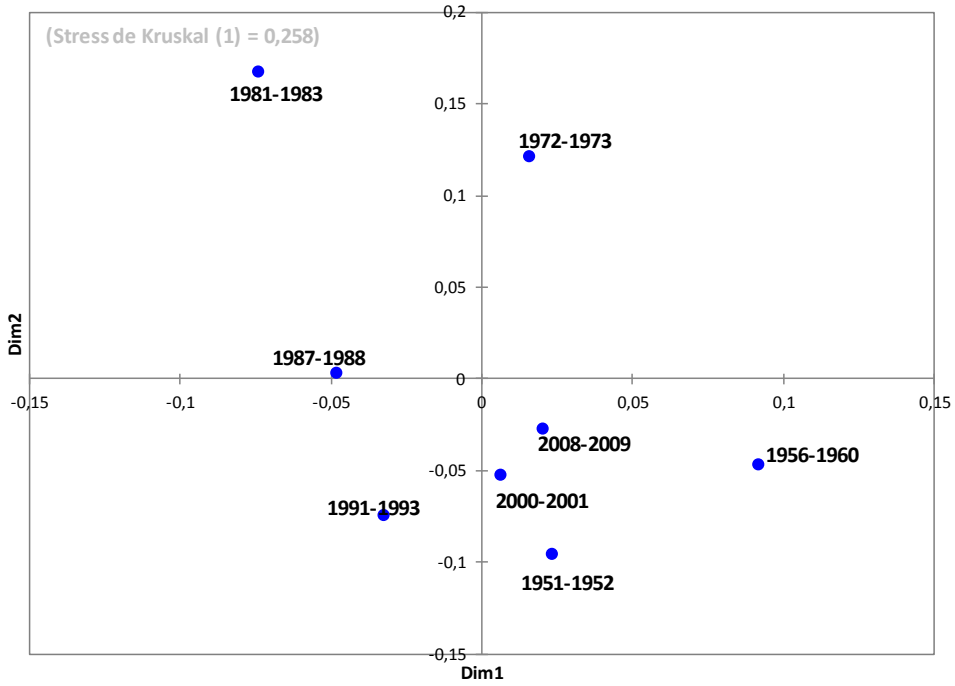


Figure S3. Sedimentary analysis of zeaxanthin and comparison with qPCR counts.

Sedimentary pigment analyses were performed from 32 sediment samples (corresponding to BF2 to BF34). The sediment samples (5 g of wet sediment) were freeze-dried and stored protected from light at -80°C. Pigment analyses were conducted in the dark on 550 mg of sediment, using ice-cold extraction solution (methanol + 0.5 mol L^{-1} ammonium acetate) (see detailed extraction protocol in Perga et al. (2010). The separation of pigments was performed on a Phenomenex Luna 5µ C18 column (250 x 4.60 mm) under a flow of three successive eluants. Flow rate was 1.0 mL min^{-1} and absorbance was read at the maximum absorbance wavelength of the targeted pigment. Peak areas were converted to concentrations by the external standard calibration method using commercially available pigment standards (Dionex Canada; DHI labproducts) for zeaxanthin (448 nm). Fossil pigment abundances were presented as dry sediment-specific concentrations (mg g^{-1} dry sediment).

The quantifications of zeaxanthin are presented with the corresponding qPCR counts obtained for total cyanobacteria (data for 32 samples presented on the graph below):