

Table S1. Spearman's rank correlation coefficients (r_s) between the dinoflagellate concentrations and the environmental variables obtained at Sfax and Carthage sites. Values in bold correspond to significant correlations ($P < 0.05$).

Variables	<i>Alexandrium minutum</i> (cells/L)	<i>Gymnodinium impudicum</i> (cells/L)
Temperature (°C)	-0.482	-0.200
Air temp Max(°C)	-0.536	-1.000
Air temp Min (°C)	-0.764	-0.400
Sea level pressure (hPa)	0.309	0.000
Wind Max (km/h)	0.074	-0.400
Wind Direction (°)	-0.535	-0.632
Day Length (h)	0.793	0.632
Sun hour	0.722	0.632
pH	-0.679	-0.400
Salinity (g/L)	0.112	0.316
NO ₂ ⁻ (μM)	0.000	0.400
NO ₃ ⁻ (μM)	-0.143	0.400
NH ₄ ⁺ (μM)	0.214	0.200
PO ₄ ³⁻ (μM)	0.703	0.800
Silicates (μM)	0.500	0.400
DIN (μM)1	-0.143	0.200

Table S2. Blast analysis on the dominant prokaryotic OTUs (>5% of total sequences in at least one sample) obtained from Sfax (Sidi Mansour, SM) and Carthage (CAR) sites during dinoflagellate blooms.

Closest cultivated relative retrieved from NCBI nucleotide database				% of sequences per sample			
OTUs	Species (Genbank accession number)	Taxonomy (Phylum or class; family)	Identity (%)	SM1	SM2	SM3	SM4
#2	<i>Halochromatium glycolicum</i> (NR_044896)	<i>Gammaproteobacteria</i> ; <i>Chromatiaceae</i>	96.15	20.15	28.99	10.35	0.91
#5	<i>Rhodovulum adriaticum</i> (NR_043404)	<i>Alphaproteobacteria</i> ; <i>Rhodobacteraceae</i>	99.53	18.83	0.75	0.65	0.14
#328	<i>Halochromatium glycolicum</i> (NR_044896)	<i>Gammaproteobacteria</i> ; <i>Chromatiaceae</i>	96.25	8.58	6.25	4.32	0.28
#8596	<i>Halochromatium glycolicum</i> (NR_044896)	<i>Gammaproteobacteria</i> ; <i>Chromatiaceae</i>	96.03	3.72	5.84	1.96	0.18
OTUs	Species (Genbank accession number)	Taxonomy	Identity (%)	CAR1	CAR2	CAR3	CAR4
#1	<i>Candidatus Pelagibacter</i> sp. HIMB1321 (LT840186)	<i>Alphaproteobacteria</i> ; <i>Pelagibacteraceae</i>	99.29	12.77	21.43	13.54	12.95
#7	<i>Candidatus Thalassoarchaea mediterranii</i> (KP211789)	<i>Candidatus Thermoplasmatota</i> ; <i>Candidatus Thalassoarchaeaceae</i>	86.55	5.79	2.23	4.23	5.98
#8	<i>Pelagibacterales</i> bacterium LSUCC0245 (KU382423)	<i>Alphaproteobacteria</i> ; <i>Pelagibacteraceae</i>	99.53	3.00	5.73	3.30	2.96