

**Isotopic compositions of Copper and Zinc in plankton from the Mediterranean Sea
(MERITE-HIPPOCAMPE campaign): trophic transfer and impact of anthropogenic
inputs**

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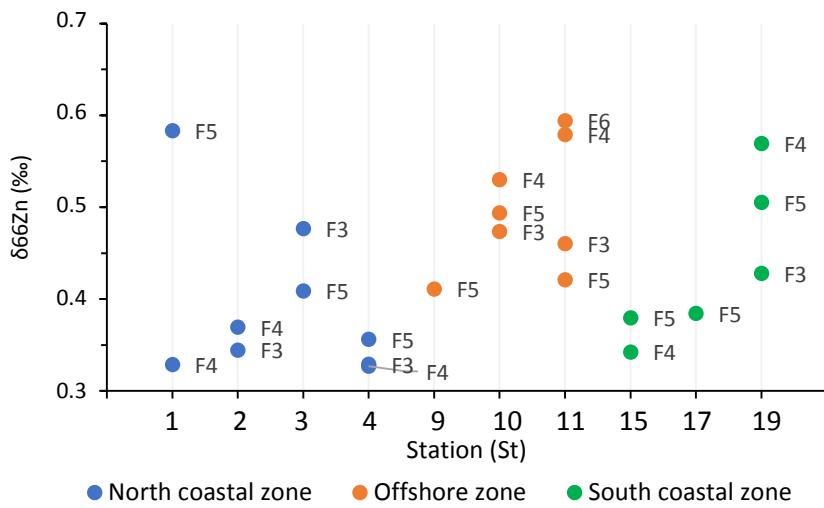
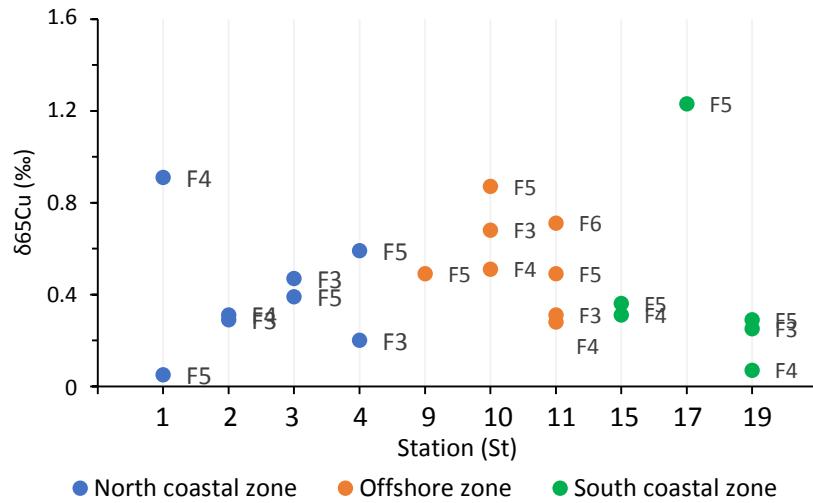


Fig. S1: Histograms showing variations of Cu and Zn isotopic compositions ($\delta^{65}\text{Cu}$ and $\delta^{66}\text{Zn}$) in plankton size fractions (F3: 60–200 μm , F4: 200–500 μm , F5: 500–1000 μm and F6: 1000–2000 μm) per stations (St1-4, St9-11, St15, St17 and St19). Values are colored according to geographical zones: the northern coastal zone (blue), the offshore zone (red) and the southern coastal zone (green).

Table S1: Spearman correlation matrix performed using $\delta^{65}\text{Cu}$ and $\delta^{66}\text{Zn}$ and the abundance (or relative abundance) of bacterial, phytoplanktonic and zooplanktonic communities in three plankton size fractions (F3: 60–200 μm , F4: 200–500 μm and F5: 500–1000 μm) and the 10 stations (St1-4, St9-11, St15, St17 and St19) with in bold a statistical significance level higher than 95% ($p < 0.05$).

Variables	$\delta^{65}\text{Cu}$	$\delta^{66}\text{Zn}$	Nanoeukaryotes	Picoeukaryotes	Nauplii	Copepods	<i>Proteobacteria</i>	<i>Cyanobacteria</i>	<i>Bacteroidota</i>	<i>Actinobacteriota</i>	<i>Firmicutes</i>	<i>Planctomycetota</i>	<i>Verrucomicrobiota</i>	<i>Synechococcus</i>	Cryptophytes	Prokaryotes	<i>Prochlorococcus</i>	Crustacea
$\delta^{65}\text{Cu}$	1																	
$\delta^{66}\text{Zn}$	-0.364	1																
Nanoeukaryotes	-0.061	0.132	1															
Picoeukaryotes	-0.222	0.180	-0.510	1														
Nauplii	-0.190	-0.001	0.003	0.505	1													
Copepods	-0.347	0.162	0.063	0.356	0.803	1												
<i>Proteobacteria</i> *	0.107	-0.061	0.132	0.103	-0.036	-0.034	1											
<i>Cyanobacteria</i> *	-0.177	0.292	-0.207	0.221	0.136	0.029	-0.703	1										
<i>Bacteroidota</i> *	0.126	-0.163	-0.257	0.007	0.057	-0.003	-0.572	0.171	1									
<i>Actinobacteriota</i> *	0.185	-0.218	0.128	-0.455	-0.412	-0.555	-0.241	0.114	0.218	1								
<i>Firmicutes</i> *	-0.155	0.267	0.328	-0.232	-0.189	0.063	0.145	-0.206	-0.024	-0.274	1							
<i>Planctomycetota</i> *	-0.446	0.109	0.131	-0.110	0.171	0.303	-0.679	0.601	-0.043	-0.082	-0.033	1						
<i>Verrucomicrobiota</i> *	-0.056	0.214	-0.159	-0.021	-0.014	0.015	-0.741	0.638	0.563	-0.001	0.216	0.425	1					
<i>Synechococcus</i>	-0.110	-0.051	-0.001	0.472	0.186	0.055	0.722	-0.293	-0.579	-0.416	-0.191	-0.338	-0.658	1				
Cryptophytes	-0.169	-0.019	0.200	0.445	0.554	0.459	0.121	0.085	-0.356	-0.197	-0.405	0.140	-0.388	0.485	1			
Prokaryotes	0.073	-0.287	0.128	-0.112	0.051	0.037	0.617	-0.635	-0.497	0.126	-0.284	-0.314	-0.807	0.396	0.352	1		
<i>Prochlorococcus</i>	0.328	0.056	-0.166	0.172	-0.216	-0.203	0.501	-0.264	-0.606	-0.151	-0.299	-0.288	-0.489	0.495	0.154	0.430	1	
Crustacea	-0.084	-0.029	0.236	-0.230	-0.498	-0.403	-0.079	-0.055	0.239	0.316	0.184	-0.144	0.093	-0.115	-0.253	-0.301	-0.121	1

*Relative abundance of prokaryotic taxa obtained by 16S rRNA gene metabarcoding analysis.

Table S2: Spearman correlation matrix performed using $\delta^{65}\text{Cu}$ and $\delta^{66}\text{Zn}$ and the abundance (or relative abundance) of bacterial, phytoplanktonic and zooplanktonic communities in three plankton size fractions (F3: 60–200 μm , F4: 200–500 μm and F5: 500–1000 μm) of the northern coastal zone (St1 to St4) with in bold a statistical significance level higher than 95% ($p < 0.05$).

Variables	$\delta^{65}\text{Cu}$	$\delta^{66}\text{Zn}$	Nanoeukaryotes	Picoeukaryotes	Nauplii	Copepods	<i>Proteobacteria</i>	<i>Cyanobacteria</i>	<i>Bacteroidota</i>	<i>Actinobacteriota</i>	<i>Firmicutes</i>	<i>Planctomycetota</i>	<i>Verrucomicrobiota</i>	<i>Synechococcus</i>	Cryptophytes	Prokaryotes	<i>Prochlorococcus</i>	Crustacea
$\delta^{65}\text{Cu}$	1																	
$\delta^{66}\text{Zn}$	-0.428	1																
Nanoeukaryotes	-0.247	-0.304	1															
Picoeukaryotes	0.305	0.327	-0.988	1														
Nauplii	0.131	-0.541	0.758	-0.740	1													
Copepods	0.145	-0.552	0.514	-0.468	0.817	1												
<i>Proteobacteria</i> *	0.329	0.350	-0.122	0.206	-0.190	0.000	1											
<i>Cyanobacteria</i> *	-0.107	0.169	0.206	-0.262	0.298	-0.064	-0.345	1										
<i>Bacteroidota</i> *	-0.277	-0.089	-0.122	0.094	0.183	0.135	-0.760	0.273	1									
<i>Actinobacteriota</i> *	-0.174	-0.034	-0.356	0.346	-0.348	-0.200	-0.462	-0.055	0.607	1								
<i>Firmicutes</i> *	0.004	0.804	-0.674	0.693	-0.657	-0.592	0.491	-0.047	-0.149	-0.069	1							
<i>Planctomycetota</i> *	-0.263	-0.216	0.262	-0.271	-0.047	-0.071	-0.273	-0.556	-0.069	-0.113	-0.265	1						
<i>Verrucomicrobiota</i> *	0.085	0.132	-0.262	0.243	-0.075	-0.235	-0.505	0.702	0.556	0.505	0.033	-0.491	1					
<i>Synechococcus</i> *	-0.247	-0.304	1.000	-0.988	0.758	0.514	-0.122	0.206	-0.122	-0.356	-0.674	0.262	-0.262	1				
Cryptophytes	-0.257	-0.313	0.988	-0.964	0.767	0.569	-0.112	0.140	-0.056	-0.262	-0.683	0.243	-0.271	0.988	1			
Prokaryotes	-0.324	-0.346	0.964	-0.952	0.758	0.578	-0.187	0.131	0.037	-0.159	-0.711	0.234	-0.262	0.964	0.988	1		
<i>Prochlorococcus</i> *	0.095	-0.047	0.337	-0.205	0.351	0.523	0.300	-0.356	0.075	0.159	-0.187	-0.009	-0.187	0.337	0.458	0.446	1	
Crustacea	0.024	0.067	-0.461	0.461	-0.463	-0.491	-0.398	-0.095	0.334	0.429	0.048	0.191	0.445	-0.461	-0.461	-0.154	1	

*Relative abundance of prokaryotic taxa obtained by 16S rRNA gene metabarcoding analysis.

Table S3: Spearman correlation matrix performed using $\delta^{65}\text{Cu}$ and $\delta^{66}\text{Zn}$ and the abundance (or relative abundance) of bacterial, phytoplanktonic and zooplanktonic communities in three plankton size fractions (F3: 60–200 μm , F4: 200–500 μm and F5: 500–1000 μm) of the offshore zone (St9 to St11) with in bold a statistical significance level higher than 95% ($p < 0.05$).

Variables	$\delta^{65}\text{Cu}$	$\delta^{66}\text{Zn}$	Nanoeukaryotes	Picoeukaryotes	Nauplii	Copepods	<i>Proteobacteria</i>	<i>Cyanobacteria</i>	<i>Bacteroidota</i>	<i>Actinobacteriota</i>	<i>Firmicutes</i>	<i>Planctomycetota</i>	<i>Verrucomicrobiota</i>	<i>Synechococcus</i>	Cryptophytes	Prokaryotes	<i>Prochlorococcus</i>	Crustacea
$\delta^{65}\text{Cu}$	1																	
$\delta^{66}\text{Zn}$	0.163	1																
Nanoeukaryotes	0.499	-0.417	1															
Picoeukaryotes	0.783	-0.126	0.500	1														
Nauplii	-0.104	-0.009	0.122	-0.486	1													
Copepods	-0.102	-0.034	0.120	-0.478	0.983	1												
<i>Proteobacteria</i> *	0.470	0.009	0.315	0.234	-0.095	-0.204	1											
<i>Cyanobacteria</i> *	-0.296	0.026	-0.153	-0.031	0.061	0.170	-0.930	1										
<i>Bacteroidota</i> *	-0.157	-0.120	-0.376	0.010	-0.234	-0.187	-0.461	0.183	1									
<i>Actinobacteriota</i> *	0.000	0.506	-0.448	0.081	-0.701	-0.732	0.304	-0.339	0.096	1								
<i>Firmicutes</i> *	-0.452	0.052	-0.122	-0.794	0.632	0.579	0.217	-0.252	-0.548	-0.235	1							
<i>Planctomycetota</i> *	-0.470	0.266	-0.397	-0.336	0.147	0.221	-0.739	0.843	-0.165	-0.148	0.165	1						
<i>Verrucomicrobiota</i> *	-0.365	-0.077	-0.234	-0.132	0.147	0.255	-0.983	0.948	0.426	-0.426	-0.252	0.722	1					
<i>Synechococcus</i>	0.499	-0.417	1.000	0.500	0.122	0.120	0.315	-0.153	-0.376	-0.448	-0.122	-0.397	-0.234	1				
Cryptophytes	0.499	-0.417	1.000	0.500	0.122	0.120	0.315	-0.153	-0.376	-0.448	-0.122	-0.397	-0.234	1.000	1			
Prokaryotes	0.499	-0.417	1.000	0.500	0.122	0.120	0.315	-0.153	-0.376	-0.448	-0.122	-0.397	-0.234	1.000	1.000	1		
<i>Prochlorococcus</i>	0.783	-0.126	0.500	1.000	-0.486	-0.478	0.234	-0.031	0.010	0.081	-0.794	-0.336	-0.132	0.500	0.500	0.500	1	
Crustacea	0.137	-0.419	0.160	0.479	-0.816	-0.842	0.359	-0.359	0.177	0.369	-0.450	-0.501	-0.359	0.160	0.160	0.160	0.479	1

*Relative abundance of prokaryotic taxa obtained by 16S rRNA gene metabarcoding analysis.

Table S4: Spearman correlation matrix performed using $\delta^{65}\text{Cu}$ and $\delta^{66}\text{Zn}$ and the abundance (or relative abundance) of bacterial, phytoplanktonic and zooplanktonic communities in three plankton size fractions (F3: 60–200 μm , F4: 200–500 μm and F5: 500–1000 μm) of the southern coastal zone (St15, St17 and St19) with in bold a statistical significance level higher than 95% ($p < 0.05$).

Variables	$\delta^{65}\text{Cu}$	$\delta^{66}\text{Zn}$	Nanoeukaryotes	Picoeukaryotes	Nauplii	Copepods	<i>Proteobacteria</i>	<i>Cyanobacteria</i>	<i>Bacteroidota</i>	<i>Actinobacteriota</i>	<i>Firmicutes</i>	<i>Planctomycetota</i>	<i>Verrucomicrobiota</i>	<i>Synechococcus</i>	Cryptophytes	Prokaryotes	<i>Prochlorococcus</i>	Crustacea
$\delta^{65}\text{Cu}$	1																	
$\delta^{66}\text{Zn}$	-0.745	1																
Nanoeukaryotes	-0.346	0.083	1															
Picoeukaryotes	-0.238	-0.238	-0.125	1														
Nauplii	-0.616	0.293	0.596	0.183	1													
Copepods	-0.940	0.731	0.388	0.183	0.569	1												
<i>Proteobacteria</i> *	0.327	0.073	-0.763	0.095	-0.402	-0.235	1											
<i>Cyanobacteria</i> *	-0.327	-0.218	0.620	0.191	0.385	0.200	-0.945	1										
<i>Bacteroidota</i> *	-0.118	0.100	0.763	-0.095	0.315	0.131	-0.436	0.273	1									
<i>Actinobacteriota</i> *	0.491	-0.418	0.286	-0.572	-0.175	-0.601	-0.473	0.345	0.309	1								
<i>Firmicutes</i> *	-0.664	0.573	0.405	0.191	0.542	0.844	0.000	-0.055	0.182	-0.709	1							
<i>Planctomycetota</i> *	-0.527	0.200	0.334	-0.095	0.350	0.514	-0.655	0.655	-0.255	-0.036	0.291	1						
<i>Verrucomicrobiota</i> *	-0.382	0.018	0.667	-0.191	0.489	0.392	-0.800	0.745	0.055	0.236	0.273	0.873	1					
<i>Synechococcus</i>	-0.238	-0.238	-0.125	1.000	0.183	0.183	0.095	0.191	-0.095	-0.572	0.191	-0.095	-0.191	1				
Cryptophytes	-0.429	-0.143	0.563	0.750	0.550	0.411	-0.429	0.572	0.429	-0.286	0.429	0.143	0.286	0.750	1			
Prokaryotes	0.405	-0.024	-0.969	-0.125	-0.642	-0.434	0.739	-0.667	-0.739	-0.143	-0.453	-0.310	-0.620	-0.125	-0.750	1		
<i>Prochlorococcus</i>	0.346	-0.083	-1.000	0.125	-0.596	-0.388	0.763	-0.620	-0.763	-0.286	-0.405	-0.334	-0.667	0.125	-0.563	0.969	1	
Crustacea	0.067	-0.315	0.150	0.600	-0.220	-0.037	0.000	0.114	0.458	-0.114	0.000	-0.458	-0.343	0.600	0.600	-0.300	-0.150	1

*Relative abundance of prokaryotic taxa obtained by 16S rRNA gene metabarcoding analysis.