**SUPPLEMENTARY MATERIAL**

**CAPTIONS -Supplementary Figures-**

Supplementary Figure S1. Average ± standard deviation (n=3) of chao1 index in each copper treatment (0, 0.01, 0.06, 0.32, 1.78 and 10 µM Cu) in function of number of sequences associated to 16S rRNA gene (A) or to the 18S rRNA gene (B).

Supplementary Figure S2. Concentration response curves for the 23 taxa identified as copper sensitive, their EC50s, standard deviation of EC50s. The taxonomy assignment of each taxon was showed in Suppl. Table 2.

Supplementary Table S1. Nominal and analysed copper concentrations (AVG ± SD; n=3) in the microcosms before and after the water renewals. The average copper concentration between before and after water renewals is also presented, as well as the percentage of analysed copper concentrations versus the nominal concentrations. Note: LoQ = 0.03 µM

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  |  |  |
| Nominal conc. (µM Cu) | Before water renewal  (µM Cu) | After water renewal  (µM Cu) | Average conc. before and after water renewals | |
| µM Cu | Analyzed as % of nominal conc. |
| 0 | < LoQ | < LoQ | < LoQ | - |
| 0.01 | < LoQ | < LoQ | < LoQ | - |
| 0.06 | 0.02 ± 0.002 | 0.02 ± 0.001 | 0.02 | 33 |
| 0.32 | 0.19 ± 0.07 | 0.15 ± 0.01 | 0.17 | 53 |
| 1.78 | 1.43 ± 0.51 | 1.61 ± 0.20 | 1.5 | 84 |
| 10 | 7.88 ± 1.84 | 8.26 ± 0.88 | 8.1 | 81 |

Sup Supplementary Table S2. The taxonomic affiliation, EC50 values (AVG) and their standard deviation (SD) in µM Cu, for the taxa classified as sensitive to Cu.

|  |  |  |  |
| --- | --- | --- | --- |
| Taxon | Taxa | EC50 (AVG) | (SD) |
| 1 | k\_\_Bacteria;p\_\_BRC1;c\_\_PRR-11;o\_\_;f\_\_ | 1.5 | 0.81 |
| 2 | k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_Cytophagia;o\_\_Cytophagales;f\_\_Cytophagaceae | 1.0 | 0.34 |
| 3 | k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_Flavobacteriia;o\_\_Flavobacteriales;Other | 1.9 | 2.5 |
| 4 | k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_Flavobacteriia;o\_\_Flavobacteriales;f\_\_Cryomorphaceae | 9.8 | 4.5 |
| 5 | k\_\_Bacteria;p\_\_Chlamydiae;c\_\_Chlamydiia;o\_\_Chlamydiales;Other | 1.8 | 0.74 |
| 6 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;Other;Other | 1.9 | 0.78 |
| 7 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;Other | 5.4 | 2.5 |
| 8 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rickettsiales;f\_\_ | 0.94 | 0.47 |
| 9 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;Other | 8.9 | 1.6 |
| 10 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_ | 8.5 | 3.7 |
| 11 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Erythrobacteraceae | 7.1 | 2.1 |
| 12 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Deltaproteobacteria;o\_\_Myxococcales;f\_\_Nannocystaceae | 0.91 | 0.37 |
| 13 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_OM60 | 6.0 | 1.1 |
| 14 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_HTCC2188;f\_\_HTCC2089 | 2.0 | 0.39 |
| 15 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Legionellales;f\_\_ | 1.6 | 0.63 |
| 16 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;Other | 9.5 | 1.1 |
| 17 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_ | 0.61 | 0.11 |
| 18 | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Marinicellales;f\_\_Marinicellaceae | 6.2 | 2.0 |
| 19 | k\_Eukarya; Archaeplastida(no rank);Rhodophyta(no rank);c\_\_Compsopogonophyceae;o\_\_Erythropeltidales;f\_\_Erythropeltidales\_X | 2.0 | 1.5 |
| 20 | k\_Eukarya; Hacrobia(no rank);Haptophyta(no rank);Pavlovophyceae(no rank);o\_\_Pavlovales;f\_\_Pavlovaceae | 1.2 | 3.7 |
| 21 | K\_Eukarya; p\_Stramenopiles; Stramenopiles\_X;\_c\_Labyrinthulea;f\_\_Thraustochytriales;g\_\_Thraustochytriaceae | 2.0 | 4.1 |
| 22 | k\_Eukarya; p\_Stramenopiles; c\_Stramenopiles\_X;MAST;MAST-3;MAST-3J | 1.8 | 0.95 |
| 23 | p\_\_Stramenopiles;Stramenopiles\_X;Other;Other;Other | 1.8 | 0.29 |

Supplementary table 3. The topological parameters of network. The topological parameters were computed by the “NetworkAnalyzer”(2.7 version) in Cytoscape 3.3.0.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | 0 | 0.01 | 0.06 | 0.32 | 1.78 | 10 |
| number of nodes | 517 | 529 | 525 | 506 | 453 | 402 |
| network heterogeneity | 1.505 | 1.497 | 1.511 | 1.652 | 1.804 | 1.782 |
| network density | 0.037 | 0.038 | 0.038 | 0.042 | 0.029 | 0.048 |
| muti-edge node pairs | 234 | 252 | 282 | 225 | 104 | 232 |
| number of neighbors | 19.277 | 20.276 | 19.73 | 21.083 | 13.223 | 19.139 |
| characteristic path length | 3.454 | 3.403 | 3.488 | 3.43 | 3.507 | 3.728 |
| network centralization | 0.231 | 0.26 | 0.24 | 0.302 | 0.277 | 0.368 |