SUPPLEMENTARY APPENDIX

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to:
Metagenomic analysis of the microbial community structure in protected wetlands in the Maritza River Basin

Ivan Iliev, Mariana Marhova, Sonya Kostadinova, Velizar Gochev, Marinela Tsankova, Angelina Ivanova, Galina Yahubyan, Vesselin Baev

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Supplemental data

Table S1. Pearson correlation matrix of the environmental parameters and alpha diversity indices established for the studied samples.

|       | obs_OTUs | ACE   | Chao1 | Shannon | Water | pH   | NH4-N | NO3-N | TN  | PO4-P | OM  |
|-------|----------|-------|-------|---------|-------|------|-------|-------|-----|-------|-----|
| obs_OTUs | 1        |       |       |         |       |      |       |       |     |       |     |
| ace    | .990**   | 1     |       |         |       |      |       |       |     |       |     |
| Chao1  | .992**   | .999**| 1     |         |       |      |       |       |     |       |     |
| Shannon| .906*    | .902* | .912* | 1       |       |      |       |       |     |       |     |
| Water  | -.210    | -.228 | -.228 | -.400   | 1    |      |       |       |     |       |     |
| pH     | .886*    | .916* | .920**| .955**  | -.440| 1    |       |       |     |       |     |
| NH4-N  | .0736    | .102  | .107  | .060    | -.484| .271 | 1     |       |     |       |     |
| NO3-N  | -.126    | -.089 | -.084 | .230    | -.843*| .262 | .337  | 1     |     |       |     |
| TN     | .259     | .330  | .328  | .352    | -.709 | .568 | .865* | .600*  | 1  |       |     |
| PO4-P  | -.641    | -.644 | -.635 | -.673   | -.691 | -.612| .068  | -.371  | -.270| 1     |     |
| OM     | .162     | .146  | .155  | .326    | -.940**| .354 | .632  | .764   | .697*| -.516 | 1   |

*. Correlation is significant at the 0.05 level (2-tailed).
**. Correlation is significant at the 0.01 level (2-tailed).
Table S2. Correlation coefficients (Pearson correlation) for the dominant genera (constitute >1% of the total abundance in the samples) and environmental parameters.

| Genus                        | pH  | NH$_2$-N | NO$_3$-N | TN  | PO$_4$-P | OM  |
|------------------------------|-----|----------|----------|-----|----------|-----|
| Bryobacter                   | -0.353 | 0.529 | -0.369 | 0.084 | **0.913** | -0.328 |
| Solibacter                   | -0.676 | 0.193 | -0.458 | -0.281 | **0.978** | -0.498 |
| Blastococcus                 | 0.617 | -0.186 | -0.304 | 0.066 | **-0.721** | -0.011 |
| Micromonospora               | 0.683 | 0.638 | 0.681 | **0.952** | -0.420 | **0.665** |
| Micromonosporaceae; UB       | -0.599 | 0.306 | 0.092 | -0.030 | **0.885** | -0.148 |
| Nocardioides                 | 0.229 | 0.148 | **0.960** | 0.514 | -0.290 | 0.564 |
| Pseudonocardia               | 0.616 | 0.657 | 0.050 | **0.722** | -0.441 | 0.524 |
| Saccharothrix                | 0.570 | 0.599 | -0.206 | **0.614** | -0.271 | 0.235 |
| Cytophagaceae; UB            | 0.289 | 0.206 | **0.981** | 0.577 | -0.392 | 0.676 |
| Flavisolibacter              | -0.636 | -0.309 | -0.669 | **-0.661** | **0.834** | -0.855 |
| Chitinophagaceae             | 0.406 | 0.946 | 0.367 | **0.904** | -0.097 | 0.702 |
| Anaerolineaceae              | -0.473 | 0.202 | -0.431 | -0.230 | **0.970** | -0.550 |
| Chloroflexi; UB              | -0.438 | 0.521 | -0.297 | 0.055 | **0.927** | -0.258 |
| Exiguobacterium              | 0.107 | -0.892 | -0.402 | **-0.684** | -0.426 | -0.500 |
| Gemmatimonas                 | -0.207 | 0.294 | -0.217 | -0.077 | **0.842** | -0.363 |
| Microvirga                   | **0.680** | 0.007 | -0.249 | 0.225 | **-0.708** | 0.120 |
| Anaeromyxobacter             | -0.638 | 0.134 | -0.507 | -0.302 | **0.985** | -0.608 |
| Acidibacter                  | 0.289 | 0.440 | 0.927 | **0.612** | -0.380 | **0.925** |
Figure S1. Alpha rarefaction plots for Chao1 and Shannon diversity estimators.
Figure S2. KRONA chart of the taxonomic diversity of the C1 sample.
Figure S3. KRONA chart of the taxonomic diversity of the C2 sample.
Figure S4. KRONA chart of the taxonomic diversity of the P1 sample.
Figure S5. KRONA chart of the taxonomic diversity of the P2 sample.
Figure S6. KRONA chart of the taxonomic diversity of the ZP1 sample.
Figure S7. KRONA chart of the taxonomic diversity of the ZP2 sample.