**Supporting Information**

Photoelectron triggered marine microorganism community succession and metabolic variety in photic zone around estuary and offshore area of Yellow Sea

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**Pretreatment and reaction system of PCR**

1 DNA samples melted on ice, centrifuged and resuspended. Quality of DNA was determined by a microvolume spectrophotometer (Nanodrop, USA). Thirty nanogram DNA was extracted for PCR.

2 PCR reaction system

|  |  |
| --- | --- |
| Reagent | Volume |
| DNA sample | X (30 ng) |
| Forward Primer (5 μM) | 1μL |
| Reverse Primer (5 μM) | 1μL |
| BSA (2 ng/μL) | 3μL |
| 2×Taq Plus Master Mix | 12.5μL |
| ddH2O | 7.5-XμL |
| Total | 25μL |



Figure S1 The pH values of each experimental setup during the reaction. The color represented different original samples: Site 1 black; Site 2 red; Site 3 blue; Site 4 green; different shape represented the potential: ■ -0.15 V; ● -0.30 V; ▲ -0.45 V; ★ open circuit.



Figure S2 Standard curves for real-time PCR assays of bacterial 16S rRNA gene (R2=0.967), archaeal 16S rRNA gene (R2=0.995) and eukaryotic 18S rRNA gene (R2=0.999).



Figure S3 Class composition of bacteria community (A) and genus composition of archaea (B).



Figure S4 Response ratio of topgenus in bacterial communities.



Figure S5 Functional prediction heatmap and Welch’s t-test difference between open circuit groups and electric-treatment groups of carbon fixation and sulfur metabolism.



Figure S6 Functional prediction heatmap of tricarboxylic acid cycle (TCA) and nitrogen metabolism.

Table S1 Index for response ratio analysis

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genus | Average RR | | | Standard Deviation (SD) | | | Variance (v) | | |
| L | M | H | L | M | H | L | M | H |
| *Methylotenera* | 0.00043 | 0.00016 | 0.00021 | 0.00050 | 0.00020 | 0.00024 | 19.32 | 19.39 | 19.29 |
| *Maricaulis* | 0.04482 | 0.00293 | 0.00135 | 0.08613 | 0.00270 | 0.00185 | 19.90 | 19.19 | 19.44 |
| *Marinobacter* | 0.00391 | 0.00653 | 0.06638 | 0.00224 | 0.00266 | 0.09270 | 19.06 | 19.01 | 19.46 |
| *Methylophaga* | 0.01713 | 0.02265 | 0.00156 | 0.02614 | 0.04280 | 0.00162 | 19.55 | 19.87 | 19.24 |
| *Denitromonas* | 0.01639 | 0.00143 | 0.00091 | 0.03200 | 0.00192 | 0.00082 | 19.93 | 19.42 | 19.18 |
| *Leeuwenhoekiella* | 0.00585 | 0.00805 | 0.00409 | 0.00675 | 0.00191 | 0.00491 | 19.31 | 18.99 | 19.33 |
| *Thalassococcus* | 0.04652 | 0.02138 | 0.00223 | 0.08964 | 0.03230 | 0.00115 | 19.90 | 19.54 | 19.03 |
| *Mesonia* | 0.02210 | 0.03394 | 0.00129 | 0.03792 | 0.04025 | 0.00053 | 19.71 | 19.32 | 19.01 |
| *Muricauda* | 0.03354 | 0.04326 | 0.00129 | 0.03650 | 0.04900 | 0.00075 | 19.27 | 19.29 | 19.06 |
| *Photobacterium* | 0.00138 | 0.00936 | 0.08280 | 0.00088 | 0.01376 | 0.00335 | 19.07 | 19.51 | 19.30 |
| *Ferrimonas* | 0.02666 | 0.08468 | 0.01262 | 0.04719 | 0.16222 | 0.00417 | 19.76 | 19.89 | 19.20 |
| *Vitellibacter* | 0.08435 | 0.02272 | 0.00235 | 0.15350 | 0.03827 | 0.00267 | 19.80 | 79.68 | 19.30 |
| *Vibrio* | 0.10389 | 0.00535 | 0.00239 | 0.20590 | 0.00891 | 0.00209 | 19.95 | 19.67 | 19.16 |
| *Oceanicaulis* | 0.08654 | 0.07455 | 0.00403 | 0.00299 | 0.15577 | 0.13430 | 19.78 | 19.78 | 18.98 |
| *Halomonas* | 0.04038 | 0.05774 | 0.24732 | 0.05606 | 0.07047 | 0.09517 | 19.45 | 19.35 | 19.01 |
| *Alteromonas* | 0.03917 | 0.20520 | 0.38348 | 0.02620 | 0.26001 | 0.15673 | 19.08 | 19.37 | 19.01 |
| Unidentified | 0.13085 | 0.21647 | 0.15891 | 0.09235 | 0.12673 | 0.12709 | 19.10 | 19.06 | 19.13 |
| Others | 0.29607 | 0.18357 | 0.11390 | 0.12346 | 0.06208 | 0.01657 | 19.02 | 19.00 | 18.98 |

Table S2 Alpha-diversity index of Archaea

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| SampleID | | chao1 | observed\_species | | PD\_whole\_tree | shannon | |
| OC1 | 116.3 | 102 | 9.34 | | 2.03 |
| OC2 | 192.2 | 191 | 16.64 | | 5.29 |
| L2 | 133.5 | 116 | 13.88 | | 2.68 |
| M2 | 128.5 | 118 | 21.83 | | 3.20 |