**Supplementary Tables**

**Genomic and metatranscriptomic analyses of carbon remineralization in an Antarctic polynya**

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**Supplementary Table S1.** Diversity and abundance of bacterial 16S rRNA gene sequences obtained by the pyrosequencing of PCR amplicons in this study. Taxa with frequencies of < 1% were omitted from all samples. N/D; not detected.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Peak-1 | Declining-1 | Declining-2 | Peak-2 | Sea ice |
| Raw reads | 8108 | 6135 | 5456 | 11467 | 7634 |
| OTU\*$ | 166 | 265 | 330 | 115 | 211 |
| Chao1 estimated richness$ | 289 | 633 | 745 | 237.2 | 476 |
| Shannon’s index for diversity$ | 2.205 | 3.181 | 3.300 | 1.774 | 3.114 |
| Simpson’s index for diversity (Inverse)$ | 0.7829 | 0.9007 | 0.9063 | 0.6945 | 0.9063 |
| Good’s coverage (%)$ | 98.5 | 97.0 | 96.4 | 98.9 | 98.1 |
| Taxonomy |  |  |  |  |  |
| *Bacteroidetes* |  |  |  |  |  |
| *Flavobacteriales* |  |  |  |  |  |
| Unclassified *Flavobacteriales* | tr | 6.95 | 9.17 | 1.47 | tr |
| Unclassifided *Cryomorphaceae* | tr | tr | tr | tr | 1.32 |
| Unclassified *Flavobacteriaceae* | 0.82 | 8.50 | 11.80 | 0.93 | 2.24 |
| *Polaribacter* | 37.37 | 9.86 | 7.76 | 50.50 | 14.49 |
| *Psychroserpens* | N/D | 1.08 | N/D | tr | N/D |
| *Proteobacteria* |  |  |  |  |  |
| *Alphaproteobacteria* |  |  |  |  |  |
| Unclassified *Alphaproteobacteria* | 0.52 | tr | tr | tr | 1.46 |
| *Rhodobacterales* |  |  |  |  |  |
| Unclassified *Rhodobacteraceae* | tr | 6.27 | 5.36 | tr | 2.74 |
| *Loktanella* | tr | 2.23 | 2.45 | tr | tr |
| *Octadecabacter* | 1.93 | 6.09 | 5.73 | 0.61 | 6.01 |
| *Pseudoruegeria* | tr | N/D | N/D | N/D | 1.37 |
| *Rickettsiales* |  |  |  |  |  |
| SAR11 clade | 11.68 | 25.00 | 23.08 | 4.04 | 22.68 |
| *Gammaproteobacteria* |  |  |  |  |  |
| Unclassified *Gammaproteobacteria* | tr | 1.11 | 1.04 | tr | tr |
| *Alteromonadales* |  |  |  |  |  |
| Unclassifided *Alteromonadales* | N/D | 2.11 | 1.45 | N/D | tr |
| Unclassifided *Alteromonadaceae* | tr | 1.85 | 0.86 | N/D | 0.53 |
| SAR92 clade | 8.49 | 2.57 | 2.98 | 6.66 | 4.72 |
| *Oceanospirillales* |  |  |  |  |  |
| Unclassified *Oceanospirillaceae* | 28.72 | 20.66 | 20.38 | 30.36 | 11.47 |
| SUP05 clade | 2.97 | tr | tr | 0.52 | 13.09 |
| *Thiotrichales* |  |  |  |  |  |
| Unclassified *Piscirickettsiaceae* | 1.12 | 2.34 | 4.07 | 3.35 | 7.04 |
| *Deltaproteobacteria* |  |  |  |  |  |
| SAR324 clade | 0.71 | N/D | tr | tr | 1.09 |

\*An OTU was defined as containing sequences with a similarity of at least 97%. tr; < 0.5% abundance.

$Alpha diversity metrics were calculated for an even sequencing depth (5456 reads subsampled per sample).

**Supplementary Table S2.** List of single marker genes from 12 bins and their phylogenetic positions determined using the NCBI NR database (Refer to Additional Excel File).

**Supplementary Table S3.** DNA reads mapped to AL1\_Pel and three *Pelagibacter* genomes.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **PK** | **DC** | **SI** |
| AL1\_Pel | 4,518,392 | 6,376,429 | 29,356,686 |
| Known *Pelagibacter* genomes\* | 1,756,367 | 2,471,753 | 11,473,960 |

\**Pelagibacter* sp. HTCC7211, *Pelagibacter* sp. IMCC9063, and *Pelagibacter ubique* HTCC1062

**Supplementary Table S4.** Abundance (phylum level) of 16S rRNA gene among DNA reads. tr, < 0.1%; N/D, not detected.

|  |  |  |  |
| --- | --- | --- | --- |
| 　 | **PK** | **DC** | **SI** |
| *Actinobacteria* | 0.4 | 0.5 | 0.6 |
| *Bacteroidetes* | 53.1 | 33.8 | 48.7 |
| *Cyanobacteria* | 1.9 | 2.1 | 2.4 |
| *Firmicutes* | 0.2 | 0.3 | 0.4 |
| *Proteobacteria* |  |  |  |
| *Alphaproteobacteria* | 0.9 | 4.4 | 4.4 |
| *Betaproteobacteria* | 0.1 | 0.1 | 0.7 |
| *Gammaproteobacteria* | 10.4 | 23.6 | 11.0 |
| *unclassified\_Proteobacteria* | 23.9 | 18.7 | 19.1 |
| *Planctomycetes* | 0.1 | N/D | N/D |
| *Spirochaetes* | tr | N/D | 0.1 |
| *Verrucomicrobia* | 0.1 | 0.1 | 0.2 |
| unclassified\_*Bacteria* | 6.8 | 16.2 | 12.4 |
| *Crenarchaeota* | 0.5 | 0.1 | tr |
| *Euryarchaeota* | 0.5 | tr | tr |
| unclassified*\_Archaea* | 1.0 | N/D | tr |

**Supplementary Table S5.** Raw read classification based on NT database using Centrifuge.

|  |  |  |
| --- | --- | --- |
|  | **DNA (%)** | **mRNA (%)** |
|  | **PK** | **DC** | **SI** | **PK** | **DC** | **SI** |
| Bacteria | 21.7 | 13.2 | 22.8 | 36.7 | 12.9 | 24.5 |
| -*Bacteroidetes* | 7.6 | 3.0 | 2.0 | 17.6 | 3.1 | 6.5 |
| -*Alphaproteobacteria* | 0.8 | 1.7 | 6.7 | 0.7 | 1.7 | 4.0 |
| -*Gammaproteobacteria* | 1.8 | 2.3 | 3.0 | 6.3 | 4.2 | 6.7 |
| Archaea | 0.2 | 0.1 | 0.2 | 0.1 | 8.5 | 0.1 |
| Environmental samples | 0.1 | 0.1 | 0.3 | 0.2 | 0.3 | 0.5 |
| Eukaryota | 8.1 | 9.6 | 9.8 | 13.3 | 19.3 | 12.2 |
| Viruses | 0.4 | 0.2 | 0.3 | 0.2 | 0.1 | 0.1 |
| No hit | 69.6 | 76.9 | 66.7 | 49.5 | 58.8 | 62.5 |

**Supplementary Table S6.** Summary of metagenome and metatranscriptome data

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 　 | DNA | mRNA | Number of scaffolds | Sum of scaffolds (bp) |
| PK | DC | SI | PK | DC | SI |
| Total reads | 337,950,538 | 212,798,116 | 170,986,196 | 50,843,842 | 59,884,236 | 56,859,202 |
| Total reads after removing Eukaroyote and virus reads$ | 309,206,576 | 191,844,778 | 153,752,466 | 43,701,612 | 47,909,398 | 49,553,468 |
| Reads mapped to binned scaffold | 95,625,154 | 31,124,872 | 30,823,615 | 18,012,957 | 3,553,189 | 6,570,980 | 3906 | 39,125,484 |
|  BC1\_Pol | 52,390,318 | 3,009,658 | 1,030,581 | 10,974,160 | 177,160 | 656,003 | 154 | 3,073,674 |
|  BC2 | 1,014,742 | 2,570,072 | 102,048 | 135,381 | 108,888 | 83,525 | 297 | 2,131,182 |
|  BC3 | 141,665 | 4,700,245 | 555,874 | 16,555 | 2,366 | 236,069 | 13 | 2,850,027 |
|  BC4 | 95,244 | 2,482,625 | 489,488 | 12,007 | 15,652 | 390,404 | 29 | 1,803,780 |
|  BC5\_Pol | 7,446,937 | 956,834 | 191,457 | 1,143,691 | 48,582 | 97,287 | 280 | 1,958,181 |
|  GM1\_Ant | 17,868,419 | 3,318,956 | 2,871,983 | 2,808,861 | 532,718 | 1,092,578 | 36 | 1,997,708 |
|  GM2\_Ant | 2,615,640 | 3,993,729 | 1,815,473 | 511,028 | 325,912 | 706,401 | 68 | 2,190,547 |
|  GM3 | 33,580 | 3,315,969 | 290,388 | 10,621 | 6,916 | 117,184 | 200 | 2,726,251 |
|  GM4\_SAR92 | 8,223,066 | 3,094,832 | 3,283,740 | 1,494,836 | 717,494 | 1,047,613 | 490 | 3,311,676 |
|  GM5 | 2,156,799 | 42,466 | 371,475 | 646,481 | 119,319 | 95,714 | 127 | 1,399,375 |
|  GM6\_SUP05 | 1,096,572 | 45,371 | 3,121,133 | 101,005 | 980,103 | 360,151 | 281 | 2,906,510 |
|  AL1\_Pel | 2,542,172 | 3,594,115 | 16,699,975 | 158,331 | 518,079 | 1,688,051 | 1931 | 10,879,719 |
| Reads mapped to un-binned scaffold\* | 76,427,515 | 50,482,954 | 86,490,648 | 9,304,687 | 8,220,363 | 22,598,370 | 32530 | 339,874,259 |
| /Reads mapped to un-binned bacterial scaffold |  |  |  |  |  |  |  |  |
| - Actinobacteria scaffolds | 77,258 | 147,766 | 363,709 | 10,108 | 11,852 | 58,868 | 219 | 2,518,644 |
| - Bacteroidetes scaffolds | 13,838,801 | 9,135,289 | 14,246,508 | 2,296,202 | 2,055,229 | 7,512,761 | 4253 | 68,142,923 |
| - Alphaproteobacteria scaffolds | 7,718,862 | 11,685,767 | 27,373,153 | 729,075 | 1,469,451 | 4,983,289 | 16927 | 142,707,927 |
| - Betaproteobacteria scaffolds | 1,084,852 | 351,233 | 1,954,142 | 89,604 | 172,787 | 398,050 | 1901 | 15,988,124 |
| - Gammaproteobacteria scaffolds | 17,963,943 | 15,901,617 | 15,725,757 | 3,574,489 | 2,316,362 | 5,704,079 | 6387 | 92,778,323 |
| - Delta/Epsilonproteobacteria scaffolds | 74,218 | 92,937 | 117,987 | 5,114 | 3,352 | 15,833 | 399 | 1,570,131 |
| - Unclassified Proteobacteria scaffolds | 16,961,893 | 1,717,512 | 4,174,737 | 948,461 | 257,851 | 400,838 | 1036 | 10,429,633 |
| - Unclassified Bacteria scaffolds | 3,486,295 | 1,651,667 | 5,298,906 | 194,995 | 176,903 | 661,456 | 1602 | 23,883,795 |
| /Reads mapped to un-binned archaeal scaffold |  |  |  |  |  |  |  |  |
| - Crenarchaeota | 546 | 1,074 | 6,081 | 3 | 35 | 214 | 21 | 91,452 |
| - Euryarchaeota | 23,471 | 20,049 | 281,441 | 312 | 2,537 | 14,410 | 158 | 2,676,693 |
| - Thaumarchaeota | 1054 | 993 | 4,553 | 25 | 133 | 257 | 25 | 59,266 |
| Reads mapped to Uniref90\*\* | 17,167,012 | 21,092,244 | 5,057,470 | 1,627,152 | 8,414,430 | 2,107,645 |  |  |
| Unmapped reads | 165,897,869 | 131,190,290 | 53,671,933 | 14,756,816 | 27,721,416 | 18,276,473 | 　 | 　 |

$Based on Centrifuge

\*Un-binned scaffold of SI metagenome

\*\*Diamond blastx against Uniref90 with unmapped read to SI metagenome

**Supplementary Table S7.** Spearman correlation coefficients for genes in the PK-mRNA-TPM and DC-mRNA-TPM datasets.

|  |  |
| --- | --- |
| Bin | Correlation coefficient(PK-mRNA-TPM: DC-mRNA-TPM) |
| BC1\_Pol | 0.74 |
| BC2 | 0.82 |
| BC3 | 0.44 |
| BC4 | 0.58 |
| BC5\_Pol | 0.72 |
| GM1\_Ant | 0.90 |
| GM2\_Ant | 0.87 |
| GM3 | 0.46 |
| GM4\_SAR92 | 0.90 |
| GM5 | 0.74 |
| GM6\_SUP05 | 0.87 |
| AL1\_Pel | 0.68 |
| 12 Selected Bins | 0.61 |

Correlation coefficients of >0.05 were considered high (marked in bold), those between 0.5 and 0.3 were medium, those between 0.3 and 0.15 were low, those between 0.15 and −0.15 indicated no correlation, and those below −0.15 were negative. [1]

**Supplementary Table S8.** Bloom phase-specific gene expression and average fold changes in expression in 12 genome bins.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Bin** | **Total gene** | **PK-specific** | **DC-specific** | **No expression** | **Average fold change\*****(PK vs. DC)** |
| **BC1\_Pol** | 2687 | 466 | 3 | 60 | 0.64 |
| **BC2** | 1669 | 65 | 17 | 86 | 0.36 |
| **BC3** | 2345 | 1033 | 53 | 759 | 0.48 |
| **BC4** | 1599 | 295 | 139 | 262 | 0.48 |
| **BC5\_Pol** | 1368 | 216 | 2 | 92 | 0.68 |
| **GM1\_Ant** | 1795 | 25 | 8 | 52 | 0.33 |
| **GM2\_Ant** | 2023 | 49 | 26 | 76 | 0.32 |
| **GM3** | 3124 | 712 | 344 | 1172 | 0.45 |
| **GM4\_SAR92** | 2489 | 42 | 31 | 150 | 0.39 |
| **GM5** | 1285 | 114 | 5 | 5 | 0.34 |
| **GM6\_SUP05** | 1900 | 1 | 174 | 91 | 0.34 |
| **AL1\_Pel** | 7287 | 63 | 2301 | 918 | 0.43 |

\*Deseq2 was used for calculation.

**Supplementary Table S9.** Summary of genes encoding representative transporters (TBDT, ABC, and TRAP) and SusD from 12 genomes.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **BC1\_****Pol** | **BC5\_****Pol** | **BC2** | **BC3** | **BC4** | **GM4\_****SAR92** | **GM1\_****Ant** | **GM2\_****Ant** | **GM3** | **GM5** | **GM6\_****SUP05** | **AL1\_****Pel** |
| **TBDT** |  |  |  |  |  |  |  |  |  |  |  |  |
| Cluster 3090 | 2 | 1 |  | 2 | 3 | 1 |  |  |  |  |  |  |
| Cluster 720 | 16 | 15 | 8 | 4 | 5 |  |  |  |  |  |  |  |
| Cluster 427 | 2 | 2 | 1 |  |  | 5 |  |  |  |  |  |  |
| Cluster 3303 | 1 | 1 | 1 | 1 | 1 | 1 |  |  |  |  |  |  |
| Cluster 410 | 1 | 1 | 1 | 2 | 1 | 14 |  |  | 1 |  |  |  |
| Cluster 973 | 1 | 3 | 7 | 5 | 5 | 1 |  |  | 1 |  | 1 |  |
| Cluster 180 | 7 | 6 | 4 | 3 | 1 |  |  |  |  |  |  |  |
| Cluster 1609 | 1 |  |  |  |  |  |  |  |  |  |  |  |
| Cluster 1856 | 4 | 1 |  | 1 |  | 2 |  |  |  |  |  |  |
| Cluster 767 | 1 |  |  | 1 |  |  |  |  |  |  |  |  |
| Unclassified TBDT | 5 | 2 | 6 | 5 | 3 | 1 | 1 |  | 3 | 6 | 1 |  |
| **SusD** |  |  |  |  |  |  |  |  |  |  |  |  |
| SusD | 10 | 5 | 3 | 1 | 2 |  |  |  |  |  |  |  |
| **ABC** |  |  |  |  |  |  |  |  |  |  |  |  |
| Amino acid | 2 | 2 | 1 | 3 |  |  | 12 | 12 | 11 | 1 | 6 | 29 |
| Branched amino acid |  |  |  |  |  |  | 14 | 7 |  |  | 3 | 36 |
| Dipeptide |  |  | 1 |  |  | 1 | 3 |  | 1 |  | 1 |  |
| Oligopeptide |  |  | 1 |  | 1 |  | 3 |  | 2 | 1 | 1 |  |
| Peptide |  |  | 2 |  | 2 | 4 | 8 |  | 5 | 1 | 14 | 5 |
| Phenylpropanoid |  |  |  |  |  |  |  | 1 |  |  |  | 4 |
| Monosaccharide | 1 | 1 |  |  |  |  | 11 | 8 | 16 |  | 31 | 47 |
| Disaccharide |  |  |  |  |  |  | 3 | 5 | 1 |  | 13 | 9 |
| Oligosaccharide |  |  |  | 1 |  |  |  | 3 | 6 |  | 5 | 1 |
| Glycoside |  |  |  |  |  |  | 1 | 3 | 1 |  |  | 4 |
| Sugar alcohol |  |  |  |  | 1 |  | 2 | 3 | 5 |  | 3 | 1 |
| Glycine betaine/Proline/Proline betaine |  |  |  |  | 1 |  | 3 | 9 | 4 |  | 18 | 25 |
| Glycerol/Glycerol-phosphate |  |  |  |  |  |  |  | 4 | 2 |  | 1 | 3 |
| Taurine |  |  |  |  |  |  | 6 |  | 2 |  | 1 | 16 |
| Opine/Polyamine |  |  |  |  | 1 | 4 | 2 | 6 |  |  | 14 | 2 |
| Steroid/lipid | 2 |  | 1 | 1 | 2 |  |  |  |  |  |  |  |
| Cyanate/Nitrite/Nitrate |  |  |  |  |  |  | 2 | 3 |  |  |  |  |
| Urea |  |  |  |  |  |  |  | 1 | 5 |  |  | 5 |
| Mo/W |  |  |  |  |  | 4 | 2 | 4 | 1 | 3 | 5 | 1 |
| Fe/Zn/Cu/Mn | 6 | 4 | 1 | 6 | 6 | 9 | 3 | 3 | 7 | 1 | 6 | 14 |
| Ferric iron-siderophore | 2 | 1 | 1 | 1 | 2 | 2 |  | 1 | 2 | 1 | 2 | 3 |
| Ferrichrome/Heme | 2 |  |  | 1 | 1 | 8 |  |  | 4 |  |  |  |
| Ni/Co | 2 |  |  |  |  |  |  | 2 |  |  | 1 | 2 |
| Vitamin B complex |  |  |  | 1 | 1 | 1 | 2 | 6 | 4 |  | 1 | 7 |
| Lipoprotein | 3 | 1 | 1 | 2 | 2 | 3 | 2 | 2 | 1 |  | 1 | 6 |
| Nucleoside |  |  |  |  |  |  | 3 | 6 | 6 |  | 8 | 2 |
| Phosphonate/Phosphate |  |  |  |  |  | 4 |  |  | 4 |  |  | 5 |
| Sugar phosphate |  | 1 |  |  |  |  | 1 | 2 | 1 |  | 5 | 2 |
| Phthalate/Protocatechuate |  |  |  |  |  |  | 1 | 1 | 2 |  |  | 2 |
| Sulfate/Thiosulfate |  |  |  |  |  | 1 | 3 | 2 |  |  | 2 |  |
| Unclassified ABC | 3 | 1 | 1 | 2 | 1 |  | 1 | 2 | 4 |  | 3 | 2 |
| **TRAP** |  |  |  |  |  |  |  |  |  |  |  |  |
| C4-dicarboxylate |  |  |  |  |  |  | 1 | 7 | 9 |  |  | 25 |
| Mannitol/chloroaromatic |  |  |  |  |  | 3 | 1 | 3 | 1 |  | 3 | 23 |
| Unclassified TRAP |  |  |  |  |  |  | 7 | 6 | 2 |  | 2 | 32 |

**Supplementary Table S10.** Genes in the pathway for vitamin B12 biosynthesis in GM1\_Ant, GM2\_Ant, and GM4\_SAR92.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genes** | **GM1\_Ant** | **GM2\_Ant** | **GM4\_****SAR92** |
| CbiB/CobD COG1270 Cobalamin biosynthesis protein | + | + | + |
| CobQ COG1492 Cobyric acid synthase | + | - | + |
| CobN COG1429 Cobalamin biosynthesis protein | + | + | - |
| CobM COG2875 Precorrin-4 methylase | + | + | - |
| CobJ COG1010 Precorrin-3B methylase | + | + | - |
| CobF COG2243 Precorrin-2 methylase | + | + | - |
| CobH COG2082 Precorrin isomerase | + | + | - |
| CobK COG2099 Precorrin-6x reductase | + | + | - |
| CbiD COG1903 Cobalamin biosynthesis protein | + | + | - |
| CobB COG1797 Cobyrinic acid a,c-diamide synthase | + | + | - |
| CobS COG0368 Cobalamin-5-phosphate synthase | + | + | + |
| CbiX Cobalamin (vitamin B12) biosynthesis CbiX domain containing protein | + | + | - |
| CobU COG2087 Adenosyl cobinamide kinase | + | + | + |
| CobC cobalamin biosynthetic protein | + | + | + |

**Supplementary Table S11.** Comparison of selected genes and pathways in GM1\_Ant, GM2\_Ant, GM4\_SAR92, GM6\_SUP05, and *Roseobacter* clades.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **GM1\_Ant** | **GM2\_Ant** | **GM4\_SAR92** | **GM6\_SUP05** | ***Planktomarina temperata*\*** | ***Octadecabacter arcticus\**** | ***Octadecabacter antarcticus\**** | ***Sulfitobacter* sp. EE-36\*** | ***Sulfitobacter* sp. NAS14.1\*** |
| **Trophic strategy** |  |  |  |  |  |  |  |  |  |
| Photosynthesis cluster | **-** | **-** | **-** | **-** | **+** | **-** | **-** | **-** | **-** |
| Proteorhodopsin | **+** | **+** | **+** | **+** | **-** | **-** | **-** | **-** | **-** |
| Xanthothodopsin | **-** | **-** | **-** | **-** | **-** | **+** | **+** | **-** | **-** |
| **Aromatic degradation** |  |  |  |  |  |  |  |  |  |
| B-ketoadipate | **-** | **-** | **-** | **-** | **+** | **-** | **-** | **+** | **+** |
| gentisate pathway | **-** | **-** | **-** | **-** | **-** | **-** | **-** | **-** | **-** |
| benzoate | **-** | **-** | **-** | **-** | **+** | **-** | **-** | **-** | **-** |
| phenylacetic acid | **+** | **+** | **+** | **+** | **+** | **-** | **-** | **+** | **+** |
| homoprotocatechuate | **-** | **-** | **-** | **-** | **+** | **-** | **-** | **-** | **-** |
| homogentisate pathway | **-** | **-** | **-** | **-** | **-** | **-** | **-** | **+** | **+** |
| **Carbon monoxide utilization** |  |  |  |  |  |  |  |  |  |
| group I CO DH | **-** | **-** | **-** | **-** | **+** | **+** | **+** | **-** | **-** |
| group II CO DH | **-** | **-** | **-** | **-** | **+** | **+** | **+** | **+** | **+** |
| **C1 compound utilization** |  |  |  |  |  |  |  |  |  |
| C1 incorp (serine) | - | - | - | **-** | **+** | **-** | **-** | **-** | **-** |
| MeOH oxidation | -? | -? | - | **-** | **-** | **-** | **-** | **-** | **-** |
| TMA oxidation | - | - | - | **-** | **-** | **+** | **+** | **-** | **-** |
| formaldehyde oxidation | **+** | **+** | **+** | **-** | **+** | **+** | **+** | **+** | **+** |
| formate oxidation | **+** | **+** | **+** | **+** | **+** | **+** | **-** | **+** | **+** |
| **C2 compound utilization** |  |  |  |  |  |  |  |  |  |
| ethylmalonyl pathway | **-** | **-** | **-** | **-** | **+** | **+** | **+** | **+** | **+** |
| glyoxylate shunt | **+** | **+** | **+** | **+** | **-** | **-** | **-** | **-** | **-** |
| **Motility, sensing, and attachment** |  |  |  |  |  |  |  |  |  |
| chemotactic ability | **-** | **+** | **-** | **-** | **+** | **-** | **-** | **-** | **-** |
| flp pilus (type IV) | +? | - | + | **-** | **-** | **-** | **+** | **+** | **+** |
| **Sulfur related** |  |  |  |  |  |  |  |  |  |
| DMSP demethylase (dmdA) | + | + | + | **+** | **+** | **+** | **+** | **-** | **-** |
| sulfur oxidation (SOX) | - | + | + | **+** | **+** | **-** | **-** | **+** | **+** |
| **vitamin related** |  |  |  |  |  |  |  |  |  |
| biotin synthesis | +? | +? | - | **+** | **-** | **-** | **-** | **-** | **-** |
| cobalamin synthesis | + | + | +? | **-** | **+** | **+** | **+** | **+** | **+** |
| thiamine synthesis | - | - | + | **-** | **-** | **+** | **+** | **+** | **+** |
| **Nitrogen related** |  |  |  |  |  |  |  |  |  |
| nitrate reduction (dis) | **-** | **-** | **-** | **-** | **-** | **-** | **-** | **-** | **-** |
| nitrate reduction (ass) | **-** | **-** | **-** | **-** | **-** | **-** | **+** | **+** | **+** |
| nitrite reduction (dis) | **-** | **-** | **-** | **-** | **-** | **-** | **+** | **-** | **-** |
| nitrite reduction (ass) | **-** | **-** | **-** | **-** | **-** | **-** | **+** | **+** | **+** |
| urease | **-** | **-** | **-** | **-** | **+** | **+** | **+** | **+** | **+** |

\*Data from Voget et al. [2] and Newton et al. [3]

? indicates that a gene cluster was not complete.

**Supplementary Table S12.** Information for the 500 most abundant genes in 12 genomes based on metatranscriptome data (a, PK; b, DC; and c, SI). Genes related to ribosome and mitochondrial biogenesis classified by KEGG and hypothetical proteins are marked in grey. (Refer to Additional Excel File)

**References**

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