**Supplementary file 1a.** Information of the Antarctic samples used in this study.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Latitude (S)** | **Longitude (W)** | **Sample description** | **Sampling date** | **Number of isolated strains** |
| 62°13′50″ | 58°58′15″ | Penguin feces, red-pigmented, agglomerated. | January 9, 2017 | 23 |
| 62°11′28″ | 58°55′0.5″ | Rotten red algae | January 10, 2017 | 11 |
| 62°11′52″ | 58°59′39″ | Intertidal sediments, soil, dark brown, muddy. | January 10, 2017 | 34 |
| 62°14′50″ | 58°58′37″ | Membrane sample filtered from 1.5 L surface seawaters | January 31, 2017 | 64 |
| 62°13′12″ | 58°51′42″ | Membrane sample filtered from 2.0 L surface seawaters | January 31, 2017 | 43 |

**Supplementary file 1b.** Homology alignment of proteins in *Psychrobacter* sp. D2 with known DMSP lyases.

|  |  |  |
| --- | --- | --- |
| **Enzymes involved in DMSP catabolism** | **Proteins of the highest similarity in *Psychrobacter*.****sp.****D2** | **Similarity** |
| DddD (*Marinomonas* sp. MWYL1) | orf01588 ([CoA transferase](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_149492825)) | 19.80% |
| DddD (*Ruegeria pomeroyi* DSS-3) | orf01588 ([CoA transferase](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_149492825)) | 23.62% |
| DddP (*Roseovarius nubinhibens* ISM) | orf00311 ([DUF3732 domain-containing protein)](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_011512582) | 4.03% |
| DddP (*Roseobacter denitrificans* OCh 114) | orf02289 ([Methionine aminopeptidase](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_AGP48063)) | 6.83% |
| DddP (*Ruegeria pomeroyi* DSS-3) | orf01862 ([MATE family efflux transporter](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_149408475)) | 4.90% |
| DddQ (*Ruegeria lacuscaerulensis* ITI-1157) | orf00350 ([1-deoxy-D-xylulose-5-phosphate synthase](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_149492468)) | 8.64% |
| DddQ (*Ruegeria pomeroyi* DSS-3) | orf01055 ([Rod shape-determining protein RodA](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_011513816)) | 7.53% |
| DddY (*Alcaligenes faecalis*) | orf01725 (N[itrite reductase small subunit NirD](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_020443516)) | 3.78% |
| DddW (*Ruegeria pomeroyi* DSS-3) | orf02427 ([TRAP transporter small permease](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_011514570)) | 9.14% |
| DddL (*Rhodobacter sphaeroides* 2.4.1) | orf02192 ([dTDP-glucose 4,6-dehydratase](https://blast.ncbi.nlm.nih.gov/Blast.cgi%22%20%5Cl%20%22alnHdr_WP_149493016%22%20%5Co%20%22Go%20to%20alignment%20for%20dTDP-glucose%204%2C6-dehydratase%20%5BPsychrobacter%20sp.%20ANT_H56B%5D%20%3Egb%7CKAA0924184.1%7C%20dTDP-glucose%204%2C6-dehydratase%20%5BPsychrobacter%20sp.%20ANT_H56B%5D)) | 6.94% |
| DddL (*Sulfitobacter* sp. EE-36) | orf01537 (Cupin domain-containing protein) | 7.96% |
| DddK (*Candidatus Pelagibacter ubique* HTCC1062) | orf01209 ([LysR family transcriptional regulator](https://blast.ncbi.nlm.nih.gov/Blast.cgi%22%20%5Cl%20%22alnHdr_WP_020443718%22%20%5Co%20%22Go%20to%20alignment%20for%20MULTISPECIES%3A%20LysR%20family%20transcriptional%20regulator%20%5BPsychrobacter%5D%20%3Egb%7CAGP49165.1%7C%20LysR%20family%20transcriptional%20regulator%20%5BPsychrobacter%20sp.%20G%5D%20%3Egb%7CASE25543.1%7C%20LysR%20family%20transcriptional%20regulator%20%5BPsychrobacter%20cryohalolentis%5D)) | 16.47% |
| Alma1 (*Emiliania huxleyi*) | orf00316 ([Molybdenum cofactor biosysynthesis protein](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_AGP47838)) | 5.77% |

**Supplementary file 1c.** Kinetic parameters of DMSP lyases and DMSP demethylase DmdA.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Protein | Organism | *K*m for DMSP (mM) | *k*cat for DMSP (s-1) | *k*cat/*K*m (M-1 s-1 ) | Reference |
| DddX | *Psychrobacter* sp. D2 | 0.4 ± 0.03 | 0.7 ± 0.02 | 1.6 × 103 | **This study** |
| DddY | *Desulfovibrio acrylicus* W218 | 0.4 | ND\* | ND | ***van der Maarel et al., 1996*** |
| *Alcaligenes* sp.M3A | 1.4 | ND | ND | ***de Souza and Yoch, 1995*** |
| *Acinetobacter bereziniae* | 5.0 ± 0.6 | 8.3 ± 0.5 × 103 | 1.7 × 106 | ***Li et al., 2017*** |
| DddK | *Pelagibacter ubique* HTCC1062 | 3.7 ± 0.6 | 0.9 ± 0.1 | 2.4 × 102 | ***Peng et al., 2019*** |
| DddW | *Ruegeria pomeroyi* DSS-3 | 8.7 ± 0.7 | 18.3 | 2.1 × 103 | ***Brummett et al., 2015*** |
| Alma1 | *Emiliania huxleyi* | 9.0 ± 0.9 | 7 ± 0.3 × 102 | 7.8 ± 0.6 × 104 | ***Alcolombri et al., 2015*** |
| DddP | *Roseovarius nubinhibens* ISM | 13.8 ± 5.5 | 0.3 ± 0.1 | 18.7 | ***Kirkwood et al., 2010*** |
| *Ruegeria lacuscaerulensis* ITI\_1157 | 17.1 ± 1.0 | ND | ND | ***Wang et al., 2015*** |
| DddQ | *Ruegeria lacuscaerulensis* ITI\_1157 | 21.5 ± 6.8 | 1.0 ± 0.3 | 46.5 | ***Li et al., 2014*** |
| DddD | *Marinomonas* sp.MWYL1 | >40\*\* | 12.6 ± 1.5 | 318 | ***Alcolombri et al., 2014*** |
| DddL | *Sulfitobacter* sp. EE-36 | ND | ND | ND | ***Curson et al., 2008*** |
| DmdA | *Ruegeria lacuscaerulensis* ITI\_1157 | 4.1 ± 0.4 | ND | ND | ***Shao et al., 2019*** |
|  | *Ruegeria pomeroyi* DSS-3 | 5.4 ± 2.3 | 2.4 | 450 | ***Reisch et al., 2008*** |
|  | *Pelagibacter ubique* HTCC1062 | 13.2 ± 2.0 | 8.1 | 618 | ***Reisch et al., 2008*** |
|  | *Roseovarius nubinhibens* ISM | 35.7 ± 2.7 | ND | ND | ***Shao et al., 2019*** |

\*No data available. \*\*Saturation was not observed at 40 mM.

**Supplementary file 1d.** Crystallographic data collection and refinement parameters of DddX.

|  |  |  |
| --- | --- | --- |
| Parameters | Se-derivative of DddX | DddX/ATP complex |
| **Diffraction data** |  |  |
| Space group | *P*212121 | C2 |
| Unit cell |  |  |
| a, b, c (Å) | 85.3, 87.5, 327.6 | 143.6, 88.8, 273.3 |
| α, β, γ (°) | 90.0, 90.0, 90.0 | 90.0, 99.9, 90.0 |
| Resolution range (Å) | 50.0-3.3 (3.36-3.30) \* | 50.0-2.25 (2.29-2.25) |
| Redundancy | 12.5 (11.6) | 3.2 (3.3) |
| Completeness (%) | 99.8 (98.4) | 97.3 (95.9) |
| *R*merge\*\* | 0.1 (0.4) | 0.1 (0.4) |
| *I*/σ*I* | 18.0 (3.9) | 13.1 (2.0) |
| **Refinement statistics** |  |  |
| R-factor |  | 0.23 |
| Free R-factor |  | 0.18 |
| RMSD from ideal geometry |  |  |
| Bond lengths (Å) |  | 0.008 |
| Bond angles (°) |  | 1.1 |
| Ramachandran plot (%) |  |  |
| Favored |  | 93.7 |
| Allowed |  | 5.1 |
| Outliers |  | 1.2 |
| Overall B-factors (Å2) |  | 42.4 |

\*Numbers in parentheses refer to data in the highest-resolution shell.

\*\**R*merge=∑*hkl*∑*i*|*I*(*hkl*)*i* -<*I*(*hkl*)>|/∑*hkl*∑*iI*(*hkl*)*i*, where *I* is the observed intensity, <*I*(*hkl*)> represents the average intensity, and *I*(*hkl*)*i* represents the observed intensity of each unique reflection.

**Supplementary file 1e.** Homology alignment of proteins in *Psychrobacter* sp. D2 with known enzymes involved in acrylate catabolism.

|  |  |  |  |
| --- | --- | --- | --- |
| **Enzymes involved in acryloyl-CoA catabolism** | **Proteins of the highest similarity in *Psychrobacter*.****sp.****D2** | **Locus tag** | **Similarity** |
| AcuH (*Ruegeria pomeroyi* DSS-3) | orf01810 (Enoyl-CoA hydratase/isomerase family protein) | H0262\_08710 | 45.58% |
| orf01692 (Enoyl-CoA hydratase/isomerase family protein) | H0262\_08180 | 34.33% |
| orf01695 (Enoyl-CoA hydratase/isomerase family protein) | H0262\_08190 | 32.48% |
| AcuI (*Ruegeria pomeroyi* DSS-3) | orf00105 (acryloyl-CoA reductase) | H0262\_00540 | 40.57% |
| orf02674 (acryloyl-CoA reductase) | H0262\_12930 | 36.15% |
| AcuN (*Halomona*s sp. HTNK1) | orf01588 ([CoA transferase](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WP_149492825)) | H0262\_07715 | 31.58% |
| AcuK (*Halomona*s sp. HTNK1) | orf01810 (Enoyl-CoA hydratase/isomerase family protein) | H0262\_08710 | 44.00% |
| PrpE (*Ruegeria pomeroyi* DSS-3) | orf01091 (propionate--CoA ligase) | H0262\_05290 | 41.98% |

**Supplementary file 1f.** Strains and plasmids used in this study.

|  |  |  |
| --- | --- | --- |
| **Strains** | **Description** | **Source** |
| *Psychrobacter* sp.D2 | Wild-type isolate | This study |
| Δ*dddX* | the *dddX* gene deletion mutant | This study |
| Δ*dddX*/pBBR1MCS-*dddX* | Δ*dddX* containing pBBR1MCS-*dddX* plasmid | This study |
| Δ*dddX*/pBBR1MCS | Δ*dddX* containing pBBR1MCS plasmid | This study |
| *Escherichia. coli* WM3064 | RP4 (tra) in chromosome, DAP-, 37°C | (***Dehio et al., 1997***) |
| *Escherichia. coli* DH5α | Used for gene cloning | Vazyme Biotech company (China) |
| *Escherichia. coli* BL21(DE3) | Used for gene expression | Vazyme Biotech company (China) |
| **Plasmids** |  |  |
| pK18*mobsacB*-Ery | pk18*mobsacB* containing the erythromycin resistant gene from pHT304, Kanr\*, Eryr\*\* | (***Wang et al., 2015***) |
| pK18Ery-*dddX* | pK18*mobsacB*-Ery containing the homologous arms of the *dddX* gene of *Psychrobacter*. sp. D2, Kanr, Eryr | This study |
| pBBR1MCS | Broad-host-range cloning vector, Kanr | (***Kovach et al., 1995***) |
| pBBR1MCS-*dddX* | pBBR1MCS containing the *dddX* gene and its promoter of *Psychrobacter*. sp. D2, Kanr | This study |
| pET-22b | Used for gene expression | Novagen (Germany) |

\* Kanr, kanamycin resistance.

\*\* Eryr, erythromycin resistance.

**Supplementary file 1g.** Composition of the basal medium (lacking the carbon source).

|  |  |
| --- | --- |
| Solution\* | Components |
| 1 | 0.05% (w/v) NH4Cl, 3% (w/v) NaCl, 0.3% (w/v) MgCl2·6H2O, 0.2% (w/v) K2SO4, 0.02% (w/v) K2HPO4, 0.001% (w/v) CaCl2, 0.0006% (w/v) FeCl3·6H2O, 0.0005% (w/v) Na2MoO4·7H2O, 0.0004% (w/v) CuCl2·2H2O, 0.6% (w/v) Tris. [1.5% (w/v) agar for solid medium] |
| 2 (***Kanagawa et al., 1982***) | 0.001% (w/v) thiamine·HCl, 0.002% (w/v) nicotinic acid, 0.002% (w/v) pyridoxine·HCl, 0.002% (w/v) riboflavin, 0.0001% (w/v) biotin, 0.0001% (w/v) cyanocobalamin, 0.001% (w/v) *p*-aminobenzoic acid, 0.002% (w/v) calcium pantothenate. |

\* Solution 1 was autoclaved at 121°C for 20 min. Solution 2 was filter-sterilized before it was combined with solution 1.

**Supplementary file 1h.** Primers used in this study.

|  |  |  |
| --- | --- | --- |
| **Primers** | **Sequence (5’-3’)** | **Purpose** |
| 27F | AGAGTTTGATCCTGGCTCAG | Amplification of cultivated strains 16S rRNA genes (***Lane et al., 1985***) |
| 1492R | GGTTACCTTGTTACGACTT |
| RT-*1696*-F | GTTGTCTGTTACTGGATT | Used for RT-qPCR of the *1696* gene |
| RT-*1696*-R | AGGTAGTCGCTAAGAATA |
| RT-*dddX*-F | GACCGCTATGGAGAAGTA | Used for RT-qPCR of the *dddX* gene |
| RT-*dddX*-R | CAAGACATCAAGTGCTACC |
| RT-*1698*-F | ATGGTTGGCGTCAATATC | Used for RT-qPCR of the *1698* gene |
| RT-*1698*-R | CAAGTCGGCATAGAGAAC |
| RT-*1699*-F | CGAATACCTAGCCTAGAAGAGA | Used for RT-qPCR of the *1699* gene |
| RT-*1699*-R | TAATGAGCGATCCATACTATTGTC |
| RT-*recA*-F | CTTCTGTGCGTATGGATATTC | Used for RT-qPCR of the *recA* gene |
| RT-*recA*-R | TGCCTTCACCGTAAGTAAT |
| *dddX*-UP-F | GTAAAACGACGGCCAGTGCCAAGCTTTAATAGCTTCAGTCCACGTTTC | Upstream homologous fragment of the *dddX* gene |
| *dddX*-UP-R | CTTATTCAATAGAAATTATACAAGCGTTTATACATTATAT |
| *dddX*-Down-F | ATATAATGTATAAACGCTTGTATAATTTCTATTGAATAAG | Downstream homologous fragment of the *dddX* gene |
| *dddX*-Down-R | GTCATAAGATTAGTCACTGGGGATCCAGGCAAACGCTGTCAGGCGCTC |
| *dddX*-1000-F | AACTAAAATTTGAAAACTCAGGCTTTTC | Confirmation of the Δ*dddX* mutant |
| *dddX*-1000-R | TGAATATGGTAATGGTACTTGTATTTATAC |
| *dddX*-300Up-F | CAGATGGCAACAATCAAAACAAATGTAGAGATGAAGATGAAC |
| *dddX*-700Down-R | TGCCGATCAAGGTGCTAAACTGGTCATCGATGGCTCTGATG |
| *dddX*-pBBR1-PF | CGGGGTACCTTATAAATTATAGATGACAATGATAG | Complementation of the Δ*dddX* mutant |
| *dddX*-pBBR1-PR | CCGCTCGAGTTTAATTACTCCTTCCTTAGAGTTAAC |
| *dddX*W-F | AAGAAGGAGATATACATATGTTGACTGGTCAGATAATTGAG | Amplification of the *dddX* gene |
| *dddX*W-R | TGGTGGTGGTGGTGCTCGAGCACCAGCTCACTACATTTTTTG |