**Table 3** Counts of genes involved in DMSP catabolism and photoheterotrophy.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Site | size µm | *dddD*  (%) | *dddL*  (%) | *dddP*  (%) | *dmdA*  (%) | Rhodopsin  (%) | *pufLM*  (%)a | *recA* |
| Organic Lake 1.7 m (GS374) | 0.1  0.8  3.0 | 2 (9)  10 (36)  11 (50) | 4 (19)  10 (**39**)  5 (21) | 0  1 (2)  2 (7) | 0\* (2)  2 (7)  9 (43) | 1 (5)  5 (20)  12 (57) | 0\* (1)  4 (14)  13 (61) | 21  26  21 |
| Organic Lake 4.2 m (GS375) | 0.1  0.8  3.0 | 5 (34)  15 (54)  23 (75) | 5 (34)  9 (31)  2 (8) | 0  0  1 (2.5) | 1 (10)  2 (6)  20 (68) | 1 (10)  7 (23)  14 (45) | 2 (16)  3 (11)  16 (53) | 14  28  30 |
| Organic Lake 5.7 m (GS376) | 0.1  0.8  3.0 | 4 (43)  6 (20)  19 (68) | 1 (7)  9 (32)  3 (12) | 0  0  0 | 1 (14)  2 (7)  13 (47) | 2 (21)  6 (22)  6 (21) | 0\* (4)  3 (12)  11 (38) | 10  29  28 |
| Organic Lake 6.5 m (GS377) | 0.1  0.8  3.0 | 10 (51)  14 (38)  42 (106) | 0\* (2)  9 (23)  5 (13) | 0  1 (2)  0 | 3 (15)  7 (20)  20 (52) | 1 (7)  6 (16)  6 (16) | 4 (22)  7 (20)  **22** (**55**) | 20  28  29 |
| Organic Lake 6.7 m (GS378) | 0.1  0.8  3.0 | 1 (7)  12 (26)  **50** (**174**) | 0\* (4)  8 (17)  5 (17) | 0  0  4 (13) | 0  2 (5)  12 (43) | 1 (7)  8 (16)  12 (43) | 2 (13)  4 (9)  14 (48) | 13  47  29 |
| Ace Lake mixolimnion | 0.1  0.8  3.0 | 0\* (2)  2 (3)  0 | 0  1 (2)  0 | 1 (2)  0  0\* (4) | 15 (56)  2 (4)  0 | 15 (53)  12 (27)  5 (42) | 0\* (1)  3 (12)  0 | 28  45  11 |
| Newcomb Bay (GS235) | 0.1  0.8  3.0 | 6 (14)  5 (12)  0 | 0  0  0 | 3 (7)  0  0 | 50 (111)  18 (41)  2 (17) | 89 (**196**)  55 (123)  4 (33) | 0  0  0 | 45  45  11 |
| Southern Ocean SZ | 0.1  0.8  3.0 | 2 (3)  3 (6)  0\* (7) | 0  0\* (0\*)  0 | 6 (9)  5 (12)  0\* (4) | 71 (101)  32 (81)  4 (66) | 98 (139)  43 (108)  5 (84) | 0  0  0 | 70  39  6 |
| Southern Ocean NZ | 0.1  0.8  3.0 | 0\* (1)  0\* (2)  0 \*(3) | 0  0  0 | 5 (7)  9 (**30**)  1 (9) | **124** (**159**)  28 (84)  7 (54) | **111** (142)  35 (107)  11 (89) | 1 (1)  2 (7)  0 (4) | 78  33  12 |
| GOS coastal | 0.1 | 0\* (0\*) | 0 | 5 (6) | 44 (52) | 74 (87) | 5 (6) | 85 |
| GOS open ocean | 0.1 | 0 | 0 | 7 (8) | 45 (50) | 66 (74) | 5 (5) | 90 |
| GOS estuary | 0.1 | 0 | 0 | 1 (1) | 29 (36) | 61 (77) | 2 (3) | 80 |
| GOS embayment (GS005) | 0.1 | 4 (8) | 0 | 6 (12) | 28 (54) | 58 (112) | 3 (6) | 52 |
| GOS Lake Gatun (GS020) | 0.1 | 0 | 0 | 0 | 4 (4) | 48 (53) | 2 (2) | 90 |
| GOS fringing reef (GS025) | 0.8 | 0 | 0 | 0 | 0 | 7 (39) | 0 | 18 |
| GOS warm seep (GS030) | 0.1 | 0 | 0 | 7 (6) | 75 (63) | 83 (69) | 6 (5) | 120 |
| GOS Upwelling, Fernandina (GS031) | 0.1 | 0 | 0 | 4 (4) | 81 (77) | 81 (76) | 4 (4) | 106 |
| GOS mangrove (GS032) | 0.1 | 0 | 0 | 2 (3) | 24 (34) | 25 (36) | 1 (1) | 71 |
| GOS Punta Cormorant Lagoon (GS033) | 0.1 | 0 | **11** (15) | **14** (21) | 4 (6) | 31 (43) | 15 (21) | 72 |
| GOS Rangirora Atoll (GS051) | 0.1 | 0 | 0 | 11 (15) | 38 (49) | 73 (94) | 3 (4) | 77 |

Counts shown for Organic Lake, Ace Lake mixolimnion, Southern Ocean and GOS metagenomes per 100 Mbp of metagenomic sequence. Percentages shown in parentheses are estimates of cells containing that marker gene, which is the percentage of the marker gene to the single-copy gene *recA*. The sample ID for each site is shown in parentheses after the site description. Values marked with an asterisk are > 0 but < 0.5. Counts for the following sites are averages of several samples: Ace Lake mixolimnion (GS232, GS231); Southern Ocean SZ (GS349, GS351–GS353, GS356–GS360); Southern Ocean NZ (GS363, GS346, GS364, GS366–GS368); GOS coastal (GS002–GS004, GS007–GS010, GS012–GS016, GS019, GS021, GS027–GS029, GS034–GS036); GOS open ocean (GS017, GS018, GS022, GS023, GS026, GS037, GS047); GOS estuary (GS006, GS011, GS012). Values shown in bold are the highest for that marker gene. SZ, Southern Zone; NZ, Northern Zone; GOS, Global Ocean Sampling.