

A Genomics-Based Discovery of Secondary Metabolite Biosynthetic Gene Clusters in the Potential Novel Strain *Streptomyces* sp. 21So2-11 Isolated from Antarctic Soil

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1 Supplementary Table

Table S1. Genome characteristics of strain 21So2-11 and 34 close related type strains used for phylogenetic analysis.

| Strain | Genome size (Mb) | G+C content (%) | Contigs number | N50 (Kb) | CDS | dDDH (%) | ANI (%) |
|--|------------------|-----------------|----------------|----------|-------|----------|---------|
| <i>Streptomyces</i> sp. 21So2-11 | 8.45 | 69.57 | 29 | 58.39 | 7,390 | 100.00 | 100.00 |
| <i>S. altiplanensis</i> HST21 ^T | 7.92 | 70.98 | 459 | 37.40 | - | 28.60 | 83.74 |
| <i>S. chryseus</i> DSM 40420 ^T | 7.08 | 71.35 | 1,451 | 9.50 | 6,500 | 28.20 | 83.68 |
| <i>S. albidochromogenes</i> DSM 41800 ^T | 7.27 | 71.47 | 795 | 18.70 | 6,526 | 27.90 | 83.35 |
| <i>S. lunaelactis</i> MM109 ^T | 8.57 | 69.75 | 1 | 8,570.00 | 7,366 | 24.70 | 83.00 |
| <i>S. poriferorum</i> P01-B04 ^T | 8.91 | 70.73 | 695 | 26.90 | 7,671 | 24.00 | 82.21 |
| <i>S. beijiangensis</i> DSM 41794 ^T | 8.40 | 69.63 | 1,769 | 21.70 | 7,802 | 23.80 | 82.10 |
| <i>S. bacillaris</i> ATCC 15855 ^T | 7.89 | 71.95 | 1 | 7,890.00 | 6,509 | 23.70 | 82.00 |
| <i>S. paludis</i> GSSD-12 ^T | 8.45 | 71.19 | 1 | 8,450.00 | 6,960 | 23.60 | 81.98 |
| <i>S. californicus</i> FDAARGOS_1209 ^T | 8.03 | 72.56 | 3 | 7,800.00 | 6,840 | 23.60 | 82.16 |
| <i>S. liangshanensis</i> QMT-12 ^T | 7.72 | 72.10 | 1 | 7,720.00 | 6,538 | 23.40 | 82.03 |
| <i>S. fulvorobeus</i> NBRC 15897 ^T | 6.63 | 70.80 | 2 | 6,600.00 | 5,321 | 23.40 | 82.03 |
| <i>S. griseus</i> subsp. <i>griseus</i> DSM 40236 ^T | 8.63 | 72.25 | 4 | 6,000.00 | 7,068 | 23.30 | 82.18 |
| <i>S. candidus</i> NBRC 12846 ^T | 7.40 | 71.15 | 64 | 349.20 | 6,430 | 23.30 | 82.11 |
| <i>S. drozdowiczii</i> NBRC 101007 ^T | 7.36 | 72.01 | 82 | 413.70 | 6,316 | 23.30 | 82.01 |
| <i>S. globisporus</i> TFH56 ^T | 7.67 | 71.54 | 3 | 7,500.00 | 6,492 | 23.30 | 82.08 |
| <i>S. nitrosporeus</i> ATCC 12769 ^T | 7.58 | 72.17 | 1 | 7,580.00 | 6,461 | 23.20 | 81.78 |
| <i>S. finlayi</i> JCM 4637 ^T | 9.49 | 71.32 | 65 | 413.30 | 8,177 | 23.10 | 81.88 |
| <i>S. cinereoruber</i> ATCC 19740 ^T | 7.52 | 72.89 | 1 | 7,520.00 | 6,545 | 23.10 | 81.74 |

| | | | | | | | |
|---|-------|-------|-----|-----------|-------|-------|-------|
| <i>S. pratensis</i> SFW ^T | 7.71 | 70.94 | 8 | 6,200.00 | 4,667 | 23.10 | 81.87 |
| <i>S.nojiriensis</i> NBRC 13794 ^T | 9.05 | 71.98 | 6 | 5,900.00 | 7,972 | 22.90 | 81.37 |
| <i>S. venezuelae</i> ATCC 10712 ^T | 8.22 | 72.46 | 1 | 8,220.00 | 7,265 | 22.90 | 81.75 |
| <i>S. vinaceus</i> ATCC 27476 ^T | 7.67 | 72.34 | 1 | 7,670.00 | 6,735 | 22.80 | 81.42 |
| <i>S. avidinii</i> NBRC 13429 ^T | 8.36 | 71.85 | 68 | 567.40 | 7,316 | 22.70 | 81.31 |
| <i>S. subutilis</i> ATCC 27467 ^T | 7.60 | 73.45 | 1 | 7,600.00 | 6,555 | 22.70 | 81.43 |
| <i>S. kanamyceticus</i> ATCC 12853 ^T | 10.13 | 71.03 | 1 | 10,130.00 | 8,529 | 22.70 | 81.41 |
| <i>S. alboniger</i> ATCC 12461 ^T | 7.96 | 71.16 | 1 | 7,960.00 | 6,741 | 22.60 | 81.39 |
| <i>S. xanthophaeus</i> NRRL B-5414 ^T | 8.62 | 72.24 | 163 | 253.50 | 7,667 | 22.50 | 81.21 |
| <i>S. fagopyri</i> QMT-28 ^T | 8.88 | 71.24 | 1 | 8,880.00 | 7,429 | 22.50 | 81.15 |
| <i>S. xanthii</i> CRXT-Y-14 ^T | 8.35 | 72.15 | 3 | 7,900.00 | 7,442 | 22.00 | 80.85 |
| <i>S. galilaeus</i> ATCC 14969 ^T | 7.76 | 71.44 | 1 | 7,760.00 | 6,808 | 22.00 | 80.78 |
| <i>S. griseochromogenes</i> ATCC 14511 ^T | 10.76 | 70.76 | 1 | 10,760.00 | 9,277 | 22.00 | 80.75 |
| <i>S. qaidamensis</i> S10 ^T | 9.08 | 71.26 | 1 | 9,080.00 | 7,871 | 21.80 | 80.54 |
| <i>S. davawensis</i> JCM 4913 ^T | 9.56 | 70.58 | 2 | 9,500.00 | 8,396 | 21.80 | 80.47 |
| <i>S. smaragdinus</i> RB5 ^T | 7.86 | 72.02 | 106 | 161.60 | 6,985 | 21.30 | 79.71 |

Table S2. Genes related to cold adaptation, ultraviolet (UV) resistance and salt tolerance in the genome of *Streptomyces* sp. 21So2-11.

| Type | Database | Scaffold No. | Start-End | Gene name |
|---|-----------------|-----------------------------|---|------------------------|
| Cold-shock protein- and RNA helicase | KEGG, SwissProt | Scaffold1, 3, 4, 10, 14, 18 | Scaffold1 (324,347-324,550); Scaffold3 (188,521-188,724); Scaffold4 (334,330-334,533); Scaffold10 (189,984-190,172); Scaffold14 (93,119-93,322); Scaffold18 (96,992-97,198) | <i>cspA</i> (6 copies) |
| | SwissProt | Scaffold1 | 294,634-295,017 | <i>cspC</i> |
| | KEGG, SwissProt | Scaffold2 | 465,520-467,667 | <i>cstA</i> |
| | KEGG | Scaffold11 | 114,067-116,622 | <i>deaD</i> |
| | KEGG, SwissProt | Scaffold5 | 65,828-67,798 | <i>dinG</i> |
| | SwissProt | Scaffold1 | 534,859-535,530 | <i>grpE</i> |
| | KEGG | Scaffold7 | 287,815-290,625 | <i>hepA</i> |
| | SwissProt | Scaffold6 | 400,848-402,167 | <i>hmgA</i> |
| | KEGG, SwissProt | Scaffold1 | 1,051,730-1,055,620 | <i>hrpA</i> |
| | KEGG, SwissProt | Scaffold7 | 242,433-245,009 | <i>hrpB</i> |
| | KEGG, SwissProt | Scaffold5, 8 | Scaffold5 (81,954-84,125); Scaffold8 (415,861-417,957) | <i>recQ</i> (2 copies) |
| | SwissProt | Scaffold17 | 106,956-108,419 | <i>rep</i> |
| | KEGG, SwissProt | Scaffold1 | 1,062,618-1,064,969 | <i>rhIE</i> |
| | KEGG, SwissProt | Scaffold14 | 26,486-27,925 | <i>rnr</i> |
| | KEGG, SwissProt | Scaffold1, 9 | 1,379,979-1,380,851; 199,270-200,151 | <i>tesB</i> (2 copies) |
| Repair of DNA damage induced by ultraviolet and | KEGG, SwissProt | Scaffold5 | 67,906-68,454 | <i>lexA</i> |
| | SwissProt | Scaffold4 | 67,576-68,256 | <i>mtcA</i> |
| | KEGG, SwissProt | Scaffold6 | 266,256-267,617 | <i>phr</i> |
| | KEGG, SwissProt | Scaffold7 | 235,422-238,079 | <i>polA</i> |

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|---|-----------------|---------------------|---|------------------------|
| ionizing radiation | KEGG, SwissProt | Scaffold5 | 30,736-31,902; 31,918-32,499 | recA; recX |
| | KEGG, SwissProt | Scaffold1 | 839,527-840,657; 1,660,666-1,661,421; 481,861-482,460 | recF; recO; recR |
| | SwissProt | Scaffold2 | 477,956-478,279 | rsr |
| | KEGG, SwissProt | Scaffold1 | 876,748-877,380 | ssb |
| | SwissProt | Scaffold1, 4, 7, 12 | Scaffold1 (1,005,377-1,007,662); Scaffold4 (430,674-433,082); Scaffold7 (317,406-320,408); Scaffold12 (18,549-21,563) | <i>uvrA</i> (4 copies) |
| | KEGG, SwissProt | Scaffold7 | 309,409-311,538; 321,917-324,004 | uvrB; uvrC |
| | KEGG, SwissProt | Scaffold1, 2, 8 | Scaffold1 (304,110-306,194); Scaffold2 (512,499-514,643); Scaffold2 (517,708-521,637); Scaffold8 (242,609-245,110) | <i>uvrD</i> (4 copies) |
| Salt and osmotic stress tolerance | KEGG | Scaffold3 | 151,729-153,300; 148,632-150,101 | betA; betB |
| | KEGG, SwissProt | Scaffold10 | 39,111-39,707; 80,783-82,528 | betI; betT |
| | KEGG | Scaffold17 | 95,111-96,637 | cvrA |
| | KEGG, SwissProt | Scaffold1 | 535,527-537,404 | dnaK |
| | SwissProt | Scaffold7 | 399,546-400,034; 397,795-398,193; 396,872-397,789 | ectA; ectC; ectD |
| | KEGG | Scaffold5, 7 | Scaffold5 (59,644-61,023); Scaffold7 (398,251-399,519) | <i>ectB</i> (2 copies) |
| | KEGG, SwissProt | Scaffold8 | 203,188-204,690 | gbsA |
| | KEGG, SwissProt | Scaffold1, 10 | Scaffold1 (1,686,327-1,687,097); Scaffold10 (37,184-38,362) | <i>gdh</i> (2 copies) |
| | KEGG, SwissProt | Scaffold7, 21 | Scaffold7 (175,646-180,265); Scaffold21 (49,449-50,735) | <i>gltB</i> (2 copies) |
| | KEGG, SwissProt | Scaffold7 | 180,399-181,718 | <i>gltD</i> |
| | KEGG, SwissProt | Scaffold5 | 240,438-242,102; 244,206-244,892; 245,113-247,656; 247,727-248,410 | kdpA; kdpC; kdpD; kdpE |
| | KEGG, SwissProt | Scaffold5 | 242,099-244,201; 548,650-550,686 | <i>kdpB</i> (2 copies) |
| | SwissProt | Scaffold1 | 1,494,450-1,495,508 | mscS |

| | | | |
|-----------------|------------------|--|------------------------|
| KEGG, SwissProt | Scaffold1 | 327,933-329,354; 329,656-330,510 | otsA; otsB |
| KEGG, SwissProt | Scaffold4, 5, 12 | Scaffold4 (293,259-293,684); Scaffold5 (419,744-420,169); Scaffold12 (70,375-70,803) | <i>osmC</i> (3 copies) |
| KEGG, SwissProt | Scaffold1 | 1,169,400-1,170,575 | prec |
| KEGG, SwissProt | Scaffold1 | 1,602,626-1,603,918; 1,600,710-1,601,843 | proA; proB |
| KEGG, SwissProt | Scaffold11 | 311,918-312,727 | proC |
| KEGG, SwissProt | Scaffold3 | 89,599-90,504 | surE |
| KEGG, SwissProt | Scaffold2 | 227,899-229,620 | treS |
| KEGG, SwissProt | Scaffold5 | 249,731-250,408 | trkA |

Table S3. Putative secondary metabolite biosynthetic gene clusters (BGCs) in *Streptomyces* sp. 21So2-11 using the antiSMASH server (<https://antismash.secondarymetabolites.org>).

| Cluster No. | Location | Type | Most similar known cluster (%) |
|-------------|------------------------------------|---------------------------|------------------------------------|
| 1.1 | Scaffold1 (405,264-433,511) | Lanthipeptide, CDPS | - |
| 1.2 | Scaffold1 (760,173-829,116) | NRPS | Vazabotide A (30%) |
| 1.3 | Scaffold1 (1,346,427-1,358,139) | Siderophore | Desferrioxamine B/E (50%) |
| 2.1 | Scaffold2 (238,400-310,876) | T2PKS, oligosaccharide | Hiroshidine (41%) |
| 3.1 | Scaffold3 (30,843-41,304) | Melanin | Melanin (100%) |
| 3.2 | Scaffold3 (242,197-370,624) | Terpene | Coelichelin (100%) |
| 4.1 | Scaffold4 (17,674-30,557) | Hydrogen-cyanide | Aborycin (14%) |
| 4.2 | Scaffold4 (390,779-431,387) | T3PKS | Capreomycin IA/IB/IIA/IIB (12%) |
| 4.3 | Scaffold4 (439,466-460,572) | Terpene | - |
| 4.4 | Scaffold4 (482,190-546,826) | T1PKS, NRPS-like | Lasalocid (11%) |
| 5.1 | Scaffold5 (47,052-79,771) | Siderophore | Kinamycin (16%) |
| 5.2 | Scaffold5 (259,617-302,430) | NRPS-like | Leucomycin (11%) |
| 5.3 | Scaffold5 (359,191-370,636) | RiPP-like | Tylactone (6%) |
| 5.4 | Scaffold5 (519,082-544,975) | Terpene | Isorenieratene (100%) |
| 7.1 | Scaffold7 (392,795-403,193) | Ectoine | Ectoine (100%) |
| 9.1 | Scaffold9 (54,588-117,493) | T1PKS, NRPS-like | Naphthomycin A (53%) |
| 9.2 | Scaffold9 (155,028-165,372) | Melanin | Melanin (28%) |

| | | | |
|------|---------------------------------|--|------------------------|
| 9.3 | Scaffold9 (228,879-239,109) | RiPP-like | Detoxin S1 (44%) |
| 9.4 | Scaffold9 (369,202-395,652) | Lanthipeptide | - |
| 10.1 | Scaffold10 (42,334-68,907) | Terpene | Hopene (84%) |
| 10.2 | Scaffold10 (233,161-255,183) | Redox-cofactor | K-252a (14%) |
| 12.1 | Scaffold12 (161,433-184,027) | Lanthipeptide | SapB (100%) |
| 13.1 | Scaffold13 (18,562-68,579) | T1PKS | Auroramycin (17%) |
| 13.2 | Scaffold13 (77,896-140,453) | T1PKS, NRPS | Neomediomycin B (28%) |
| 16.1 | Scaffold16 (1,657-36,499) | Thiopeptide, LAP | - |
| 19.1 | Scaffold19 (25,480-97,962) | T2PKS, butyrolactone | Gaudimycin A/C/D (54%) |
| 21.1 | Scaffold21 (3,367-73,812) | Lanthipeptide, NRPS, T1PKS, blactam | Streptolydigin (13%) |
| 25.1 | Scaffold25 (5,829-37,472) | T1PKS, PKS-like | Enteromycin (20%) |

2 Supplementary Figures



Figure S1. Annotations of the genome of *Streptomyces* sp. 21So2-11 using the COG (A) and KEGG (B) databases.

