**Supplementary Material**

**Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat**

Stefan Spring, Dimitry Y. Sorokin, Susanne Verbarg, Manfred Rohde, Tanja Woyke, Nikos C. Kyrpides

**Contents Page**

Supplementary Tables S1 to S5 2 - 11

Supplementary Figures S1 to S3 12 - 14

**TABLE S1.** Specifications of genomes used for the reconstruction of phylogenetic relationships within the *Desulfovibrionales*.

|  |  |  |  |
| --- | --- | --- | --- |
| Accession No. a | Strain Designation b | G+C (mol%) | Size (Mb) |
| JOMJ00000000 | L21-Syr-ABT | 65.47 | 3.39 |
| JNJP00000000 | *Bilophila wadsworthia* ATCC 49260T (DsrBD fusion) | 59.22 | 4.63 |
| CM001488 | *Desulfobacter postgatei* 2ac9T | 47.17 | 3.97 |
| JAEX00000000 | *Desulfocurvus vexinensis* DSM 17965T | 69.66 | 3.63 |
| CP001734, CP001735 | *Desulfohalobium retbaense* DSM 5692T | 57.33 | 2.91 |
| CP001629 | *Desulfomicrobium baculatum* DSM 4028T | 58.65 | 3.94 |
| ACJN00000000 | *Desulfonatronospira thiodismutans* ASO3-1T | 51.33 | 3.97 |
| JMKT00000000 | *Desulfonatronovibrio hydrogenovorans* DSM 9292T | 50.33 | 2.94 |
| JAFE00000000 | *Desulfonatronum lacustre* DSM 10312T | 59.32 | 3.76 |
| FNIN00000000 | *Desulfonauticus submarinus* DSM 15269T | 32.47 | 2.10 |
| BDFE00000000 | *Desulfoplanes formicivorans* Pf12BT | 49.81 | 3.00 |
| JIAK00000000 | *Desulfovermiculus halophilus* DSM 18834T | 56.81 | 3.24 |
| AULZ00000000 | *Desulfovibrio africanus* subsp. *africanus* DSM 2603T | 61.10 | 4.41 |
| CP000112 | *Desulfovibrio alaskensis* G20 | 57.84 | 3.73 |
| JNJA00000000 | *Desulfovibrio alcoholivorans* DSM 5433T | 64.70 | 5.13 |
| ATHI00000000 | *Desulfovibrio alkalitolerans* DSM 16529T | 64.48 | 3.11 |
| AUMA00000000 | *Desulfovibrio aminophilus* DSM 12254T | 66.16 | 3.42 |
| AUCX00000000 | *Desulfovibrio bastinii* DSM 16055T | 43.06 | 3.91 |
| FUYA00000000 | *Desulfovibrio bizertenis* DSM 18304T | 52.09 | 3.27 |
| BBCB00000000 | *“Desulfovibrio brasiliensis”* JCM 12178 | 59.65 | 3.56 |
| AUCY00000000 | *Desulfovibrio cuneatus* DSM 11391T | 53.50 | 3.36 |
| ATUZ00000000 | *Desulfovibrio desulfuricans* DSM 642T | 57.36 | 3.39 |
| CP014229 | *“Desulfovibrio fairfieldensis”* CCUG 45958 | 60.90 | 3.70 |
| FNGA00000000 | *Desulfovibrio ferrireducens* DSM 16995T | 42.78 | 3.87 |
| JONL00000000 | *Desulfovibrio frigidus* DSM 17176T | 42.75 | 4.19 |
| AECZ00000000 | *Desulfovibrio fructosivorans* JJT | 63.85 | 4.67 |
| CP006585, CP006586 | *Desulfovibrio gigas* DSM 1382T | 63.63 | 3.79 |
| FUYC00000000 | *Desulfovibrio gracilis* DSM 16080T | 58.43 | 3.18 |
| IMG 2571042916 | *Desulfovibrio halophilus* DSM 5663T | 60.96 | 3.38 |
| FO203522, FO203523 | *Desulfovibrio hydrothermalis* DSM 14728T | 45.09 | 3.66 |
| IMG 2574180452 | *Desulfovibrio idahonensis* DSM 15450T | 64.99 | 3.57 |
| AUBP00000000 | *Desulfovibrio inopinatus* DSM 10711T | 49.09 | 5.77 |
| FNBX00000000 | *Desulfovibrio legallii* KHC7 | 64.80 | 2.70 |
| FRDI00000000 | *Desulfovibrio litoralis* DSM 11393T | 36.87 | 2.74 |
| ATVA00000000 | *Desulfovibrio longus* DSM 6739T | 63.64 | 3.70 |
| AP010904, AP010905, AP010906 | *Desulfovibrio magneticus* RS-1T | 62.67 | 5.32 |
| FZOC00000000 | *Desulfovibrio mexicanus* DSM 13116T | 65.60 | 3.54 |
| AQXE00000000 | *Desulfovibrio oxyclinae* DSM 11498T | 59.11 | 3.33 |
| IMG 2571042346 | *Desulfovibrio paquesii* DSM 16881T | 62.98 | 4.21 |
| LT630450 | *Desulfovibrio piger* FI11049 | 64.20 | 2.81 |
| AUBQ00000000 | *Desulfovibrio putealis* DSM 16056T | 62.79 | 4.71 |
| CP001649 | *Desulfovibrio salexigens* DSM 2638T | 47.09 | 4.29 |
| DIXN00000000 | *Desulfovibrio* sp. MAG UBA6079 | 67.30 | 4.54 |
| ATHV00000000 | *Desulfovibrio* sp. X2 | 67.99 | 3.91 |
| AZAO00000000 | *Desulfovibrio termitidis* HI1T | 66.07 | 4.26 |
| IMG 2574179706 | *Desulfovibrio vietnamensis* DSM 10520T (*D. senezii* DSM 8436T) c | 61.39 | 3.99 |
| AE017285, AE017286 | *Desulfovibrio vulgaris* HildenboroughT | 63.28 | 3.77 |
| AUDC00000000 | *Desulfovibrio zosterae* DSM 11974T | 41.75 | 4.10 |
| AULY00000000 | *Halodesulfovibrio aestuarii* DSM 10141 | 45.02 | 3.41 |
| FSRG00000000 | *Halodesulfovibrio marinisediminis* DSM 17456T | 44.95 | 3.71 |
| JXMS00000000 | *Halodesulfovibrio spirochaetisodalis* JC271T | 46.19 | 3.61 |
| CP004029, CP004030, CP004031, CP004032 | *Lawsonia intracellularis* N343 | 33.08 | 1.72 |
| CP002431 | *Pseudodesulfovibrio aespoeensis* Aspo-2T | 62.56 | 3.63 |
| LKAQ00000000 | *Pseudodesulfovibrio hydrargyri* BerOc1T | 63.80 | 4.08 |
| CP014206 | *Pseudodesulfovibrio indicus* J2T | 63.50 | 3.97 |
| FO203427 | *Pseudodesulfovibrio piezophilus* C1TLV30T | 49.93 | 3.65 |

a All accession numbers are from NCBI GenBank, except IMG numbers, which are from the JGI IMG/M database.

b Superscript T denotes a type strain. Species names in quotation marks have been effectively published but not validly published under the rules of the International Code of Nomenclature of Bacteria.

c It turned out that the determined sequences of the *Desulfovibrio senezii* dissimilatory sulfite-reductase genes obtained by cloning (JF830006) are 100% identical to the respective genes in the genome deposited under the name *Desulfovibrio vietnamensis* in the JGI IMG database, which is not possible due to the large phylogenetic distance of both species. Therefore, we conclude that the genomes of both species were mixed up at IMG and use in this study the designation *D. senezii* for the genome with the IMG ID 2574179706.

**TABLE S2.** Assembly statistics and sources of genomes representing a clade of sulfate-reducing bacteria containing the newly isolated strain L21-Syr-ABT.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Organism | Unclassified species | Unclassified species | *D. alkalitolerans* | Metagenome | *D. africanus* subsp. *africanus* |
| Strain | L21-Syr-ABT | X2 | DSM 16529T | UBA6079 | DSM 2603T |
| Source | hypersaline mat | estuarine sediment | biofilm growing in alkaline waters of a district heating system | oil sand tailings pond | well water |
| Assembly accession no. | GCA\_ 000711295 | GCA\_ 000422205 | GCA\_ 000422245 | GCA\_ 002428705 | GCA\_ 000422545 |
| Total length (bp) | 3,390,909 | 3,912,295 | 3,202,328 | 4,541,696 | 4,402,525 |
| Ungapped length (bp) | 3,390,909 | 3,912,295 | 3,202,328 | 4,541,423 | 4,400,400 |
| Contig count | 5 | 66 | 32 | 78 | 44 |
| Contig N50 | 2,531,670 | 125,439 | 202,204 | 112,272 | 162,267 |
| Contig L50 | 1 | 10 | 6 | 15 | 9 |
| Scaffold count | - | - | - | 72 | 41 |

**TABLE S3.** Cellular fatty acid compositions of strain L21-Syr-ABT and the related type strains *D. alkalitolerans* DSM 16259T and *D. africanus* subsp. *africanus* DSM 2603T.

Values are percentages of total fatty acids. Major fatty acids (>5% of total amount) are given in bold; fatty acids that were detected only in trace amounts (<1.0% of the total amount) in all samples are not shown. Abbreviations: -, not detected; tr, trace amounts (<1.0% of the total amount); *c*, *cis* isomer; *i* and *ai* indicate *iso*- and *anteiso*-branched fatty acids, respectively.

|  |  |  |  |
| --- | --- | --- | --- |
| Fatty acid | L21-Syr-ABT | DSM 16529T | DSM 2603T |
| *i*-C14:0 | 1.8 | tr | 1.0 |
| C14:0 | 2.6 | tr | 3.6 |
| *i*-C15:1 F a | - | - | 2.2 |
| *ai*-C15:1 A a | - | - | 1.2 |
| *i*-C15:0 | 7.1 | **30.4** | 3.0 |
| *ai*-C15:0 | **39.3** | **24.8** | **5.4** |
| *i*-C16:1 H a | - | - | **7.6** |
| *i*-C16:0 | **10.7** | 1.5 | 1.8 |
| C16:1 *c*9 | - | tr | **23.1** |
| C16:1 *c*11 | - | - | 1.6 |
| C16:0 | **21.5** | **7.4** | **8.6** |
| C16:0 10 methyl | 1.9 | - | - |
| *i*-C17:1 *c*7 | - | **14.6** | **7.6** |
| *ai*-C17:1 *c*7 | - | **6.7** | **5.4** |
| *i*-C17:0 | 3.5 | **7.0** | tr |
| *ai*-C17:0 | **6.3** | 1.1 | tr |
| C17:1 *c*11 | - | - | 1.2 |
| C18:1 *c*11 | - | tr | **21.2** |
| C18:0 | 3.8 | 1.3 | tr |
| *i*-C17:0 3OH | 1.0 | 2.8 | - |

a Positions of double bonds were not determined.

**TABLE S4.** Classification, number and predicted activities of carbohydrate-active protein domains identified in the L21-Syr-ABT genome.

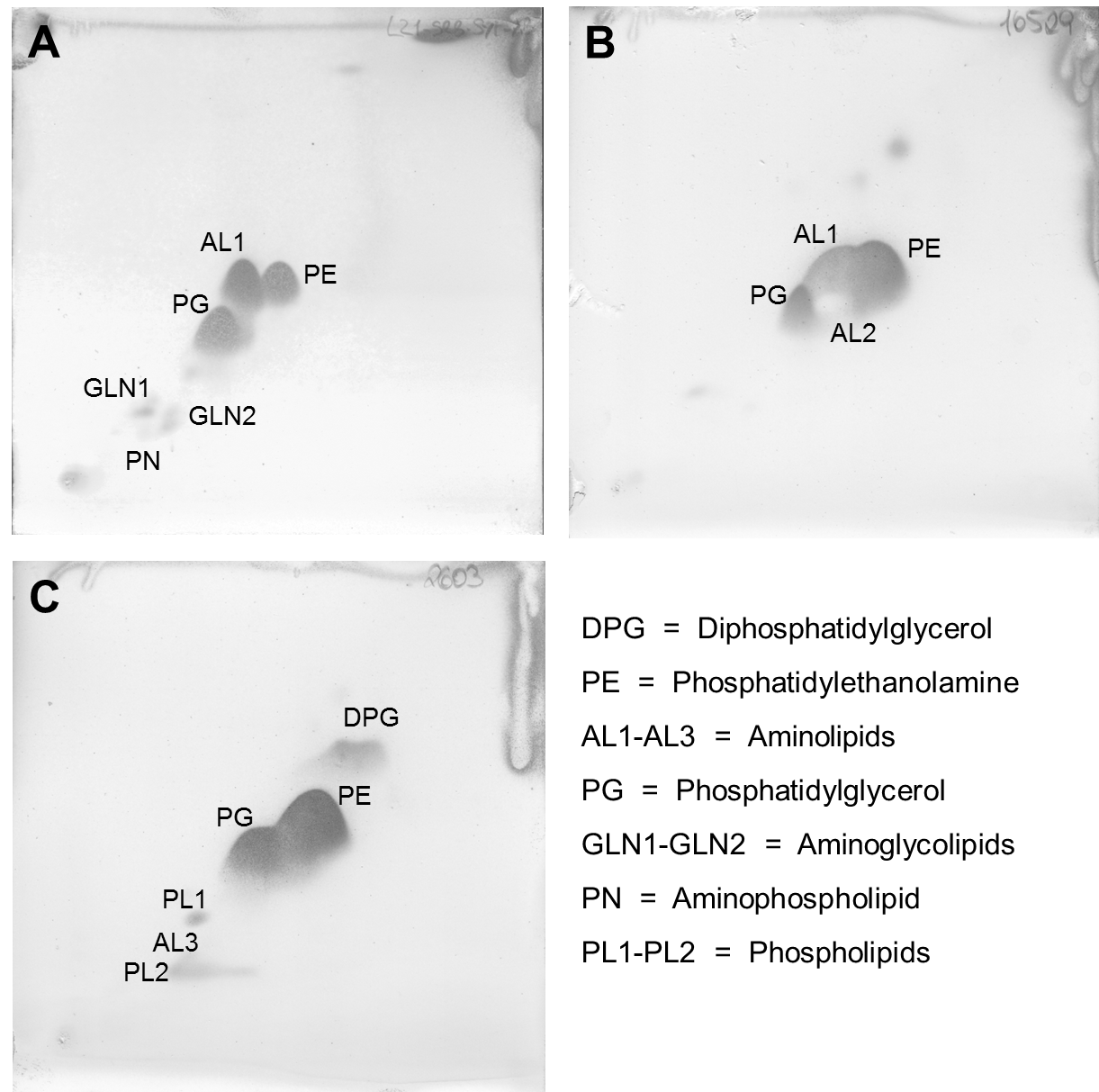
|  |  |  |
| --- | --- | --- |
| Carbohydrate-active enzymes or modules | No. of sequences a | Predicted activities |
| *Carbohydrate-Binding Modules* |  |  |
| CBM48 | 2 | Glycogen-binding |
| *Carbohydrate Esterases* |  |  |
| CE4 | 1 | Polysaccharide deacetylase |
| CE11 | 1 | UDP-3-O-acyl-N-acetylglucosamine deacetylase |
| CE14 | 1 | GlcNAc-PI de-N-acetylase |
| *Glycoside Hydrolases* |  |  |
| GH3 | 1 | Beta-N-acetylhexosaminidase |
| GH13\_3 | 1 | Alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase |
| GH13\_9 | 2 | 1,4-Alpha-glucan branching protein |
| GH13\_10 | 2 | Malto-oligosyltrehalose trehalohydrolase |
| GH13\_16 | 2 | Trehalose synthase |
| GH13\_26 | 2 | Malto-oligosyltrehalose synthase |
| GH15 | 1 | Putative glucoamylase |
| GH23 | 2 | Lytic transglycosylase, Lytic murein transglycosylase C |
| GH57 | 2 | Alpha-amylase/alpha-mannosidase |
| GH65 | 1 | Beta-phosphoglucomutase |
| GH77 | 1 | 4-Alpha-glucanotransferase |
| GH102 | 1 | Membrane-bound lytic murein transglycosylase A |
| GH103 | 2 | Membrane-bound lytic murein transglycosylase B |
| *Glycosyltransferases* |  |  |
| GT1 | 1 | unknown |
| GT2 | 6 | Exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase, Undecaprenyl-phosphate mannosyltransferase |
| GT4 | 11 | GDP-mannose-dependent alpha-(1-6)-phosphatidylinositol monomannoside mannosyltransferase, Glycosyltransferase involved in cell wall biosynthesis, Alpha-D-QuiNAc alpha-1,3-galactosyltransferase, GDP-mannose-dependent alpha-mannosyltransferase, Trehalose synthase |
| GT5 | 1 | Glycogen synthase |
| GT9 | 6 | ADP-heptose:LPS heptosyltransferase, Lipopolysaccharide heptosyltransferase II |
| GT19 | 1 | Lipid-A-disaccharide synthase |
| GT20 | 1 | Trehalose 6-phosphate synthase |
| GT26 | 1 | Exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase |
| GT28 | 2 | UDP-2,4-diacetamido-2,4, 6-trideoxy-beta-L-altropyranose hydrolase, UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase |
| GT30 | 1 | 3-deoxy-D-manno-octulosonic-acid transferase |
| GT35 | 2 | Alpha-1,4 glucan phosphorylase |
| GT51 | 1 | Penicillin-binding protein |
| GT83 | 2 | Dolichyl-phosphate-mannose-mannosyltransferase, Phospholipid carrier-dependent glycosyltransferase |

a Note that the total number is higher than the number of genes due to the occurrence of genes encoding more than one activity.

**TABLE S5.** Manually annotated genes with a potential function in the energy metabolism of strain L21-Syr-ABT. Assumed operons are highlighted with gray or blue shading. The IMG locus tags of the L21-Syr-ABT genome are labelled with N911DRAFT\_.

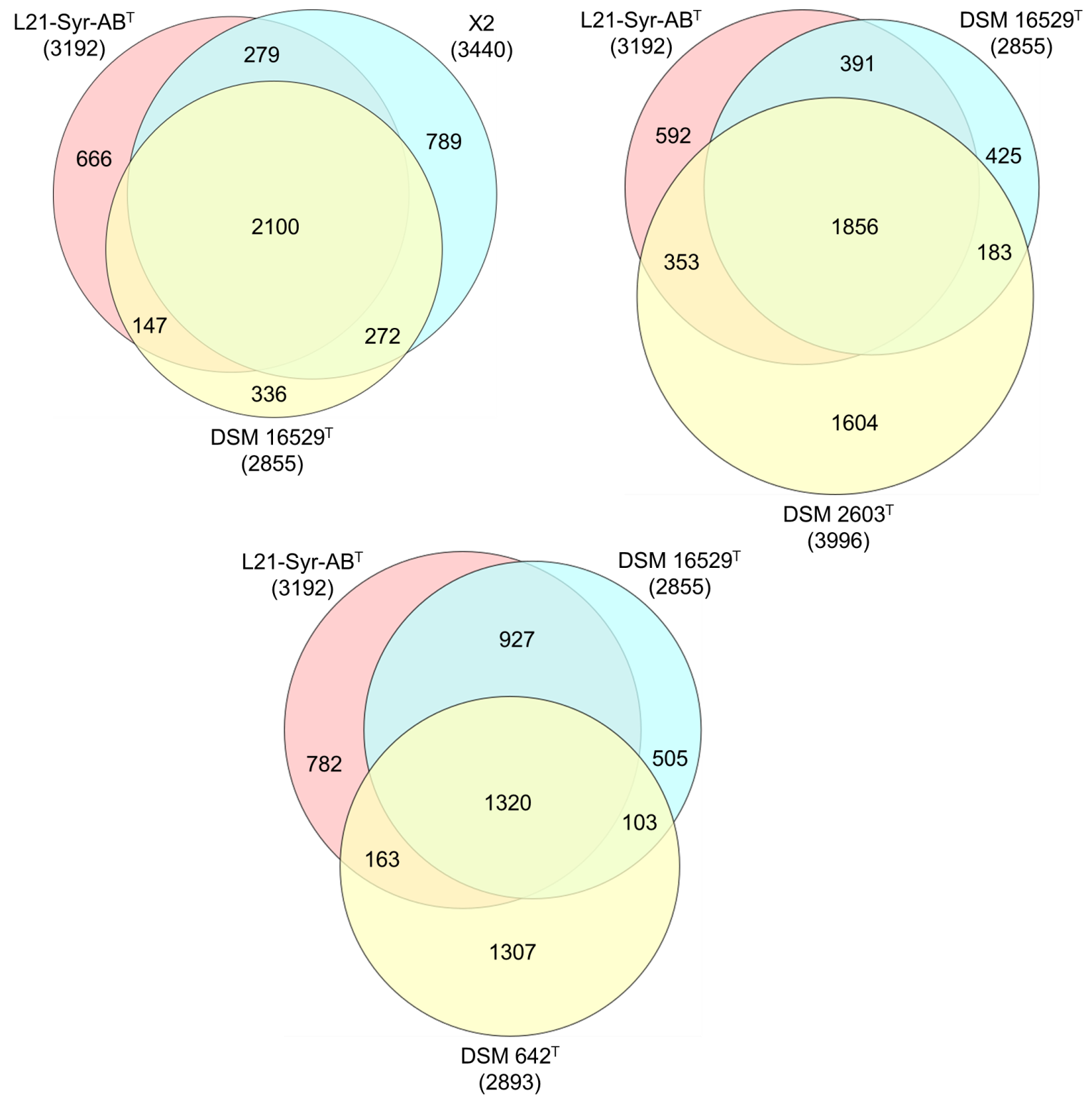
|  |  |  |  |
| --- | --- | --- | --- |
| Predicted protein | Gene Symbol | Amino Acids | IMG Locus Tag |
| Electron donor utilization |  |  |  |
| *Hydrogen* |  |  |  |
| Heterodisulfide reductase subunit A | *hdrA* | 669 | 3172 |
| Heterodisulfide reductase subunit C | *hdrC* | 169 | 3173 |
| Heterodisulfide reductase subunit B | *hdrB* | 305 | 3174 |
| F420-non-reducing [NiFe] hydrogenase iron-sulfur subunit | *mvhD* | 139 | 3175 |
| F420-non-reducing [NiFe] hydrogenase small subunit | *mvhG* | 325 | 3176 |
| F420-non-reducing [NiFe] hydrogenase large subunit | *mvhA* | 488 | 3177 |
| Hydrogenase maturation protease | *hybD* | 149 | 3178 |
| Membrane-bound Ech [NiFe] hydrogenase subunit F | *echF* | 193 | 0900 |
| Membrane-bound Ech [NiFe] hydrogenase subunit E | *echE* | 358 | 0901 |
| Membrane-bound Ech [NiFe] hydrogenase subunit D | *echD* | 120 | 0902 |
| Membrane-bound Ech [NiFe] hydrogenase subunit C | *echC* | 149 | 0903 |
| Membrane-bound Ech [NiFe] hydrogenase subunit B | *echB* | 282 | 0904 |
| Membrane-bound Ech [NiFe] hydrogenase subunit A | *echA* | 634 | 0905 |
| Periplasmic [NiFe] hydrogenase small subunit | *hynA* | 317 | 0964 |
| Periplasmic [NiFe] hydrogenase large subunit | *hynB* | 569 | 0965 |
| Periplasmic [NiFe] hydrogenase maturation factor | *hynC* | 178 | 0966 |
| Periplasmic [NiFe] hydrogenase assembly chaperone | *hynD* | 85 | 0967 |
| Type I cytochrome *c*3 | *cycA* | 132 | 3216 |
| *Formate* |  |  |  |
| Formate dehydrogenase maturation protein | *fdhE* | 292 | 1353 |
| Formate dehydrogenase assembly factor | *fdhD* | 231 | 1354 |
| Molybdopterin-guanine dinucleotide biosynthesis protein A | *mobA* | 200 | 1355 |
| Molybdenum cofactor biosynthesis enzyme | *moaA* | 330 | 1356 |
| Transposase |  | 296 | 1357 |
| Hypothetical protein |  | 67 | 1358 |
| Formate dehydrogenase major subunit | *fdhA* | 1005 | 1359 |
| Formate dehydrogenase iron-sulfur subunit | *fdhB* | 239 | 1360 |
| Formate dehydrogenase major subunit | *fdhA* | 1014 | 2430 |
| Formate dehydrogenase iron-sulfur subunit | *fdhB* | 248 | 2431 |
| Formate dehydrogenase maturation protein | *fdhE* | 316 | 2432 |
| Formate dehydrogenase assembly factor | *fdhD* | 253 | 2433 |
| *Ethanol* |  |  |  |
| Aldehyde:ferredoxin oxidoreductase | *aor* | 489 | 0054 |
| Rubrerythrin | *rbr* | 162 | 0055 |
| NAD(P)H-flavin reductase | *flxA* | 282 | 0056 |
| Fe-S oxidoreductase | *flxB* | 351 | 0057 |
| 4Fe-4S ferredoxin iron-sulfur binding domain-containing protein | *flxC* | 316 | 0058 |
| Methyl-viologen-reducing hydrogenase subunit D | *flxD* | 154 | 0059 |
| Heterodisulfide reductase subunit A | *hdrA* | 659 | 0060 |
| Heterodisulfide reductase subunit B | *hdrB* | 297 | 0061 |
| Heterodisulfide reductase subunit C | *hdrC* | 185 | 0062 |
| Alcohol dehydrogenase, class IV | *adh1* | 393 | 2511 |
| Two-component system response regulator, NtrC family |  | 451 | 2512 |
| PAS domain-containing protein |  | 401 | 2513 |
| Alcohol dehydrogenase, class IV | *adh2* | 379 | 2514 |
| *Pyruvate and Lactate* |  |  |  |
| L-Lactate utilization protein BA | *lutBA* | 727 | 1388 |
| L-Lactate utilization protein C | *lutC* | 210 | 1389 |
| Acetate kinase | *ackA* | 404 | 1390 |
| Phosphate acetyltransferase | *pta* | 704 | 1391 |
| D-Lactate dehydrogenase, iron-sulfur-binding domain | *glcF* | 426 | 1392 |
| D-Lactate dehydrogenase, FAD-binding domain | *glcD* | 461 | 1393 |
| Lactate permease | *lctP* | 570 | 1394 |
| Pyruvate:ferredoxin oxidoreductase | *por* | 1218 | 1395 |
| Two-component system response regulator, NtrC family |  | 477 | 1396 |
| PAS domain-containing protein |  | 848 | 1397 |
| FMN-dependent L-lactate dehydrogenase | *lldD* | 343 | 1398 |
| Sulfate reduction |  |  |  |
| Sulfate adenylyltransferase | *sat* | 426 | 0238 |
| Adenylylsulfate reductase beta subunit | *aprB* | 169 | 0239 |
| Adenylylsulfate reductase alpha subunit | *aprA* | 667 | 0240 |
| Quinone-modifying oxidoreductase, subunit A | *qmoA* | 411 | 0241 |
| Quinone-modifying oxidoreductase, subunit B | *qmoB* | 764 | 0242 |
| Quinone-modifying oxidoreductase, subunit C | *qmoC* | 415 | 0243 |
| Hypothetical protein |  | 228 | 0244 |
| Sulfite reductase-associated electron transfer protein DsrP | *dsrP* | 383 | 1528 |
| Sulfite reductase-associated electron transfer protein DsrO | *dsrO* | 257 | 1529 |
| Sulfite reductase-associated electron transfer protein DsrJ | *dsrJ* | 131 | 1530 |
| Sulfite reductase-associated electron transfer protein DsrK | *dsrK* | 535 | 1531 |
| Sulfite reductase-associated electron transfer protein DsrM | *dsrM* | 339 | 1532 |
| Hypothetical protein |  | 201 | 1533 |
| Dissimilatory sulfite reductase, subunit A | *dsrA* | 437 | 1562 |
| Dissimilatory sulfite reductase, subunit B | *dsrB* | 381 | 1563 |
| Dissimilatory sulfite reductase, subunit D | *dsrD* | 80 | 1564 |
| Cobyrinate a,c-diamide synthase | *cbiA* | 475 | 1565 |
| Hypothetical protein |  | 562 | 1566 |
| Sulfur relay protein DsrC | *dsrC* | 105 | 0568 |
| Membrane complexes involved in energy metabolism |  |  |  |
| *NADH-quinone oxidoreductase-like complex* |  |  |  |
| Subunit A | *nuoA* | 126 | 2747 |
| Subunit B | *nuoB* | 181 | 2748 |
| Subunit C | *nuoC* | 183 | 2749 |
| Subunit D | *nuoD* | 382 | 2750 |
| Subunit H | *nuoH* | 324 | 2751 |
| Subunit I | *nuoI* | 217 | 2752 |
| Subunit J | *nuoJ* | 169 | 2753 |
| Subunit K | *nuoK* | 102 | 2754 |
| Subunit L | *nuoL* | 494 | 2755 |
| Hypothetical protein |  | 87 | 2756 |
| Subunit N | *nuoN* | 596 | 2757 |
| Subunit M | *nuoM* | 522 | 2758 |
| Subunit N | *nuoN2* | 473 | 2759 |
| *Qrc complex* |  |  |  |
| Class III cytochrome *c* | *qrcA* | 186 | 2946 |
| Molybdopterin oxidoreductase | *qrcB* | 714 | 2947 |
| Molybdopterin oxidoreductase, iron-sulfur binding subunit | *qrcC* | 267 | 2948 |
| Molybdopterin oxidoreductase, membrane subunit | *qrcD* | 416 | 2949 |
| *Tmc complex* |  |  |  |
| Type II cytochrome *c*3 | *tmcA* | 132 | 2787 |
| Iron-sulfur oxidoreductase | *tmcB* | 448 | 2788 |
| Tmc subunit C | *tmcC* | 219 | 2789 |
| Tmc subunit D | *tmcD* | 420 | 2790 |
| *Rnf complex (ferrredoxin:NAD+ oxidoreductase)* |  |  |  |
| Class III cytochrome *c* |  | 251 | 0456 |
| Rnf electron transport complex subunit C | *rnfC* | 395 | 0457 |
| Rnf electron transport complex subunit D | *rnfD* | 312 | 0458 |
| Rnf electron transport complex subunit G | *rnfG* | 193 | 0459 |
| Rnf electron transport complex subunit E | *rnfE* | 242 | 0460 |
| Rnf electron transport complex subunit A | *rnfA* | 191 | 0461 |
| Rnf electron transport complex subunit B | *rnfB* | 710 | 0462 |
| Flavin transferase, ApbE-like |  | 324 | 0463 |
| *Ohc complex* |  |  |  |
| Iron-sulfur binding subunit | *ohcB1* | 335 | 1515 |
| Membran subunit | *ohcB2* | 159 | 1516 |
| Octaheme cytochrome *c* | *ohcA* | 547 | 1517 |
| Transmembrane cytochrome *b* | *ohcC* | 215 | 1518 |
| *F-type ATP synthase* |  |  |  |
| F0 subcomplex membrane subunit b’ | *atpF2* | 138 | 2300 |
| F0 subcomplex membrane subunit b | *atpF1* | 191 | 2301 |
| F1 subcomplex delta subunit | *atpH* | 183 | 2302 |
| F1 subcomplex alpha subunit | *atpA* | 502 | 2303 |
| F1 subcomplex gamma subunit | *atpG* | 298 | 2304 |
| F1 subcomplex beta subunit | *atpD* | 466 | 2305 |
| F1 subcomplex epsilon subunit | *atpC* | 142 | 2306 |
| F1 subcomplex beta subunit | *atpD2* | 461 | 3189 |
| F1 subcomplex epsilon subunit | *atpC2* | 127 | 3190 |
| F-type ATP Synthase membrane subunit I | *atpI* | 99 | 3191 |
| F-type ATP Synthase membrane subunit 2 | *atpR* | 96 | 3192 |
| F0 subcomplex membrane subunit a | *atpB* | 243 | 3193 |
| F0 subcomplex membrane subunit c | *atpE* | 93 | 3194 |
| F0 subcomplex membrane subunit b | *atpF3* | 282 | 3195 |
| F1 subcomplex alpha subunit | *atpA2* | 543 | 3196 |
| F1 subcomplex gamma subunit | *atpG2* | 300 | 3197 |
| *V-type proton ATPase* |  |  |  |
| V1 subcomplex subunit E | *ntpE* | 230 | 1707 |
| Hypothetical protein |  | 179 | 1708 |
| V1 subcomplex subunit A | *ntpA* | 577 | 1709 |
| V1 subcomplex subunit B | *ntpB* | 449 | 1710 |
| V1 subcomplex subunit D | *ntpD* | 201 | 1711 |
| V0 subcomplex subunit I | *ntpI* | 597 | 1712 |
| V0 subcomplex subunit K | *ntpK* | 160 | 1713 |

**FIGURE S1.** Polar lipid patterns of strain L21-Syr-ABT and two related type strains after two-dimensional thin layer chromatography.



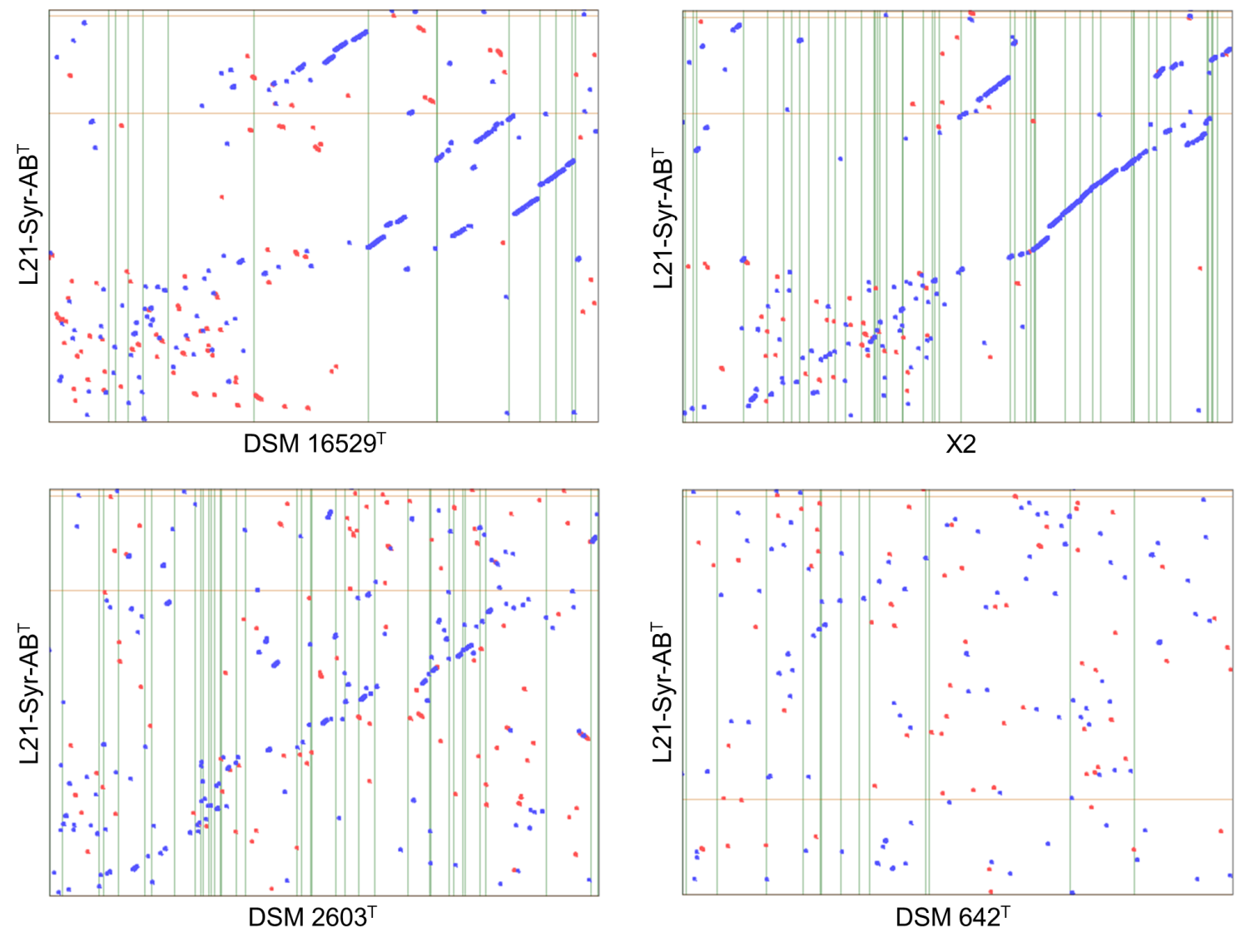
Chromatograms are shown for strain L21-Syr-ABT **(A)**, *D. alkalitolerans* DSM 16529T **(B)** and *D. africanus* subsp. *africanus* DSM 2603T **(C)**. Staining of the chromatograms was done with molybdatophosphoric acid. Specific spray reagents were used to detect the functional head groups of the lipids.

**FIGURE S2.** Venn diagrams showing the shared gene content among strains of the L21-Syr-ABT clade and the type species *D. desulfuricans*.



The number of overlapping protein genes is given inside the areas of the circles and the total number of protein genes used for each strain is shown in parentheses. Strain L21-Syr-ABT was compared with *Desulfovibrio* sp. X2, *D. alkalitolerans* DSM 16529T, *D.* *africanus* subsp. *africanus* DSM 2603T and *D.* *desulfuricans* DSM 642T. Diagrams were created using the Venn diagram plotter available from the Pacific Northwest National Laboratory Software Distribution Centre (<https://omics.pnl.gov/software/venn-diagram-plotter>).

**FIGURE S3.** Synteny plots of the L21-Syr-ABT genome against related strains and the type strain of the type species *D. desulfuricans*.



Strain designations given on the x-axis refer to *D. alkalitolerans* DSM 16529T, strain X2, *D. africanus* subsp. *africanus* DSM 2603T and *D. desulfuricans* DSM 642T. The six frame amino acid translation of the DNA input sequences were used for comparing genomes using PROmer software. Blue dots represent regions of similarity found on parallel strands and red dots show regions of similarity found on anti-parallel strands.