**Apendix A: Supplementary data**

**Taxonomic identification and antagonistic mechanism of *Streptomyces luomodiensis* sp. nov. against phytopathogenic fungi**

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**Tables**

Table S1. Allele sequence accession numbers of *Streptomyces* used for the present study

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Strains** | **atpD** | **gyrB** | **recA** | **rpoB** | **trpB** |
| *Streptomyces luomodiensis* | SCA4-21T | CP117522 | CP117522 | CP117522 | CP117522 | CP117522 |
| *Streptomyces iranensis* | HM 35T | MW197742.1 | MW197743.1 | MW197744.1 | MW197745.1 | MW197746.1 |
| *Streptomyces rapamycinicus* | NRRL B-5491T | NC\_022785.1 | NC\_022785.1 | NC\_022785.1 | NC\_022785.1 | NC\_022785.1 |
| *Streptomyces hygroscopicus* subsp.*hygroscopicus* | NBRC 13472T | NZ\_BBOX01000262.1 | NZ\_BBOX01000097.1 | NZ\_BBOX01000200.1 | NZ\_BBOX01000138.1 | NZ\_BBOX01000120.1 |
| *Streptomyces demainii* | NRRL B-1478(DSM 41600)T | FJ406182.1 | FJ406238.1 | FJ406294.1 | FJ406349.1 | FJ406405.1 |
| *Streptomyces melanosporofaciens* | DSM 40318T | NZ\_FNST01000002.1 | NZ\_FNST01000002.1 | NZ\_FNST01000002.1 | NZ\_FNST01000002.1 | NZ\_FNST01000002.1 |
| *Streptomyces antimycoticus* | NBRC 12839T | NZ\_BJHV01000001.1 | NZ\_BJHV01000001.1 | NZ\_BJHV01000001.1 | NZ\_BJHV01000001.1 | NZ\_BJHV01000001.1 |
| *Streptomyces himastatinicus* | ATCC 53653T | NZ\_GG657754.1 | NZ\_GG657754.1 | NZ\_GG657754.1 | NZ\_GG657754.1 | NZ\_GG657754.1 |
| *Streptomyces lydicamycinicus* | NBRC 110027T | BBNO01000001.1 | BBNO01000002.1 | BBNO01000008.1 | BBNO01000005.1 | BBNO01000012.1 |
| *Streptomyces caniferus* | NBRC 15389T | NZ\_BLIN01000002.1 | NZ\_BLIN01000005.1 | NZ\_BLIN01000002.1 | NZ\_BLIN01000005.1 | NZ\_BLIN01000005.1 |
| *Streptomyces platensis* | JCM 4662 (DSM 40041)T | NZ\_MIGA01000003.1 | NZ\_MIGA01000008.1 | NZ\_MIGA01000021.1 | NZ\_MIGA01000026.1 | NZ\_MIGA01000017.1 |
| *Streptomyces celluloflavu* | NRRL B-2493T | NZ\_JOEL01000012.1 | NZ\_JOEL01000017.1 | NZ\_JOEL01000056.1 | NZ\_JOEL01000011.1 | NZ\_JOEL01000004.1 |
| *Streptomyces morookaense* | LMG 20074 (DSM40503)T | NZ\_JABBXF010000065.1 | NZ\_JABBXF010000006.1 | NZ\_JABBXF010000043.1 | NZ\_JABBXF010000039.1 | NZ\_JABBXF010000021.1 |
| *Streptomyces lacticiproducens* | GIMN4.001 (NRRL B-24800)T | KT384614.1 | KT384963.1 | KT385313.1 | KT388934.1 | KT389283.1 |
| *Streptomyces palmae* | MU-AB 204 (JCM31289)T | MH534869.1 | MH534870.1 | MH534871.1 | MH534872.1 | MH534873.1 |
| *Streptomyces cuspidosporus* | NBRC 12378 (NRRL B-5620)T | KT384533.1 | KT384882.1 | KT385230.1 | KT388852.1 | KT389202.1 |
| *Streptomyces sparsogenes* | ATCC 25498T | NZ\_MAXF01000096.1 | NZ\_MAXF01000061.1 | NZ\_MAXF01000107.1 | NZ\_MAXF01000083.1 | NZ\_MAXF01000016.1 |

Table S2. Physiological and biochemical characteristics of strain SCA4-21T

|  |  |  |  |
| --- | --- | --- | --- |
| **Characteristics** | **Result** | **Characteristics** | **Result** |
| **Morphological** |  | **Antibiotic sensitivity (μg/slice)** |  |
| Aerial mycelium | Branched | Clindamycin (2) | S |
| Spore chain shape | Spiral | Chloramphenicol (30) | S |
| Spore shape | Cylindrical | Furazolidone (300) | R |
| Spore surface |  Shrinkage | Compound sulfamethoxazole (1.25) | R |
| **Biochemical** |  | Polymyxin B (300 IU/slice) | R |
| Urease test | + | Vancomycin (30) | R |
| Twain-20 | + | Penicillin (10 U/slice) | S |
| Twain-40 | - | Erythromycin (15) | R |
| Twain-60 | - | Minocycline (30) | R |
| Gelatin liquefaction | - | Kanamycin (30) | R |
| Starch hydrolysis | + | Gentamicin (10) | R |
| Nitrate reduction | - | Cefepime (75) | S |
| Degradation of cellulose | - | Ceftriaxone (30) | R |
| Melanoid pigment | + | Cefotaxime (30) | S |
| H2S production | - | Cefuroxime (30) | R |
| Siderophores | + | Cefamandole (30) | S |
| **Physiological** |  | Midecamycin (30) | S |
| pH range for growth | 6-9 | Carbenicillin (100) | S |
| Optimum pH for growth | 7 | Ampicillin (10) | S |
| NaCl tolerance (%) | 1-3 | Benzylpenicillin (1) | S |
| Optimum NaCl toleranc (%) | 2.00 | Piperacillin (100) | S |

Note: Note: “+” means positive; “-” means negative; S, sensitivity; R, resistance.

Table S3. The carbon and nitrogen utilization of strain SCA4-21T

|  |  |
| --- | --- |
| **Characteristic** | **Results** |
| *Carbon source utilization* |  |
| D- mannose | +++ |
| D- trehalose | ++ |
| L- arabinose | - |
| Sorbose | +++ |
| D- fructose | ++ |
| α- Lactose | + |
| D- ribose | +++ |
| Mannitol | ++ |
| Xylan | + |
| Raffinose | - |
| Inositol | - |
| *Nitrogen source utilization* |  |
| L- phenylalanine | + |
| L- asparagine | ++ |
| Anhydrous inositol | - |
| L- methionine | + |
| L- valine | +++ |
| L- histidine | + |
| L- glutamic acid | - |
| L- tryptophan | ++ |
| L- tyrosine | - |
| D- cellobiose | +++ |
| L- arginine | - |
| L- hydroxyproline | + |
| L- cysteine | + |
| Glycine | - |

Note: “+++” represented that the strain grew well; “+ +” represented the general growth of the strain; “+” represented that the strain can grow; ‘-’ represented the strain cannot grow.

Table S4. COG functional cluster of predicted genes in strain SCA4-21T

|  |  |  |  |
| --- | --- | --- | --- |
| **COG functional categories** | **Type** | **Gene****No.** | **% of Gene****No**. |
| **Information storage and processing** |  | **1489** | **19.7%** |
| RNA processing and modification | A | 1 |  |
| Translation, ribosomal structure and biogenesis | J | 296 |  |
| Transcription | K | 1032 |  |
| Replication, recombination and repair | L | 160 |  |
| **Metabolism** |  | **3578** | **47.4%** |
| Energy production and conversion | C | 441 |  |
| Amino acid transport and metabolism | E | 589 |  |
| Nucleotide transport and metabolism | F | 138 |  |
| Carbohydrate transport and metabolism | G | 772 |  |
| Coenzyme transport and metabolism | H | 484 |  |
| Lipid transport and metabolism | I | 568 |  |
| Inorganic ion transport and metabolism | P | 309 |  |
| Secondary metabolites biosynthesis, transport andcatabolism | Q | 277 |  |
| **Cellular processes and signaling** |  | **1528** | **20.2%** |
| Cell cycle control, cell division, chromosomepartitioning | D | 86 |  |
| Cell wall/membrane/envelope biogenesis | M | 310 |  |
| Cell motility | N | 20 |  |
| Posttranslational modification, protein turnover,chaperones | O | 255 |  |
| Signal transduction mechanisms | T | 484 |  |
| Intracellular trafficking, secretion, and vesiculartransport | U | 53 |  |
| Defense mechanisms | V | 212 |  |
| Extracellular structures | W | 14 |  |
| Cytoskeleton | Z | 5 |  |
| Mobilome: prophages, transposons | X | 89 |  |
| **Poorly characterized** |  | **953** | **12.6%** |
| General function prediction only | R | 794 |  |
| Function unknown | S | 159 |  |

Table S5. Family and gene ID of strain SCA4-21T CAZymes

|  |  |  |
| --- | --- | --- |
| **Family**  | **Genes No.** | **Gene ID** |
| **Auxiliary Activities（AA）** | **36**  |  |
| AA1 | 2 | gene0968, gene2542 |
| AA2 | 1 | gene6975 |
| AA3 | 11 | gene0094, gene0190, gene1355, gene1407, gene1519, gene2924, gene3679, gene3692, gene4873, gene6812, gene7011 |
| AA3\_2 | 3 | gene1526, gene3647, gene6518 |
| AA4 | 3 | gene3323, gene7037, gene7935 |
| AA5 | 1 | gene3264 |
| AA6 | 5 | gene0059, gene0636, gene7628, gene7709, gene8112 |
| AA7 | 3 | gene1000, gene4505, gene6047 |
| AA10 | 7 | gene0624, gene1675, gene1780, gene2049, gene3257, gene5523, gene6167 |
| **Carbohydrate-Binding Modules (CBM)** | **6** |  |
| CBM2 | 1 | gene2825 |
| CBM13 | 2 | gene5170, gene7842 |
| CBM35 | 1 | gene3777 |
| CBM66 | 2 | gene6392, gene7306 |
| **Carbohydrate Esterases (CE)** | **74** |  |
| CE1 | 24 | gene0176, gene0177, gene0396, gene0570, gene0767, gene1439, gene1563, gene1656, gene1898, gene2671, gene3543, gene3567, gene3714, gene3914, gene4651, gene4833, gene5174, gene5350, gene5357, gene7311, gene7724, gene7864, gene7996, gene8217 |
| CE2 | 2 | gene0498, gene0681 |
| CE3 | 6 | gene1102, gene2034, gene3277, gene3491, gene6265, gene6586 |
| CE4 | 7 | gene2216, gene4634, gene4840, gene6952, gene7425, gene7656, gene8060 |
| CE7 | 5 | gene0562, gene4053, gene7026, gene7877, gene8194 |
| CE8 | 1 | gene0661 |
| CE9 | 1 | gene3774 |
| CE10 | 21 | gene0003, gene0081, gene0199, gene0305, gene0476, gene1047, gene1138, gene1175, gene1685, gene1712, gene3597, gene4022, gene4408, gene5315, gene5675, gene6198, gene6272, gene6316, gene6361, gene7673, gene7840 |
| CE12 | 2 | gene2218, gene7487 |
| CE14 | 4 | gene1650, gene5187, gene5317, gene6111 |
| CE15 | 1 | gene7746 |
| **Glycoside Hydrolases (GH)** | **155** |  |
| GH1 | 2 | gene1587, gene3177 |
| GH2 | 8 | gene0100, gene0974, gene6895, gene6996, gene7224, gene7387, gene8209, gene8222 |
| GH3 | 4 | gene3119, gene5445, gene6959, gene8067 |
| GH4 | 3 | gene3020, gene6988, gene0953 |
| GH5\_1 | 1 | gene3947 |
| GH5\_8 | 1 | gene7006 |
| GH5\_18 | 1 | gene8068 |
| GH5\_19 | 1 | gene6958 |
| GH5\_40 | 1 | gene3171 |
| GH5\_43 | 1 | gene0548 |
| GH6 | 7 | gene0172, gene1998, gene3172, gene3265, gene3949, gene5764, gene6217 |
| GH8 | 1 | gene3962 |
| GH9 | 1 | gene7050 |
| GH10 | 2 | gene1734, gene6953 |
| GH11 | 1 | gene4355 |
| GH12 | 1 | gene5893 |
| GH13\_3 | 1 | gene5658 |
| GH13\_9 | 1 | gene5655 |
| GH13\_10 | 1 | gene6165 |
| GH13\_11 | 2 | gene5690, gene6169 |
| GH13\_13 | 1 | gene2526 |
| GH13\_16 | 1 | gene5657 |
| GH13\_26 | 1 | gene6168 |
| GH13\_30 | 2 | gene2532, gene7053 |
| GH13\_32 | 1 | gene2527 |
| GH15 | 3 | gene2098, gene2175, gene7351 |
| GH16 | 4 | gene0917, gene5654, gene6893, gene7651 |
| GH18 | 10 | gene1565, gene1638, gene2872, gene2907, gene3179, gene5217, gene5218, gene5259, gene5648, gene6873 |
| GH19 | 1 | gene6597 |
| GH20 | 3 | gene3148, gene3345, gene3624 |
| GH23 | 3 | gene1828, gene2670, gene4503 |
| GH25 | 3 | gene4119, gene5503, gene5697 |
| GH26 | 1 | gene0108 |
| GH27 | 1 | gene0179 |
| GH30\_5 | 2 | gene4557, gene4926 |
| GH30\_7 | 1 | gene2753 |
| GH31 | 2 | gene1301, gene3371 |
| GH33 | 4 | gene1036, gene2559, gene6377, gene7662 |
| GH35 | 1 | gene7807 |
| GH36 | 3 | gene0101, gene0376, gene6585 |
| GH42 | 1 | gene5892 |
| GH43 | 1 | gene1515 |
| GH43\_3 | 1 | gene7226 |
| GH43\_5 | 1 | gene0563 |
| GH43\_10 | 1 | gene7070 |
| GH43\_24 | 1 | gene0553 |
| GH43\_26 | 2 | gene0554, gene6994 |
| GH43\_34 | 2 | gene0507, gene0555 |
| GH44 | 1 | gene7198 |
| GH46 | 1 | gene6600 |
| GH48 | 1 | gene3170 |
| GH51 | 3 | gene2748, gene6815, gene6831 |
| GH54 | 1 | gene0178 |
| GH55 | 1 | gene0843 |
| GH62 | 2 | gene0173, gene1735 |
| GH63 | 1 | gene2853 |
| GH64 | 2 | gene2099, gene7246 |
| GH65 | 2 | gene0539, gene0972 |
| GH67 | 1 | gene0266 |
| GH74 | 1 | gene1467 |
| GH76 | 2 | gene6995, gene7247 |
| GH77 | 1 | gene3010 |
| GH78 | 2 | gene0515, gene2612 |
| GH85 | 1 | gene8066 |
| GH87 | 4 | gene1641, gene7052, gene7828, gene7829 |
| GH89 | 1 | gene2524 |
| GH92 | 4 | gene0931, gene6109, gene6112, gene7344 |
| GH93 | 3 | gene2646, gene7412, gene8210 |
| GH95 | 1 | gene0583 |
| GH106 | 2 | gene0514, gene0516 |
| GH109 | 4 | gene0602, gene2576 |
| GH113 | 1 | gene7311 |
| GH114 | 2 | gene2359, gene6983 |
| GH127 | 2 | gene0557, gene8140 |
| GH128 | 1 | gene7213 |
| GH135 | 1 | gene5362 |
| GH145 | 1 | gene6910 |
| GH146 | 3 | gene0517, gene0552, gene8139 |
| GH152 | 1 | gene7212 |
| GH154 | 2 | gene1022, gene7690 |
| **Glycosyl Transferases (GT)** | **65** |  |
| GT1 | 5 | gene0005, gene1180, gene3194, gene3883, gene6414 |
| GT2\_Glycos\_transf\_2 | 12 | gene0098, gene1210, gene1211, gene3460, gene3581, gene3863, gene4092, gene6148, gene6560, gene6827, gene6879, gene7922 |
| GT2\_Glyco\_tranf\_2\_3 | 11 | gene0027, gene0030, gene1219, gene1383, gene1997, gene2580, gene3613, gene3952, gene6830, gene6852, gene7308  |
| GT4 | 15 | gene0925, gene1215, gene1216, gene1333, gene1334, gene1987, gene1996, gene2081, Gene2100, gene2448, gene2614, gene3874, gene6502, gene6711, gene7874 |
| GT5 | 1 | gene1807 |
| GT9 | 3 | gene1212, gene1217, gene6836 |
| GT20 | 1 | gene3769 |
| GT28 | 3 | gene2400, gene5130, gene7422 |
| GT35 | 1 | gene5662 |
| GT39 | 1 | gene5075 |
| GT41 | 2 | gene2299, gene3007 |
| GT76 | 2 | gene2068, gene4393 |
| GT81 | 1 | gene3768 |
| GT83 | 4 | gene0158, gene3953, gene4091, gene7362 |
| GT87 | 3 | gene2632, gene4908, gene7459 |
| **Polysaccharide Lyases (PL)** | **12** |  |
| PL1 | 1 | gene7071 |
| PL1\_5 | 1 | gene0392 |
| PL1\_6 | 1 | gene2217 |
| PL3\_4 | 1 | gene5660 |
| PL7\_3 | 2 | gene7568, gene7569 |
| PL8 | 1 | gene7236 |
| PL9 | 1 | gene6336 |
| PL9\_3 | 1 | gene2215 |
| PL11 | 1 | gene5661 |
| PL26 | 1 | gene6698 |
| PL31 | 1 | gene2302 |
| **Total No.** | **348** | 　 |

Figures



Fig. S1. The analysis of high-performance liquid chromatography (Shimadzu LabSolutions) showed that strain SCA4-21T mainly contained dominant menaquinones composed of MK9 (H8) (65.50%) and MK10 (H2) (34.50%).



Fig. S2. Maximum-parsimony tree based on 16S rRNA gene showing position of strain SCA4-21T among its phylogenetic neighbors in the genus *Streptomyces*. Bootstrap percentages (based on 1000 replications) were shown at branching points. Bar, 5 base changes between nodes.



Fig. S3. Maximum-likelihood tree based on 16S rRNA gene showing position of strain SCA4- 21T among its phylogenetic neighbors in the genus *Streptomyces*. Bootstrap percentages (based on 1000 replications) were shown at branching points. Bar, 0.002 substitutions per nucleotide position.



Fig. S4. Maximum-likelihood tree based on five housekeeping genes (*atpD*, *gyrB*, *recA*, *rpoB*, and *trpB*) showing position of strain SCA4-21T among its phylogenetic neighbors in the genus *Streptomyces*. Bootstrap percentages (based on 1000 replications) were shown at branching points. Bar, 0.1 substitutions per nucleotide position.



Fig. S5. Maximum-parsimony tree based on five housekeeping genes (*atpD*, *gyrB*, *recA*, *rpoB*, and *trpB*) showing position of strain SCA4-21T among its phylogenetic neighbors in the genus *Streptomyces*. Bootstrap percentages (based on 1000 replications) were shown at branching points. Bar, Bar, 200 base changes between nodes.