**Supplementary Table 1.** Composition of media used for isolation of sulfur oxidizing bacteria in this study

|  |  |  |
| --- | --- | --- |
| **S. No.** | **Ingredient** | **Quantity used** |
| **Thiosulfate media** |
|  | Sodium Thiosulfate | 5 g |
|  | Sodium Bicarbonate | 200 mg |
|  | Ammonium Chloride | 100 mg |
|  | Potassium Hydrogen Phosphate | 100 mg |
|  | Bromophenol blue | 100 mg |
|  | Agar | 20 g |
|  | Water | 1000 ml |
|  | pH | 8.0 |
| **Starkey Broth** |
|  | KH2PO4 | 3.0 g |
|  | MgSO4×7H2O | 0.2 g |
|  | CaCl2×2H2O | 0.2 g |
|  | (NH4)2SO4 | 0.5 g |
|  | Traces of FeSO4 in 1000 ml |  |
|  | Bromo cresol purple was the indicator used |  |
|  | pH | 8.0 |
| **NCL Broth** |
|  | MgSO4×7H2O | 0.5g |
|  | CaCl2×2H2O | 0.25g |
|  | (NH4)2SO4 | 0.2g |
|  | traces of FeSO4 in 1000 ml |  |
|  | Bromo cresol purple was the indicator used |  |
|  | pH  | 8.0 |

**Supplementary Table 2.** Physico-chemical characteristics of experimental soil

|  |  |  |
| --- | --- | --- |
| S.N. | Soil Properties | Values |
| 1. | Soil separatesa (%) |  |
| (i) | Coarse sand (0.2-2.0 mm) | 11.43 |
| (ii) | Fine sand (0.02-0.2 mm) | 17.10 |
| (iii) | Silt (0.002-0.02mm) | 49.60 |
| (iv) | Clay(< 0.002 mm) | 21.87 |
| 2. | Textural class | Silt loam |
| 3. | pHb | 7.6 |
| 4. | EC (dS m-1) | 1.25 |
| 5. | OC (g kg-1) | 5.2 |
| 6. | OM (g kg-1) | 9.04 |
| 7. | Bulk density (Mg m-3) | 1.45 |
| 8. | Particle density (Mg m-3)  | 2.55 |
| 9. | Total CEC [cmol (P+) kg-1] | 14.36 |
| 10. |  CaCO3 (%) | 6.50 |
| 11. | Available macronutrients (kg ha-1) |  |
|  | N | 195.25 |
|  | P | 47.56 |
| (iii) | K | 145.50 |
| (iv) | S | 8.35 |
| 12. | Available micronutrients (mg kg-1) |  |
| (i) | Fe | 12.68 |
| (ii) | Zn | 0.74 |

a Hydrometer methods, b Water:soil= 2.5:1, EC- Electrical conductivity, OC- organic carbon, OM -organic matter, CEC- cation exchange capacity

**Supplementary Table 3.** List of primers used in qPCR analyses

|  |  |  |
| --- | --- | --- |
| **Gene** | **Forward Primer** | **Reverse Primer** |
| **1. Potassium transporters** |
| Cajanus cajan potassium transporter6 (CcPoT 6) | CATGTTTGCTGGTCTTGGGC | CAGAACAGGCCACCTCAACT |
| Cajanus cajan putative potassium transporter 12 (CcPoT 12) | TATGTCCCTGTCCCTGTGGT | TGCACGGTGATCTTCCTTCC |
| Cajanus cajan potassium transporter 3(CcPoT 3) | GTTTGAGGCAATTTCGCGGT | CCTCGTTCTCTACTCGCGTC |
| Cajanus cajan potassium transporter 7 (CcPoT 7) | GTTCCCGGTGCTCAGAGAAA | ACAAAGGGCTCGTTCCAACA |
| Cajanus cajan probable potassium transporter 17 (CcPoT 17) | ACTTATGCGGGACAGACAGC | ACGACTGGCTAGCAACAACA |
| **2. Phosphorous transporters** |  |  |
| Cajanus cajan phosphate transporter PHO1 homolog 3 (CcPhT PHO1-3) | CAGAGCTTTCAGTGGCCTCA | TCTGCGGCCATGAGAAAAGT |
| Cajanus cajan phosphate transporter (CcPhT PHO1) | TCACCACACACACACACCAA | TGAGCTGCCTGTAGTTGACG |
| Cajanus cajan inorganic phosphate transporter 1-4 (CcPh(i)T 1-4) | TCTCCACACAGTTCCTTCGC | GGCTATGAGGGTCTGTGCTC |
| Cajanus cajan probable inorganic phosphate transporter 1-3 (CcPh(i)T 1-3) | GCTTGGCTTTGGGATTGGTG | AAGGCCACTATTCCACCAGC |
| Cajanus cajan phosphate transporter PHO1 homolog 9 (CcPhT PHO1-9) | AGCACTTGAACAACGTTGGC | ATGGCTCCCTCCTCCTCATT |
| **3. Sulfur transporters** |  |  |
| Cajanus cajan sulfate transporter 1.1 (CcSULTR1;1) | CTTGGCATTGAAGCCATTTT | CCACTGCCACTGGTCCTATT |
| Cajanus cajan sulfate transporter 1.2 (CcSULTR1;2) | GCATCCAAGCCTTTGAAGAG | CCTCAACCACCTTTGGAGAA |
| Cajanus cajan high affinity sulfate transporter 2.1 (CcSULTR2;1) | GGGAAATTCAAGAAGCACCA | CCGATTTTGCCAACAAAGTT |
| Cajanus cajan probable sulfate transporter 3.4 (CcSULTR3;4) | TGGAAAGCTCAGCCTTGATT | TCCCTCTAGCAAAAGCCAAA |
| Cajanus cajan sulfate transporter 4.1 (CcSULTR4;1) | TTGGCTTCCCACCATTTTCT | CAGCCAACACCAAGACCAAC |
| Cajanus cajan sulfate transporter 4.2(CcSULTR4;2) | GCTGCTTCGTTTCATTAGCC | TCGATTTTCCCAGGTGTTTC |

**Supplementary Table 4.** Details of GenBank accession number of bacterial isolates with their nearest matching strain.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Strain** | **Identified As** | **Accession Number** | **Similarity (%)** | **Completeness (%)** | **E Value** | **Nearest match with Accession Number** |
| DRC-18-7A | *Stenotrophomonas maltophilia* | MZ436650 | 99.7 | 100 | 0.0 | [*Stenotrophomonas maltophilia* TRMK2](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1821463289)([CP049956](https://www.ncbi.nlm.nih.gov/nucleotide/CP049956.1?report=genbank&log$=nucltop&blast_rank=1&RID=DE90GAMV01R)) |
| DRC-18-10 | *Stenotrophomonas maltophilia* | MZ436652 | 99.8 | 100 | 0.0 | *Stenotrophomonas maltophilia* IPN-TD (KP165415) |
| DRC-18-7B | *Stenotrophomonas pavanii* | MZ436651 | 100 | 100 | 0.0 | [*Stenotrophomonas pavanii* IITRCS146](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2022709784) ([MW879704](https://www.ncbi.nlm.nih.gov/nucleotide/MW879704.1?report=genbank&log$=nucltop&blast_rank=1&RID=DE8GZ7G001R)) |
| DRC-18-11 | *Stenotrophomonas pavanii* | MZ436648 | 100 | 100 | 0.0 | [*Stenotrophomonas pavanii* IITRCS146](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2022709784) ([MW879704](https://www.ncbi.nlm.nih.gov/nucleotide/MW879704.1?report=genbank&log$=nucltop&blast_rank=1&RID=DE8GZ7G001R)) |
| DSC-18-101 | *Rhizobium pusense* | MZ436813 | 100 | 100 | 0.0 | *Rhizobium pusense* NRCPB10 (NR116874) |
| DRC-18-25 | *Rhizobium pusense* | MZ436814 | 99.5 | 100 | 0.0 | *Rhizobium pusense* YEBPT8 (MN082414) |
| DSC-18-5 | *Rhizobium pusense* | MZ436815 | 99.8 | 100 | 0.0 | *Rhizobium pusense* GRD S2 (MK559541) |
| DJC-18-21 | *Rhizobium pusense* | MZ436816 | 100 | 100 | 0.0 | *Rhizobium pusense* BN-23 (AB969785) |
| DRC-18-15 | *Rhizobium pusense* | MZ436817 | 99.5 | 100 | 0.0 | *Rhizobium pusense* BN-23 (AB969785) |
| DSC-18-501 | *Bacillus velezensis* | MZ436658 | 99.8 | 100 | 0.0 | *Bacillus velezensis* FZB42 (NR075004) |
| DJC-18-02J | *Bacillus velezensis* | MZ436658 | 99.6 | 100 | 0.0 | *Bacillus velezensis* CBMB205 (NR116240) |
| DRC-18-101A | *Paenibacillus massiliensis* | MZ447860 | 99.8 | 100 | 0.0 | *Paenibacillus massiliensis* EB373 (MH127819) |
| DSC-18-77D | *Paenibacillus massiliensis* | MZ447860 | 100 | 100 | 0.0 | *Paenibacillus massiliensis* 2301065 (NR115175) |

**Supplementary Table 5.** Antibiotic susceptibility of the sulphur oxidizing bacteria expressed as zone of inhibition (mm diameter)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Isolate | Kanamycin 30 | Streptomycin 10 | Ampicillin 10 | Chloramphenicol 30 | Rifampicin 5 | Nalidixic acid 30 |
| Diameter of inhibition zone(mm) |
| *S. maltophilia* DRC-18-7A | S(17) | S(23) | R(-) | I(19) | I(14) | R(-) |
| *S. maltophilia* DRC-18-10 | I(19) | S(26) | R(-) | S(21) | I(12) | R(-) |
| *S. pavanii* DRC-18-7B | S(21) | S(23) | R(-) | S(23) | I(15) | R(-) |
| *S. pavanii* DRC-18-11 | S(32) | I(15) | R(-) | S(20) | I (14) | R(-) |
| *R. pusense* DRC-18-25 | I(15) | S(23) | R(-) | I(13) | I (12) | R(-) |
| *R. pusense* DSC-18-5 | I(14) | S(27) | R(-) | S(16) | I (13) | R(-) |
| *R. pusense* DJC-18-21 | I(16) | I(15) | R(-) | S(21) | I (14) | R(-) |

Note: Degree of susceptibility: S=sensitive (≥21mm); I=intermediate (12-20mm); R=resistant (≤12mm).

**Supplementary Table 6.** Biochemical properties of selected sulfur oxidixing bacterial strains used in this study

|  |  |
| --- | --- |
| Properties/ characteristics | Microbial strains |
| DRC-18-7A | DRC-18-10 | DRC-18-7B | DRC-18-11 | DRC-18-25 | DSC-18-5 | DJC-18-21 |
| Amylase production | +ve | +ve | +ve | +ve | +ve | -ve | +ve |
| IAA production | +ve | +ve | +ve | -ve | +ve | +ve | -ve |
| P solubilization | +ve | +ve | +ve | +ve | -ve | -ve | -ve |
| H2O2  production | -ve | -ve | -ve | -ve | +ve | -ve | -ve |
| Catalase test | +ve | -ve | -ve | -ve | -ve | +ve | +ve |
| Starch hydrolysis | +ve | +ve | +ve | -ve | +ve | -ve | +ve |
| Siderophore production | +ve | +ve | +ve | +ve | +ve | +ve | -ve |
| Ammonia production | +ve | +ve | +ve | +ve | +ve | -ve | -ve |
| Chitinase production | -ve | -ve | -ve | +ve | -ve | -ve | +ve |
| Protease production | +ve | +ve | +ve | +ve | -ve | +ve | -ve |

**Supplementary Table 7.** Quantitative estimation of P solubilization, Siderophore and IAA production by SOB

|  |  |  |  |
| --- | --- | --- | --- |
| **Bacterial strains** | **P solubilization (µg ml-1)** | **Siderophore production (%)** | **IAA Production (µg ml-1)** |
| DRC-18-7A | 24.39 | 12.37 | 11.25 |
| DRC-18-10 | 21.25 | 14.25 | 10.50 |
| DRC-18-7B | 20.75 | 10.75 | 8.75 |
| DRC-18-11 | 18.36 | 9.66 | - |
| DRC-18-25 | - | 4.25 | 13.33 |
| DSC-18-5 | - | 5.33 | 15.21 |
| DJC-18-21 | - | - | - |