**Supplementary material**

**Supplementary Table S1.** Biochemical analysis of strains PIC28, PIC73 and PIC167 using Biolog GEN III Microplat**e** including utilization of carbon sources and chemical sensibilities.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Carbon source**  **utilization assays** | PIC28 | PIC73 | PIC167 | **Chemical sensitivity assays** | PIC28 | PIC73 | PICF167 | |
| Dextrin | + | + | + | pH 6 | + | + | + | |
| D-Maltose | + | + | + | pH 5 | - | + | - | |
| D-Trehalose | + | + | + | 1% NaCl | + | + | + | |
| D-Cellobiose | - | + | + | 4% NaCl | - | + | - | |
| Gentiobiose | - | + | + | 8% NaCl | - | - | - | |
| Sucrose | - | + | + | 1% Sodium Lactate | + | + | + | |
| D-Turanose | - | + | + | Fusidic Acid | - | - | - | |
| Stachyose | - | + | + | D-Serine | + | - | - | |
| D-Raffinose | - | + | + | Troleandomycin | - | - | - | |
| α-D-Lactose | - | + | + | Rifamycin SV | - | +/- | - | |
| D-Melibiose | - | + | + | Minocycline | - | - | - | |
| β-Methyl-D- Glucoside | + | + | + | Lincomycin | - | +/- | - | |
| D-Salicin | + | + | + | Guanidine HCl | - | + | - | |
| N-Acetyl-D- Glucosamine | + | - | - | Niaproof 4 | - | +/- | - | |
| N-Acetyl-β-D- Mannosamine | - | - | - | Vancomycin | - | - | - | |
| N-Acetyl-D- Galactosamine | - | - | - | Tetrazolium Violet | - | - | - | |
| N-Acetyl Neuraminic Acid | - | - | - | Tetrazolium Blue | - | - | - | |
| α-D-Glucose | + | + | + | Nalidixic Acid | - | - | - | |
| D-Mannose | - | + | + | Lithium Chloride | + | + | + | |
| D-Fructose | +/- | + | + | Potassium Tellurite | + | + | + | |
| D-Galactose | - | + | + | Aztreonam | - | - | - | |
| 3-Methyl Glucose | - | - | - | Sodium Butyrate | + | + | + | |
| D-Fucose | - | - | - | Sodium Bromate | - | - | - | |
| L-Fucose | - | - | - |  |  |  |  | |
| L-Rhamnose | - | - | - |  |  |  |  | |
| Inosine | +/- | - | - |  |  |  |  | |
| D-Sorbitol | - | - | - |  |  |  |  | |
| D-Mannitol | - | + | + |  |  |  |  | |
| D-Arabitol | - | - | - |  |  |  |  | |
| myo-Inositol | - | - | - |  |  |  |  | |
| Glycerol | + | + | + |  |  |  |  | |
| D-Glucose- 6-PO4 | + | - | - |  |  |  |  | |
| D-Fructose- 6-PO4 | + | - | - |  |  |  |  | |
| D-Aspartic Acid | - | - | - |  |  |  |  | |
| D-Serine | + | - | - |  |  |  |  | |
| Gelatin | + | - | - |  |  |  |  | |
| Glycyl-L-Proline | - | - | - |  |  |  |  | |
| L-Alanine | - | - | - |  |  |  |  | |
| L-Arginine | - | - | - |  |  |  |  | |
| L-Aspartic Acid | +/- | - | + |  |  |  |  | |
| L-Glutamic Acid | +/- | - | - |  |  |  |  | |
| L-Histidine | + | - | - |  |  |  |  | |
| L-Pyroglutamic Acid | - | - | - |  |  |  |  | |
| L-Serine | + | - | - |  |  |  |  | |
| Pectin | + | + | + |  |  |  |  | |
| D-Galacturonic Acid | - | + | + |  |  |  |  |
| L-Galactonic Acid Lactone | - | + | + |  |  |  |  | |
| D-Gluconic Acid | - | +/- | + |  |  |  |  | |
| D-Glucuronic Acid | - | - | - |  |  |  |  | |
| Glucuronamide | - | - | - |  |  |  |  | |
| Mucic Acid | - | - | - |  |  |  |  | |
| Quinic Acid | - | - | - |  |  |  |  | |
| D-Saccharic Acid | - | - | - |  |  |  |  | |
| p-Hydroxy- Phenylacetic Acid | - | - | - |  |  |  |  | |
| Methyl Pyruvate | + | - | +/- |  |  |  |  | |
| D-Lactic Acid Methyl Ester | - | - | - |  |  |  |  | |
| L-Lactic Acid | + | - | - |  |  |  |  | |
| Citric Acid | - | - | - |  |  |  |  | |
| α-Keto-Glutaric Acid | - | - | - |  |  |  |  | |
| D-Malic Acid | - | - | - |  |  |  |  | |
| L-Malic Acid | - | - | + |  |  |  |  | |
| Bromo-Succinic Acid | - | - | + |  |  |  |  | |
| Tween 40 | - | - | - |  |  |  |  | |
| γ-Amino-Butryric Acid | - | - | - |  |  |  |  | |
| α-Hydroxy- Butyric Acid | - | - | - |  |  |  |  | |
| β-Hydroxy-D,L- Butyric Acid | - | - | - |  |  |  |  | |
| α-Keto-Butyric Acid | - | - | - |  |  |  |  | |
| Acetoacetic Acid | + | - | - |  |  |  |  | |
| Propionic Acid | - | - | - |  |  |  |  | |
| Acetic Acid | + | - | + |  |  |  |  | |
| Formic Acid | + | - | - |  |  |  |  | |
|  |  |  |  |  |  |  |  | |

+, ability to use this carbon source or no sensitivity to the inhibitory chemical; –, no ability to use this carbon source or significant sensitivity to the inhibitory chemical; ±, one replicate showed positive result and the other negative and.

**Supplementary Table S2.** General information of the three sequencing projects.

|  |  |  |
| --- | --- | --- |
| **MIGS ID** | **Property** | **Term** |
| MIGS-28 | Libraries used | PCR-free 550 pb |
| MIGS-29 | Sequencing platforms | Illumina Miseq |
| MIGS-30 | Assemblers | Megahit v1.0.3 |
| MIGS-31 | Finishing quality | Draft |
| MIGS-31.2 | Fold coverage | 168 x (PIC28)  193x (PIC73)  130x (PICF167) |
| MIGS-32 | Gene calling method | NCBI Prokaryotic Genome Annotation Pipeline |
|  | Locus Tag | PIC28  PIC73  PIC167 |
|  | Genbank ID | PZPM00000000 (PIC28)  PNXP00000000 (PIC73)  PNXQ00000000 (PIC167) |
|  | BIOPROJECT | PRJNA428872 |
|  | NCBI taxon ID | 994873 (PIC28)  1406 (PIC73)  159743 (PIC167) |
|  | Project relevance | Plant-bacteria interaction,  Agricultural, Environmental |

MIGS, minimum information about a genome sequence (Field et al., 2008).

**Supplementary Table S4.** Number of genes associated with GO functional categories.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Strain** | | | | | | | |  | |
|  | **PIC28** | | **PIC73** | | | **PIC167** | | |  | |
| **Code** | **Value** | **% of total** | | **Value** | **% of total** | | **Value** | **% of total** | | **Group\_Description** | |
| A | 4 | 0.1268633048 | | 0 | 0 | | 0 | 0 | | RNA processing and modification | |
| B | 1 | 0.0317158262 | | 0 | 0 | | 0 | 0 | | Chromatin structure and dynamics | |
| C | 173 | 5.4868379321 | | 123 | 3.8163201986 | | 117 | 3.6885245902 | | Energy production and conversion | |
| D | 59 | 1.8712337456 | | 58 | 1.7995656221 | | 54 | 1.7023959647 | | Cell cycle control, cell division, chromosome partitioning | |
| E | 312 | 9.8953377735 | | 272 | 8.4393422277 | | 284 | 8.9533417402 | | Amino acid transport and metabolism | |
| F | 90 | 2.8544243578 | | 81 | 2.5131864722 | | 90 | 2.8373266078 | | Nucleotide transport and metabolism | |
| G | 158 | 5.0111005392 | | 348 | 10.7973937325 | | 358 | 11.2862547289 | | Carbohydrate transport and metabolism | |
| H | 177 | 5.6137012369 | | 165 | 5.1194539249 | | 165 | 5.2017654477 | | Coenzyme transport and metabolism | |
| I | 121 | 3.8376149699 | | 99 | 3.0716723549 | | 86 | 2.711223203 | | Lipid transport and metabolism | |
| J | 165 | 5.2331113225 | | 204 | 6.3295066708 | | 203 | 6.3997477932 | | Translation, ribosomal structure and biogenesis | |
| K | 254 | 8.0558198541 | | 328 | 10.1768538629 | | 323 | 10.1828499369 | | Transcription | |
| L | 105 | 3.3301617507 | | 119 | 3.6922122246 | | 120 | 3.7831021438 | | Replication, recombination and repair | |
| M | 198 | 6.2797335871 | | 185 | 5.7399937946 | | 168 | 5.2963430013 | | Cell wall/membrane/envelope biogenesis | |
| N | 48 | 1.5223596575 | | 64 | 1.985727583 | | 64 | 2.0176544767 | | Cell motility | |
| O | 123 | 3.9010466223 | | 118 | 3.6611852312 | | 106 | 3.341740227 | | Posttranslational modification, protein turnover, chaperones | |
| P | 206 | 6.5334601966 | | 206 | 6.3915606578 | | 213 | 6.7150063052 | | Inorganic ion transport and metabolism | |
| Q | 83 | 2.6324135744 | | 68 | 2.1098355569 | | 49 | 1.5447667087 | | Secondary metabolites biosynthesis, transport and catabolism | |
| R | 319 | 10.1173485569 | | 269 | 8.3462612473 | | 256 | 8.0706179067 | | General function prediction only | |
| S | 214 | 6.7871868062 | | 141 | 4.3748060813 | | 129 | 4.0668348045 | | Function unknown | |
| T | 199 | 6.3114494133 | | 240 | 7.4464784362 | | 245 | 7.7238335435 | | Signal transduction mechanisms | |
| U | 30 | 0.9514747859 | | 25 | 0.7756748371 | | 25 | 0.7881462799 | | Intracellular trafficking, secretion, and vesicular transport | |
| V | 100 | 3.1715826197 | | 87 | 2.6993484331 | | 95 | 2.9949558638 | | Defense mechanisms | |
| W | 3 | 0.0951474786 | | 0 | 0 | | 1 | 0.0315258512 | | Extracellular structures | |
| X | 9 | 0.2854424358 | | 20 | 0.6205398697 | | 19 | 0.5989911728 | | Mobilome: prophages, transposons | |
| Y | 0 | 0 | | 0 | 0 | | 0 | 0 | | Nuclear structure | |
| Z | 2 | 0.0634316524 | | 3 | 0.0930809805 | | 2 | 0.0630517024 | | Cytoskeleton | |

aThe total is based on the total number of protein coding genes in the annotated genome.