**Label-free** **Quantitative Proteomic Analysis of the Global Response to Indole-3-acetic Acid in Newly Isolated *Pseudomonas* sp. strain LY1**

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**Supplementary Table 1 Primers used in this study.**

|  |  |  |
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| Primer Name | Sequence (5′–3′) | Function Description (可选) |
| *iadA*-RT-F | GCCCCTGGAGACGCTGGACAA | Used to quantify the expression level of *iadA* genes in RT-qPCR reactions |
| *iadA*-RT-R | TTTCCCGTGGCATCACGGCC |
| *iadB*-RT-F | CCCACGTGAGGAGCAGCTGG | Used to quantify the expression level of *iadB* genes in RT-qPCR reactions |
| *iadB*-RT-R | GGTGGTGCGGAACAGGTTGC |
| *iadC*-RT-F | GATCTGGAAGCCGACCTGGA | Used to quantify the expression level of *iadC* genes in RT-qPCR reactions |
| *iadC*-RT-R | CGCGTGGTGGATCTCGGTCT |
| *iadD*-RT-F | GAGACCGATTTCGAGAACAC | Used to quantify the expression level of *iadD* genes in RT-qPCR reactions |
| *iadD*-RT-R | CTTGAGCACGTCCTTGCGGA |
| *iadE*-RT-F | GCTGCGATGACCCGCACCAC | Used to quantify the expression level of *iadE* genes in RT-qPCR reactions |
| *iadE*-RT-R | CGATGGCGCCCTTGGAGGCC |
| 16S-RT-F | GGTAGTCCACGCCGTAAACGA | Used to quantify the expression level of 16S rRNA gene genes in RT-qPCR reactions |
| 16S-RT-R | CCAATCCATCTCTGGAAAGT |
| *iadA*-Mu-UF | TATGACATGATTACGAATTAGGCGGCGGATTTCGCACAG | Used for the construction of double crossover homologous recombination plasmid pK18MST-Δ*iadA* |
| *iadA*-Mu-UR | CGCTCACCACGCCGTTGGCGTACACCTT |
| *iadA*-Mu-DF | CGCCAACGGCGTGGTGAGCGTCGAGCAG |
| *iadA*-Mu-DR | CGGGTACCGAGCTCGAATTTGGTCATCCTCGACACGG |
| *iadB*-Mu-UF | TATGACATGATTACGAATTATTCTGCGAGATGGTGGAGG | Used for the construction of double crossover homologous recombination plasmid pK18MST-Δ*iadB* |
| *iadB*-Mu-UR | GTCTCGATGTCCGGCACGTCGGCCACCGCCCAGACTTCCAGCTGC |
| *iadB*-Mu-DF | AGCAGCTGGAAGTCTGGGCGGTGGCCGACGTGCCGGACATC |
| *iadB*-Mu-DR | AGGATCCCCGGGTACCGAGCTCGTCGCCCTTGTCCAGGCAGTC |
| *iadE*-Mu-UF | TATGACATGATTACGAATTTCCACCACGCGGTGATCA | Used for the construction of double crossover homologous recombination plasmid pK18MST-Δ*iadE* |
| *iadE*-Mu-UR | GGGGGCGATGGCGTTGACGATGGACAGACCGAGGC |
| *iadE*-Mu-DF | GCCTCGGTCTGTCCATCGTCAACGCCATCGCCCCC |
| *iadE*-Mu-DR | CGGGTACCGAGCTCGAATTTGCGTATCGCCTTCGTCAT |

**Supplementary Figure 1**

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**Neighbour-joining tree based on analysis of the 16S rRNA gene showing relationship between strain LY1 and relative *Pseudomonas* sp. strains.** 16S rRNA genes from *Moraxella* were used as outgroup. Bootstrap probabilities (as percentages) are determined from 1,000 resamplings. Bar 0.005 substitutions per nucleotide position.

**Supplementary Figure 2**

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**Growth of strain LY1 under different conditions.** a. Effect of pH on the growth of strain LY1; b. Effect of temperature on the growth of strain LY1. c. Effect of IAA concentration on the growth of strain LY1. d. The changes of IAA concentrations in LY1 cultures. Each value is the mean from three parallel replicates ± SD.

**Supplementary Figure 3**



**Identification of dioxindole-3-acetic acid as the IAA degradation intermediate.** a. HPLC analysis of the collected new intermediate. b. LC-MS analysis of the new intermediate.

**Supplementary Figure 4**



RNM results. (a) structure of **M#1**. (b) ESIMS spectrum of **M#1**; (c) 1H-NMR spectrum of (**1**) in DMSO-*d*6 (d) 13C-NMR spectrum of **M#1** in DMSO-*d*6. Compound **M#1** was obtained as white amorphous powder. The molecular formula was C10H9NO4 on the basis of a ESIMS peak at m/z 206.6[M-H]- and NMR data, indicating 7 degrees of unsaturation. The observed signals in 1H NMR spectrum of **M#1** for two doublet aromatic protons at δH 7.31 (d, J = 7.3) and 6.81 (d, J = 7.6), and two triplet aromatic protons at δH 6.94 (t, J = 7.4) and 7.19 (t, J = 7.5) were indicative of a 1,2-disubstituted benzene ring system . The 13C NMR spectra revealed the presence of 10 carbon atoms, which were clarified into five non-protonated carbons (including one carboxyl, one amide carbonyl, two olefinic and one oxygenated sp3 carbons), four olefinic methines and one methylenes. Thus, compound **M#1** was identified as 2,3-dihydro-3-hydroxy-2-oxo-1H-indole-3-acetic acid.

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| NMR data of compounds **1** in DMSO-*d*6 (500 MHz for 1H and 125 MHz for 13C, *δ* in ppm, *J* in Hz) |
|  | *δ*c | *δ*H |
| 2 | 178.6, C |  |
| 3 | 73.1, C |  |
| 3a | 131.8, C | - |
| 4 | 124.1, CH | 7.31, d (7.3) |
| 5 | 121.6 CH | 6.94, t (7.4,) |
| 6 | 129.3, CH | 7.19, t (7.5) |
| 7 | 109.8, CH | 6.81,d (7.6) |
| 7a | 142.8, C | - |
| 8 | 42.2, CH2 | 2.90, d (15.6); 2.83, d (15.6) |
| 9 | 171.3, C |  |
| 1-NH |  | 10.27, s |

**Supplementary Figure 5**



**Identification of isatin and 2-aminophenyl glyoxylic acid as the IAA degradation intermediate.** a. HPLC analysis of the collected new intermediate. b. LC-MS analysis of the new intermediate.

**Supplementary Figure 6**



**Isatin transformation by IAA induced resting cells of strain LY1.** The signal at 254 nm was recorded. Isatin (with a retention time of 6.4 min) was transformed to a new compound (M#2, isatinic acid) with a retention time of 3.1 min. The arrow indicated UV spectrum of M#2. The mobile phase was 35% (v/v) methanol and 65% (v/v) 0.05% formic acid. The HPLC column was Agilent XBD C18 (4.6 mm × 250 mm, 5 μm).

**Supplementary Figure 7**



**Identification of anthranilate as the IAA degradation intermediate by strain LY1.** a. HPLC analysis of the sample of IAA transformation by IAA-grown resting cells of strain LY1. Spectra of the instinct peaks from HPLC DAD detector were also shown. b. LC-MS analysis of the purified compound with the retention time of 6.59 min in HPLC analysis (a). c. GC-MS analysis of the purified compound.