Supplementary Material

Enhanced bacterial growth and gene expression of D-amino acid dehydrogenase with D-glutamate as a sole carbon source

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**Supplementary Table S2**. Tabularized dataset of expression levels of four target genes (*dadA*, *murI*, *dao* and *murD*) sub-sampled at four timings (1, 2, 3 and 4) from the cultures of strain A25 (left), *Raoultella ornithinolytica* JCM 6096T (middle) and *Pseudomonas aeruginosa* JCM 5962T (right).determined by RT-RT-qPCR.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Gene | A25 | *Raoultella ornithinolytica* JCM 6096 | *Pseudomonas aeruginosa* JCM 5962 |
| 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 |
| Doublerelative value | *dadA*\*1 | 60.9  | 30.8  | 3.1  | 1.7  | 87.9  | 39.8  | 2.1  | 5.1  | 　0\*5 | 4.6  | 4.5  | 14.6  |
| *murI*\*2 | 1.6  | 0.8  | 0.4  | 0.0  | 1.2  | 0.5  | 0.5  | 0.9  | 1.4  | 1.7  | 1.4  | 1.3  |
| *dao*\*3 | 　0 | 0.3  | 0.3  | 　0 | 　0 | 0.5  | 0.6  | 1.6  | 0.8  | 1.0  | 1.5  | 0.6  |
| *murD*\*4 | 0.9  | 0.6  | 0.2  | 0.8  | 1.0  | 0.3  | 0.5  | 0.7  | 1.5  | 1.5  | 2.0  | 1.4  |
| Standard deviation | *dadA* | 23.9  | 6.5  | 0.4  | 1.2  | 34.3  | 17.1  | 0.5  | 0.2  | 　0\*6 | 4.0  | 3.5  | 6.2  |
| *murI* | 0.8  | 0.2  | 0.1  | 0.6  | 0.2  | 0.1  | 0.1  | 0.0  | 0.2  | 0.2  | 0.2  | 0.1  |
| *dao* | 　0 | 0.1  | 0.1  | 　0 | 　0 | 0.1  | 0.2  | 0.5  | 0.2  | 0.3  | 0.7  | 0.2  |
| *murD* | 0.3  | 0.2  | 0.1  | 0.2  | 0.1  | 0.1  | 0.1  | 0.3  | 0.3  | 0.7  | 0.9  | 0.1  |

\*1 D-amino acid dehydrogenase gene (*dadA*); \*2 glutamate racemase gene (*murI*); \*3 D-glutamate oxidase or D-glutamate (*dao*); and, \*4 gene of UDP-N-acetyl-α-D-muramoyl -L-alanyl-D-glutamate ligase involved in the synthesis of a cell-wall peptide in bacteria (*murD*); \*5 uncalculated due to less than threshold counts (*C*t); and, \*6 accordingly uncalculated.