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.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Gene | A25 | | | | *Raoultella ornithinolytica* JCM 6096 | | | | *Pseudomonas aeruginosa* JCM 5962 | | | |
| 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 |
| Double  relative 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.