Production of poly(3-hydroxyalkanoate) from benzoate and lignin-derived aromatic compounds using metabolically engineered *Pseudomonas putida* H

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**Supplementary Material**

**Table S1. Oligos employed in this work.**

| Oligos (5´→3´) | Sequence | Source |
|----------------|----------|--------|
| catAUpFw       | GAATTCGCACCATGCTCGAAGGTT | Fermelo Biotec, Santiago, Chile |
| catAUpRv       | CACAGTGACATAACCTCGAACCCTGTCATTACCTCGATTGGTTC | Fermelo Biotec, Santiago, Chile |
| catADwFw       | GTTCGAGGTTATGCTACTGTG | Fermelo Biotec, Santiago, Chile |
| catADwRv       | GGATCCCTCACAGAAGTTGAGCAAG | Fermelo Biotec, Santiago, Chile |
| catA2UpFw      | GAATTCGTCTACGCCCCTAGCTCCT | Fermelo Biotec, Santiago, Chile |
| catA2UpRv      | AAACAGCCCACTCGGTGAGGGGTTACCTCGTTTGTT | Fermelo Biotec, Santiago, Chile |
| catA2DwFw      | TCCACCGAGTGGGCTGTTT | Fermelo Biotec, Santiago, Chile |
| catA2DwRv      | GGATCCATGCAAGATCTGAGAGGATT | Fermelo Biotec, Santiago, Chile |
| catAKOFw       | CCGTGAATTTCCCACACT | Fermelo Biotec, Santiago, Chile |
| catAKORv       | GGGTCGAATCGAAGTACGAA | Fermelo Biotec, Santiago, Chile |
| catA2KOFw      | CATACTCGCGAGGTACAGCA | Fermelo Biotec, Santiago, Chile |
| catA2KORv      | GTCCCCGACAGGTATCT | Fermelo Biotec, Santiago, Chile |
S2. In-silico model of Pseudomonas putida H

### Transport Reactions
- **'biomass(c) →**
- **'CAT_ex(e) →**
- **'HMS_ex(e) →**
- **'MUC_ex(e) →**
- **'ATP_maintenance(c) →**
- **'CO2(c) →**

### Benzoate uptake and conversion to catechol
- **'BEN(e) → BEN(p)'
- **'BEN(p) → BEN(c)'
- **'BEN(c) + NADH(c) + O2(c) → BENDIO(c) + NAD(c)'
- **'BENDIO(c) + NAD(c) → CAT(c) + CO2(c) + NADH(c)'

### Ortho pathway
- **'CAT(c) + O2(c) → MUC(c)'
- **'MUC(c) → MUC_ex(e)'
- **'MUC(c) → MUCLAC(c)'
- **'MUCLAC(c) → KAD(c)'
- **'KAD(c) + SUCC-CoA(c) → KAD-CoA(c) + SUCC(c)'
- **'KAD-CoA(c) → AcCoA(c) + SUCC-CoA(c)'

### Meta pathway
- **'CAT(c) + O2(c) → HMS(c)'
- **'HMS(c) + NAD(c) → HM(c) + NADH(c)'
- **'HMS(c) → HMS_ex(e)'
- **'HMS(c) → FOR(c) + 2KPE(c)'
- **'FOR(c) + NAD(c) → CO2(c) + NADH(c)'
- **'HM(c) → 2KHE(c)'
- **'2KHE(c) → 2KPE(c) + CO2(c)'
- **'2KPE(c) → 4KPE(c)'
- **'4KPE(c) → acetA(c) + PYR(c)'
- **'acetA(c) + NAD(c) → AcCoA(c) + NADH(c)'

### Pentose phosphate pathway
- **'RIB-5P(c) ↔ XYL-5P(c)'
- **'RIB-5P(c) ↔ RIBO-5P(c)'
- **'S7P(c) + GAP(c) ↔ RIBO-5P(c) + XYL-5P(c)'
- **'S7P(c) + GAP(c) ↔ E4P(c) + F6P(c)'
- **'F6P(c) + GAP(c) ↔ E4P(c) + XYL-5P(c)'

### Entner-Doudoroff pathway
- **'6PG(c) → KDPG(c)'
- **'KDPG(c) → GAP(c) + PYR(c)'

### Embden-Meyerhof-Parnas pathway
- **'G6P(c) ↔ F6P(c)'
- **'FBP(c) ↔ F6P(c)'
- **'FBP(c) ↔ GAP(c) + DHAP(c)'
- **'DHAP(c) ↔ GAP(c)'
- **'GAP(c) + NAD(c) ↔ 13-PG(c) + NADH(c)'
- **'13-PG(c) ↔ 2-PG(c)'
- **'2-PG(c) ↔ PEP(c)'
- **'PEP(c) + ADP(c) → PYR(c) + ATP(c)'
- **'PYR(c) + NAD(c) → AcCoA(c) + NADH(c) + CO2(c)'
- **'PYR(c) + 2 ATP(c) → 2 ADP(c) + PEP(c)'

### TCA cycle
- **'AcCoA(c) + OAA(c) → CIT(c)'
- **'CIT(c) ↔ KIC(c)'
- **'I(c) + NADP(c) → AKG(c) + CO2(c) + NADPH(c)'
- **'AKG(c) + NAD(c) → SUCC-CoA(c) + NADH(c) + CO2(c)'
- **'SUCC-CoA(c) + ADP(c) ↔ SUCC(c) + ATP(c)'
- **'SUCC(c) + Q(c) ↔ FUM(c) + QH2(c)'
- **'FUM(c) → MAL(c)'
- **'MAL(c) + NAD(c) ↔ OAA(c) + NADH(c)'

### Glyoxylate metabolism
- **'I(c) + Glyoxy(c) + SUCC(c)'
- **'Glyoxy(c) + AcCoA(c) → MAL(c)'

### Amphibolic metabolism
- **'PYR(c) + ATP(c) + CO2(c) → OAA(c) + ADP(c)'
- **'MAL(c) + NADP(c) → PYR(c) + NADPH(c) + CO2(c)'
- **'OAA(c) → PYR(c) + CO2(c)'
- **'PEP(c) + CO2(c) → OAA(c)'

### PHA synthesis
- **'[5] AcCoA(c) + (4) ATP(c) + (7) NADPH(c) → PHA(c) + (4) ADP(c) + (7) NADP(c)'
- **'PHA(c) → '
Energy metabolism

\[ \text{NADPH}(c) + \text{NAD}(c) \rightarrow \text{NADP}(c) + \text{NADH}(c) \]

\[ (3) \text{NADH}(c) + (3) \text{NADP}(c) + \text{ATP}(c) \rightarrow (3) \text{NAD}(c) + (3) \text{NADPH}(c) + \text{ADP}(c) \]

\[ (0.5) \text{O}_2(c) + \text{NADH}(c) + (1.33) \text{ADP}(c) \rightarrow \text{NAD}(c) + (1.33) \text{ATP}(c) \]

\[ (0.5) \text{O}_2(c) + \text{QH}_2(c) + (0.66) \text{ADP}(c) \rightarrow \text{Q}(c) + (0.66) \text{ATP}(c) \]

\[ \text{ATP}(c) \rightarrow \text{ADP}(c) + \text{ATP}_\text{maintenance}(c) \]

\[ \text{SO}_4(c) + (3) \text{NADPH}(c) + (4) \text{ATP}(c) \rightarrow \text{H}_2\text{S}(c) + (3) \text{NADP}(c) + (4) \text{ADP}(c) \]

Biomass production

\[ (1.481) \text{OAA}(c) + (1.338) \text{PG}(c) + (0.627) \text{RIBO-5P}(c) + (17.821) \text{ATP}(c) + (16.548) \text{NADPH}(c) + (6.965) \text{NH}_3(c) + (3.548) \text{NAD}(c) + (2.930) \text{AcCoA}(c) + (2.861) \text{PYR}(c) + (1.078) \text{AKG}(c) + (0.361) \text{E4P}(c) + (0.72) \text{PEP}(c) + (0.233) \text{H}_2\text{S}(c) + (0.072) \text{F6P}(c) + (0.206) \text{G6P}(c) + (0.129) \text{GAP}(c) \rightarrow \text{biomass}(c) + (16.548) \text{NADP}(c) + (3.548) \text{NADH}(c) + (17.821) \text{ADP}(c) + (1.678) \text{CO}_2(c) \]

S3. Robustness analysis of the catechol branch of *P. putida* H with a benzoate uptake rate set at 2.4 [mmol (gCDW·h)^{-1}].