

FIG S1 Genomic comparisons of *P. veronii* strain 1YdBTEX2 and 1YB2 with *P. fluorescens* SBW25, A506, F113 and Pf0-1, *P. brassicacearum* NFM421, *P. protegens* CHA0 and Pf-5 and *P. aeruginosa* PAO1 at the amino acid level (A) and at the nucleotide level (B). Similarity matrices taking into consideration all proteins (A) or coding nucleotide sequences (B) as described in the Experimental procedures were generated using the Bray–Curtis coefficient (1) and dendrograms calculated by group-average agglomerative hierarchical clustering.

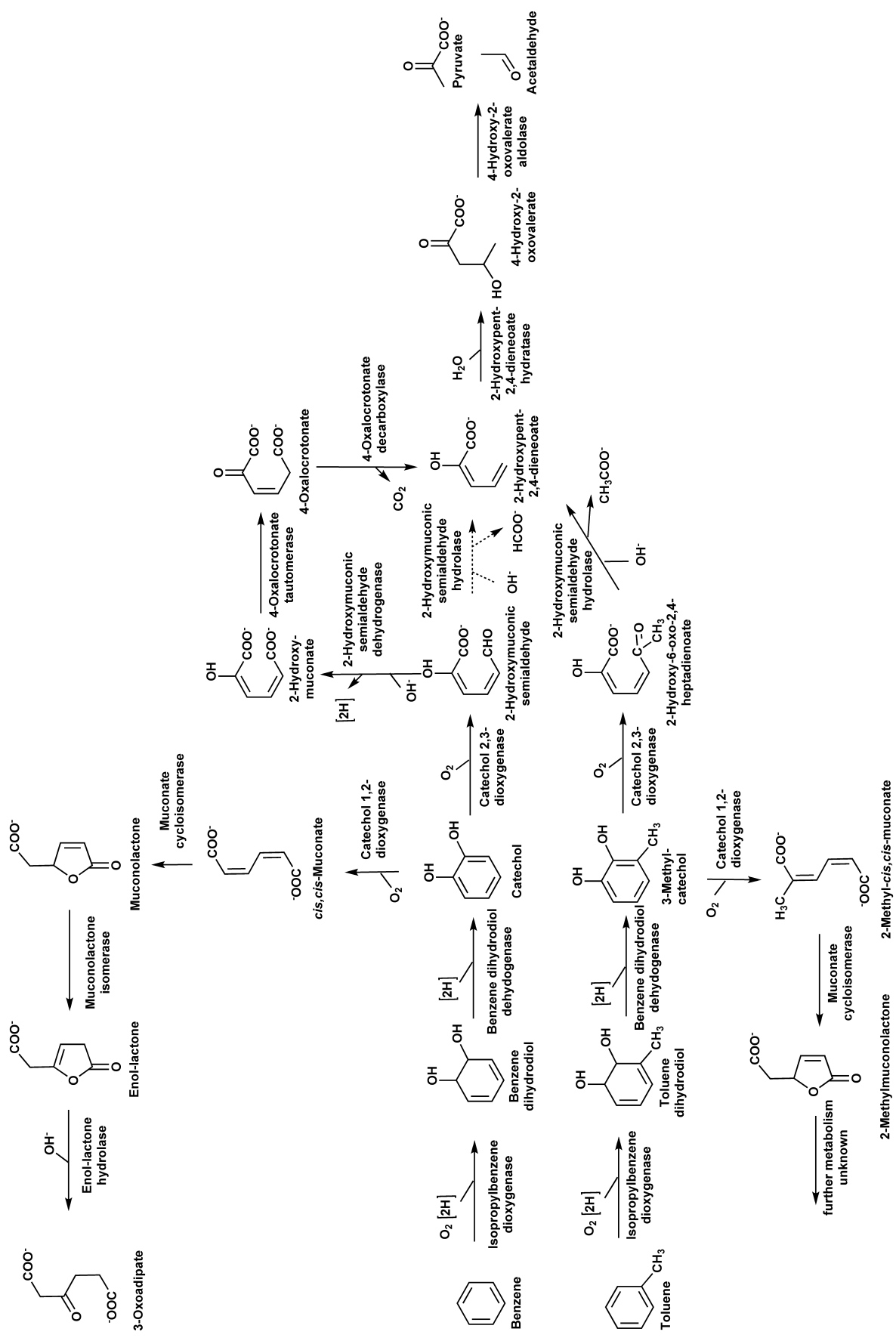


FIG S2 Metabolic routes for the degradation of benzene and toluene after dioxygenolytic activation. Major metabolic routes are indicated by solid arrows.

Tab. S1. Genome information of selected isolates of the *Pseudomonas fluorescens* group.

species	strain	Number of contigs	Genome size (Mb)	Gene count	Protein coding genes	GC content (%)	Reference
<i>P. veronii</i>	1YdBTEX2	63	6.68	6052	5981	59	(2)
	1YB2	115	7.64	6943	6879	60	
<i>P. fluorescens</i>	SBW25	1	7.14	6492	6395	60	(8)
	A506	1	5.96	5426	5323	60	(4)
	Pf0-1	1	6.44	5829	5722	61	(8)
	F113	1	6.85	5962	5862	61	(7)
<i>P. protegens</i>	Pf-5	1	7.07	6257	6142	63	(6)
	CHA0	1	6.86	6199	6116	63	(3)
<i>P. brassicacearum</i>	NFM421	1	6.84	6176	6095	61	(5)

REFERENCES

1. **Bray JR, Curtis JT.** 1957. An ordination of the upland forest communities of southern Wisconsin. *Ecol Monogr* **27**:325-349.
2. **de Lima-Morales D, Chaves-Moreno D, Jarek M, Vilchez-Vargas R, Jauregui R, Pieper DH.** 2013. Draft genome sequence of *Pseudomonas veronii* strain 1YdBTEX2. *Genome Announc* **1**:e00258-00213.
3. **Jousset A, Schuldes J, Keel C, Maurhofer M, Daniel R, Scheu S, Thuermer A.** 2014. Full-genome sequence of the plant growth-promoting bacterium *Pseudomonas protegens* CHA0. *Genome Announc* **2**.
4. **Loper JE, Hassan KA, Mavrodi DV, Davis EW, 2nd, Lim CK, Shaffer BT, Elbourne LD, Stockwell VO, Hartney SL, Breakwell K, Henkels MD, Tetu SG, Rangel LI, Kidarsa TA, Wilson NL, van de Mortel JE, Song C, Blumhagen R, Radune D, Hostetler JB, Brinkac LM, Durkin AS, Kluepfel DA, Wechter WP, Anderson AJ, Kim YC, Pierson LS, 3rd, Pierson EA, Lindow SE, Kobayashi DY, Raaijmakers JM, Weller DM, Thomashow LS, Allen AE, Paulsen IT.** 2012. Comparative genomics of plant-associated *Pseudomonas* spp.: insights into diversity and inheritance of traits involved in multitrophic interactions. *PLoS Genet* **8**:e1002784.
5. **Ortet P, Barakat M, Lalaouna D, Fochesato S, Barbe V, Vacherie B, Santaella C, Heulin T, Achouak W.** 2011. Complete genome sequence of a beneficial plant root-associated bacterium, *Pseudomonas brassicacearum*. *J Bacteriol* **193**:3146.
6. **Paulsen IT, Press CM, Ravel J, Kobayashi DY, Myers GS, Mavrodi DV, DeBoy RT, Seshadri R, Ren Q, Madupu R, Dodson RJ, Durkin AS, Brinkac LM, Daugherty SC, Sullivan SA, Rosovitz MJ, Gwinn ML, Zhou L, Schneider DJ, Cartinhour SW, Nelson WC, Weidman J, Watkins K, Tran K, Khouri H, Pierson EA, Pierson LS, 3rd, Thomashow LS, Loper JE.** 2005. Complete genome sequence of the plant commensal *Pseudomonas fluorescens* Pf-5. *Nat Biotechnol* **23**:873-878.

7. **Redondo-Nieto M, Barret M, Morrisey JP, Germaine K, Martinez-Granero F, Barahona E, Navazo A, Sanchez-Contreras M, Moynihan JA, Giddens SR, Coppoolse ER, Muriel C, Stiekema WJ, Rainey PB, Dowling D, O'Gara F, Martin M, Rivilla R.** 2012. Genome sequence of the biocontrol strain *Pseudomonas fluorescens* F113. *J Bacteriol* **194**:1273-1274.
8. **Silby MW, Cerdano-Tarraga AM, Vernikos GS, Giddens SR, Jackson RW, Preston GM, Zhang XX, Moon CD, Gehrig SM, Godfrey SA, Knight CG, Malone JG, Robinson Z, Spiers AJ, Harris S, Challis GL, Yaxley AM, Harris D, Seeger K, Murphy L, Rutter S, Squares R, Quail MA, Saunders E, Mavromatis K, Brettin TS, Bentley SD, Hothersall J, Stephens E, Thomas CM, Parkhill J, Levy SB, Rainey PB, Thomson NR.** 2009. Genomic and genetic analyses of diversity and plant interactions of *Pseudomonas fluorescens*. *Genome Biol* **10**:R51.