



Fig. 3. Two amino acid decarboxylase enzymes encoded by the *Providencia* genome act redundantly to modulate octanol avoidance.

a) Cartoons depicting the *tyrDC* locus (top) in *Lactobacillales* (left) and JUb39 (right) and the *adcA* locus (bottom) in *Morganella* (left) and JUb39 (right).

b) Presence of *tyrDC* and *adcA* among complete genomes in *Gammaproteobacteria*. Linked boxes indicate organization in an operon. Hatched shading indicates variable presence among genera. Colored triangles indicate taxa of interest.

c) Presence of *tyrDC*, *adcA*, *E.coli*-type *tyrP* and *Morganella*-type *tyt-1* at the family and genus level among *Enterobacteriales*. Linked boxes indicate organization in an operon.

d) Homology-based model of the TyrDC catalytic domain in *Providencia* based on the *Lb*-TyrDC crystal structure³⁴ using SWISS-MODEL (https://swissmodel.expasy.org). Residues in magenta, green and yellow are from *Lb*-TyrDC, JUb39-TyrDC, and JUb39-AdcA, respectively. PLP is depicted in red and L-Tyr (manually docked for illustration) is indicated in light blue. Position of A600/S586³⁴ in JUb39 TyrDC and *Lb*-TyrDC are indicated.

e, g) Reversal response latency of animals of wild-type *C. elegans* grown on the indicated bacterial genotypes in either control conditions of NGM + 0.5% L-Tyr (**e**) or supplemented with the indicated concentrations of TA (**g**) to 100% octanol using SOS assays. Each dot is the response time of a single worm. Y-axis is log₁₀-scaled for these log-normal distributed data, and normalized to the indicated control group for each experimental day, indicated by the gray horizontal line. Numbers in parentheses indicate the number of worms tested in assays over at least 3 independent days. Boxplot indicates median and quartiles, whiskers indicate the data range, excluding outliers. Gray thin and thick vertical bars at right indicate Bayesian 95% and 66% credible intervals for the difference of means, respectively. *P*-values between indicated conditions are from a LMM with Tukey-type multivariate-*t* adjustment.

f) Quantification of succinyl-TA in *tdc-1* mutant animals grown on the indicated bacterial strains. OP50 and JUb39 data are repeated from Fig. 2d. Data are averaged from three independent replicates each. ND, not detected.