Bioremediation of complex organic pollutants by engineered Vibrio natriegens

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Industrial wastewater, petroleum pollution and plastic contamination are significant threats to global marine biosecurity because of their toxic, mutagenic and persistent nature1. The use of microorganisms in bioremediation has been constrained by the complexity of organic pollutants and limited tolerance to saline stress2. In this study, we used synthetic biology to engineer Vibrio natriegens into a strain capable of bioremediating complex organic pollutants in saline wastewater and soils. The competence master regulator gene tfoX was inserted into chromosome 1 of the V. natriegens strain Vmax and overexpressed to enhance DNA uptake and integration. Degradation gene clusters were chemically synthesized and assembled in yeast. We developed a genome engineering method (iterative natural transformation based on Vmax with amplified tfoX effect) to transfer five gene clusters (43 kb total) into Vmax. The engineered strain has the ability to bioremediate five organic pollutants (biphenyl, phenol, naphthalene, dibenzofuran and toluene)

covering a broad substrate range, from monocyclic to multicyclic compounds, in industrial wastewater samples from a chlor–alkali plant and a petroleum refinery.

The genome assembly generated in this study was deposited in NCBI under the BioProject PRJNA1240198. All other data are presented in the paper and Supplementary Information. The public data used in this study included function annotations of non-essential genes in the genome of Vmax and degradation gene clusters from

the NCBI database (https://www.ncbi.nlm.nih.gov). The accession numbers of the genes are listed in Supplementary Tables 4 and 5.

Duarte, C. M. et al. Rebuilding marine life. Nature 580, 39–51 (2020).

Article ADS CAS PubMed Google Scholar

Li, X. et al. High salinity inhibits soil bacterial community mediating nitrogen cycling. Appl. Environ. Microbiol. 87, e01366–21 (2021).

Article CAS PubMed PubMed Central Google Scholar

Reddy, C. M. et al. Composition and fate of gas and oil released to the water column during the Deepwater Horizon oil spill. Proc. Natl Acad. Sci. USA 109, 20229–20234 (2011).

Article ADS PubMed PubMed Central Google Scholar

Huynh, B. Q. et al. Public health impacts of an imminent Red Sea oil spill. Nat. Sustainability 4, 1084–1091 (2021).

Article MathSciNet Google Scholar

Dvo ž ²À P. et al. Bioremediation 3.0: engineering pollutant-removing bacteria in the times of systemic biology. Biotechnol. Adv. 35, 845–866 (2017).

Article PubMed Google Scholar

Bhatt, P. et al. Biotechnological basis of microbial consortia for the removal of pesticides from the environment. Crit. Rev. Biotechnol. 41, 317–338 (2021).

Article PubMed Google Scholar

Atlas, R. M. & Hazen, T. C. Oil biodegradation and bioremediation: a tale of the two worst spills in U.S. history. Environ. Sci. Technol. 45, 6709–6715 (2011).

Article ADS CAS PubMed PubMed Central Google Scholar

Lin, J. et al. Environmental impacts and remediation of dye-containing wastewater. Nat. Rev. Earth Environ. 4, 785–803 (2023).

Article ADS CAS Google Scholar

Ahmadizadeh, R., Shokrollahzadeh, S., Latifi, S. M., Samimi, A. & Pendashteh, A. Application of halophilic microorganisms in osmotic membrane bioreactor (OMBR) for reduction of volume and organic load of produced water. J. Water Process Eng. 37, 101422 (2020).

Article Google Scholar

Weinstock, M. T. et al. Vibrio natriegens as a fast-growing host for molecular biology. Nat. Methods 13, 849–851 (2016).

Article CAS PubMed Google Scholar

Eagon, R. G. Pseudomonas natriegens, a marine bacterium with a generation time of less than 10 minutes. J. Bacteriol. 83, 736–737 (1962).

Article CAS PubMed PubMed Central Google Scholar

Ellis, G. A. et al. Exploiting the feedstock flexibility of the emergent

synthetic biology chassis Vibrio natriegens for engineered natural product production. Mar. Drugs 17, 679 (2019).

Article CAS PubMed PubMed Central Google Scholar

Teufel, M. et al. A multifunctional system for genome editing and large-scale interspecies gene transfer. Nat. Commun. 13, 3430 (2022).

Article ADS CAS PubMed PubMed Central Google Scholar

Stukenberg, D. et al. NT-CRISPR, combining natural transformation and CRISPR-Cas9 counterselection for markerless and scarless genome editing in Vibrio natriegens. Commun. Biol. 5, 265 (2022).

Article CAS PubMed PubMed Central Google Scholar

Dalia, T. N. et al. Multiplex genome editing by natural transformation (MuGENT) for synthetic biology in Vibrio natriegens. ACS Synth. Biol. 6, 1650–1655 (2017).

Article CAS PubMed PubMed Central Google Scholar

Lim, H. G. et al. Vibrio sp. dhg as a platform for the biorefinery of brown macroalgae. Nat. Commun. 10, 2486 (2019).

Article ADS PubMed PubMed Central Google Scholar

Denkin, S. M. & Nelson, D. R. Induction of protease activity in Vibrio anguillarum by gastrointestinal mucus. Appl. Environ. Microbiol. 65, 3555–3560 (1999).

Article ADS CAS PubMed PubMed Central Google Scholar

Mutanda, I. et al. Bacterial membrane transporter systems for aromatic compounds: regulation, engineering, and biotechnological applications. Biotechnol. Adv. 59, 107952 (2022).

Article CAS PubMed Google Scholar

Ramos, J. L. et al. Mechanisms of solvent tolerance in gram-negative bacteria. Annu. Rev. Microbiol. 56, 743–768 (2002).

Article CAS PubMed Google Scholar

Hoff, J. et al. Vibrio natriegens: an ultrafast-growing marine bacterium as emerging synthetic biology chassis. Environ. Microbiol. 22, 4394–4408 (2020).

Article PubMed Google Scholar

Tschirhart, T. et al. Synthetic biology tools for the fast-growing marine bacterium Vibrio natriegens. ACS Synth. Biol. 8, 2069–2079 (2019).

Article CAS PubMed Google Scholar

Lee, H. H. et al. Functional genomics of the rapidly replicating bacterium Vibrio natriegens by CRISPRi. Nat. Microbiol. 4, 1105–1113 (2019).

Article CAS PubMed Google Scholar

Fong, K. P., Goh, C. B. & Tan, H. M. Characterization and expression of the plasmid-borne bedD gene from Pseudomonas putida ML2, which codes for a NAD+-dependent cis-benzene dihydrodiol dehydrogenase. J. Bacteriol. 178, 5592–5601 (1996).

Article CAS PubMed PubMed Central Google Scholar

Assinder, S. J. & Williams, P. A. in Advances in Microbial Physiology, Vol. 31 (eds Rose, A. H. & Tempest, D. W.) 1–69 (Academic, 1990).

Kasai, Y., Inoue, J. & Harayama, S. The TOL plasmid pWW0 xylN gene product from Pseudomonas putida is involved in m-xylene uptake. J. Bacteriol. 183, 6662–6666 (2001).

Article CAS PubMed PubMed Central Google Scholar

Liu, Y. et al. Phenol biodegradation by Acinetobacter radioresistens APH1 and its application in soil bioremediation. Appl. Environ. Microbiol. 104, 427–437 (2020).

CAS Google Scholar

Simon, M. J. et al. Sequences of genes encoding naphthalene dioxygenase in Pseudomonas putida strains G7 and NCIB 9816-4. Gene 127, 31–37 (1993).

Article CAS PubMed Google Scholar

Tang, H. et al. Genome sequence of Pseudomonas putida strain B6-2, a superdegrader of polycyclic aromatic hydrocarbons and dioxin-like compounds. J. Bacteriol. 193, 6789–6790 (2011).

Article CAS PubMed PubMed Central Google Scholar

Kasuga, K. et al. Cloning of dfdA genes from Terrabacter sp. strain DBF63 encoding dibenzofuran 4,4a-dioxygenase and heterologous expression in Streptomyces lividans. Appl. Microbiol. Biotechnol. 97,

4485–4498 (2013).

Article CAS PubMed Google Scholar

Denome, S. A., Olson, E. S. & Young, K. D. Identification and cloning of genes involved in specific desulfurization of dibenzothiophene by Rhodococcus sp. strain IGTS8. Appl. Environ. Microbiol. 59, 2837–2843 (1993).

Article ADS CAS PubMed PubMed Central Google Scholar

Jiang, S. et al. Efficient de novo assembly and modification of large DNA fragments. Sci. China Life Sci. 65, 1445–1455 (2022).

Article CAS PubMed Google Scholar

Richardson, S. M. et al. Design of a synthetic yeast genome. Science 355, 1040–1044 (2017).

Article ADS CAS PubMed Google Scholar

Seeger, M. et al. Regiospecificity of dioxygenation of di- to pentachlorobiphenyls and their degradation to chlorobenzoates by the bph-encoded catabolic pathway of Burkholderia sp. strain LB400. Appl. Environ. Microbiol. 65, 3614–3621 (1999).

Article ADS CAS PubMed PubMed Central Google Scholar

de Lorenzo, V., Pérez-Pantoja, D. & Nikel, P. I. Pseudomonas putida KT2440: the long journey of a soil-dweller to become a synthetic biology chassis. J. Bacteriol. 206, e00136-24 (2024).

Article PubMed PubMed Central Google Scholar

Huang, L. et al. Establishment of a salt-induced bioremediation platform from marine Vibrio natriegens. Commun. Biol. 5, 1352 (2022).

Article CAS PubMed PubMed Central Google Scholar

Sandberg, T. E. et al. The emergence of adaptive laboratory evolution as an efficient tool for biological discovery and industrial biotechnology. Metab. Eng. 56, 1–16 (2019).

Article CAS PubMed PubMed Central Google Scholar

Yang, M. et al. Comparative toxicity of chlorinated saline and freshwater wastewater effluents to marine organisms. Environ. Sci. Technol. 49, 14475–14483 (2015).

Article ADS CAS PubMed Google Scholar

Lu, Q., Liang, Q. & Wang, S. Burning question: rethinking organohalide degradation strategy for bioremediation applications. Microb. Biotechnol. 17, e14539 (2024).

Article PubMed PubMed Central Google Scholar

Isobe, A. et al. Abundance of non-conservative microplastics in the upper ocean from 1957 to 2066. Nat. Commun. 10, 417 (2019).

Article ADS CAS PubMed PubMed Central Google Scholar

Si, J. et al. Porous composite architecture bestows Fe-based glassy alloy with high and ultra-durable degradation activity in decomposing

azo dye. J. Hazard. Mater. 388, 122043 (2020).

Article CAS PubMed Google Scholar

Khandare, S. D. et al. Biodegradation and decolorization of trypan blue azo dye by marine bacteria Vibrio sp. JM-17. Biocatal. Agric. Biotechnol. 51, 102802 (2023).

Article CAS Google Scholar

Peng, P. et al. Organohalide-respiring Desulfoluna species isolated from marine environments. ISME J. 14, 815–827 (2020).

Article CAS PubMed PubMed Central Google Scholar

Zhang, Z. et al. Polyvinyl chloride degradation by a bacterium isolated from the gut of insect larvae. Nat. Commun. 13, 5360 (2022).

Article ADS CAS PubMed PubMed Central Google Scholar

Liu, H. et al. An intelligent synthetic bacterium for chronological toxicant detection, biodegradation, and its subsequent suicide. Adv. Sci. 10, 2304318 (2023).

Article ADS CAS Google Scholar

Specht, D. A. et al. Efficient natural plasmid transformation of Vibrio natriegens enables zero-capital molecular biology. PNAS Nexus 3, pgad444 (2024).

Article PubMed PubMed Central Google Scholar

Lu, Q. Seamless cloning and gene fusion. Trends Biotechnol. 23, 199–207 (2005).

Article CAS PubMed PubMed Central Google Scholar

Zheng, W. et al. Precise genome engineering in Pseudomonas using phage-encoded homologous recombination and the Cascade–Cas3 system. Nat. Protoc. 18, 2642–2670 (2023).

Article CAS PubMed Google Scholar

Bopp, L. H., Chakrabarty, A. M. & Ehrlich, H. L. Chromate resistance plasmid in Pseudomonas fluorescens. J. Bacteriol. 155, 1105–1109 (1983).

Article CAS PubMed PubMed Central Google Scholar

Gal-Mor, O. et al. A novel secretion pathway of Salmonella enterica acts as an antivirulence modulator during salmonellosis. PLoS Pathog. 4, e1000036 (2008).

Article PubMed PubMed Central Google Scholar

Chan, L. Y., Kosuri, S. & Endy, D. Refactoring bacteriophage T7. Mol. Syst. Biol. 1, 2005.0018 (2005).

Article PubMed PubMed Central Google Scholar

Gai, Z. et al. Cometabolic degradation of dibenzofuran and dibenzothiophene by a newly isolated carbazole-degrading Sphingomonas sp. strain. Appl. Environ. Microbiol. 73, 2832–2838 (2007).

Article ADS CAS PubMed PubMed Central Google Scholar

Liu, Y. et al. A Pseudomonas sp. strain uniquely degrades PAHs and heterocyclic derivatives via lateral dioxygenation pathways. J. Hazard. Mater. 403, 123956 (2021).

Article CAS PubMed Google Scholar

Gressel, S. et al. CDK9-dependent RNA polymerase II pausing controls transcription initiation. eLife 6, e29736 (2017).

Article PubMed PubMed Central Google Scholar

Biglari, N. et al. Functionally distinct POMC-expressing neuron subpopulations in hypothalamus revealed by intersectional targeting. Nat. Neurosci. 24, 913–929 (2021).

Article CAS PubMed PubMed Central Google Scholar

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H.T. and J.D. designed and supervised the overall research framework

and provided acquired funding. C.S., Y. Liu, C.W. and L.Q. conducted molecular biology experiments, including bacterial strain construction, transcriptomic analyses and qPCR gene expression analysis. C.S., H.C. and P.Z. performed bacterial growth characterization and pollutant degradation assays, including optimization of culture conditions, growth curve measurement and degradation testing. H.C., W.W., Z.C., M.Y., Y. Li and S.H. collected and processed industrial wastewater and soil samples and conducted pollutant degradation experiments under practical environmental conditions. C.S., H.C., W.W., Z.C., M.Y., Y. Li, P.X. and H.T. performed chromatographic and mass spectrometric analyses (HPLC, gas chromatography, UPLC–QTOF-MS and HRGC–MS) and conducted data analysis. H.C., W.W., Z.C., M.Y. and Y. Li conducted microbial diversity analyses of environmental samples and performed statistical analyses, data organization and significance testing. C.S., H.C., W.W., Z.C., M.Y., Y. Li, Y.C., S.H., J.Z., P.X., J.D. and H.T. wrote the paper. All authors contributed to reviewing the draft of the paper and approving the final paper.

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a, Heatmap of differentially expressed genes related to aromatic

compound resistance, detected based on RNA-seq of V. natriegens Vmax in the presence or absence of the indicated mixture of complex organic pollutants. Transcription factors are in green; energy metabolism genes are in black; multidrug-resistance-related genes are in purple; ABC transporter genes are in blue. b, qPCR analysis of expression of the indicated genes. Data are represented as the mean of three biological triplicates ± SD.

a, NT efficiency testing between VCOD-1 and the original strain with a linear fragment (xxxx) as the donor. b, NT efficiency testing between VCOD-1 and the original strain with the p15A plasmid. c. NT efficiency of VCOD-1 with the indicated quantity of the 9Gv&dc£¤6Õ donor DNA fragment containing the indicated length (in kbp) of homology arms on each side of the mutation. Statistical analysis: a-c, data are represented as the mean ± SD. n = 3 independent experiments. Statistical significance was assessed using one-way ANOVA with Tukey’s multiple comparisons tests.

a, NT efficiency of VCOD-2 with the indicated quantities of the 9Gv&dc£¤6Õ donor DNA fragment (with 0.5 kbp/0.5 kbp homology arms). b, NT efficiency of VCOD-2 in the indicated bacterial growth states (measured by OD600) with 200 ng 9Gv&dc£¤6Õ (with 2 kbp/2 kbp homology arms) of the donor DNA fragment. c, NT efficiency of VCOD-2 induced by the indicated concentrations of IPTG with 200 ng of the 9Gv&dc£¤6Õ (2 kbp/2 kbp) donor DNA fragment. d, NT efficiency of VCOD-2 with 200 ng of the 9Gv&dc£¤6Õ donor DNA fragment (containing the indicated lengths for homology arms). e, NT efficiency of VCOD-2 with different incubation times after adding 200 ng of the 9Gv&dc£¤6Õ (2 kbp/2 kbp) donor DNA fragment. Statistical analysis: a-e, data are represented as the mean ± SD. n = 3

independent experiments. Statistical significance was assessed using one-way ANOVA with Tukey's multiple comparisons tests.

a-e, Catabolic pathways and LC-MS spectra for degradation intermediates produced by the VCOD-3 (a), VCOD-4 (b), VCOD-5 (c), VCOD-6 (d), and VCOD-7 (e) strains. The organic pollutants were added to resting cell suspensions in nine-salt solution (see Supplementary Information Table 2 for the detailed composition); metabolites were extracted by ethyl acetate after six-hour incubation of cultures with the pollutants (see Methods and Materials for details). Detected biphenyl degradation intermediates included: biphenyl-2,3-diol (2), 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate (3), and benzoic acid (4). Catechol was detected as a phenol degradation intermediate (6). Detected naphthalene degradation intermediates included naphthalene-1,2-diol (8) and salicylic acid (9). Detected dibenzofuran degradation intermediates included 2,2',3-trihydroxybiphenyl (11) and salicylic acid (9). Detected toluene degradation intermediates included benzyl alcohol (13) and benzoic acid (4).

a-e, Cultures of all strains were induced using 1 mM IPTG. The analyte genes (as indicated) were assessed with qPCR for strains VCOD-3 (a), VCOD-4 (b), VCOD-5 (c), VCOD-6 (d), and VCOD-7 (e) strains. Data are represented as the mean ± SD. n = 3 independent experiments.

a, Schematic for the organization of gene clusters in VCOD-12. Two gene clusters were inserted into the neutral site chr2_297. The screening marker kanamycin resistance gene KanR was present at the end of the dmp gene cluster. b, qPCR analysis of the indicated genes from the complex pollutant degrading gene cluster in

VCOD-12, induced with 1 mM IPTG. c-d, Complex organic pollutant remediation efficiency of VCOD-12 in nine-salt solution. e, Growth of the VCOD-2 and VCOD-12 strains in LB3 medium. Statistical analysis: b-e, data are represented as the mean ± SD. n = 3 independent experiments. Statistical significance was assessed using unpaired t-tests with Welch's correction.

a, Schematic for the organization of gene clusters in VCOD-13. Three gene clusters were inserted into the neutral site chr2_297. The screening marker chloramphenicol resistance gene CmR was present at the end of the nah gene cluster. b, qPCR analysis of the indicated genes from the complex pollutant degrading gene cluster in VCOD-13, induced with 1 mM IPTG. c-e, Complex organic pollutant remediation efficiency of VCOD-13 in nine-salt solution. f, Growth of the VCOD-2 and VCOD-13 strains in LB3 medium. Statistical analysis: b-f, data are represented as the mean ± SD. n = 3 independent experiments. Statistical significance was assessed using unpaired t-tests with Welch's correction.

a, Schematic for the organization of gene clusters in VCOD-14. Four gene clusters were inserted into the neutral site chr2_297. The screening marker kanamycin resistance gene KanR was present at the end of the nah gene cluster. b, qPCR analysis of the indicated genes from the complex pollutant degrading gene cluster in transformed V. natriegens cultures, induced with 1 mM IPTG. c-f, Complex organic pollutant remediation efficiency of VCOD-14 in nine-salt solution. g, Bacterial growth of strains VCOD-2 and VCOD-14 in LB3 medium. Statistical analysis: b-g, data are represented as the mean ± SD. n = 3 independent experiments. Statistical significance was assessed using unpaired t-test with Welch's correction.

a-e, Catabolic pathways and LC-MS spectra for degradation intermediates of biphenyl (1) (a), phenol (6) (b), naphthalene (8) (c), dibenzofuran (15) (d), and toluene (18) (e). The organic pollutants were added to resting cell suspensions in nine-salt solution; metabolites were extracted by ethyl acetate after six hours (see Methods and Materials for details). Detected biphenyl degradation intermediates included biphenyl-2,3-diol (3), 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate (4), and benzoic acid (5). Catechol was a detected degradation intermediate from phenol (7). Detected naphthalene degradation intermediates included naphthalene-1,2-diol (10) and salicylic acid (14). Detected dibenzofuran degradation intermediates included 2,2',3-trihydroxybiphenyl (16) and salicylic acid (14). Detected toluene degradation intermediates included benzyl alcohol (19) and benzoic acid (5).

a, Photograph of the multi-parallel bioreactors. Industrial wastewater samples were treated with VCOD-15. b-f, Complex organic pollutant bioremediation efficiency of VCOD-15 in industrial wastewater samples. g, The relative abundance of microbial genera in the wastewater samples' microbial communities was measured at 0, 24, and 48 h during the bioremediation process (n = 3). b-f, Data are represented as the mean of three biological triplicates ± SD.

This file contains Supplementary Figs. 1–21 and Tables 1–10. Supplementary figures: schematic of the workflow of gene cluster assembly and insertion, as well as growth curve, promoter strength, transformation/recombination efficiency, pollutant remediation efficiency and metabolite analysis in this study. Supplementary tables: strains, broths, genes, primers, wastewater samples and selected genome insertion targets used in this study.

Raw data for Figs. 1–5, Extended Data Figs. 1–10 and Supplementary Figs. 1, 6, 8, 9, 12 and 14–21.

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