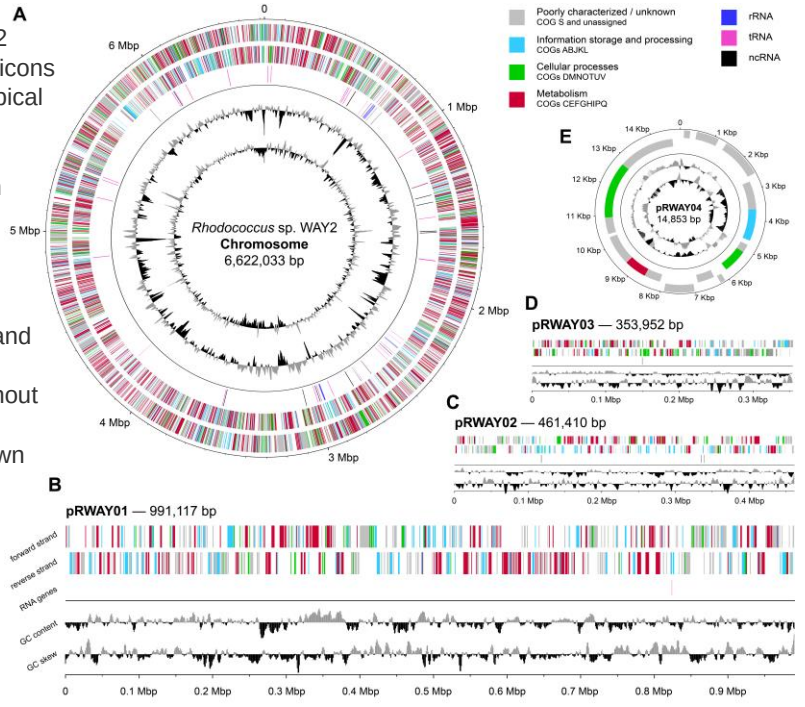
MICROBIAL GENOMICS
Volume 6, Issue 4, e000363
10.1099/mgen.0.000363

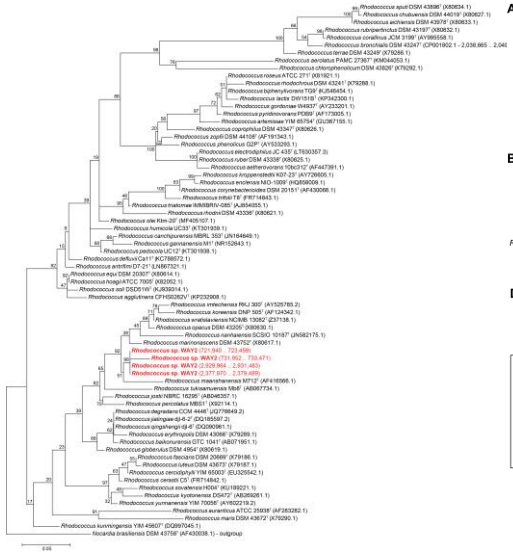
Analysis of the biodegradative and adaptive potential of the novel polychlorinated biphenyl degrader *Rhodococcus* sp. WAY2 revealed by its complete genome sequence

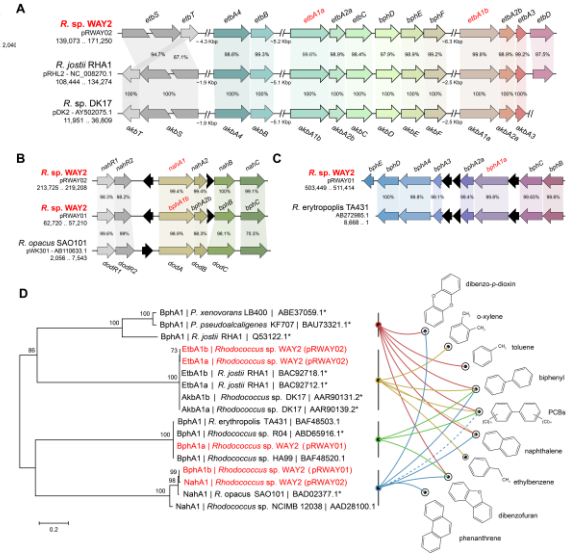
Daniel Garrido-Sanz[1], Paula Sansegundo-Lobato[1], Miguel Redondo-Nieto[1], Jachym Suman[2], Tomas Cajthaml[3], Esther Blanco-Romero[1], Marta Martin[1], Ondrej Uhlik[2], Rafael Rivilla[1]

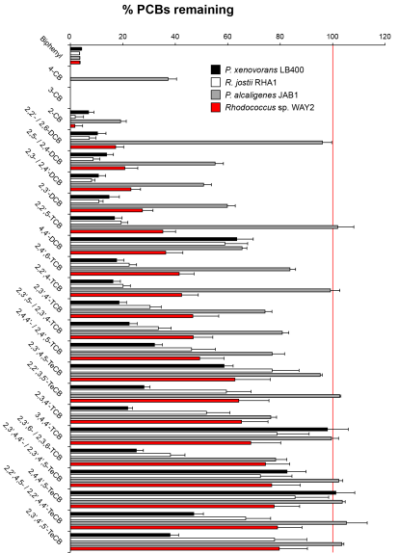
[1]Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid, C/ Darwin 2, 28049 Madrid, Spain | [2]Department of Biochemistry and Microbiology, Faculty of Food and Biochemical Technology, University of Chemistry and Technology Prague, Technika 3, 16628 Prague, Czech Republic | [3] Laboratory of Environmental Biotechnology, Institute of Microbiology, Czech Academy of Sciences v.v.i., Vídeňská 1083, 14200 Prague, Czech Republic

The complete genome sequence of *Rhodococcus* sp. WAY2 (WAY2) consists of a circular chromosome, three linear replicons and a small circular plasmid. The linear replicons contain typical actinobacterial invertron-type telomeres with the central CGTXCGC motif. Comparative phylogenetic analysis of the 16S rRNA gene along with phylogenomic analysis based on the genome-to-genome BLAST distance phylogeny (GBDP) algorithm and digital DNA–DNA hybridization (dDDH) with other *Rhodococcus* type strains resulted in a clear differentiation of WAY2, which is likely a new species. The genome of WAY2 contains five distinct clusters of *bph*, *etb* and *nah* genes, putatively involved in the degradation of several aromatic compounds. These clusters are distributed throughout the linear plasmids. The high sequence homology of the ring-hydroxylating subunits of these systems with other known enzymes has allowed us to model the range of aromatic substrates they could degrade. Further functional characterization revealed that WAY2 was able to grow with biphenyl, naphthalene and xylene as sole carbon and energy sources, and could oxidize multiple aromatic compounds, including ethylbenzene, phenanthrene, dibenzofuran and toluene. In addition, WAY2 was able to co-metabolize 23 polychlorinated biphenyl congeners, consistent with the five different ring-hydroxylating systems encoded by its genome. WAY2 could also use n-alkanes of various chain-lengths as a sole carbon source, probably due to the presence of alkB and ladA gene copies, which are only found in its chromosome. These results show that WAY2 has a potential to be used for the biodegradation of multiple organic compounds.









This research was funded by GREENER-H2020 (EU), grant number 826312, and MICINN/FEDER EU, grant number RTI2018-0933991-B-I00. D.G.-S. was supported by a MECD FPU fellowship program, grant number FPU14/03965. P.S.-L. was supported by the MICINN FPU fellowship program, grant number FPU18/02169. E.B.-R. was supported by the MECD FPU fellowship program, grant number FPU16/05513. J.S., T.C. and O.U. acknowledge Czech Science Foundation grant number 17–00227S, which enabled PCB co-metabolism experiments to be undertaken.