

Resveratrol as a growth substrate for bacteria from the rhizosphere.

Zohre Kurt, Marco Minoia and Jim C. Spain*

Supplementary figures and tables

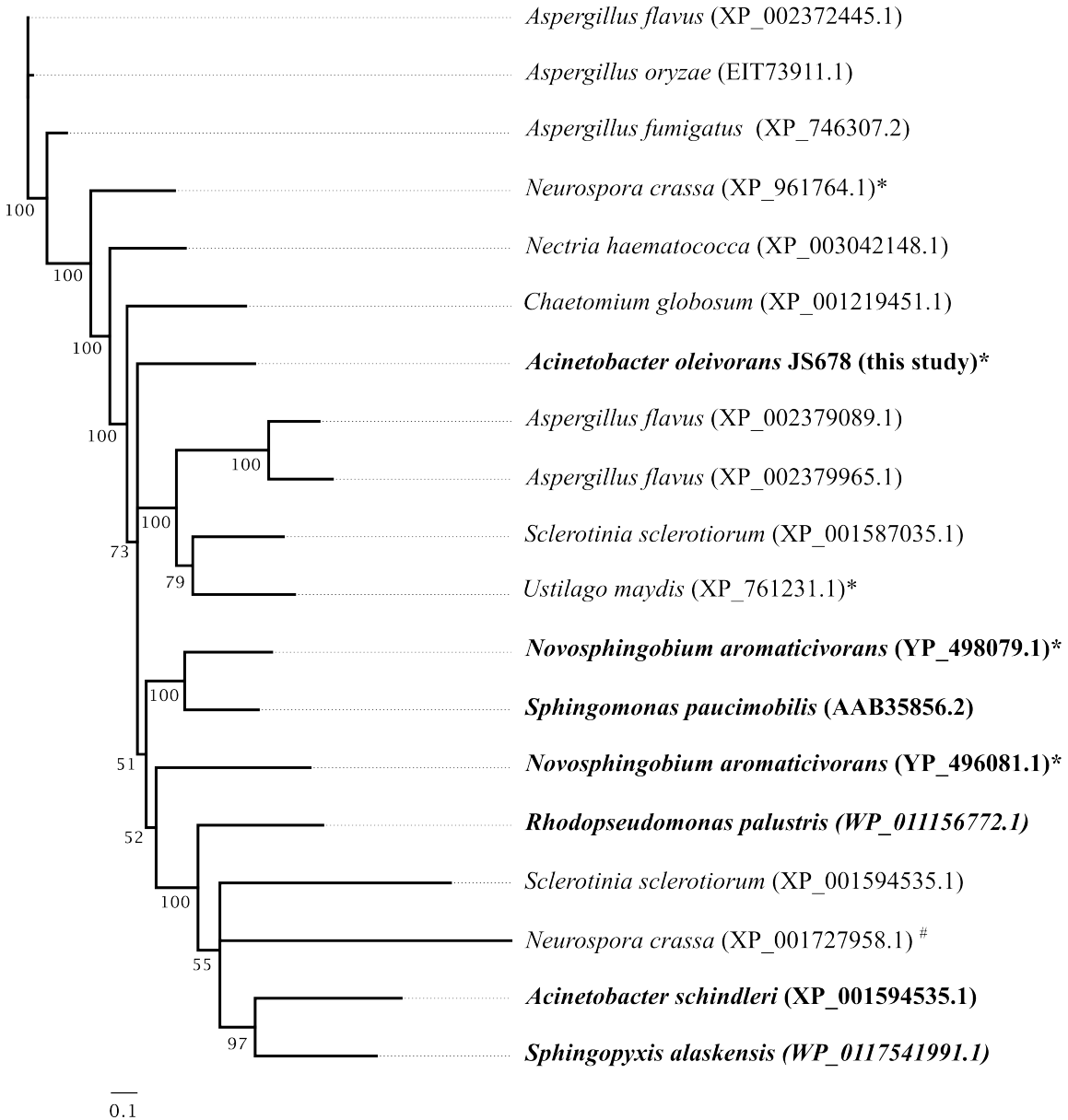


Figure S1. Phylogenetic tree of functionally characterized carotenoid cleaving oxygenases from fungi and bacteria (bold)(1-6). Enzymes that transform resveratrol are marked as * and enzymes that were tested but could not transform resveratrol are marked

as #. The tree was constructed based on neighbor joining method and bootstrap values are included in nodes and the alignment for the tree was made with ClustalW2.

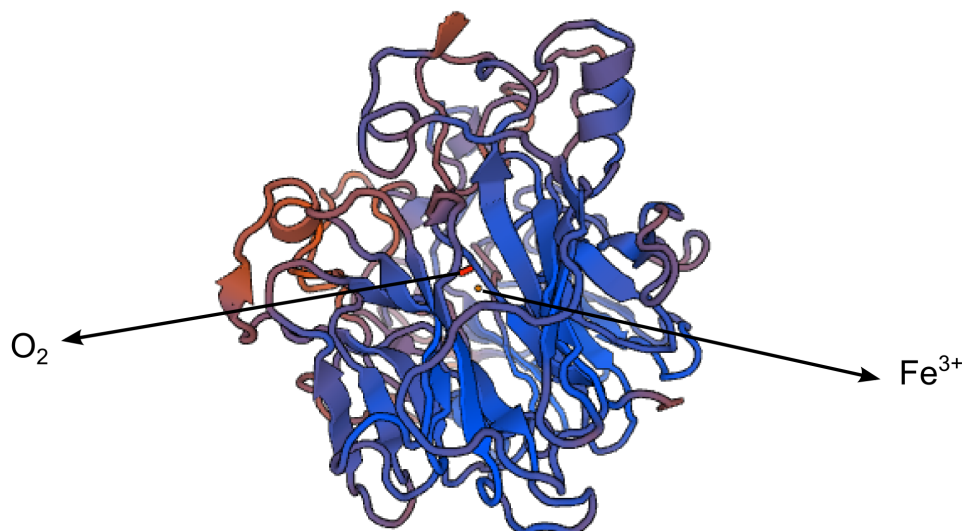


Figure S3. Model of Rzo using SWISS-MODEL (7-9).

Table S1. Strains isolated from peanut, identified by their 16S rDNA sequences using 8F and 1492R primers (10) and their closest relative.

Strain	Fragment length	Strain	% Identity
JS678	1400 bp	<i>Acinetobacter</i> sp. DR1	99 %
JS679	1386 bp	<i>Pseudomonas</i> sp. 130(2zx)	99 %
JS680	1381 bp	<i>Pseudomonas putida</i> strain AS90	98 %
JS681	1391 bp	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A	98 %
JS682	1387 bp	<i>Pseudomonas syringae</i> pv. <i>aesculi</i> str. 0893_23	99 %
JS683	1385 bp	<i>Burkholderia cenocepacia</i> HI2424	100 %

Table S2. Key genes encoding putative enzymes of the resveratrol degradation pathway in the JS678 genome. The sequences of JS678 were specified based on the contig numbers they were annotated in the draft genome (SUB1068911).

Genes	Amino acid similarity to nearest homolog ^a	Contig	Primers used for RT-PCR
16S rRNA gene	100 % to 16S rRNA from <i>Acinetobacter</i> sp. DR1 (CP002080.1)	401	5' GGTTGGCGCTAATATCTGGA 3' & 5' TCTGAATCAACGCTGTCTGG 3'
Resveratrol oxygenase (<i>rzo</i>)	73 % to dioxygenase from <i>Marinomonas profundimaris</i> (WP_024022327.1)	2366	5' GGGTGAAGGCCGTGTTAGTA 3' & 5' GATCCAATGCCCATGGTAAG 3'
4-Hydroxybenzaldehyde dehydrogenase (<i>pchA</i>)	97 % to aldehyde dehydrogenase from <i>Acinetobacter baumannii</i> Naval-82 (WP_002123484.1)	2302	5' CTTGGAATTGGCCATTTGTT 3' & 5' GAACCTGCGGATGTTTCAGTT 3'
4-Hydroxybenzoate hydroxylase (<i>pobA</i>)	92 % to 4-hydroxybenzoate 3-monoxygenase from <i>Acinetobacter oleivorans</i> JCM 1667 (YP_003732665.1)	5608	5' TGAATTCCGAATAGCCGAAC 3' & 5' GGTTTAGAGGGGCAACTTCC 3'
Protocatechuate 3,4-dioxygenase (<i>pcd</i>)	85 % to protocatechuate 3,4-dioxygenase from <i>Acinetobacter calcoaceticus</i> ANC 3811 (WP_016137964.1)	4965	5' GTGCTTACGCCCAACGTAAT 3' & 5' GGGCCAAACAAATTTGAAGA 3'
3,5-Dihydroxybenzaldehyde dehydrogenase (<i>ken6</i>)	39 % to benzaldehyde dehydrogenase from <i>Streptomyces violaceoruber</i> (CAQ52616.1)	1739	5' CCTTGCTTTAGCCAACCAAA 3' & 5' GAGATCCAGTGGTCGGTTGT 3'

^a The similarity was compared using UniProt database

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