

ПРИЛОЖЕНИЕ

к статье Ю.А. Марковой, И.С. Петрушина, Л.А. Беловежец «Обнаружение генных кластеров биодеструкции алканов и ароматических соединений в геноме *Rhodococcus qingshengii* VKM Ac-2784D»

SUPPLEMENTARY MATERIAL

to the article Yu.A. Markova, I.S. Petrushin, L.A. Belovezhets «Detection of gene clusters for biodegradation of alkanes and aromatic compounds in the *Rhodococcus qingshengii* VKM Ac-2784D genome»

Таблица S1. Сведения о генных кластерах метаболических путей

название гена	аннотация в NCBI	№ локуса в геноме R. qingshengii VKM Ac-2784D	% идентичности	описание гена в статье с описанием метаболического пути	3D	5Ap	ATCC-17895	ATCC-BAA870	B403	BCP1	ВН4	dfl-6-2	DK17	Eu-32	FUR100	NCIMB-2038	P14	P2117036	PD630	PR4	Q1	R1	R7	RHA1	S2-17	S8	USK10	VER34	VT6	WAY2	WB9	WY	Yc-YT1
ketoacidipate pathway																																	
catR	IclR family transcriptional regulator	RHA1_RS11600	73,6%	transcriptional regulator CatR	96	65	74	64	65	75	73	73	100	46	74	96	73	46	98	74	64	73	98	100	41	96	97	73	73	94	96	46	73
catA	catechol 1,2-dioxygenase	RHA1_RS11595	73,2%	catechol 1,2-dioxygenase	99	70	73	69	69	70	73	73	100	0	73	98	70	42	98	73	69	70	99	100	95	99	97	73	72	95	99	42	73
catB	chloromuconate cycloisomerase	RHA1_RS11590	84,5%	muconate cycloisomerase	97	75	84	75	75	78	84	84	100	30	84	95	79	26	97	84	75	78	98	100	94	97	95	84	84	93	98	26	84
catC	muconolactone Delta-isomerase	RHA1_RS11585	81,7%	muconolactone isomerase	97	88	81	88	87	87	82	82	100	0	82	96	87	0	96	82	89	87	96	100	92	97	98	81	82	92	95	0	82
pcaJ	CoA transferase subunit B	RHA1_RS06455	78,6%	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit	99	76	78	76	76	79	78	100	74	78	98	76	76	99	78	76	76	99	100	96	99	97	78	78	95	99	75	79	
pcaL	CoA transferase subunit A	RHA1_RS06460	81,1%	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit	100	81	81	81	81	80	81	100	66	81	99	80	81	100	81	80	80	98	100	98	100	81	81	81	80	98	100	81	81
pcaH	protocatechuate 3,4-dioxygenase subunit b	RHA1_RS06465	73,4%	protocatechuate 3,4-dioxygenase β chain	97	48	73	48	48	71	73	73	100	0	73	95	74	73	97	72	49	74	97	100	96	97	95	73	73	96	97	73	73
pcaG	protocatechuate 3,4-dioxygenase subunit alp	RHA1_RS06470	62,8%	protocatechuate 3,4-dioxygenase α chain	98	40	61	40	40	57	63	62	99	0	60	95	58	64	96	62	41	58	99	100	87	97	95	62	62	87	98	64	63
pcaB	3-carboxy-cis,cis-muconate cycloisomerase	RHA1_RS06475	63,1%	3-carboxy-cis,cis-muconate cycloisomerase	96	59	62	59	59	61	62	63	99	28	62	94	62	62	98	100	84	97	94	62	63	85	97	63	62	85	97	63	62
pcaL / pcaD	3-oxoadipate enol-lactonase	RHA1_RS06480	63,6%	4-carboxymuconolactone decarboxylase	97	63	63	63	63	63	63	99	40	63	94	65	64	97	63	65	97	100	88	97	93	63	63	89	97	64	63		
pcaR	helix-turn-helix domain-containing protein	RHA1_RS06485	72,8%	Pca regulon regulatory protein	98	70	72	70	70	68	72	72	99	72	72	98	70	98	100	86	98	72	72	86	98	68	72	72	86	98	68	72	
pcaF	acetyl-CoA C-acetyltransferase	RHA1_RS06490	82,4%	β-ketoadipyl-CoA thiolase	99	81	81	80	82	82	82	99	80	81	98	81	81	99	98	98	82	82	95	99	81	82	82	95	99	81	82		
phenylacetic acid pathway																																	
paaF	phenylacetate--CoA ligase	RHA1_RS13900	87,7%	phenylacetate-CoA ligase	98	0	88	28	0	29	88	87	100	85	88	95	25	0	98	88	0	25	98	100	85	98	87	87	29	99	0	88	
paaK	phenylacetate-CoA oxygenase/reductase sub	RHA1_RS13905	80,7%		99	37	80	38	37	41	80	80	100	80	80	95	42	35	99	80	37	42	96	100	81	98	85	80	40	99	35	80	
paaJ	phenylacetate-CoA oxygenase subunit PaaJ	RHA1_RS13910	74,6%		97	0	77	0	0	30	74	77	100	73	76	94	0	27	98	77	0	0	98	100	75	94	77	77	30	98	27	74	
paaC	phenylacetate-CoA oxygenase subunit PaaC	RHA1_RS13915	80,3%	3-hydroxybutyryl-CoA dehydrogenase	99	0	79	0	0	0	79	80	99	88	80	97	0	0	99	80	0	0	100	100	91	99	99	80	80	0	99	0	80
paaB	1,2-phenylacetyl-CoA epoxidase subunit B	RHA1_RS13920	81,0%	2-cyclohexenylcarbonyl CoA isomerase; PaaE	99	0	82	0	0	0	80	80	99	88	89	98	0	0	99	89	0	0	99	100	91	99	98	89	89	0	99	0	89
paaA	1,2-phenylacetyl-CoA epoxidase subunit A	RHA1_RS13925	89,7%	enoyl-CoA hydratase	99	0	89	0	0	0	89	89	99	88	89	98	0	0	99	89	0	0	99	100	91	99	98	89	89	0	99	0	89
paaI	hydroxypheylacetyl-CoA thioesterase Paal	RHA1_RS13960	75,4%		97	0	75	0	0	0	75	73	98	69	74	93	0	0	97	74	0	0	97	100	71	97	92	75	75	0	97	0	75
2-hydroxypentadenoate pathway																																	
xylF	alpha/beta fold hydrolase	RHA1_RS28300	71,6%	2-hydroxymuconic semialdehyde hydrolase	98	71	71	72	71	73	71	71	99	39	71	97	74	68	98	71	71	71	99	100	91	98	96	71	92	98	68	71	
kstD	FAD-binding protein	RHA1_RS28305	46,9%		97	49	46	49	49	46	56	59	47	46	94	49	80	97	46	49	49	98	100	90	97	94	56	56	91	98	80	46	
hsaE	2-keto-4-pentenoate hydratase	RHA1_RS28310	65,0%	2-hydroxypentadenoate hydratase	97	47	65	32	45	83	65	64	99	60	65	95	83	36	97	65	32	85	97	100	90	97	94	65	65	91			