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Supplementary Information

Rhodosporidium toruloides-1588 as a tool to biodegrade furfural as well as accumulate lipid and carotenoids: A enzyme identification study

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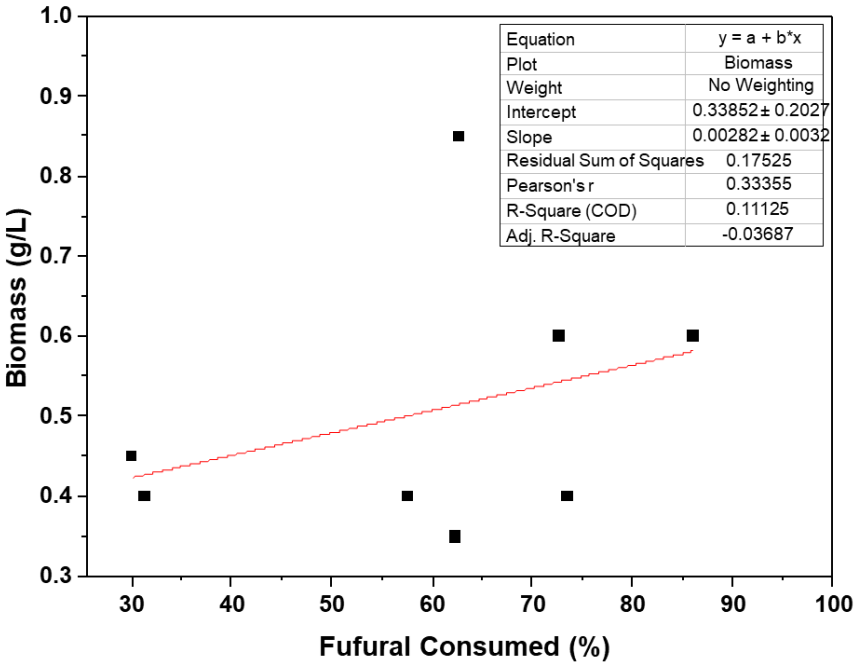

Fig. S1. Pearson correlation between furfural consumed (%) with respect to the biomass produced (g/L)

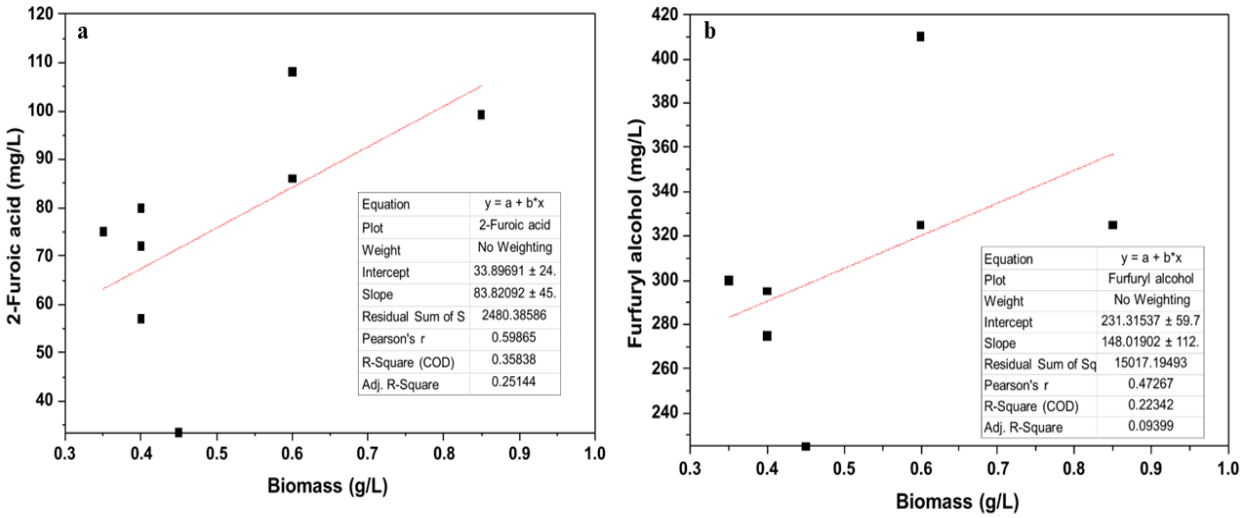

Fig. S2. Illustration of Pearson correlation between biomass with 2-furoic acid (2a) and furfuryl alcohol (2b) production.

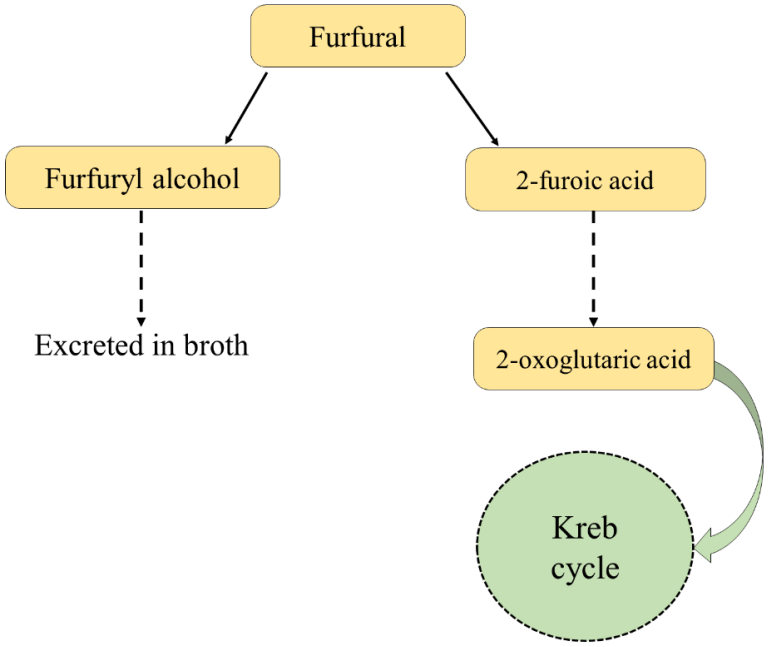

Fig. S3. Illustration of Furfural degradation pathway adapted from Nieves et al.[1] , Osorio Gonzalez et al.[2] , Wierckx et al.[3].

Table S1. Peptide profile identified in the samples from glucose, furfural and furfural-glucose media using LCMS/MS and corresponding enzyme accession number from UniProt databank.

S. No.	Enzyme	UniProt ID	Molecular Weight (kDa)	Coverage (%)
1	FGENESH: predicted gene_1.797 protein (Fragment)	A0A0K3CCP2	5.9	42
2	Nucleoside diphosphate kinase	A0A0K3CM94	16.5	31
3	Voltage-dependent ion-selective channel	A0A0K3CMF3	30.6	24
4	ATP synthase subunit alpha	A0A0K3CJN0	56.4	11
5	Elongation factor 1-alpha	A0A0K3C7H5	48.7	10
6	40S ribosomal protein s20	A0A061B3U3	13.7	10
7	Superoxide dismutase	A0A0K3CIK6	23.7	8
8	ADP/ATP translocase	A0A0K3C7I2	33.2	6
9	Citrate synthase	A0A0K3CN89	50.2	5
10	Glyceraldehyde-3-phosphate	A0A0K3CP51	31.3	5
11	Peroxiredoxin	A0A0K3CAW1	24.9	5
12	S-adenosylmethionine synthase	A0A0K3CCG4	41.4	4
13	Inorganic diphosphatase	A0A0K3CIY4	31.9	3
14	Heat shock protein 70 family	A0A0K3C908	70.8	2
15	Amine oxidase	A0A0K3CAM7	87.5	1
16	ATP-citrate synthase	A0A0K3CJ29	125.7	1

References

1. L. M. Nieves, L. A. Panyon and X. Wang, *Frontiers in Bioengineering and Biotechnology*, 2015, **3**.
2. C. S. Osorio-González, K. Hegde, S. K. Brar, A. Kermanshahipour and A. Avalos-Ramírez, *Biofuel Boprod Bior*, 2018, **0**.
3. N. Wierckx, F. Koopman, H. J. Ruijssenaars and J. H. de Winde, *Appl. Microbiol. Biotechnol.*, 2011, **92**, 1095-1105.