

phenolic acid inhibitors by adaptive laboratory evolution

SynBioForum 2019 Improved tolerance of Saccharomyces cerevisiae to lignin-derived Hanqi Gu*, Xiaoguang Liu, Yanyan Xu, Ran Liu, Yanfang Peng, Jie Li Department of Biology and Food Science, Hebei Normal University for Nationalities, Hebei 067000, China

Summary

Phenolic acids are the lignin-derived fermentation inhibitors and wildly exist in the various pretreated lignocellulosic hydrolysates. In this study, the effect of phenolic acids (vanillic, phydroxybenzoic and syringic acids as model compounds) on S. cerevisiae was investigated. Adaptive laboratory evolution was used to improve tolerance to the phenolic acid inhibitors. Tolerant mechanism was analyzed at the morphological and physiological level.

The results show that the phenolic acids caused the synergistic inhibitory effect on the yeast cell growth and ethanol fermentation. The evolved strains presented more tolerance than those of the parental strain by comparing the kinetic parameters of growth and fermentation in synthetic media with different phenolic acids.

Inhibitory effect of individual phenolic acids on S. cerevisiae								
Phenolic acids	Concentration (g/L)	µ _{max} b (h⁻¹)	GI ^b (%)	Lag phase (h)	Y _{x/s} b (g/g)	Q _{glucose} (g/L/h)	Q _{etOH} (g/L/h)	Y _{etOH} (%)
Vanillic acid	0	0.38	0	3	0.24	3.03	1.37	84.34
	0.33	0.35	7.78	3	0.21	3.07	1.25	81.17
	0.75	0.36	6.64	3	0.19	2.68	1.13	80.80
	1.5	0.33	13.99	3	0.16	2.47	0.88	84.65
	2.25	0.18	53.60	9	0.11	1.15	0.51	80.55
	3.0	0.00	99.55	15	0.03	0.78	0.24	61.14
	0	0.37	0	3	0.25	3.00	1.27	82.79
р-	2.0	0.36	5.48	3	0.20	3.07	1.23	78.01
hydroxybenzo	2.5	0.33	12.20	3	0.18	3.00	1.25	80.36
ic acid	3.0	0.30	21.63	3	0.17	2.02	0.82	79.29
	4.0	0.20	45.88	9	0.14	1.17	0.50	82.62
	5.0	0	100	15	0.02	0.75	0.19	49.02
Syringic acid	0	0.38	0	3	0.26	2.87	1.26	85.96
	0.25	0.36	6.01	3	0.26	2.80	1.23	86.25
	0.5	0.36	5.05	3	0.23	2.62	1.17	84.62
	1.0	0.34	11.19	3	0.22	2.45	0.82	86.48
	1.5	0.30	20.98	3	0.20	2.40	0.61	83.11
	2.0	0.27	29.03	3	0.18	2.23	0.63	87.77
V-H-S ^a	0	0.37	0	3	0.26	2.82	1.27	86.06
	0.5-0.3-0.25	0.33	9.83	3	0.25	2.82	1.09	75.76
	1.0-0.6-0.5	0.23	38.77	3	0.20	1.92	1.05	71.06
	1.5-0.9-0.75	0.16	57.39	9	0.08	0.72	0.22	59.62
	2.0-1.2-1.0	0	100	15	0.03	0.10	0.08	21.36
	2.5-1.5-1.25	0	100	24	0.02	0	0	0

the yeast cell growth and ethanol fermentation.



The adaptative evolution under stress of phenolic acids could efficiently improve the growth and fermentation performance of the yeast strain not only in the synthetic media with phenolic acids



Figure 2. Cytoplasmic membrane integrity of yeast strains under phenolic acids stress. (a) leakage of intracellular 260 nm-absorbing substances; (b) relative electric conductivity; (c) PI stained cells rate; PS represents the parental strain cells; A-50H, A-50V and A-50M were the adapted strains which obtained by adaptative evolution under stress of p-hydroxybenzoic acid, vanillic acid and mixed phenolic acids at 50% inhibitory concentration.



Figure 3. SEM and TEM of S. cerevisiae after treatment of phenolic acids. the parental strain cells (a, c) and the adapted strain (b, d). All above strain cells were inoculated in the medium with phenolic acids mixture at concentration of IC50 at 30 °C with agitation at 150 rpm for 9 h.

Phenolic acids caused the parental strain to generate many cytoplasmic membrane invaginations with crack at the top of these sites.



Conclusion

The cytoplasmic membrane integrity of yeast strain was disrupted by the phenolic acids and the evolved strain exhibited change in cell structure, especially, the cytoplasmic membrane and wall. The evolved strains improved the cytoplasmic membrane integrity of yeast cell under the phenolic acids stress was found by testing the leakage of intracellular substance and the permeability of fluorescent probe. The change of lipid composition induced the structural change of cell membrane might contribute the improvement membrane integrity. The adaptive laboratory evolution will contribute to the development of robust microbials for biofuels production from lignocellulosic biomass.

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