

Understanding of metabolic flexibility of lactic acid bacteria under severe impertinence

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International Society of Biocatalysis and Agricultural Biotechnology (<http://www.isbab.org>)

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and

President Jei-Fu Shaw of the National Chung Hsing University (NCHU), Taichung, Taiwan

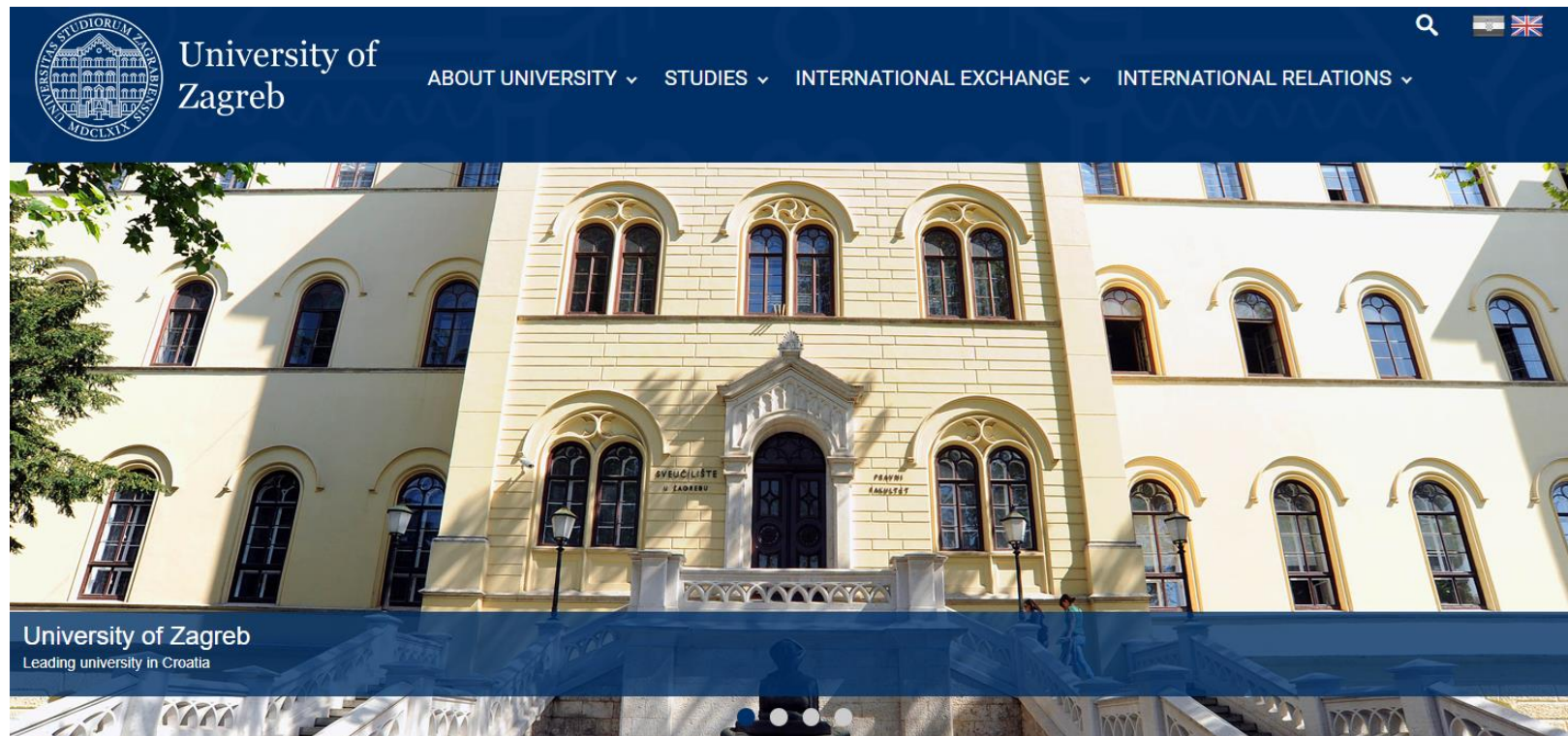
Professor Milan Čertík, PhD, Slovak University of Technology, Slovak Republic,

Chair of the 18thISBAB PS

Thank you for your kind invitation!

University of Zagreb Faculty of Food Technology and Biotechnology

- . University of Zagreb (<https://www.unizg.hr>); the oldest university in Southeast Europe established in 1669
- . University of Zagreb Faculty of Food Technology and Biotechnology (<http://www.pbf.unizg.hr/>)



. overview

. stressors

.. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531

... proteolytic, amylolytic and fermentative activity

... production of different ratios of D-/L-lactic acid by three *Lactobacillus* sp.

(*L. amylovorus* DSM 20531, *L. rhamnosus* DSM 20021, and *L. coryniformis* subsp. *torquens* DSM 20004)

... doors of opportunity - manufacturing of high-value chemicals from sustainably produced D-/L-lactic acid

.. effect of dissolved oxygen concentration on acetate production by *L. coryniformis* subsp. *torquens* DSM 20004

.. encapsulation of *L. amylovorus* DSM 20531 with polymeric substrate - towards integrated process for ethyl lactate production

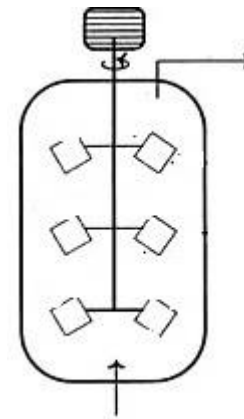
.. production of α -D-glucosylglycerol by *Leuconostoc mesenteroides* LMG 7954 under osmotic stress

future plans

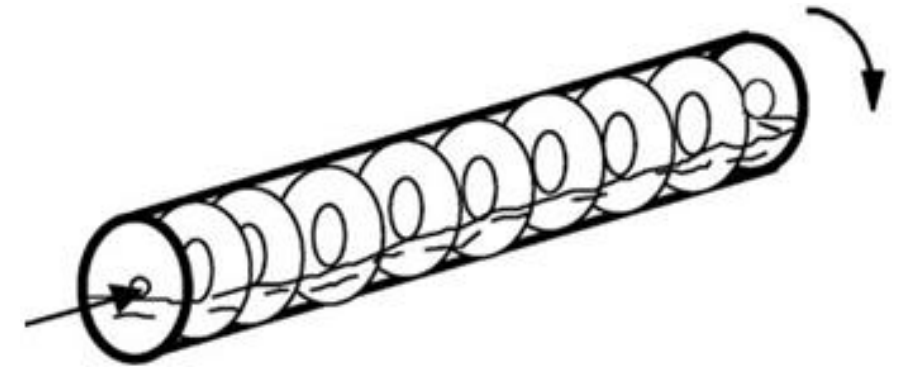
. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531



polenta



STB



HRTB

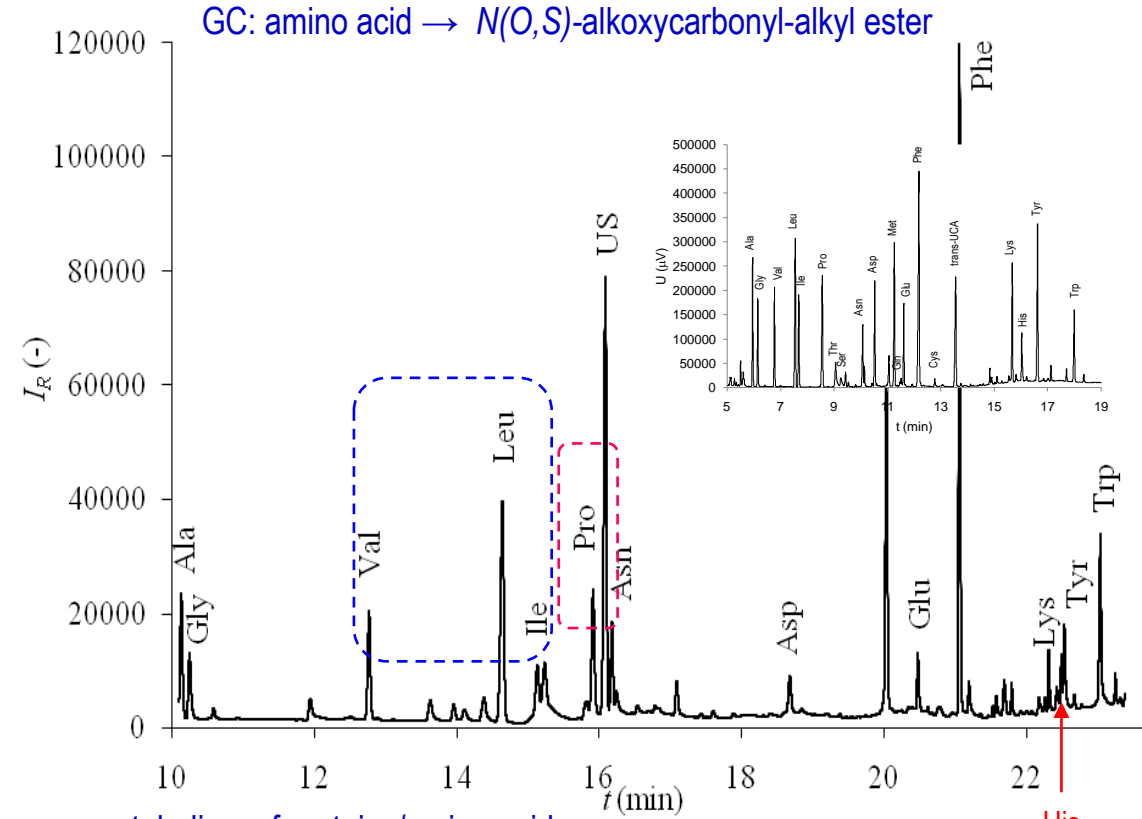
cultivations:

- . batch
- . fed-batch
- . semicontinuous
- . continuous

. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: proteolytic activity



polenta



. metabolism of proteins/amino acids :

accumulation of Pro (osmotic stress);

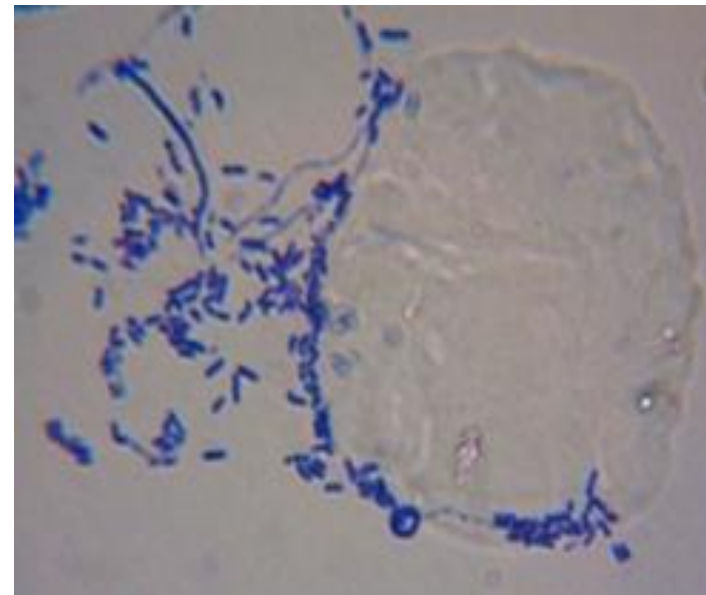
His concentration below detection level;

very low concentration of branched-chain amino acids.

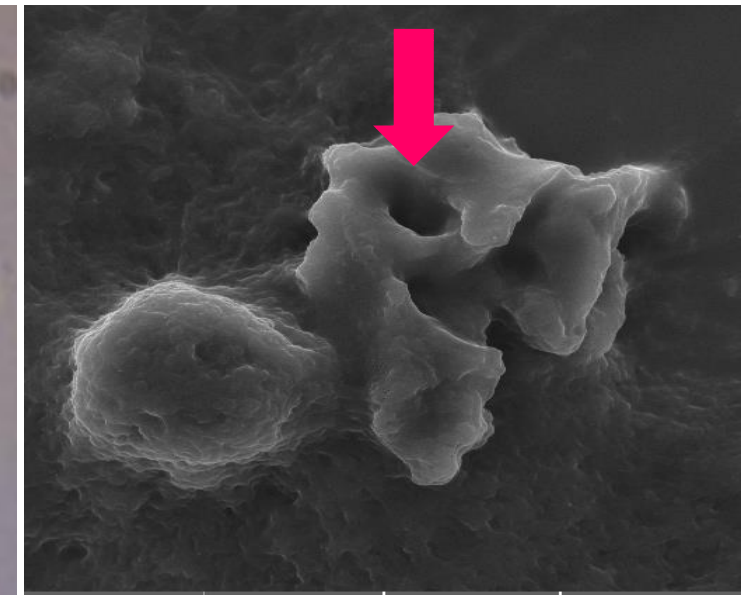
. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: amylolytic activity



polenta



microscopic image of *L. amylovorus* DSM 20531 attached to starch granules



SEM image of starch granules obtained during hydrolysis by *L. amylovorus* DSM 20531 amylases

unpublished data

. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: amylolytic activity

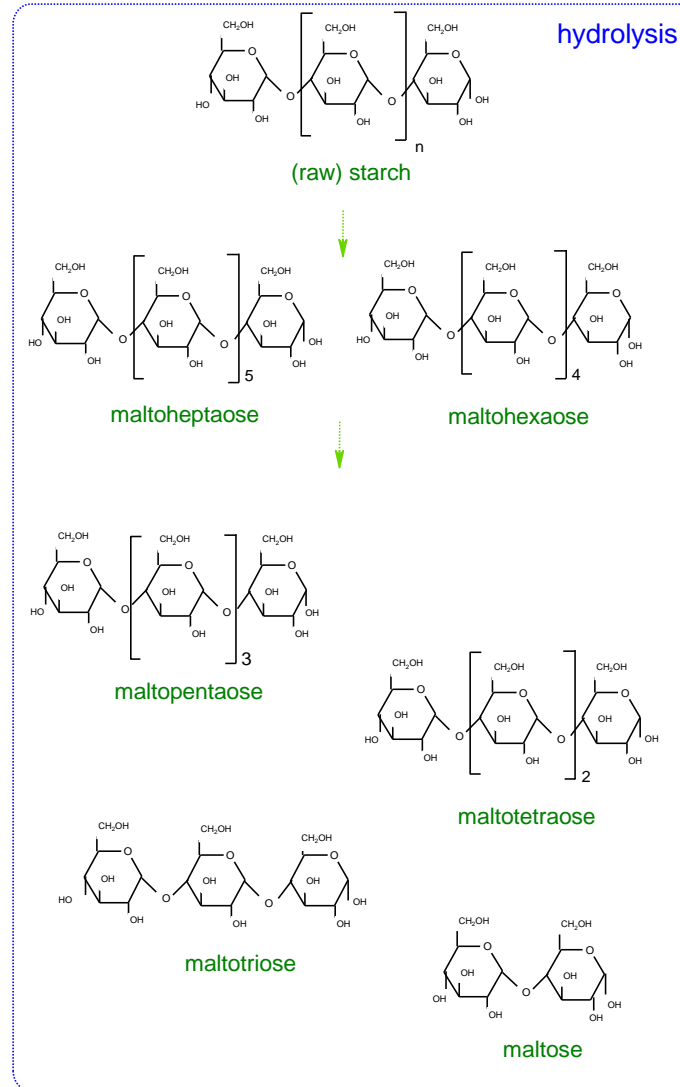


polenta

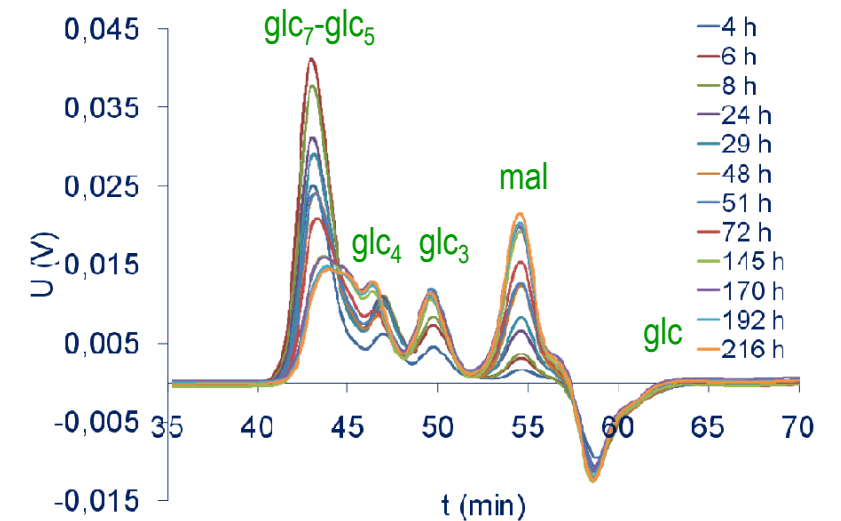
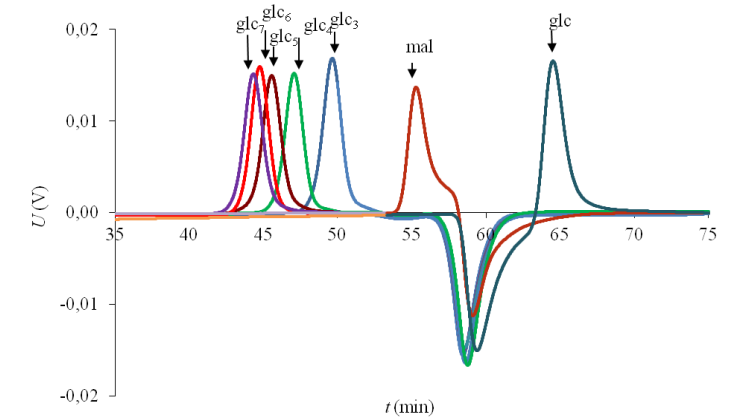
. complete hydrolysis of linear and branched chains of (raw) starch to maltooligosaccharides and maltose

. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: amylolytic activity

- . complete hydrolysis of linear and branched chains of (raw) starch to maltooligosaccharides and maltose
- . mixture of maltooligosaccharides - a platform mixture to be used in numerous enzymatic and whole-cell catalyzed reactions

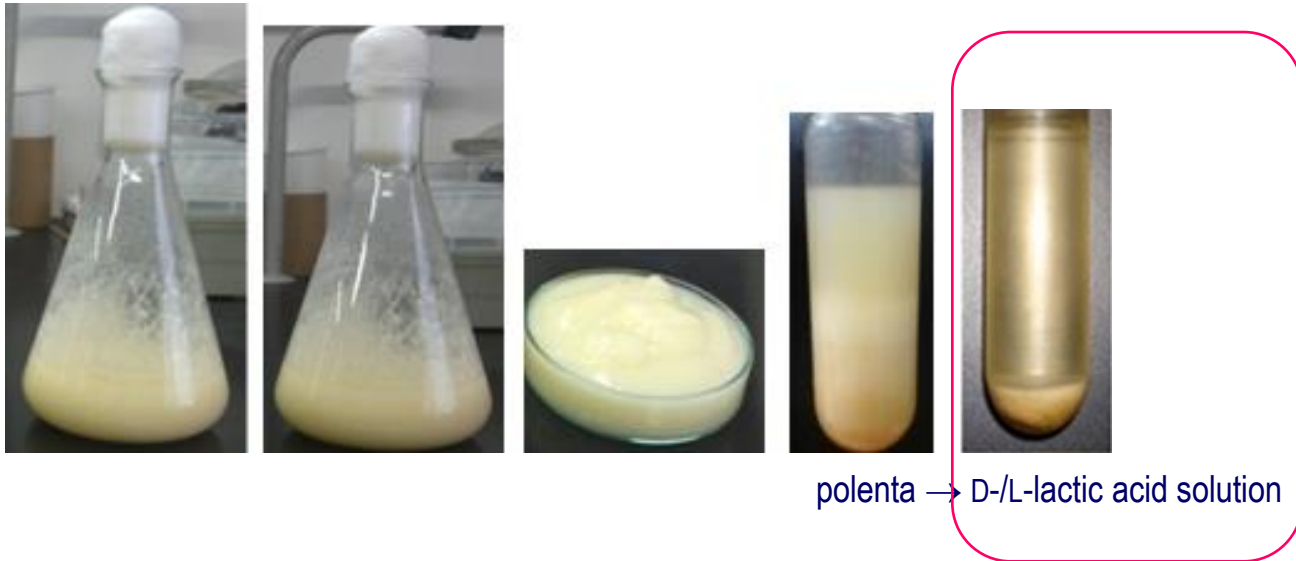


IEX-HPLC



unpublished data

. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: proteolytic, amylolytic and fermentative activity



. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: **proteolytic, amylolytic and fermentative activity**



polenta



→ D-/L-lactic acid solution



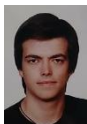
I. Inkret, I. Jakša



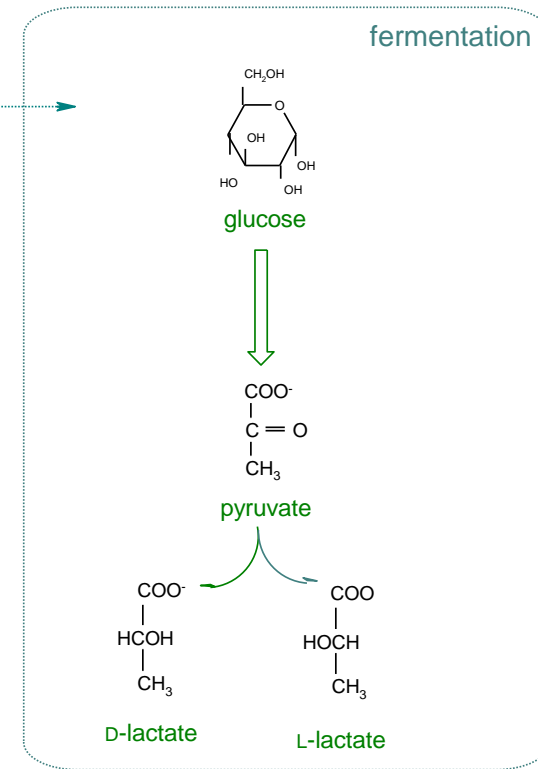
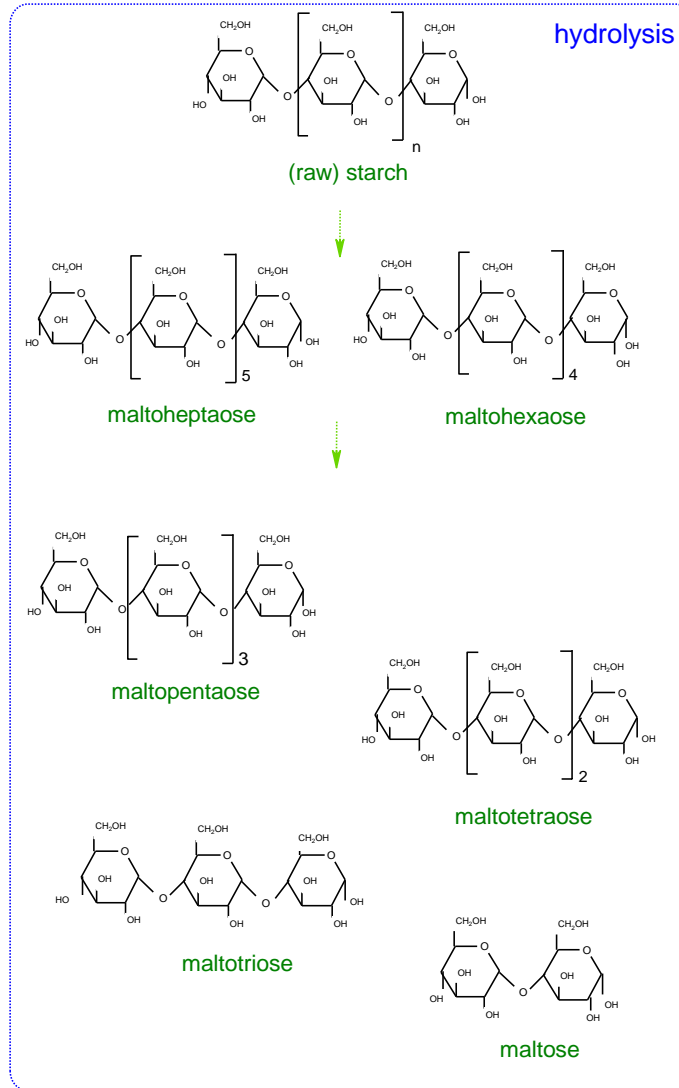
D. Kolanović



D. Kostelac



D. Švec



A. Trontel



I. Dusper



V. Tadić



A. Polenus

unpublished data

$$\begin{aligned} \left(\frac{d\gamma_{glc}}{dt}\right)_{s_5f} &= \left(\frac{d\gamma_{glc}}{dt}\right)_h + \left(\frac{d\gamma_{glc}}{dt}\right)_f & \left(\frac{d\gamma_{glc_7}}{dt}\right)_h &= r_{\check{s}krob/gl_{c_7}} + r_{gl_{c_7}/gl_{c_7}} - r_{gl_{c_7}/gl_{c_3}+gl_{c_4}} - r_{gl_{c_7}/gl_{c_6}} - r_{gl_{c_7}/mal+gl_{c_5}} - r_{gl_{c_7}/gl_{c_3}+gl_{c_4}} \\ \left(\frac{d\gamma_{mal}}{dt}\right)_{s_5f} &= \left(\frac{d\gamma_{mal}}{dt}\right)_h + \left(\frac{d\gamma_{mal}}{dt}\right)_f & \left(\frac{d\gamma_{glc_{5-7}}}{dt}\right)_h &= \left(\frac{d\gamma_{glc_5}}{dt}\right)_h + \left(\frac{d\gamma_{glc_6}}{dt}\right)_h + \left(\frac{d\gamma_{glc_7}}{dt}\right)_h \\ \left(\frac{d\gamma_{glc}}{dt}\right)_h &= r_{gl_{c_7}/gl_{c_3}+gl_{c_6}} + r_{gl_{c_6}/gl_{c_3}+gl_{c_5}} + r_{gl_{c_5}/gl_{c_3}+gl_{c_4}} + r_{gl_{c_4}/gl_{c_3}+gl_{c_3}} & \left(\frac{d\gamma_{\check{s}krob}}{dt}\right)_h &= -r_{\check{s}krob/gl_{c_7}} - r_{\check{s}krob/gl_{c_n}} \\ \left(\frac{d\gamma_{mal}}{dt}\right)_h &= r_{gl_{c_7}/mal+gl_{c_5}} + r_{gl_{c_6}/mal+gl_{c_4}} + r_{gl_{c_5}/mal+gl_{c_3}} + r_{gl_{c_4}/mal+mal} & r_{\check{s}krob/gl_{c_7}} &= k_{\check{s}krob,gl_{c_7}} \cdot \gamma_{\check{s}krob} \\ \left(\frac{d\gamma_{glc_3}}{dt}\right)_h &= r_{\check{s}krob/gl_{c_3}} + r_{gl_{c_7}/gl_{c_3}} + r_{gl_{c_7}/gl_{c_3}+gl_{c_4}} + r_{gl_{c_6}/gl_{c_3}+gl_{c_3}} + r_{gl_{c_5}/mal+gl_{c_3}} + r_{gl_{c_4}/gl_{c_3}+gl_{c_3}} & r_{\check{s}krob/gl_{c_n}} &= \sum_3^7 k_{\check{s}krob,gl_{c_n}} \cdot \gamma_{\check{s}krob} \\ \left(\frac{d\gamma_{glc_4}}{dt}\right)_h &= r_{\check{s}krob/gl_{c_4}} + r_{gl_{c_7}/gl_{c_4}} + r_{gl_{c_7}/gl_{c_3}+gl_{c_4}} + r_{gl_{c_6}/mal+gl_{c_4}} + r_{gl_{c_5}/gl_{c_3}+gl_{c_4}} - r_{gl_{c_4}/mal+mal} & r_{gl_{c_7}/gl_{c_n}} &= \sum_{n=3}^7 k_{gl_{c_7},gl_{c_n}} \cdot \gamma_{gl_{c_7}} \\ & - r_{gl_{c_4}/gl_{c_3}+gl_{c_3}} & r_{gl_{c_7}/gl_{c_n}+gl_{c_{7-n}}} &= \sum_{n=1}^3 k_{gl_{c_7},gl_{c_n}+gl_{c_{7-n}}} \cdot \gamma_{gl_{c_7}} \\ \left(\frac{d\gamma_{glc_5}}{dt}\right)_h &= r_{\check{s}krob/gl_{c_5}} + r_{gl_{c_7}/gl_{c_5}} + r_{gl_{c_7}/mal+gl_{c_5}} + r_{gl_{c_6}/gl_{c_3}+gl_{c_5}} - r_{gl_{c_5}/mal+gl_{c_3}} - r_{gl_{c_5}/gl_{c_3}+gl_{c_4}} & r_{gl_{c_6}/gl_{c_n}+gl_{c_{6-n}}} &= \sum_{n=1}^3 k_{gl_{c_6},gl_{c_n}+gl_{c_{6-n}}} \cdot \gamma_{gl_{c_6}} \\ \left(\frac{d\gamma_{glc_6}}{dt}\right)_h &= r_{\check{s}krob/gl_{c_6}} + r_{gl_{c_7}/gl_{c_6}} + r_{gl_{c_7}/gl_{c_3}+gl_{c_6}} - r_{gl_{c_6}/gl_{c_3}+gl_{c_3}} - r_{gl_{c_6}/mal+gl_{c_4}} - r_{gl_{c_6}/gl_{c_3}+gl_{c_5}} & r_{gl_{c_5}/gl_{c_n}+gl_{c_{5-n}}} &= \sum_{n=1}^2 k_{gl_{c_5},gl_{c_n}+gl_{c_{5-n}}} \cdot \gamma_{gl_{c_5}} \\ & & r_{gl_{c_4}/gl_{c_n}+gl_{c_{4-n}}} &= \sum_{n=1}^2 k_{gl_{c_4},gl_{c_n}+gl_{c_{4-n}}} \cdot \gamma_{gl_{c_4}} \end{aligned}$$

. a high initial concentration of polymeric substrates - case of *Lactobacillus amylovorus* DSM 20531: mathematical model (B) - fermentative production of lactic acid

$$\left(\frac{d\gamma_{glcNH}}{dt}\right)_{s_5f} = \left(\frac{d\gamma_{glc}}{dt}\right)_{s_5f} + \left(\frac{d\gamma_{mal}}{dt}\right)_{s_5f} + \left(\frac{d\gamma_{glc_3}}{dt}\right)_h + \left(\frac{d\gamma_{glc_4}}{dt}\right)_h + \left(\frac{d\gamma_{glc_{5-7}}}{dt}\right)_h + \left(\frac{d\gamma_{glc_{\gamma 7}}}{dt}\right)_h + \left(\frac{d\gamma_{škrob}}{dt}\right)_h$$

$$\left(\frac{d\gamma_{glc}}{dt}\right)_f = -\frac{1}{Y_{X_1/gl c}} \cdot \frac{d\gamma_{X_1}}{dt} - m_s \cdot \gamma_{X_1}$$

$$\left(\frac{d\gamma_{mal}}{dt}\right)_f = -\frac{1}{Y_{X_1/mal}} \cdot \frac{d\gamma_{X_1}}{dt} - m_s \cdot \gamma_{X_1}$$

$$\frac{d\gamma_{UH}}{dt} = -\frac{1}{Y_{X/UH}} \cdot \frac{d\gamma_X}{dt} - m_s \cdot \gamma_X$$

$$\frac{d\gamma_X}{dt} = \mu \cdot \gamma_X - k_D \cdot \gamma_X$$

$$\mu = \mu_m \cdot \frac{\gamma_{UH}}{K_{UH} + \gamma_{UH}} \cdot \frac{K_i}{K_i + \gamma_{MK}}$$

$$k_D = k_{D_0} \cdot (1 + C \cdot \gamma_{MK})$$

$$\frac{d\gamma_{MK}}{dt} = \alpha_{MK} \cdot \frac{d\gamma_X}{dt} + \beta_{MK} \cdot \gamma_X$$

production of different ratios of D-/L-lactic acid

substrate

glc, glucose
starch
cgs, corn grits
suc, sucrose
mal, maltose

strains of lactic acid bacteria

L.a., *L. amylovorus* DSM 20531
L.r., *L. rhamnosus* DSM 20021
L.c.t., *L. coryniformis* subsp. *torquens* DSM 20004

bioreactor

STB, Stirred Tank Bioreactor
HRTB, Horizontal Rotating Tubular Bioreactor

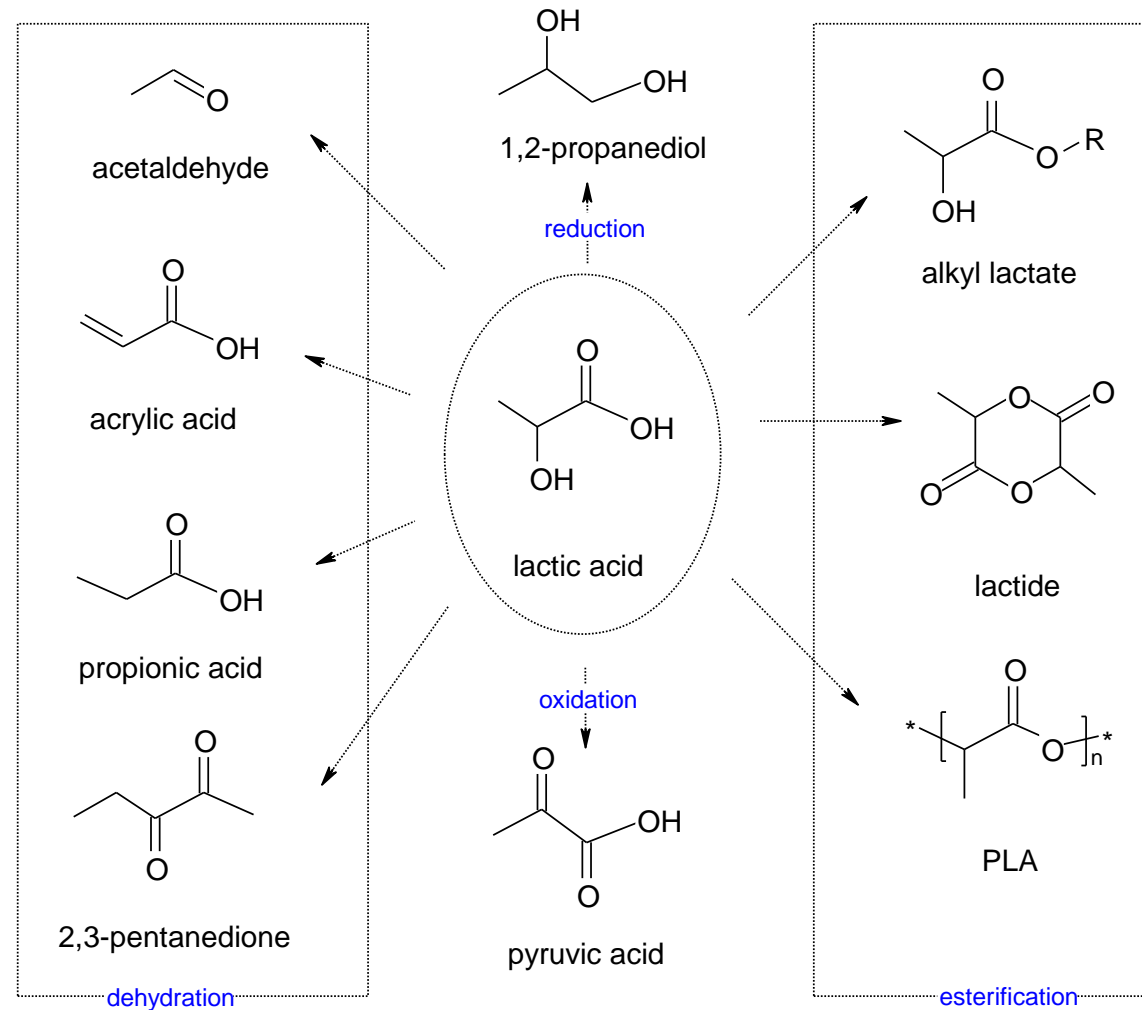
product(s)

LA, lactic acid
AA, acetic acid

batch systems (carbon source _{concentration} / LAB / temperature (°C / bioreactor)	w _{D-LA} (%)	w _{L-LA} (%)	product(s)
glc ₂₀ /L. r./40/STB	7.4	92.6	D-/L-LA
starch ₁₀ /L. a.+L. r./40/STB co-culture	27.2	72.8	D-/L-LA
cgs ₆₀ /L. a./20.5-34.7/HRTB	30.0	70.0	D-/L-LA
cgs ₁₀₀ /L. a./45/STB	33.3	66.7	D-/L-LA
starch ₁₀ /L. a./35/STB	43.7	56.3	D-/L-LA
suc ₁₀ /L. a./40/STB	48.4	51.6	D-/L-LA
starch ₁₀ /L. a./30/STB	49.1	50.9	D-/L-LA
starch ₁₀₀ /L. a./45/STB	49.5	50.5	D-/L-LA
starch ₁₀ /L. a./45/STB	49.7	50.3	D-/L-LA
glc ₂₀ /L. a./40/STB	50.1	49.9	D-/L-LA
cgs ₁₀₀ /L. a./45/STB	50.8	49.2	D-/L-LA
glc ₁₀ /L. a./40/STB	50.8	49.2	D-/L-LA+AA
starch ₁₀ /L. a./40/STB	52.0	48.0	D-/L-LA
mal ₁₀ /L. a./40/STB	52.2	47.8	D-/L-LA+AA
starch ₁₀ /L. a./50/STB	62.9	37.1	D-/L-LA
glc ₂₀ /L. c. t./30/STB	100.0	0.0	D-LA+AA
glc ₂₀ /L. c. t./30-50/STB	100.0	0.0	D-LA

unpublished data

. doors of opportunity - manufacturing of high-value chemicals from sustainably produced D-/L-lactic acid

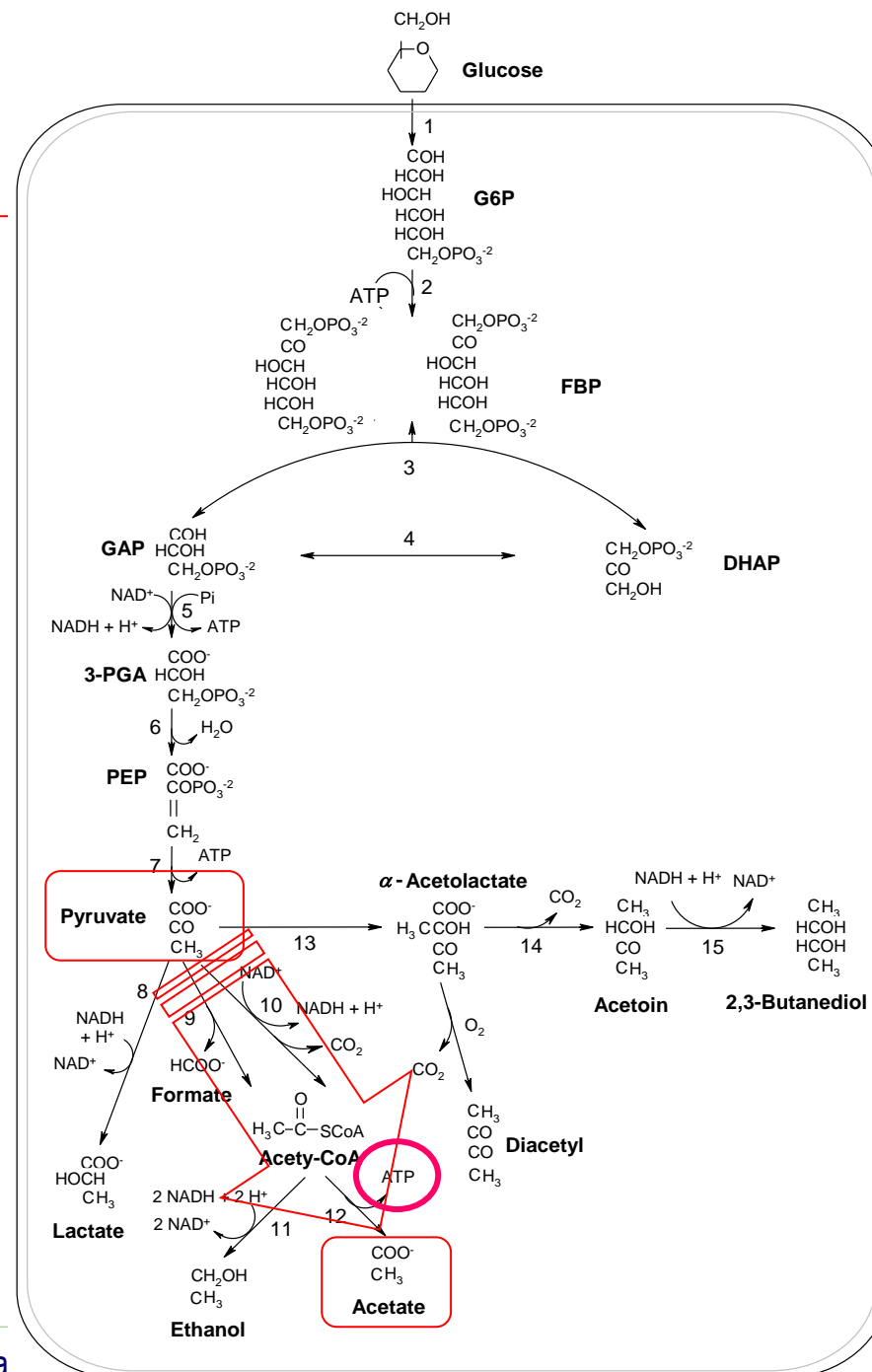
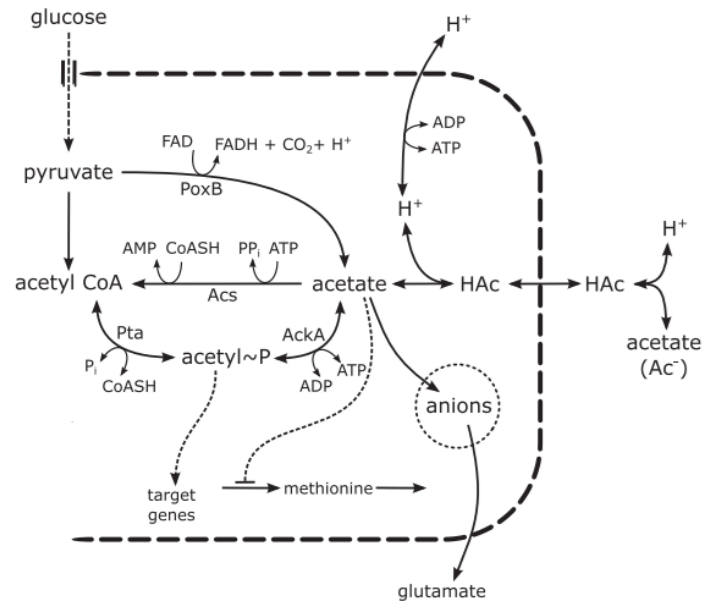


production of different ratios of D-/L-lactic acid

		batch systems (carbon source _{concentration} / LAB / temperature (°C / bioreactor))	w _{D-LA} (%)	w _{L-LA} (%)	product(s)	
substrate glc, glucose starch cgs, corn grits suc, sucrose mal, maltose		glc ₂₀ /L. r./40/STB	7.4	92.6	D-/L-LA	
		starch ₁₀ /L. a.+L. r./40/STB co-culture	27.2	72.8	D-/L-LA	
		cgs ₆₀ /L. a./20.5-34.7/HRTB	30.0	70.0	D-/L-LA	
		cgs ₁₀₀ /L. a./45/STB	33.3	66.7	D-/L-LA	
		starch ₁₀ /L. a./35/STB	43.7	56.3	D-/L-LA	
	strains of lactic acid bacteria L.a., <i>L. amylovorus</i> DSM 20531 L.r., <i>L. rhamnosus</i> DSM 20021 L.c.t., <i>L. coryniformis</i> subsp. <i>torquens</i> DSM 20004		suc ₁₀ /L. a./40/STB	48.4	51.6	D-/L-LA
		starch ₁₀ /L. a./30/STB	49.1	50.9	D-/L-LA	
		starch ₁₀₀ /L. a./45/STB	49.5	50.5	D-/L-LA	
	bioreactor STB, Stirred Tank Bioreactor HRTB, Horizontal Rotating Tubular Bioreactor		starch ₁₀ /L. a./45/STB	49.7	50.3	D-/L-LA
		glc ₂₀ /L. a./40/STB	50.1	49.9	D-/L-LA	
	cgs ₁₀₀ /L. a./45/STB	50.8	49.2	D-/L-LA		
product(s) LA, lactic acid AA, acetic acid	homofermentative	glc ₁₀ /L. a./40/STB	50.8	49.2	D-/L-LA+AA	glc below 35.52 mM (6.40 g/L)
		starch ₁₀ /L. a./40/STB	52.0	48.0	D-/L-LA	
		mal ₁₀ /L. a./40/STB	52.2	47.8	D-/L-LA+AA	mal below 27.64 mM (9.46 g/L)
		starch ₁₀ /L. a./50/STB	62.9	37.1	D-/L-LA	
	facultatively heterofermentative	glc ₂₀ /L. c. t./30/STB	100.0	0.0	D-LA+AA	glc below 38.41 mM (6.92 g/L)
		glc ₂₀ /L. c. t./30-50/STB	100.0	0.0	D-LA	

. acetate in the growth medium (glc₂₀) without growth inhibition

- . acetate switch in *Escherichia coli*
- . intracellular osmotic pressure
- . synthesis of methionine
- . pool of glutamate
- . more organic acids in growth medium



Wolfe, Microbiol Mol Biol Rev. 2005 <https://doi.org/10.1128/MMBR.69.1.12-50.2005>.

Pinhal S, Ropers D, Geiselmann J, de Jong H. 2019. J Bacteriol <https://doi.org/10.1128/JB.00147-19>.

production of different ratios of D-/L-lactic acid

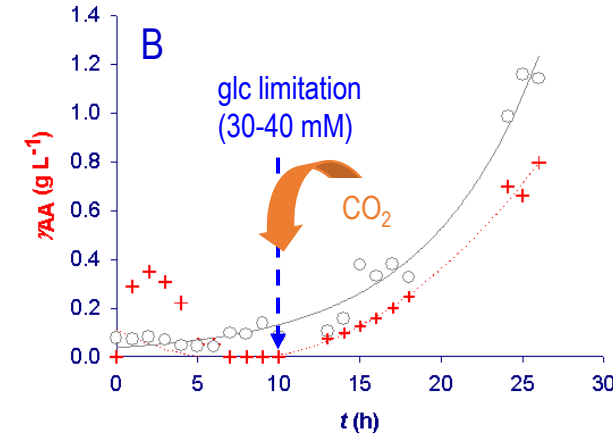
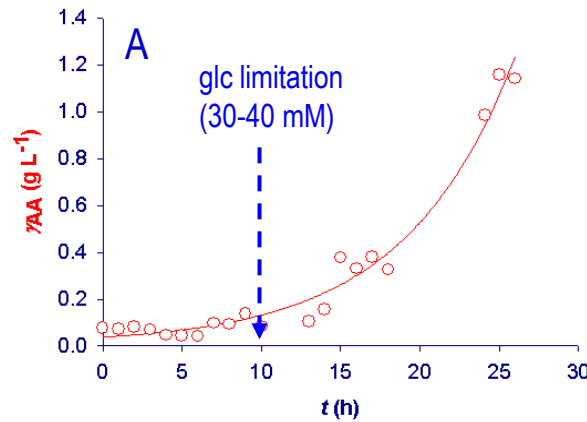
Acetate can be produced from:
 (1) **pyruvate** in reactions catalyzed by pyruvate dehydrogenase, phosphotransacetylase and acetate kinase;
 (2) **lactate** by the LDH-POX-ACK pathway; and/or
 (3) **amino acids**: Ser, Asp, Val, Leu and Ile.

Drops in the concentration of three amino acids, **Asp, Val and Ile**, were connected with the start of the **acetate** production. Further increase in the acetate concentration was extended in the **stationary phase** of *L. c. t.* Molar ratios of utilized or produced **lactate, acetate** and **three amino acids** obtained in experiments do not correspond to stoichiometric ratios of metabolic pathways considered above.

batch systems (carbon source _{concentration} / LAB / temperature (°C / bioreactor)	w _{D-LA} (%)	w _{L-LA} (%)	product(s)	
glc ₂₀ /L. r./40/STB	7.4	92.6	D-/L-LA	
starch ₁₀ /L. a.+L. r./40/STB co-culture	27.2	72.8	D-/L-LA	
cgs ₆₀ /L. a./20.5-34.7/HRTB	30.0	70.0	D-/L-LA	
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suc ₁₀ /L. a./40/STB	48.4	51.6	D-/L-LA	
starch ₁₀ /L. a./30/STB	49.1	50.9	D-/L-LA	
starch ₁₀₀ /L. a./45/STB	49.5	50.5	D-/L-LA	
starch ₁₀ /L. a./45/STB	49.7	50.3	D-/L-LA	
glc ₂₀ /L. a./40/STB	50.1	49.9	D-/L-LA	
cgs ₁₀₀ /L. a./45/STB	50.8	49.2	D-/L-LA	
glc ₁₀ /L. a./40/STB	50.8	49.2	D-/L-LA+AA	glc below 35.52 mM (6.40 g/L)
starch ₁₀ /L. a./40/STB	52.0	48.0	D-/L-LA	
mal ₁₀ /L. a./40/STB	52.2	47.8	D-/L-LA+AA	mal below 27.64 mM (9.46 g/L)
starch ₁₀ /L. a./50/STB	62.9	37.1	D-/L-LA	
glc ₂₀ /L. c. t./30/STB	100.0	0.0	D-LA+AA	glc below 38.41 mM (6.92 g/L)
glc ₂₀ /L. c. t./30-50/STB	100.0	0.0	D-LA	

effect of dissolved oxygen concentration on acetate production by *L. coryniformis* subsp. *torquens* DSM 20004

- STB (working volume of 10 L)
- glc₂₀
- 28°C, pH 5.5 -6.1, 100 rpm
- D-LA + AA

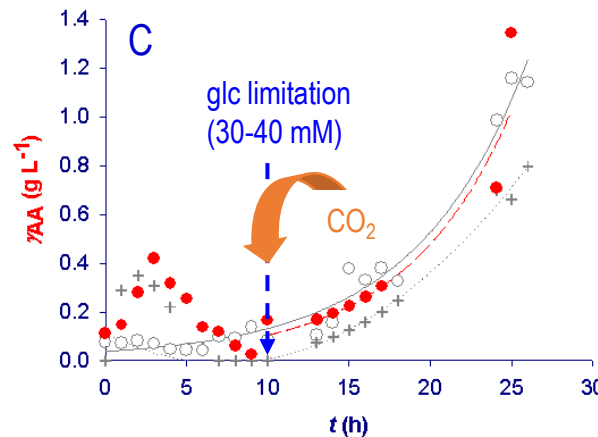


- (A) $\rho_{O_2} = 80-100\%$; $\mu_{max} = 0.21 \text{ h}^{-1}$
- (B) $\rho_{O_2} = 20-30\%$; $\mu_{max} = 0.17 \text{ h}^{-1}$
- (C) $\rho_{O_2} = 0-10\%$; $\mu_{max} = 0.21 \text{ h}^{-1}$



reoxidation of NADH + H⁺

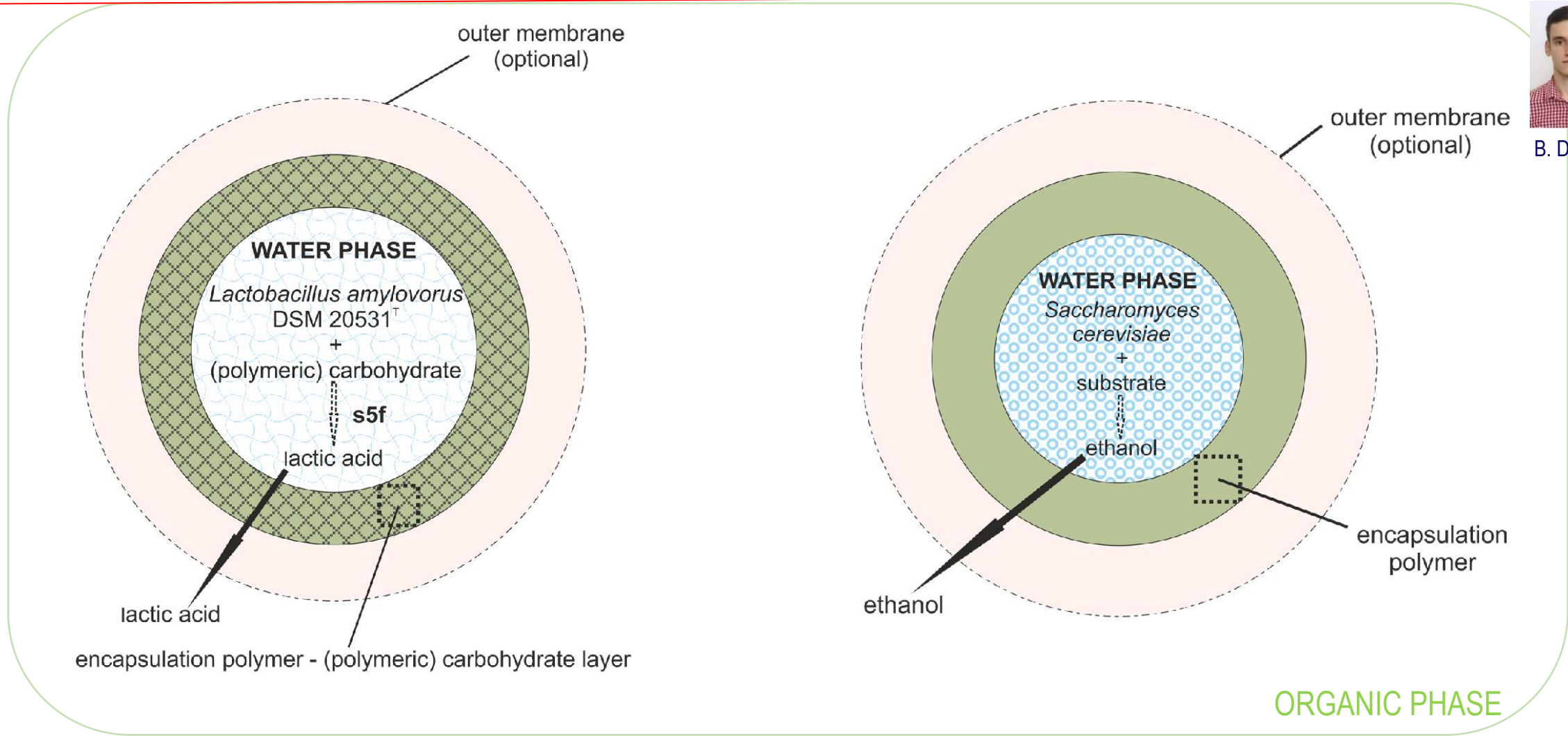
CO₂ → acety-CoA



. encapsulation of *L. amylovorus* DSM 20531 with polymeric substrate

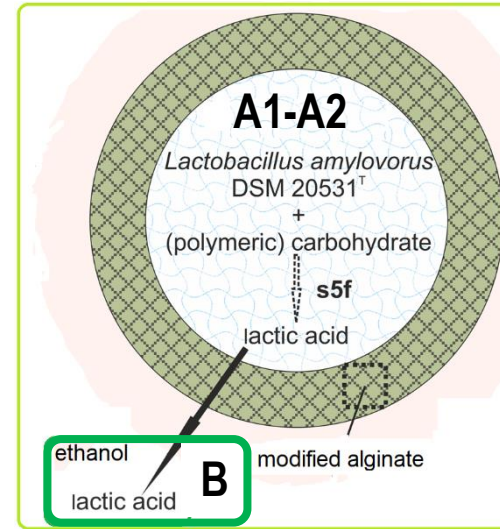
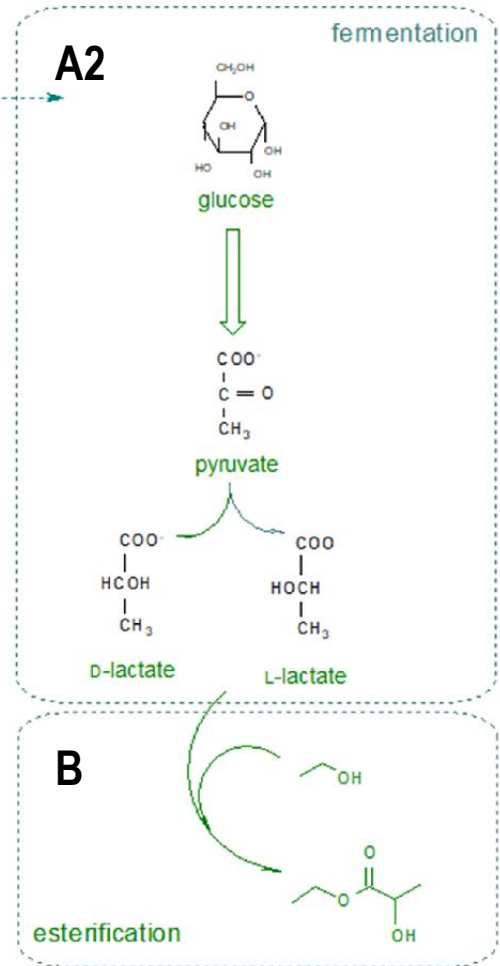
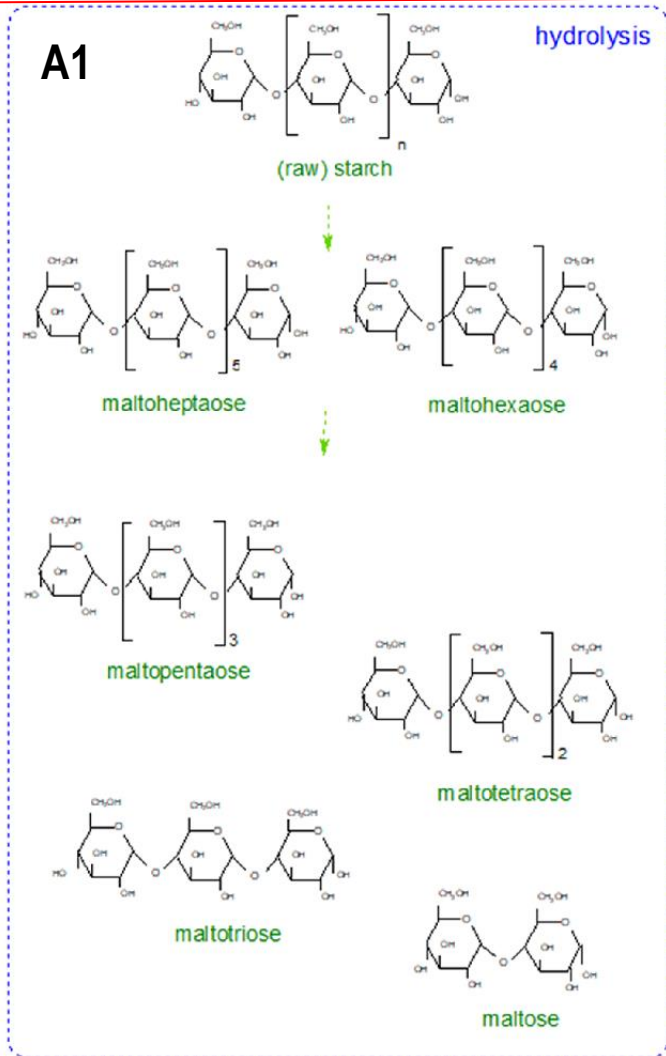


B. Duić



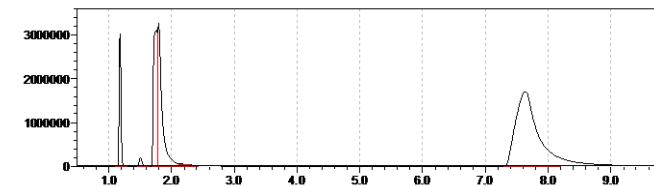
unpublished data

. encapsulation of *L. amylovorus* DSM 20531 with polymeric substrate - development of an integrated bioprocesses



Leo Moguš

MS detection of ethyl lactate

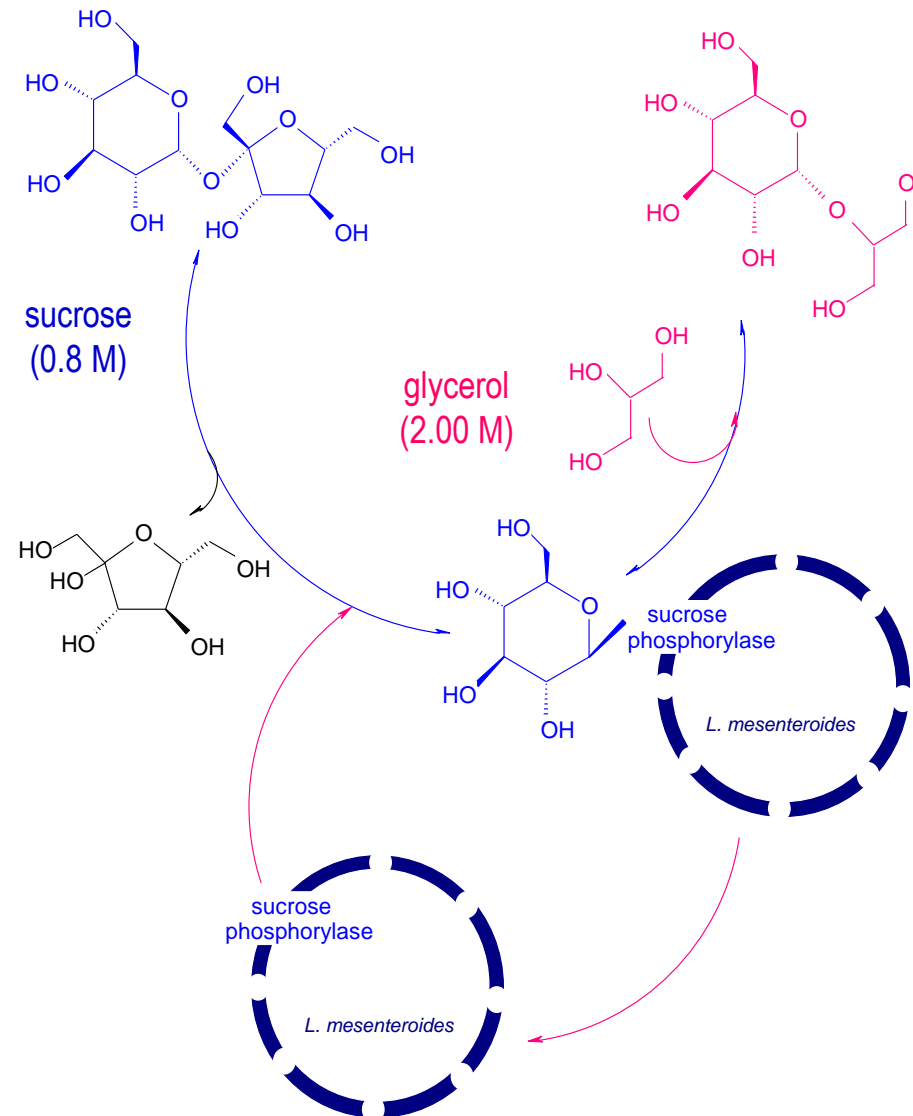


Hit#	Similarity	RegIn	Compound Name	Mol Wt	Formula	Library
1	98	12	Propanoic acid, 2-hydroxy-, ethyl ester; L-lactic acid, ethyl	118	C9H18O3	NIST08.LIB
2	118		Propanoic acid, 2-hydroxy-, ethyl ester, (S)-; Ethyl (S)-lactate; Ethyl 2-hydroxypropanoate; S			

unpublished data

Leuconostoc mesenteroides LMG 7954 whole-cell catalysed glycosylation

- ultrasound-assisted *L. mesenteroides* LMG 7954 permeabilization
- sucrose phosphorylase (EC 2.4.1.7)
- < 100 mM α -D-glucosylglycerol



α -D-glucosylglycerol



I. Vučenić



Iva Blašković
Ana-Marija Gručić
Lucija Vrtodušić

unpublished data

26 **Abstract**

27 Yeast *Saccharomyces cerevisiae* is widely recognized as a versatile chassis for constructing microbial
28 cell factories. However, producing chemicals from toxic, highly concentrated, or cell-impermeable
29 substrates, or chemicals dependent on enzymatic reactions incompatible with the yeast's intracellular
30 environment, remains challenging. In this study, we engineered a yeast microbial cell factory that, in a
31 single-step reaction, produces 2-O-(α -D-glucopyranosyl)-sn-glycerol (glucosyl glycerol, α GG), a
32 natural osmolyte used in the cosmetics and healthcare industries. For this purpose, we employed sucrose
33 phosphorylase (SucP) from *Leuconostoc mesenteroides*, a glucosyl transferase that, in a low-water,
34 glycerol-rich, phosphate-free environment, transfers the glucosyl moiety from sucrose to glycerol. To
35 accomplish this, we utilised surface display methodology to engineer yeast cells that covalently bind
36 SucP to their cell wall, thus converting their outer surface into a self-sustaining α GG-producing catalyst.
37 To efficiently anchor SucP near its C-terminus, we developed a miniature Ccw12-tag, derived from the
38 abundant yeast GPI-anchored cell wall protein Ccw12. This tag adds only 1.1 kDa to the enzyme of
39 interest while enabling its covalent attachment to the cell wall. The C-terminally anchored SucP
40 produced extracellularly 37.3 g l⁻¹ (146 mM) of α GG in five days, while the host cells metabolised
41 reaction by-products, thereby simplifying downstream processing.

42

43 **Keywords:** glucosyl glycerol, osmolyte, sucrose phosphorylase, *Saccharomyces cerevisiae*, surface
44 display, Ccw12

Stability Increase of Phenolic Acid Decarboxylase by a Combination of Protein and Solvent Engineering Unlocks Applications at Elevated Temperatures

Kamela Myrtollari, Elia Calderini, Daniel Kracher, Tobias Schöngaßner, Stela Galušić, Anita Slavica, Andreas Taden, Daniel Mokos, Anna Schrüfer, Gregor Wirnsberger, Karl Gruber, Bastian Daniel,* and Robert Kourist*

 Cite This: *ACS Sustainable Chem. Eng.* 2024, 12, 3575–3584

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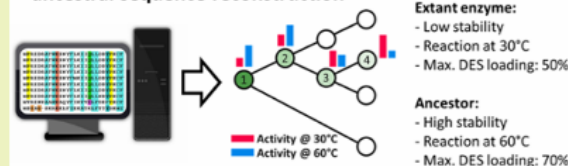
 Article Recommendations

 Supporting Information

ABSTRACT: Enzymatic decarboxylation of biobased hydroxycinnamic acids gives access to phenolic styrenes for adhesive production. Phenolic acid decarboxylases are proficient enzymes that have been applied in aqueous systems, organic solvents, biphasic systems, and deep eutectic solvents, which makes stability a key feature. Stabilization of the enzyme would increase the total turnover number and thus reduce the energy consumption and waste accumulation associated with biocatalyst production. In this study, we used ancestral sequence reconstruction to generate thermostable decarboxylases. Investigation of a set of 16 ancestors resulted in the identification of a variant with an unfolding temperature of 78.1 °C and a half-life time of 45 h at 60 °C. Crystal structures were determined for three selected ancestors. Structural attributes were calculated to fit different regression models for predicting the thermal stability of variants that have not yet been experimentally explored. The models rely on hydrophobic clusters, salt bridges, hydrogen bonds, and surface properties and can identify more stable proteins out of a pool of candidates. Further stabilization was achieved by the application of mixtures of natural deep eutectic solvents and buffers. Our approach is a straightforward option for enhancing the industrial application of the decarboxylation process.

KEYWORDS: *biocatalysis, enzymatic decarboxylation, biobased polymers, deep eutectic solvents, ancestral sequence reconstruction*

ancestral sequence reconstruction





. the workflow

WP1. Design and developing of connection between nonthermal processing techniques (high power ultrasound and pulsed electric field) with Internet of Things (IoT) hardware and software.

WP2. Optimisation of nonthermal IoT green extraction processes (NT-IoT-P) of proteins (RuBisCO): analytical and sustainable procedures.

WP3. Optimisation of electrospinning, electrospraying and encapsulation techniques of extracted proteins (RuBisCO): analytical procedures.

WP4. Developing and setting bioinformatic in-silico modeling in protein and peptide extraction.

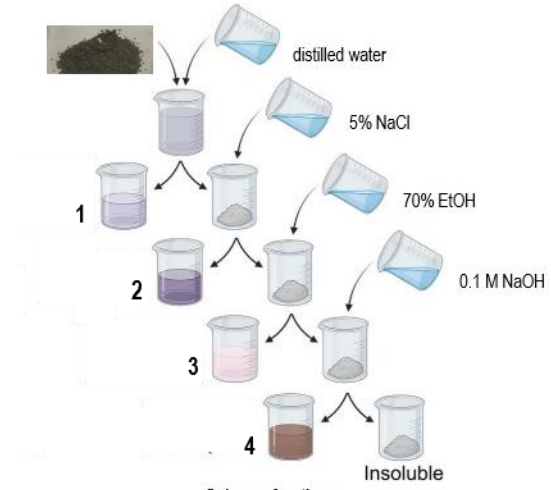
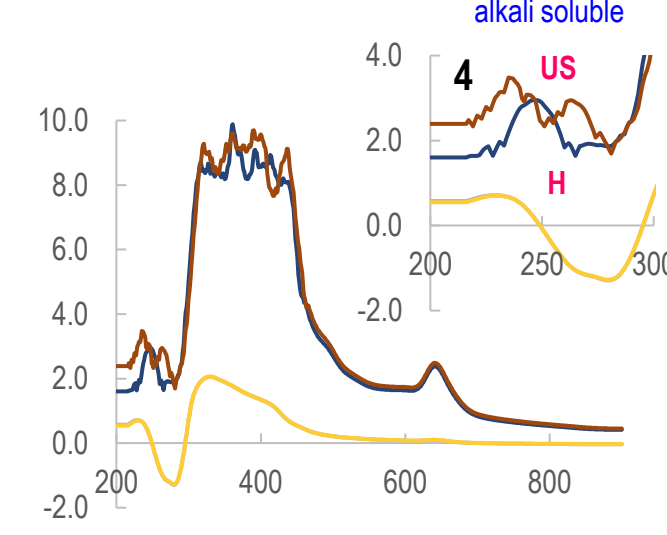
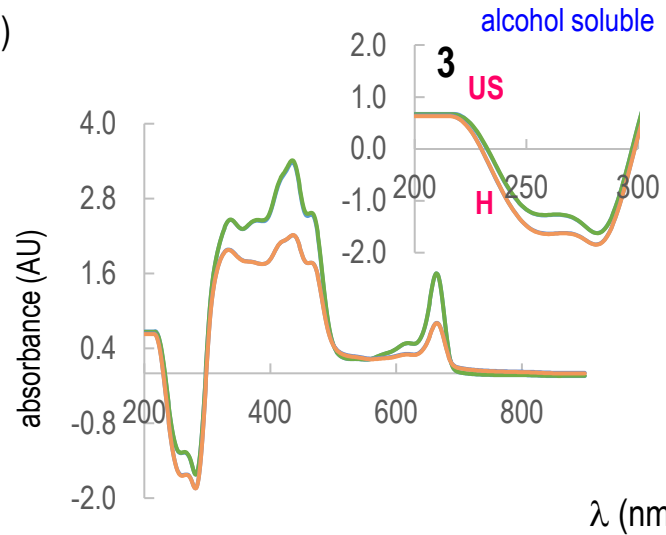
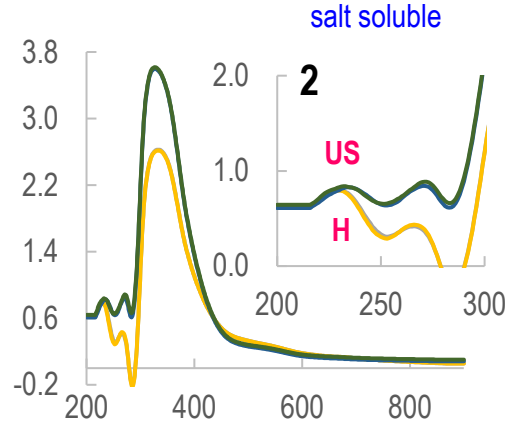
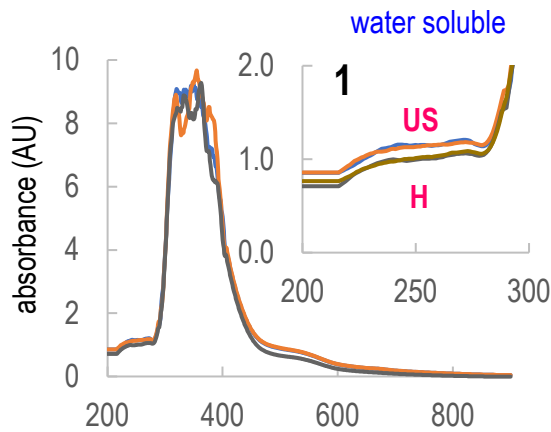
WP5. Economic and sustainable assessment on NT-IoT-P in green extraction of proteins (RuBisCO).

WP 6. Dissemination and knowledge transfer.

new challenges and opportunities - DEEP project



- heat (H)- vs ultrasound (US)-assisted Osborne fractionation of proteins (RuBISCo) and other bioactive compounds from Beta vulgaris L. (beetroot) leaves - preliminary data



acknowledgment



Bernd Nidetzky, Univ.-Prof. Dipl.-Ing. Dr.techn. Dr.h.c

Univ.-Prof. Dr.rer.nat. Robert Kourist



Digitalisation of nonthermal Extraction of proteins from plant by-products and Electroforming as output Product (DEEP; IP-2022-10-2207)



Biotechnological application of incorporation of heterologous proteins into yeast cell walls (IP-2019-04-2891)



Ministry of Science, Education and Youth of the Republic of Croatia, Application of integrated bioprocesses in the production of lactic acid (058-0581990-1997)

Thank you for your kind attention!

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