Alterations in the transcription factors GntR1 and RamA enhance the growth and central metabolism of Corynebacterium glutamicum

Evolution, i.e. the change in heritable characteristics of biological populations over successive generations, has created the diversity of life that exists today. In this study we have harnessed evolution to create faster growing mutants of Corynebacterium glutamicum, i.e. to debottleneck growth rate of this highly important industrial workhorse. After approximately 1500 generations of Adaptive Laboratory Evolution (ALE) in defined minimal medium with glucose, we obtained faster growing mutants with specific growth rate as high as 0.64h⁻¹ as compared with 0.45h⁻¹ for the wild type, and this 42% improvement is the highest reported for C. glutamicum to date. By genome resequencing and inverse metabolic engineering, we were able to pinpoint two mutations contributing to most of the growth improvement, and these resided in the transcriptional regulators GntR1 (gntR1-E70K) and RamA (ramA-A52V). We confirmed that the two mutations lead to alteration rather than elimination of function, and their introduction in the wild-type background resulted in a specific growth rate of 0.62h⁻¹. The glycolytic and pentose phosphate pathway fluxes had both increased significantly, and a transcriptomic analyses supported this to be associated with increased capacity. Interestingly, the observed fast growth phenotype was not restricted to glucose but was also observed on fructose, sucrose and xylose, however, the effect of the mutations could only be seen in minimal medium, and not rich BHI medium, where growth was already fast. We also found that the mutations could improve the performance of resting cells, under oxygen-deprived conditions, where an increase in sugar consumption rate of around 30% could be achieved. In conclusion, we have demonstrated that it is feasible to reprogram C. glutamicum into growing faster and thus enhance its industrial potential.
A bacterial cell factory for efficient production of ethanol from whey

The invention relates to a method for homo-ethanol production from lactose using a genetically modified lactic acid bacterium of the invention, where the cells are provided with a substrate comprising dairy waste supplemented with an amino nitrogen source (such as acid hydrolysed corn steep liquor). The invention further relates to genetically modified lactic acid bacterium and its use for homo-ethanol production from lactose in dairy waste. The lactic acid bacterium comprises both genes (lacABCD, LacEF, lacG) encoding enzymes catalysing the lactose catabolism pathway; and transgenes (pdc and adhB) encoding enzymes catalysing the conversion of pyruvate to ethanol. Additionally a number of genes (Idh, pta and adhE) are deleted in order to maximise homo-ethanol production as compared to production of lactate, acetoin and acetate production.

General information
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Organisations: National Food Institute, Research Group for Microbial Biotechnology and Biorefining
Contributors: Jensen, P. R., Liu, J., Solem, C., Dantoft, S. H.
Publication date: 31 Aug 2017

Publication information
IPC: C12N 15/75 A1
Patent number: WO2017144672
High-level production of diacetyl in a metabolically engineered lactic acid bacterium

The present invention provides a genetically modified lactic acid bacterium capable of producing diacetyl under aerobic conditions. Additionally, the invention provides a method for producing diacetyl using the genetically modified lactic acid bacterium under aerobic conditions in the presence of a source of iron-containing porphyrin and a metal ion selected from Fe3+, Fe2+, and Cu2+. The lactic acid bacterium is genetically modified by deletion of those genes in its genome that encode polypeptides having lactate dehydrogenase (EC 1.1.1.27/EC.1.1.1.28); α-acetolactate decarboxylase (EC 4.1.1.5); water-forming NADH oxidase (EC 1.6.3.4); phosphotransacetylase (EC 2.3.1.8) activity; and optionally devoid of or deleted for genes encoding polypeptides having diacetyl reductase ((R)-acetoin forming; EC: 1.1.1.303); D-acetoin reductase; butanediol dehydrogenase ((R,R)-butane-2,3-diol forming; EC: 1.1.1.4/1.1.1.1) and alcohol dehydrogenase (EC 1.2.1.10) activity. The invention provides for use of the genetically modified lactic acid bacterium for the production of diacetyl and a food product.

General information
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Organisations: National Food Institute, Research Group for Microbial Biotechnology and Biorefining
Contributors: Solem, C., Jensen, P. R., Liu, J.
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Priority number: EP20160157443
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Research output: Research › Patent – Annual report year: 2017

Engineering Lactococcus lactis into a cell factory for production of butanol isomers

General information
State: Published
Organisations: National Food Institute, Research Group for Microbial Biotechnology and Biorefining, Novo Nordisk Foundation Center for Biosustainability, iLoop, University of Copenhagen
Contributors: Andersen, J. M., Mar, M. J., Kandasamy, V., Liu, J., Brock-Nannestad, T., Solem, C., Jensen, P. R.
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Research output: Research › peer-review › Conference abstract in proceedings – Annual report year: 2017
Harnessing the respiration machinery for high-yield production of chemicals in metabolically engineered Lactococcus lactis

When modifying the metabolism of living organisms with the aim of achieving biosynthesis of useful compounds, it is essential to ensure that it is possible to achieve overall redox balance. We propose a generalized strategy for this, based on fine-tuning of respiration. The strategy was applied on metabolically engineered Lactococcus lactis strains to optimize the production of acetoin and (R,R)-2,3-butanediol (R-BDO). In the absence of an external electron acceptor, a surplus of two NADH per acetoin molecule is produced. We found that a fully activated respiration was able to efficiently regenerate NAD+, and a high titer of 371 mM (32 g/L) of acetoin was obtained with a yield of 82% of the theoretical maximum. Subsequently, we extended the metabolic pathway from acetoin to R-BDO by introducing the butanediol dehydrogenase gene from Bacillus subtilis. Since one mole of NADH is consumed when acetoin is converted into R-BDO per mole, only the excess of NADH needs to be oxidized via respiration. Either by fine-tuning the respiration capacity or by using a dual-phase fermentation approach involving a switch from fully respiratory to non-respiratory conditions, we obtained 361 mM (32 g/L) R-BDO with a yield of 81% or 365 mM (33 g/L) with a yield of 82%, respectively. These results demonstrate the great potential in using finely-tuned respiration machineries for bio-production.

General information
State: Published
Organisations: National Food Institute, Research Group for Microbial Biotechnology and Biorefining, Novo Nordisk Foundation Center for Biosustainability, New Bioactive Compounds
Contributors: Liu, J., Wang, Z., Kandasamy, V., Lee, S. Y., Solem, C., Jensen, P. R.
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  Web of Science (2017): Impact factor 7.674
  Web of Science (2017): Indexed yes
  BFI (2016): BFI-level 2
  Scopus rating (2016): CiteScore 8.33 SJR 3.626 SNIP 1.865
  Web of Science (2016): Impact factor 8.142
  Web of Science (2016): Indexed yes
  BFI (2015): BFI-level 2
  Scopus rating (2015): CiteScore 8.2 SJR 3.6 SNIP 1.809
  Web of Science (2015): Impact factor 8.201
  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 2
  Scopus rating (2014): CiteScore 7.23 SJR 3.395 SNIP 2.009
  Web of Science (2014): Impact factor 6.767
  Web of Science (2014): Indexed yes
  BFI (2013): BFI-level 2
  Scopus rating (2013): CiteScore 8.43 SJR 4.036 SNIP 2.164
  Web of Science (2013): Impact factor 8.258
  ISI indexed (2013): ISI indexed yes
  Web of Science (2013): Indexed yes
  BFI (2012): BFI-level 2
  Scopus rating (2012): CiteScore 6.72 SJR 2.989 SNIP 1.847
  Web of Science (2012): Impact factor 6.859
  ISI indexed (2012): ISI indexed yes
  Web of Science (2012): Indexed yes
  BFI (2011): BFI-level 1
  Scopus rating (2011): CiteScore 6.75 SJR 3.049 SNIP 2.038
  Web of Science (2011): Impact factor 5.614
Metabolic characterization and transformation of the non-dairy Lactococcus lactis strain KF147, for production of ethanol from xylose

The non-dairy lactic acid bacterium Lactococcus lactis KF147 can utilize xylose as the sole energy source. To assess whether KF147 could serve as a platform organism for converting second generation sugars into useful chemicals, we characterized growth and product formation for KF147 when grown on xylose. In a defined medium KF147 was found to co-metabolize xylose and arginine, resulting in bi-phasic growth. Especially at low xylose concentrations, arginine significantly improved growth rate. To facilitate further studies of the xylose metabolism, we eliminated arginine catabolism by deleting the arcA gene encoding the arginine deiminase. The fermentation product profile suggested two routes for xylose degradation, the phosphoketolase pathway and the pentose phosphate pathway. Inactivation of the phosphoketolase pathway redirected the entire flux through the pentose phosphate pathway whereas over-expression of phosphoketolase increased the flux through the phosphoketolase pathway. In general, significant amounts of the mixed-acid products, including lactate, formate, acetate and ethanol, were formed irrespective of xylose concentrations. To demonstrate the potential of KF147 for converting xylose into useful chemicals we chose to redirect metabolism towards ethanol production. A synthetic promoter library was used to drive the expression of codon-optimized versions of the Zymomonas mobilis genes encoding pyruvate decarboxylase and alcohol dehydrogenase, and the outcome was a strain producing ethanol as the sole fermentation product with a high yield corresponding to 83% of the theoretical maximum. The results clearly indicate the great potential of using the more metabolically diverse non-dairy L. lactis strains for bio-production based on xylose containing feedstocks.
Micro-organism for the production of stereo-specific s, s-2,3-butanediol
The invention relates to a genetically modified lactic acid bacterium capable of producing (S,S)-2,3-butanediol stereo specifically from glucose under aerobic conditions. Additionally, the invention relates to a method for producing (S,S)-2,3-butanediol and L-acetoin using the genetically modified lactic acid bacterium, under aerobic conditions in the presence of a source of iron-containing porphyrin or a source of metal ions (Fe³⁺/Fe²⁺). The lactic acid bacterium is genetically modified to express heterologous genes encoding enzymes catalysing the stereo-specific synthesis of (S,S)-2,3-butanediol, and additionally a number of genes are deleted in order to maximise the production of (S,S)-2,3-butanediol as compared to other products of oxidative fermentation.

General information
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Organisations: Systems Biotechnology, National Food Institute, Research Group for Microbial Biotechnology and Biorefining
Contributors: Solem, C., Jensen, P. R., Chen, J., Liu, J.
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Priority number: EP20150191703
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Electronic versions:
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Source: espacenet
Source-ID: WO2016097268
Research output: Research - Patent – Annual report year: 2016

AcetoIn and 2,3 butanediol isomers synthesis in metabolically engineered Lactococcus lactis
Harnessing the biosynthetic machinery of living cells is a common approach used for producing a broad range of useful chemicals. Here, we divert inherent metabolic routes in L. lactis to produce (3R)-acetoin and the derived 2,3 butanediol isomers. Efficient production of (3R)-acetoin was accomplished using a strain where the competing lactate, acetate and ethanol forming pathways had been blocked. By introducing different alcohol dehydrogenases into this strain, either EcBdh from Enterobacter cloacae or SadB from Achromobacter xylosoxidans, it was possible to achieve high-yield production of m-BDO or R-BDO respectively. To achieve biosustainable production of these chemicals from dairy waste, we transformed the above strains with the lactose plasmid pLP712. This enabled efficient production of (3R)-acetoin, m-BDO and R-BDO from processed whey waste, with titers of 27, 51, and 32.1 g/L respectively. The corresponding yields obtained were 0.42, 0.47 and 0.40 g/g lactose, which is 82%, 89%, and 76% of maximum theoretical yield respectively. These results clearly demonstrate that L. lactis is an excellent choice as a cell factory for transforming lactose containing dairy waste into value added chemicals.

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State: Published
Organisations: National Food Institute, Research Group for Microbial Biotechnology and Biorefining, Systems Biotechnology
Contributors: Kandasamy, V., Liu, J., Dantoft, S. H., Solem, C., Jensen, P. R.
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URLs:
http://www.sustain.dtu.dk/

Bibliographical note
Sustain Abstract B-6
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2016
A novel cell factory for efficient production of ethanol from dairy waste

Sustainable and economically feasible ways to produce ethanol or other liquid fuels are becoming increasingly relevant due to the limited supply of fossil fuels and the environmental consequences associated with their consumption. Microbial production of fuel compounds has gained a lot of attention and focus has mostly been on developing bio-processes involving non-food plant biomass feedstocks. The high cost of the enzymes needed to degrade such feedstocks into its constituent sugars as well as problems due to various inhibitors generated in pretreatment are two challenges that have to be addressed if cost-effective processes are to be established. Various industries, especially within the food sector, often have waste streams rich in carbohydrates and/or other nutrients, and these could serve as alternative feedstocks for such bio-processes. The dairy industry is a good example, where large amounts of cheese whey or various processed forms thereof are generated. Because of their nutrient-rich nature, these substrates are particularly well suited as feedstocks for microbial production. We have generated a Lactococcus lactis strain which produces ethanol as its sole fermentation product from the lactose contained in residual whey permeate (RWP), by introducing lactose catabolism into a L. lactis strain CS4435 (MG1363 Δ(3) ldh, Δpta, ΔadhE, pCS4268), where the carbon flow has been directed toward ethanol instead of lactate. To achieve growth and ethanol production on RWP, we added corn steep liquor hydrolysate (CSLH) as the nitrogen source. The outcome was efficient ethanol production with a titer of 41 g/L and a yield of 70 % of the theoretical maximum using a fed-batch strategy. The combination of a low-cost medium from industrial waste streams and an efficient cell factory should make the developed process industrially interesting. A process for the production of ethanol using L. lactis and a cheap renewable feedstock was developed. The results demonstrate that it is possible to achieve sustainable bioconversion of waste products from the dairy industry (RWP) and corn milling industry (CSLH) to ethanol and the process developed shows great potential for commercial realization.
Combining metabolic engineering and biocompatible chemistry for efficient production of food ingredients

Biocompatible chemistry, that is non-enzymatic chemical reactions compatible with living organisms, is gaining increasing attention because of its potential within biotechnology for expanding the repertoire of biological transformations carried out by enzymes. Here we demonstrate how biocompatible chemistry can be used for synthesizing valuable food ingredients as well as for linking metabolic pathways to achieve redox balance and rescued growth. By comprehensive rerouting of metabolism, activation of respiration, and finally metal ion catalysis, we successfully managed to convert the homolactic bacterium *Lactococcus lactis* into a homo-diacetyl producer with high titer (95 mM or 8.2 g/L) and high yield (87% of the theoretical maximum). Subsequently, the pathway was extended to (S,S)-2,3-butanediol (S-BDO) through efficiently linking two metabolic pathways via chemical catalysis. This resulted in efficient homo-S-BDO production with a titer of 74 mM (6.7 g/L) S-BDO and a yield of 82%. The diacetyl and S-BDO production rates and yields obtained are the highest ever reported, demonstrating the promising combination of metabolic engineering and biocompatible chemistry as well as the great potential of *L. lactis* as a new production platform.

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Peer-reviewed: Yes
URLs:
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Bibliographical note
Sustain Abstract B-1
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Combining metabolic engineering and biocompatible chemistry for high-yield production of homo-diacetyl and homo-(S,S)-2,3-butanediol
Biocompatible chemistry is gaining increasing attention because of its potential within biotechnology for expanding the repertoire of biological transformations carried out by enzymes. Here we demonstrate how biocompatible chemistry can be used for synthesizing valuable compounds as well as for linking metabolic pathways to achieve redox balance and rescued growth. By comprehensive rerouting of metabolism, activation of respiration, and finally metal ion catalysis, we...
successfully managed to convert the homolactic bacterium Lactococcus lactis into a homo-diacetyl producer with high titer (95mM or 8.2g/L) and high yield (87% of the theoretical maximum). Subsequently, the pathway was extended to (S,S)-2,3-butanediol (S-BDO) through efficiently linking two metabolic pathways via chemical catalysis. This resulted in efficient homo-S-BDO production with a titer of 74mM (6.7g/L) S-BDO and a yield of 82%. The diacetyl and S-BDO production rates and yields obtained are the highest ever reported, demonstrating the promising combination of metabolic engineering and biocompatible chemistry as well as the great potential of L. lactis as a new production platform.

**General information**
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Organisations: National Food Institute, Research Group for Microbial Biotechnology and Biorefining, University of Copenhagen, Korean Advanced Institute of Science and Technology (KAIST)
Contributors: Liu, J., Chan, S. H. J., Brock-Nannestad, T., Chen, J., Lee, S. Y., Solem, C., Jensen, P. R.
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BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 8.33 SJR 3.626 SNIP 1.865
Web of Science (2016): Impact factor 8.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 8.2 SJR 3.6 SNIP 1.809
Web of Science (2015): Impact factor 8.201
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 7.23 SJR 3.395 SNIP 2.009
Web of Science (2014): Impact factor 6.767
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 8.43 SJR 4.036 SNIP 2.164
Web of Science (2013): Impact factor 8.258
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 6.72 SJR 2.989 SNIP 1.847
Web of Science (2012): Impact factor 6.859
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 6.75 SJR 3.049 SNIP 2.038
Web of Science (2011): Impact factor 5.614
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.375 SNIP 1.786
Web of Science (2010): Impact factor 5.512
Integrating biocompatible chemistry and manipulating cofactor partitioning in metabolically engineered Lactococcus lactis for fermentative production of (3S)-acetoin

Biocompatible chemistry (BC), i.e. non-enzymatic chemical reactions compatible with living organisms, is increasingly used in conjunction with metabolically engineered microorganisms for producing compounds that do not usually occur naturally. Here we report production of one such compound, (3S)-acetoin, a valuable precursor for chiral synthesis, using a metabolically engineered Lactococcus lactis strain growing under respiratory conditions with ferric iron serving as a BC component. The strain used has all competing product pathways inactivated, and an appropriate cofactor balance is achieved by fine-tuning the respiratory capacity indirectly via the hemin concentration. We achieve high-level (3S)-acetoin production with a final titer of 66 mM (5.8 g/L) and a high yield (71% of the theoretical maximum). To the best of our knowledge, this is the first report describing production of (3S)-acetoin from sugar by microbial fermentation, and the results obtained confirm the potential that lies with BC for producing useful chemicals.

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Contributors: Liu, J., Solem, C., Jensen, P. R.
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BFI (2017): BFI-level 1
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Web of Science (2017): Impact factor 3.952
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.14 SJR 1.447 SNIP 1.178
Web of Science (2016): Impact factor 4.481
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.44 SJR 1.632 SNIP 1.355
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.16 SJR 1.612 SNIP 1.395
Web of Science (2014): Impact factor 4.126
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.44 SJR 1.637 SNIP 1.427
Web of Science (2013): Impact factor 4.164
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.04 SJR 1.62 SNIP 1.364
Web of Science (2012): Impact factor 3.648
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.08 SJR 1.668 SNIP 1.481
Web of Science (2011): Impact factor 3.946
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.551 SNIP 1.354
Web of Science (2010): Impact factor 3.7
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.498 SNIP 1.358
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
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Scopus rating (2007): SJR 1.363 SNIP 1.356
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.467 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.135 SNIP 1.23
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.105 SNIP 1.245
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.052 SNIP 1.228
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.117 SNIP 1.263
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.059 SNIP 1.16
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.428 SNIP 1.529
Web of Science (2000): Indexed yes
Stimulation of acetoin production in metabolically engineered Lactococcus lactis by increasing ATP demand

Having a sufficient supply of energy, usually in the form of ATP, is essential for all living organisms. In this study, however, we demonstrate that it can be beneficial to reduce ATP availability when the objective is microbial production. By introducing the ATP hydrolyzing F1-ATPase into a Lactococcus lactis strain engineered into producing acetoin, we show that production titer and yield both can be increased. At high F1-ATPase expression level, the acetoin production yield could be increased by 10%; however, because of the negative effect that the F1-ATPase had on biomass yield and growth, this increase was at the cost of volumetric productivity. By lowering the expression level of the F1-ATPase, both the volumetric productivity and the final yield could be increased by 5% compared to the reference strain not overexpressing the F1-ATPase, and in batch fermentation, it was possible to convert 176 mM (32 g/L) of glucose into 146.5 mM (12.9 g/L) acetoin with a yield of 83% of the theoretical maximum. To further demonstrate the potential of the cell factory developed, we complemented it with the lactose plasmid pLP712, which allowed for growth and acetoin production from a dairy waste stream, deproteinized whey. Using this cheap and renewable feedstock, efficient acetoin production with a titer of 157 mM (14 g/L) acetoin was accomplished.

General information
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 1.2 SNIP 1.182
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.43 SJR 1.256 SNIP 1.221
Web of Science (2015): Impact factor 3.376
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.71 SJR 1.332 SNIP 1.448
Web of Science (2014): Impact factor 3.337
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.3 SJR 1.54 SNIP 1.43
Synthesis of (3R)-acetoin and 2,3-butanediol isomers by metabolically engineered Lactococcus lactis

The potential that lies in harnessing the chemical synthesis capabilities inherent in living organisms is immense. Here we demonstrate how the biosynthetic machinery of Lactococcus lactis, can be diverted to make (3R)-acetoin and the derived 2,3-butanediol isomers meso-(2,3)-butanediol (m-BDO) and (2R,3R)-butanediol (R-BDO). Efficient production of (3R)-acetoin was accomplished using a strain where the competing lactate, acetate and ethanol forming pathways had been blocked. By introducing different alcohol dehydrogenases into this strain, either EcBDH from Enterobacter cloacae or SadB from Achromobacter xylosoxidans, it was possible to achieve high-yield production of m-BDO or R-BDO respectively. To achieve biosustainable production of these chemicals from dairy waste, we transformed the above strains

Additional ATP consumption, F1-ATPASE, Acetoin, Lactococcus lactis

Original language: English

Keywords: Additional ATP consumption, F1-ATPASE, Acetoin, Lactococcus lactis

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Research output: Research - peer-review › Journal article – Annual report year: 2016
with the lactose plasmid pLP712. This enabled efficient production of (3R)-acetoin, m-BDO and R-BDO from processed whey waste, with titers of 27, 51, and 32 g/L respectively. The corresponding yields obtained were 0.42, 0.47 and 0.40 g/g lactose, which is 82%, 89%, and 76% of maximum theoretical yield respectively. These results clearly demonstrate that L. lactis is an excellent choice as a cell factory for transforming lactose containing dairy waste into value added chemicals.

**General information**

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Contributors: Kandasamy, V., Liu, J., Dantoft, S. H., Solem, C., Jensen, P. R.
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Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Impact factor 4.259
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.3 SJR 2.034 SNIP 1.597
Web of Science (2015): Impact factor 5.228
Web of Science (2015): Indexed yes
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Scopus rating (2014): CiteScore 4.75 SJR 2.163 SNIP 1.554
Web of Science (2014): Impact factor 5.578
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.06 SJR 1.998 SNIP 1.57
Web of Science (2013): Impact factor 5.078
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.44 SJR 1.531 SNIP 0.962
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