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# pH and base counterion affect succinate production in dual-phase *Escherichia coli* fermentations

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Abstract Succinate production was studied in Escherichia coli AFP111, which contains mutations in pyruvate formate lyase (pfl), lactate dehydrogenase (ldhA) and the phosphotransferase system glucosephosphotransferase enzyme II (ptsG). Two-phase fermentations using a defined medium at several controlled levels of pH were conducted in which an aerobic cell growth phase was followed by an anaerobic succinate production phase using 100% (v/v) CO<sub>2</sub>. A pH of 6.4 yielded the highest specific succinate productivity. A metabolic flux analysis at a pH of 6.4 using <sup>13</sup>C-labeled glucose showed that 61% of the PEP partitioned to oxaloacetate and 39% partitioned to pyruvate, while 93% of the succinate was formed via the reductive arm of the TCA cycle. The flux distribution at a pH of 6.8 was also analyzed and was not significantly different compared to that at a pH of 6.4. Ca(OH)<sub>2</sub> was superior to NaOH or KOH as the base for controlling the pH. By maintaining the pH at 6.4 using 25% (w/v) Ca(OH)<sub>2</sub>, the process achieved an average succinate productivity of 1.42 g/l h with a yield of 0.61 g/g.

Keywords Succinic acid  $\cdot$  CO<sub>2</sub>  $\cdot$  Calcium

# Introduction

Succinic acid (succinate) and its derivatives are widely used as specialty chemicals in foods, pharmaceuticals and cosmetics [10], and it can serve as a starting material for

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Center for Molecular BioEngineering, University of Georgia, Athens, GA 30602, USA e-mail: eiteman@engr.uga.edu many commercially important products [37]. Some anaerobic bacteria, such as Anaerobiospirillum succiniciproducens [13, 14], Actinobacillus succinogenes [11, 31] and Mannheimia succiniciproducens [15], produce succinate as the major fermentation product. During anaerobic fermentation, these organisms fix the greenhouse gas CO<sub>2</sub> via carboxylation reactions and convert C<sub>3</sub> to C<sub>4</sub> metabolites. Recombinant Escherichia coli can also generate a high concentration of succinate. For example, an anaerobic process generates 15.6 g/l succinate with a yield of 0.85 g/g glucose through overexpression of pyruvate carboxylase in an alcohol dehydrogenase and lactate dehydrogenase mutant [25]. Aerobically, E. coli generates 6.7 g/l succinate at a yield of 0.71 g/g glucose, although in this case CO<sub>2</sub> is not fixed [16, 17]). A dual-phase *E. coli* process (aerobic growth followed by an anaerobic succinate production phase) generates nearly 100 g/l succinate at a productivity of 1.3 g/l h and a yield of 1.1 g/g glucose [34].

A few studies have investigated the effect of pH on succinate production. For example, Van der Werf et al. [32] found that succinate was produced in the pH range of 6.0-7.4 by Actinobacillus sp., but pH was not controlled. Samuelov et al. [24] reported that for A. succiniciproducens a pH of 6.2 was better than a pH of 7.2 using NaOH. Optimal anaerobic succinate production by E. coli was reported to occur with a 0.2 M sodium phosphate buffer having a pH of 6.5 at the beginning of the fermentation [1], though pH was not controlled. Similarly, a 0.2 M sodium phosphate buffer at an initial pH of 6.5 was found to provide the optimal initial conditions for succinate production by Bacteroides fragilis [12]. Other studies select a pH rather than optimize it, and universally use either Na<sub>2</sub>CO<sub>3</sub> or NaOH for pH control, resulting in sodium ion accumulation.

The highest reported succinate concentration has been generated by *E. coli* AFP111 and its derivatives using a dual-phase process [34]. We selected this strain to study the influence of pH, and also compared its metabolism at two different values of pH using flux analysis with <sup>13</sup>C-labeled glucose. The formation of succinate requires the use of base in order to maintain the pH. When NaOH was used in initial experiments, we observed a decrease in the rate of succinate formation during the course of the anaerobic phase. To determine whether the Na<sup>+</sup> specifically is detrimental to succinate formation, we compared three common bases [NaOH, KOH and Ca(OH)<sub>2</sub>] and elucidated their effects as base counterions.

#### Materials and methods

#### Bacterial strain

*Escherichia coli* AFP111 ( $F^+ \lambda^- rpoS396$  (Am) *rph*-1  $\Delta pfIAB::Cam ldhA::Kan ptsG$ ) was used in this study [3, 5].

Media and fermentation conditions

All fermentations used a defined medium containing (per liter): 40.0 g glucose, 3.0 g citric acid, 3.0 g Na<sub>2</sub> HPO<sub>4</sub>·7H<sub>2</sub>O, 8.00 g KH<sub>2</sub>PO<sub>4</sub>, 8.00 g (NH<sub>4</sub>)<sub>2</sub>HPO<sub>4</sub>, 0.20 g NH<sub>4</sub>Cl, 0.75 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.84 g NaHCO<sub>3</sub>, 1.00 g MgSO<sub>4</sub>·7H<sub>2</sub>O, 10.0 mg CaCl<sub>2</sub>·2H<sub>2</sub>O, 0.5 mg ZnSO<sub>4</sub>·7H<sub>2</sub>O, 0.25 mg CuCl<sub>2</sub>·2H<sub>2</sub>O, 2.5 mg MnSO<sub>4</sub>·H<sub>2</sub>O, 1.75 mg CoCl<sub>2</sub> 6H<sub>2</sub>O, 0.12 mg H<sub>3</sub>BO<sub>3</sub>, 1.77 mg Al<sub>2</sub>(SO<sub>4)3</sub>·xH<sub>2</sub>O, 0.5 mg Na<sub>2</sub>MoO<sub>4</sub>·2H<sub>2</sub>O, 16.1 mg Fe(III) citrate, 20 mg thiamine HCl and 2 mg biotin.

Dual-phase fermentations operating in batch mode with an initial volume of 1.2 l in 2.5-l fermentors (Bioflow III, New Brunswick Scientific, Edison, NJ) were inoculated using 50 ml grown for 10-12 h to an optical density  $(OD_{600})$  of about 2–4 in the same medium in 250-ml shake flasks. Oxygen-enriched air as necessary was sparged at 1.0 l/min with an agitation of 200-500 rpm to maintain the dissolved oxygen (DO) above 40% as measured by an online probe (Mettler-Toledo Process Analytical Instruments, Wilmington, MA). During growth, the pH was controlled at 7.0 with 20% (w/v) NaOH, and the temperature was maintained at 37°C. When the OD<sub>600</sub> reached about 20, the aerobic growth phase was terminated by switching the inlet gas composition to 100% (v/v) CO<sub>2</sub>. Simultaneously, the total flow rate was reduced to 500 ml/min (dry basis, 0°C and 1 atm), the agitation reduced to 200 rpm, and 120 ml of 550 g/l glucose was added. During this anaerobic phase, the pH was controlled with either 25% (w/v) NaOH, 25% (w/v) KOH or 25% (w/v) Ca(OH)<sub>2</sub> as indicated.

Analysis of glucose and products

Samples were diluted by 1% H<sub>2</sub>SO<sub>4</sub> as necessary and centrifuged ( $10,000 \times g$  for 10 min at 4°C) and the supernatant analyzed for glucose, succinate, pyruvate, acetate and ethanol by high performance liquid chromatography (HPLC) as previously described [6]. When calcium succinate was generated, the total succinate (dissolved plus precipitate) was determined by diluting the sample with 1% H<sub>2</sub>SO<sub>4</sub> and sonicating prior to analysis.

For metabolic flux analysis involving [1-<sup>13</sup>C] glucose, dual-phase fermentations were repeated as described above except the initial volume was 0.6 l in 1.0-L fermentors (Bioflow III, New Brunswick Scientific, Edison, NJ), the inoculum volume was reduced to 25 ml, and the initial glucose concentration was 30 g/l. The glucose concentration was monitored using a glucose analyzer (YSI 2700 SELECT<sup>TM</sup>, Yellow Springs Instrument, Inc, Yellow Springs, OH). When the glucose concentration reached about 2 g/l, the system was switched to anaerobic conditions by sparging CO<sub>2</sub>. When the glucose concentration reached about 1 g/l, 10 ml of 450 g/l  $[1-^{13}C]$ glucose (99%, Cambridge Isotope Laboratories, Andover, MA) was added into the fermentor, and the pH was reduced within a couple minutes to the desired value with 20% (v/v) H<sub>2</sub>SO<sub>4</sub>. Samples were then collected every 30 min, centrifuged at 0°C (10,000×g for 10 min) and the supernatants stored at -4°C for later LC-MS and NMR analyses.

# LC-MS analysis of succinate

The supernatant was filtered by a 0.2-µM syringe filter (Cole-Parmer Instrument Co., Vernon Hills, IL) prior to LC-MS analysis. The liquid chromatography was performed at 25°C (140B Solvent Delivery System, Applied Biosystems, Foster City, CA) using a C18 column (Kromasil,  $250 \times 1$  mm, 5-µm particles, 100-Å pore space, Keystone Scientific, Inc., Bellefonte, PA). The mobile phase at 50 µl/min was a gradient of aqueous acetic acid (0.1% w/v, pH 3.23) and methanol. Electrospray ionization mass spectrometry was performed using a single quadrupole instrument with an electrospray ion source (PE Sciex API 1 Plus, Concord, ON, Canada). The operating conditions were: nebulizer gas (N<sub>2</sub>) at a flow rate of 0.6 l/min and pressure of 30 psi, curtain gas (N<sub>2</sub>) at a flow rate of 0.8 l/min and interface temperature 50°C. Data were acquired in negative ion mode with a capillary voltage of 3,500 V. Mass peak heights were determined using the BioTool Box Version B software package (Applied Biosystems/PE Sciex, Foster City, CA). The relative concentrations of M + 0, M + 1, M + 2 and M + 3 (M + 0represents succinate without <sup>13</sup>C label having a m/z of 117,

etc.) were calculated by the fractions of each peak heights after correcting for naturally occurring  $^{13}$ C (1.109%) and  $^{18}$ O (0.20%) [22].

# Metabolic modeling and flux analysis

An overall flux balance was developed using stoichiometric analysis and the pseudo-steady-state condition for intracellular metabolites [27]. The balance equations for *E. coli* AFP111 metabolism have been developed previously [34], and this model was further extended by including the pentose phosphate pathway (Fig. 1). Flux partitions ( $\phi$ ) were defined as fractional fluxes ( $\nu$ ) into one of two key branches. The fraction of flux into the pentose phosphate pathway ( $\phi_{PPP}$ ) is defined as

$$\phi_{\rm PPP} = \frac{v_3}{v_2 + v_3}$$

The fraction of flux through anaplerotic carboxylation at the PEP node ( $\phi_{PPC}$ ) is defined as:

$$\phi_{\rm PPC} = \frac{v_{13}}{v_{13} + v_{14}}$$

The model contained 27 fluxes and 21 metabolites (Fig. 1 and Appendix A). Since insignificant growth occurs during the anaerobic process [34], glucose consumption and product formation rates were essentially constant (e.g., Fig. 2); thus, the process exhibited a metabolic pseudosteady state. Although five fluxes are known, the balance equations represent an underdetermined set. In order to calculate the optimal solution for the flux model, LC-MS results with 1-<sup>13</sup>C-glucose were used. Specifically, we wrote analogous balance equations for isotopomers of each metabolite [28]. We calculated the distribution of succinate isotopomers for a given set of fluxes and calculated the mole fraction  $(X_{calc})$  of each isotopomer *i*. These calculated values were compared with the mole fractions of each isotopomer observed from the LC-MS results ( $X_{obs}$ ). The optimal solution for the flux model was then determined by minimizing the weighted sum of squared residuals over the four mass peaks [33]:

$$\text{error} = \sqrt{\sum_{i=0}^{3} \frac{\left(X_{\text{calc},i} - X_{\text{obs},i}\right)^{2}}{s_{i}^{2}}}$$

where *s* is the standard deviation of the observed mole fraction determined by three LC-MS analyses of each sample. The isotopomer analysis cannot determine whether flux occurred through the malic enzyme and/or pyruvate oxidase because these pathways do not alter the <sup>13</sup>C-labeled distribution compared, respectively, with PEP carboxylase and acetate formation via acetyl CoA. Therefore, the model did not include these two pathways.

#### NMR analysis of succinate

The sample supernatant was filtered by a 0.2-µM syringe filter, and then the filtered supernatant was mixed with 15% volume of deuterium dioxide (D<sub>2</sub>O) for NMR analysis. Proton-coupled <sup>13</sup>C NMR spectra (500 NMR spectroscopy; Varian Inc., Palo Alto, CA) at 125.7 MHz were obtained with the following spectral parameters: 45° pulses, 31.4-kHz spectral width and 45-s relaxation delay. Field stabilization was achieved by locking on the D<sub>2</sub>O frequency. <sup>13</sup>C chemical shift assignments for succinate were determined by comparison with the natural abundance standard.

NMR was not used to calculate fluxes, but was employed to complement the LC-MS results. Specifically, since the LC-MS results did not provide information about the position of the label, we were able to use NMR to observe the total <sup>13</sup>C enrichment at C-1 position (S1) and that at C-2 position of succinate (S2). The enrichment ratio of S2/S1 was calculated from the ratio of the peak area of the methylene group to the carboxyl group of succinate. This observed enrichment ratio was compared to the enrichment ratio calculated from the optimized metabolic flux model. We also calculated the redox ratio as the fluxes through NAD(P)H formation steps in the pathways divided by fluxes through NAD(P)H consumption steps.

We chose for all metabolic flux analyses the interval between the time  $1-{}^{13}$ C-glucose was added and the time that the succinate concentration reached about 4 g/l (approximately 2 h).

#### Results

Effect of pH on succinate production

E. coli AFP111 accumulates significant amounts of succinate during an anaerobic non-growth phase after growing to a high cell density under aerobic conditions at a pH of 7.0. During succinate generation,  $CO_2$  is incorporated into the central metabolism through the action of the enzyme PEP carboxylase (PPC) [8]. We first examined the effect of pH on succinate formation. We controlled the pH at a constant level in the range of 5.8-7.0 using 25% Ca(OH)<sub>2</sub> as the neutralizing agent. Figure 2 shows the generation of several products during the anaerobic process when the pH was maintained at 6.4. Over the course of 14-16 h, succinate was generated to 25-30 g/l, pyruvate to 7-10 g/l, ethanol to about 1 g/l and acetate to less than 1 g/l. For each pH studied, the glucose consumption rate  $(q_G)$ , the volumetric succinate productivity (Qs), specific succinate productivity  $(q_{\rm S})$  and mass product yields of succinate, acetate, ethanol and pyruvate were calculated during the 14 h of the anaerobic phase, and the values reported are the means of Fig. 1 Biochemical pathways for the synthesis of succinate from glucose in E. coli. Not all enzymatic steps or intermediates are shown. Key enzymes in the pathways are as follows: (1) glucokinase, (2) phosphoglucoisomerase; (3) 6-phosphogluconate dehydrogenase; (4) phosphopentose epimerase; (5) phosphopentose epimerase; (6) transketolase; (7) transaldolase; (8) transketolase; (9) phosphofructokinase; (10) fructose biphosphate aldolase; (11) glyceraldehyde 3phosphate dehydrogenase and phosphoglycerate kinase; (12) phosphoglycerate mutase and enolase; (13) PEP carboxylase; (14) pyruvate kinase; (16) pyruvate dehydrogenase complex; (17)phosphoacetyltransferase; (18) acetate kinase; (19) acetaldehyde dehydrogenase and alcohol dehydrogenase; (20) citrate synthase; (21)aconitase; (22) isocitrate lyase; (23) malate synthase; (24) malate dehydrogenase; (25) fumarase; (26) fumarate reductase



two to three experiments (Table 1). In the pH range of 5.8– 6.4,  $q_G$  and  $q_S$  increased with increasing pH, but the yields of succinate and other products did not significantly change. When controlled pH was greater than 6.6,  $q_G$  and  $q_S$ decreased. Fermentations in which the pH was controlled at 6.4 resulted in the highest specific succinate productivity. Moreover, the volumetric succinate productivity at a pH of 6.4 or 6.6 remained high throughout the course of the anaerobic production phase (about 1.2–1.8 g/l h), resulting in the highest mean succinate productivity (Table 1). For a pH above 6.6, the productivity declined over the course of the anaerobic phase (from about 2.0 to 0.5 g/l h). Since pure (acidic) CO<sub>2</sub> was sparged into the fermenter during the anaerobic phase and three acid products were formed, base was required to maintain the pH (Fig. 3). Indeed, an unacceptably large quantity of base was needed above a pH of about 6.6. The observed reduction in specific productivity, which would account for any "dilution effect," demonstrates that the cells generated a maximal rate of succinate at the intermediate pH. Because of these results, a pH controlled at 6.4 during the anaerobic production phase was selected for the subsequent study.

### Metabolic flux analysis

Succinate is formed through two pathways: the reductive arm of the tricarboxylic acid cycle (TCA) via the anaplerotic enzyme PPC and the glyoxylate shunt [35]. To



Fig. 2 Production of succinate (*filled square*), pyruvate (*open diamond*), ethanol (*open triangle*) and acetate (*open square*) from glucose (*filled circle*) during the anaerobic non-growth production phase for *E. coli* AFP111 using 25% Ca(OH)<sub>2</sub> to control pH at 6.4

understand whether pH affects the distribution of these two pathways, we compared the metabolic fluxes at a pH of 6.4 to that at a pH of 6.8. We first determined the flux distribution at a pH of 6.4. Table 3 compares the observed mass distribution of succinate and the calculated mass distribution by the optimal metabolic model (i.e., least error as defined in "Materials and methods"). Two methods were used to validate the metabolic model. First, we compared the enrichment ratio S2/S1 observed in the NMR results with that ratio predicted from the metabolic model obtained from independent LC-MS results (Table 2). In addition, we calculated the redox balance based on the metabolic model, and the value was very close to 1 (Table 2). The resulting metabolic fluxes for the process operating at a pH of 6.4 showed that 93% of the 1.25 mol succinate formed per mole glucose was generated via the reductive arm of the TCA cycle and 7% via the glyoxylate shunt (Fig. 4a). At the PEP node,  $\phi_{PPC}$  was 0.61 (i.e., about 61% of PEP partitioned to the reductive branch of the TCA cycle). Although 39% of the PEP formed pyruvate, most of the



Fig. 3 Volume of 25% Ca(OH)<sub>2</sub> consumption during 14 h of an anaerobic non-growth production phase for *E. coli* AFP111 under different levels of controlled pH

pyruvate ultimately became by-products (external pyruvate, acetate and ethanol), and only 12% of the pyruvate became succinate via the glyoxylate shunt (either directly or from malate).

During succinate accumulation  $CO_2$  was released via 6-phosphogluconate dehydrogenase and pyruvate dehydrogenase (or pyruvate oxidase) but sequestered via PPC (Fig. 1). At a pH of 6.4, the net  $CO_2$  consumption rate was 1.10 mmol/g h. The overall stoichiometric coefficient for  $CO_2$  (i.e., the ratio of net  $CO_2$  consumption to glucose consumption) was 0.62 (Fig. 4a).

We similarly determined the metabolic fluxes at a pH of 6.8 (Table 2). Although the higher pH significantly reduced the glucose consumption rate and succinate production rate (Fig. 4b), it did not alter the carbon partitioning compared to a pH of 6.4: succinate yield was 1.24 mol/mol glucose,  $\phi_{\rm PPP}$  of 0.15 and  $\phi_{\rm PPC}$  of 0.62 (Table 2). Also, 38% of the intermediate PEP formed pyruvate, and about 10% of the pyruvate became succinate via the glyoxylate shunt; the CO<sub>2</sub> stoichiometric coefficient was 0.59 (Fig. 4b).

**Table 1** The volumetric productivity (Q), specific consumption or production rates (q) and product mass yields (Y) of *E. coli* AFP111 during 14 h of an anaerobic non-growth phase using Ca(OH)<sub>2</sub> as the base to control pH

pН	$q_G (mg/g h)$	Q <sub>S</sub> (g/l h)	q <sub>S</sub> (mg/g h)	$Y_{S}$ (g/g)	$Y_A (g/g)$	$Y_{P}(g/g)$	$Y_E (g/g)$
5.8	108.7 <sup>a</sup>	0.67 <sup>a</sup>	76.5 <sup>a</sup>	0.71 <sup>a</sup>	0.01 <sup>a</sup>	0.24 <sup>a</sup>	$0.00^{a}$
6.0	189.3 <sup>b</sup>	1.02 <sup>b</sup>	126.0 <sup>b</sup>	$0.67^{\rm a}$	0.01 <sup>a</sup>	0.21 <sup>a</sup>	$0.02^{a}$
6.2	192.6 <sup>b</sup>	1.18 <sup>bc</sup>	125.7 <sup>b</sup>	0.65 <sup>a</sup>	$0.02^{\mathrm{a}}$	0.24 <sup>a</sup>	$0.02^{a}$
6.4	284.6 <sup>c</sup>	1.42 <sup>c</sup>	174.3 <sup>c</sup>	0.61 <sup>a</sup>	$-0.01^{a}$	0.24 <sup>a</sup>	0.03 <sup>a</sup>
6.6	257.4 <sup>bc</sup>	1.49 <sup>c</sup>	169.3 <sup>c</sup>	0.66 <sup>a</sup>	$0.00^{\mathrm{a}}$	0.16 <sup>a</sup>	0.03 <sup>a</sup>
6.8	166.3 <sup>b</sup>	0.99 <sup>b</sup>	119.4 <sup>ab</sup>	$0.72^{\rm a}$	0.01 <sup>a</sup>	0.19 <sup>a</sup>	0.03 <sup>a</sup>
7.0	85.7 <sup>d</sup>	0.36 <sup>d</sup>	47.4 <sup>d</sup>	0.55 <sup>b</sup>	$0.06^{b}$	0.05 <sup>b</sup>	0.02 <sup>a</sup>

Different letters were statistically significantly different at the 90% confidence level

G glucose, S succinate, A acetate, P pyruvate, E ethanol

$M + 2$ $M + 3$ $(S2/S1)^a$	R/O
$0.014 \pm 0.008$ $0.002 \pm 0.002$ 19.56	
0.022 0.003 18.32	0.97
$0.018 \pm 0.005$ $0.009 \pm 0.006$ 18.76	
0.022 0.003 18.79	1.06
	$M + 2$ $M + 3$ $(S2/S1)^a$ $0.014 \pm 0.008$ $0.002 \pm 0.002$ 19.56 $0.022$ $0.003$ 18.32 $0.018 \pm 0.005$ $0.009 \pm 0.006$ 18.76 $0.022$ $0.003$ 18.79

Table 2 Comparison of the mass distributions of succinate formed by *E. coli* AFP111 as observed by mass spectrometry and as calculated by the optimal metabolic model

The enrichment ratio (S2/S1) was observed from NMR results. The redox ratio R/O was calculated from the optimal metabolic model Observed values are shown as mean  $\pm$  standard deviation from three analyses

<sup>a</sup> The standard deviation for NMR measurements was 4-10%



Fig. 4 Metabolic fluxes (mmol/g h) during an anaerobic non-growth production phase of E. coli AFP111 at a pH of 6.4 (a) and a pH of 6.8 (b)

#### Effect of base counterion

Using a pH of 6.4 and 100%  $CO_2$  in the gas phase, we next examined the effect of the type of neutralizing agent used on succinate production. Three different bases were compared: 25% KOH, 25% NaOH or 25% Ca(OH)<sub>2</sub>. The effects of K<sup>+</sup> and Na<sup>+</sup> appeared to be similar, with the succinate productivity declining during the anaerobic phase (from about 1.7 to 0.3 g/l h). The difference in volume used (Table 3) was due to the unequal molar base concentrations, and the total moles of KOH or NaOH added during the 14-h anaerobic phase were similar. When  $Ca(OH)_2$  was used for pH control, some calcium succinate precipitated, and the volumetric succinate productivity remained high during 14 h of an anaerobic production phase (about 1.2–1.8 g/l h), resulting in the highest mean

	-		-				
$q_G \; (mg/g \; h)$	Q <sub>S</sub> (g/l h)	$q_{S} (mg/g h)$	$Y_{S} \; (g\!/g)$	$\mathrm{Y}_{\mathrm{P}}\left(\mathrm{g}/\mathrm{g}\right)$	$Y_A (g/g)$	$\mathrm{Y_{E}}~(\mathrm{g/g})$	V <sub>base</sub> (ml)
$248.6\pm31.8$	$1.42\pm0.19$	$174.3\pm40.2$	$0.61\pm0.13$	$0.24\pm0.04$	$-0.01 \pm 0.02$	$0.03\pm0.02$	$135\pm18$
$177.9\pm19.0$	$0.88\pm0.07$	$95.3\pm5.8$	$0.54\pm0.08$	$0.37\pm0.01$	$-0.01\pm0.02$	$0.01\pm0.03$	$113\pm7$
$176.2\pm28.2$	$0.99\pm0.19$	$101.6\pm23.9$	$0.57\pm0.04$	$0.21\pm0.08$	$0.02\pm0.01$	$0.00\pm0.02$	$66 \pm 15$
	$\begin{array}{c} q_{G} \ (mg/g \ h) \\ \\ 248.6 \pm 31.8 \\ 177.9 \pm 19.0 \\ \\ 176.2 \pm 28.2 \end{array}$	$\begin{array}{ll} q_{G} \ (mg/g \ h) & Q_{S} \ (g/l \ h) \\ \\ 248.6 \pm 31.8 & 1.42 \pm 0.19 \\ 177.9 \pm 19.0 & 0.88 \pm 0.07 \\ 176.2 \pm 28.2 & 0.99 \pm 0.19 \end{array}$	$\begin{array}{c} q_{G} \mbox{ (mg/g h)} & Q_{S} \mbox{ (g/l h)} & q_{S} \mbox{ (mg/g h)} \\ 248.6 \pm 31.8 & 1.42 \pm 0.19 & 174.3 \pm 40.2 \\ 177.9 \pm 19.0 & 0.88 \pm 0.07 & 95.3 \pm 5.8 \\ 176.2 \pm 28.2 & 0.99 \pm 0.19 & 101.6 \pm 23.9 \end{array}$	$ \begin{array}{c c} q_G \ (mg/g \ h) & Q_S \ (g/l \ h) & q_S \ (mg/g \ h) & Y_S \ (g/g) \\ \hline \\ 248.6 \pm 31.8 & 1.42 \pm 0.19 & 174.3 \pm 40.2 & 0.61 \pm 0.13 \\ 177.9 \pm 19.0 & 0.88 \pm 0.07 & 95.3 \pm 5.8 & 0.54 \pm 0.08 \\ 176.2 \pm 28.2 & 0.99 \pm 0.19 & 101.6 \pm 23.9 & 0.57 \pm 0.04 \\ \end{array} $	$ \begin{array}{c ccccc} q_G \ (mg/g \ h) & Q_S \ (g/l \ h) & q_S \ (mg/g \ h) & Y_S \ (g/g) & Y_P \ (g/g) \\ \hline \\ 248.6 \pm 31.8 & 1.42 \pm 0.19 & 174.3 \pm 40.2 & 0.61 \pm 0.13 & 0.24 \pm 0.04 \\ 177.9 \pm 19.0 & 0.88 \pm 0.07 & 95.3 \pm 5.8 & 0.54 \pm 0.08 & 0.37 \pm 0.01 \\ 176.2 \pm 28.2 & 0.99 \pm 0.19 & 101.6 \pm 23.9 & 0.57 \pm 0.04 & 0.21 \pm 0.08 \\ \end{array} $	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$

**Table 3** The volumetric productivity (Q), specific consumption or production rates (q) and product mass yields (Y) of *E. coli* AFP111 during 14 h of an anaerobic non-growth phase using three different bases to control pH at 6.4

Data were presented as mean  $\pm$  standard deviation from two to three replications

G glucose, S succinate, A acetate, P pyruvate, E ethanol

succinate productivity ( $q_S$ ) (Table 3). The small reduction in succinate productivity over the course of the anaerobic phase for Ca(OH)<sub>2</sub> can be attributed to a dilution of fermenter contents (i.e., adding base to a non-growing population). Twenty-five percent Ca(OH)<sub>2</sub> and 25% NaOH have similar OH<sup>-</sup> molar concentrations (0.67 M for Ca(OH)<sub>2</sub> and 0.63 M for NaOH). However, during the 14-h anaerobic phase about twice the amount of Ca(OH)<sub>2</sub> was consumed compared to NaOH (Table 3), which is consistent with the higher q<sub>S</sub> for Ca(OH)<sub>2</sub>. The values of  $q_G$  and  $Y_S$ using Ca(OH)<sub>2</sub> were also higher than those at NaOH or KOH as a base counterion (Table 3).

## Discussion

Between the pH range of 5.8-6.8, the specific succinate formation and glucose consumption rates achieved their maximum values, although the fermentation product yields were not significantly affected by the external pH (Table 1). Most aerobic and facultatively anaerobic bacteria stringently regulate the cytoplasmic pH (pH<sub>i</sub>), and the pH<sub>i</sub> of *E. coli* is unaffected by large variations in the medium pH (pH<sub>ex</sub>) [2]. Olsen et al. [21] found that the  $pH_i$ of E. coli (7.0–8.0) did not vary significantly over the  $pH_{ex}$ ranging from 5.5 to 8.0. However, the pH gradient  $(\Delta pH = pH_i - pH_{ex})$  is approximately 1.5 at a pH<sub>ex</sub> of 5.5 and decreases with increasing pHex, ultimately reaching 0 at a pH<sub>ex</sub> of 8.0 [21]. A large  $\Delta$ pH is associated with more active transport of H<sup>+</sup> and other ions across the membrane to maintain pH homeostasis [2]. One might anticipate that the increased maintenance requirement resulting from reduced pH might reduce the product yield. Although no product yield reduction was observed, the burden of maintaining  $\Delta pH$  at low pH may be responsible for the reduced rates of substrate utilization and succinate formation.

The succinate formation rate did not increase indefinitely with increasing pH; it decreased above a pH of 6.4. The quantity of buffer required to maintain the pH increased with increasing pH (Fig. 3). Thus, when the pH was above 6.4, the ionic strength increased more quickly during the succinate formation phase, an effect that may have been detrimental to the rate of succinate formation. Two mechanisms may exist that result in the observed optimum pH: a  $\Delta$ pH effect that reduces succinate formation at low pH and an ionic strength effect that reduces the succinate formation rate at higher pH. Interestingly, the optimal pH for succinate productivity observed in this study (6.4) corresponds closely with the pK<sub>a</sub> of the carbonic acid/bicarbonate equilibrium (6.35). Our optimal pH for succinate production by *E. coli* AFP111 near 6.4 is also consistent with other succinate-producing bacteria, including *A. succiniciproducens* at a pH of 6.2 [24] and *Bacteroides fragilis* at a pH of 6.5 [12].

The results demonstrate that <sup>13</sup>C-labeling can be successfully applied to calculate metabolic fluxes during nongrowth succinate production. For this process, the reductive branch of the TCA cycle was the most important pathway for succinate formation. This result is consistent with other succinate-producing E. coli strains, including a ptsG mutant TUQ2 [36] and E. coli strains that overexpress Lactococcus lactis pyruvate carboxylase [26]. Surprisingly, the flux distribution/carbon distribution was not significantly different between a pH of 6.4 and 6.8. In particular, the pH of the medium, which in this pH range would have a large impact on the  $CO_2/HCO_3^-$  ratio [7, 29], did not affect the flux partition at the PEP node (Fig. 4). Similar to our results with E. coli, the distribution of fermentation products by Actinobacillus sp. 130z [32] did not differ in the pH range of 6.0-7.4. The key enzyme PPC uses bicarbonate as the form of  $CO_2$  [20], and flux through this pathway could be expected to depend on the external availability of  $CO_2/HCO_3^-$ . Indeed, in the presence of limiting concentrations of CO2, E. coli AFP111 formed less succinate (data not shown); however, in this study 100% CO<sub>2</sub> was used. Under these circumstances, the yield and flux results support the conclusion that CO<sub>2</sub> was not limiting despite the dissociation between the dissolved gas and bicarbonate in this pH range. Consequently, under these non-limiting conditions, increasing the total quantity of CO<sub>2</sub> (i.e., CO<sub>2</sub> plus  $HCO_3^-$ ) as a result of increasing the pH would not lead to an increase in the PPC flux and associated succinate formation. Furthermore, as the previous research described above would suggest, pH<sub>i</sub> is likely unchanged over the pH range studied, and pH would therefore not affect the

activities of the various enzymes in the glucose to succinate metabolic pathways.

The results demonstrate that  $Ca^{2+}$  is superior to  $Na^+$  or K<sup>+</sup> as a base counterion to control the pH during the fermentation. Although the specific cause for this difference is unknown, the calcium succinate has a solubility of only 11.8 g/l at 40°C [19], which is far lower than sodium succinate or potassium succinate. Thus, the use of  $Ca(OH)_2$ would have the double benefit of removing both the cation Ca<sup>2+</sup> and the anion succinate from the solution. The observed removal of succinate by the precipitation of calcium succinate could relieve the inhibition of PPC [4] and isocitrate lyase [18], two key enzymes in succinate formation [35]. Removal of the cation would reduce osmotic stress. At the end of the processes studied, the concentration of  $Na^+$  or  $K^+$  was about 0.5 M, while the remaining concentration of dissociated Ca<sup>2+</sup> would have been only about 0.18 M. High ion strength leads to osmotic stress, and under aerobic conditions E. coli exports some  $Na^+$  as a response [23]. However, under anaerobic conditions, Na<sup>+</sup> extrusion activity may decrease [30]. Moreover, in our study the high ionic strength only occurred under anaerobic non-growth conditions, potentially limiting the cellular ability to respond to that stress. A recent study on lactate generation similarly demonstrated that monovalent cations reduce acid formation by E. coli compared to  $Ca^{2+}$  [38]. Gouesbet et al. [9] found that about 0.24 M KCl (osmolarity of 820 mOsm) had inhibitory and repressive effects on anaerobic enzymes and the corresponding genes in E. coli due to osmotic stress.

In summary, although the pH does affect the production rate, the pH within the range of 5.8-6.8 does not affect yield or the flux distribution of products in a two-phase succinate production process using *E. coli*. The negative impact of osmotic stress during succinate accumulation can at least partly be alleviated by using calcium as the product counterion.

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# Appendix A: Metabolic reactions for succinate production

- $v_1$  Glucose + ATP  $\equiv$  glucose 6-phosphate + ADP
- $v_2$  Glucose 6-phosphate  $\leftrightarrows$  fructose 6-phosphate
- $v_3$  Glucose 6-phosphate + 2 NADP<sup>+</sup> + H<sub>2</sub>O ⇒ ribulose 5-phosphate + CO<sub>2</sub> + 2 NADPH + 2 H<sup>+</sup>

# Appendix continued

- $v_4$  Ribulose 5-phosphate  $\leftrightarrows$  ribose-5-phosphate
- $v_5$  Ribulose 5-phosphate  $\leftrightarrows$  xylulose 5-phosphate
- $v_6$  Ribose 5-phosphate + xylulose 5-phosphate  $\leftrightarrows$  glyceraldehyde 3-phosphate + sedoheptulose 7-phosphate
- $v_7$  Glyceraldehyde 3-phosphate + sedoheptulose-7-phosphate  $\leftrightarrows$  fructose 6-phosphate + erythrose 4-phosphate
- $v_8$  Xylulose 5-phosphate + erythrose 4-phosphate  $\leftrightarrows$  fructose 6-phosphate + glyceraldehydes 3-phosphate
- $v_9$  Fructose 6-phosphate + ATP  $\leftrightarrows$  fructose 1,6bisphosphate + ADP
- $v_{10}$  Fructose 1,6-bisphosphate  $\leftrightarrows$  dihydroxyacetone phosphate + glyceraldehyde 3-phosphate
- $v_{11}$  Glyceraldehyde 3-phosphate + NAD<sup>+</sup> + ADP + Pi  $\leftrightarrows$  3-phosphoglycerate + NADH + H<sup>+</sup> + ATP
- $v_{12}$  3-Phosphoglycerate  $\leftrightarrows$  PEP + H<sub>2</sub>O
- $v_{13}$  PEP + CO<sub>2</sub> + H<sub>2</sub>O  $\leftrightarrows$  oxaloacetate + Pi
- $v_{14}$  Phosphoenolpyruvate + ADP  $\leftrightarrows$  pyruvate + ATP
- $v_{15}$  Pyruvate (intracellular)  $\leftrightarrows$  pyruvate (extracellular)
- $v_{16}$  Pyruvate + NAD<sup>+</sup> + CoA  $\leftrightarrows$  acetyl-CoA + CO<sub>2</sub> + NADH + H<sup>+</sup>
- $v_{17}$  Acetyl-CoA + ADP + Pi  $\leftrightarrows$  acetate + CoA + ATP
- $v_{18}$  Acetate (intracellular)  $\leftrightarrows$  acetate (extracellular)
- $v_{19}$  Acetyl-CoA + 2 NADH + 2 H<sup>+</sup>  $\leftrightarrows$  ethanol + 2 NAD<sup>+</sup>
- $v_{20}$  Oxaloacetate + acetyl-CoA + H<sub>2</sub>O  $\leftrightarrows$  citrate + CoA
- $v_{21}$  Citrate  $\leftrightarrows$  isocitrate
- $v_{22}$  Isocitrate  $\leq$  glyoxylate + succinate
- $v_{23}$  Glyoxylate + acetyl-CoA + H<sub>2</sub>O  $\leftrightarrows$  malate + CoA
- $v_{24}$  Oxaloacetate + NADH + H<sup>+</sup>  $\leq$  malate + NAD<sup>+</sup>
- $v_{25}$  Malate  $\leftrightarrows$  fumarate + H<sub>2</sub>O
- $\textit{v}_{26} \;\; Fumarate + NADH + H^+ \leftrightarrows succinate + NAD^+$
- $v_{27}$  Succinate (intracellular)  $\leftrightarrows$  succinate (extracellular)

#### References

- Agarwal L, Isar J, Meghwanshi GK, Saxena RK (2006) A cost effective fermentative production of succinic acid from cane molasses and corn steep liquor by *Escherichia coli*. J Appl Microbiol 100:1348–1354. doi:10.1111/j.1365-2672.2006.02894.x
- Booth IR (1985) Regulation of cytoplasmic pH in bacteria. Microbiol Rev 49:359–378
- Chatterjee R, Millard CS, Champion K, Clark DP, Donnelly MI (2001) Mutation of the *ptsG* gene results in increased production of succinate in fermentation of glucose by *Escherichia coli*. Appl Environ Microbiol 67:148–154. doi:10.1128/AEM.67.1.148-154. 2001
- Corwin LM, Fanning GR (1968) Studies of parameters affecting the allosteric nature of phosphoenolpyruvate carboxylase of *Escherichia coli*. J Biol Chem 243:3517–3525
- Donnelly MI, Millard CS, Clark DP, Chen MJ, Rathke JW (1998) A novel fermentation pathway in an *Escherichia coli* mutant producing succinic acid, acetic acid, and ethanol. Appl Biochem Biotechnol 70–72:187–198. doi:10.1007/BF02920135
- Eiteman MA, Chastain MJ (1997) Optimization of the ionexchange analysis of organic acids from fermentation. Anal Chim Acta 338:69–75. doi:10.1016/S0003-2670(96)00426-6

- Frahm B, Blank HC, Cornand P, Oelssner W, Guth U, Lane P, Munack A, Johannsen K, Portner R (2002) Determination of dissolved CO<sub>2</sub> concentration and CO<sub>2</sub> production rate of mammalian cell suspension culture based on off-gas measurement. J Biotechnol 99:133–148. doi:10.1016/S0168-1656(02)00180-3
- Gokarn RR, Eiteman MA, Altman E (2000) Metabolic analysis of *Escherichia coli* in the presence and absence of carboxylating enzymes phosphoenolpyruvate carboxylase and pyruvate car- boxylase. Appl Environ Microbiol 66:1844–1850. doi:10.1128/ AEM.66.5.1844-1850.2000
- Gouesbet G, Abaibou H, Wu LF, Mandrand-Berthelot MA, Blanco C (1993) Osmotic repression of anaerobic metabolic systems in *Escherichia coli*. J Bacteriol 175:214–221
- Guettler MV, Jain MK, Soni BK (1998) Process for making succinic acid, microorganisms for use in the process and methods of obtaining the microorganisms. US patent 5,723,322, 3 March 1998
- Guettler MV, Rumler D, Jain MK (1999) Actinobacillus succinogenes sp. nov., a novel succinic-acid-producing strain from the bovine rumen. Int J Syst Bacteriol 49:207–216
- Isar J, Agarwal L, Saran S, Saxena RK (2006) Succinic acid production from *Bacteroides fragilis*: process optimization and scale up in a bioreactor. Anaerobe 12:231–237. doi:10.1016/ j.anaerobe.2006.07.001
- Lee PC, Lee WG, Kwon S, Lee SY, Chang HN (2000) Batch and continuous cultivation of *Anaerobiospirillum succiniciproducens* for the production of succinic acid from whey. Appl Microbiol Biotechnol 54:23–27. doi:10.1007/s002530000331
- Lee PC, Lee WG, Lee SY, Chang HN (2001) Succinic acid production with reduced by-product formation in the fermentation of *Anaerobiospirillum succiniciproducens* using glycerol as a carbon source. Biotechnol Bioeng 72:41–48. doi:10.1002/1097-0290(20010105)72:1<41::AID-BIT6>3.0.CO;2-N
- Lee SJ, Song H, Lee SY (2006) Genome-based metabolic engineering of *Mannheimia succiniciproducens* for succinic acid production. Appl Environ Microbiol 72:1939–1948. doi:10.1128/ AEM.72.3.1939-1948.2006
- Lin H, Bennett GN, San KY (2005) Genetic reconstruction of the aerobic central metabolism in *Escherichia coli* for the absolute aerobic production of succinate. Biotechnol Bioeng 89:148–156. doi:10.1002/bit.20298
- Lin H, Bennett GN, San KY (2005) Metabolic engineering of aerobic succinate production systems in *Escherichia coli* to improve process productivity and achieve the maximum theoretical succinate yield. Metab Eng 7:116–127. doi:10.1016/ j.ymben.2004.10.003
- MacKintosh C, Nimmo HG (1988) Purification and regulatory properties of isocitrate lyase from *Escherichia coli* ML308. Biochem J 250:25–31
- Miczynski ZN (1886) Uber die Bestimmung der Loslichkeit einiger Sauren und Salze der Oxalsaurereihe in Wasser bei verschiedenen Temperaturen. Monatsh Chem 7:255–272. doi: 10.1007/BF01516575
- O'Leary MH (1982) Phosphoenolpyruvate carboxylase: an enzymologist's view. Annu Rev Plant Physiol 33:297–315. doi: 10.1146/annurev.pp.33.060182.001501
- Olsen K, Budde B, Siegumfeldt H, Rechinger K, Jakobsen M, Ingmer H (2002) Noninvasive measurement of bacterial intracellular pH on a single-cell level with green fluorescent protein and fluorescence ratio imaging microscopy. Appl Environ Microbiol 68:4145–4147. doi:10.1128/AEM.68.8.4145-4147.2002
- Rosman KJR, Taylor PDP (1998) Isotopic compositions of the elements. Pure Appl Chem 70:217–230. doi:10.1351/pac 199870010217
- 23. Sakuma T, Yamada N, Saito H, Kakegawa T, Kobayashi H (1998) pH dependence of the sodium ion extrusion systems in

*Escherichia coli*. Biochim Biophys Acta 1363:231–237. doi: 10.1016/S0005-2728(97)00102-3

- Samuelov N, Lamed R, Lowe S, Zeikus JG (1991) Influence of CO2–HCO3- levels and pH on growth, succinate production, and enzyme activities of *Anaerobiospirillum succiniciproducens*. Appl Environ Microbiol 57:3013–3019
- 25. Sanchez AM, Bennett GN, San KY (2005) Efficient succinic acid production from glucose through overexpression of pyruvate carboxylase in an *Escherichia coli* alcohol dehydrogenase and lactate dehydrogenase mutant. Biotechnol Prog 21:358–365. doi: 10.1021/bp049676e
- Sanchez AM, Bennett GN, San KY (2006) Batch culture characterization and metabolic flux analysis of succinate-producing *Escherichia coli* strains. Metab Eng 8:209–226. doi:10.1016/ j.ymben.2005.11.004
- Savinell JM, Palsson BO (1992) Network analysis of intermediary metabolism using linear optimization. I. Development of mathematical formalism. J Theor Biol 154:421–454. doi:10.1016/ S0022-5193(05)80161-4
- Schmidt K, Carlsen M, Nielsen J, Villadsen J (1997) Modeling isotopomer distributions in biochemical networks using isotopomer mapping matrices. Biotechnol Bioeng 55:831–840. doi: 10.1002/(SICI)1097-0290(19970920)55:6<831::AID-BIT2>3.0. CO;2-H
- 29. Stumm W, Morgan J (1996) Dissolved carbon dioxide. In: Aquatic chemistry, John Wiley, New York, p 192
- Trchounian A, Kobayashi H (1999) Fermenting *Escherichia coli* is able to grow in media of high osmolarity, but is sensitive to the presence of sodium ion. Curr Microbiol 39:109–114. doi: 10.1007/s002849900429
- Urbance S, Pometto AIII, Dispirito A, Denli Y (2004) Evaluation of succinic acid continuous and repeat-batch biofilm fermentation by *Actinobacillus succinogenes* using plastic composite support bioreactors. Appl Microbiol Biotechnol 65:664–670. doi: 10.1007/s00253-004-1634-2
- Van der Werf MJ, Guettler MV, Jain MK, Zeikus JG (1997) Environmental and physiological factors affecting the succinate product ratio during carbohydrate fermentation by *Actinobacillus sp.* 130z. Arch Microbiol 167:332–342. doi:10.1007/s0020300 50452
- Van Dien SJ, Strovas T, Lidstroml ME (2003) Quantification of central metabolic fluxes in the facultative methylotroph *methylobacterium extorquens* AM1 using <sup>13</sup>C-label tracing and mass spectrometry. Biotechnol Bioeng 84:45–55. doi:10.1002/bit. 10745
- Vemuri GN, Eiteman MA, Altman E (2002) Succinate production in dual-phase *Escherichia coli* fermentations depends on the time of transition from aerobic to anaerobic conditions. J Ind Microbiol Biotechnol 28:325–332. doi:10.1038/sj.jim.7000250
- 35. Vemuri GN, Eiteman MA, Altman E (2002) Effects of growth mode and pyruvate carboxylase on succinic acid production by metabolically engineered strains of *Escherichia coli*. Appl Environ Microbiol 68:1715–1727. doi:10.1128/AEM.68.4.1715-1727.2002
- Wang Q, Chen X, Yang Y, Zhao X (2006) Genome-scale in silico aided metabolic analysis and flux comparisons of *Escherichia coli* to improve succinate production. Appl Microbiol Biotechnol 73:887–894. doi:10.1007/s00253-006-0535-y
- Zeikus JG, Jain MK, Elankovan P (1999) Biotechnology of succinic acid production and markets for derived industrial products. Appl Microbiol Biotechnol 51:545–552. doi:10.1007/ s002530051431
- Zhu Y, Eiteman MA, DeWitt K, Altman E (2007) Homolactate fermentation by metabolically engineered *Escherichia coli* strains. Appl Environ Microbiol 73:456–464. doi:10.1128/AEM. 02022-06