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## 3-Amino-4-hydroxybenzoic acid production from sweet sorghum juice by recombinant Corynebacterium glutamicum



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## highlights and the state of the

The stalk juice of sweet sorghum contained fermentable sugars and amino acids.

Recombinant Corynebacterium glutamicum produced 3,4-AHBA from sorghum juice.

Components of sweet sorghum juice were fractionated by membrane separation.

Amino acids of Leu or Cys in sweet sorghum juice enhanced 3,4-AHBA production.

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#### ARSTRACT

The production of the bioplastic precursor 3-amino-4-hydroxybenzoic acid (3,4-AHBA) from sweet sorghum juice, which contains amino acids and the fermentable sugars sucrose, glucose and fructose, was assessed to address the limitations of producing bio-based chemicals from renewable feedstocks. Recombinant Corynebacterium glutamicum strain KT01 expressing griH and griI derived from Streptomyces griseus produced 3,4-AHBA from the sweet sorghum juice of cultivar SIL-05 at a final concentration  $(1.0 g<sup>-1</sup>)$  that was 5-fold higher than that from pure sucrose. Fractionation of sweet sorghum juice by nanofiltration (NF) membrane separation (molecular weight cut-off 150) revealed that the NF-concentrated fraction, which contained the highest concentrations of amino acids, increased 3,4-AHBA production, whereas the NF-filtrated fraction inhibited 3,4-AHBA biosynthesis. Amino acid supplementation experiments revealed that leucine specifically enhanced 3,4-AHBA production by strain KT01. Taken together, these results suggest that sweet sorghum juice is a potentially suitable feedstock for 3,4-AHBA production by recombinant C. glutamicum.

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#### 1. Introduction

Sorghum (Sorghum bicolor (L.) Moench) is a  $C_4$  grass with high biomass yield. Compared to other biomass crops, such as corn and sugar cane, sorghum is drought-tolerant, requires less fertilizer, and has a large geographical distribution [\(Rooney et al.,](#page--1-0) [2007\)](#page--1-0). Juice extracted from the stalks of sweet sorghum predominantly consists of the fermentable sugar sucrose (>150 g  $1^{-1}$ ), but also contains variable concentrations of the reducing sugars glucose and fructose ([Kawahigashi et al., 2013\)](#page--1-0). The high content of glucose and fructose in sorghum juice as compared to that found in sugar cane extract inhibits crystallization, which limits the processing of sugar for use in foods. However, sweet sorghum juice is a potentially suitable feedstock for bioethanol production ([Laopaiboon et al., 2009; Ratnavathi et al., 2010](#page--1-0)), although its

Abbreviations: 3,4-AHBA, 3-amino-4-hydroxybenzoic acid; GABA,  $\gamma$ -amino butyric acid; MWCO, molecular weight cut-off; NF, nanofiltration; UF, ultrafiltration.

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utilization for biochemical production has been poorly characterized to date.

3-Amino-4-hydroxybenzoic acid (3,4-AHBA) is a metabolic intermediate of grixazone biosynthesis in Streptomyces griseus ([Suzuki et al., 2006](#page--1-0)) and is synthesized by the activities of the enzymes GriI and GriH, which are encoded by griI and griH, respectively. GriI catalyzes an aldol condensation reaction between L-aspartate-4-semialdehyde and dihydroxyacetone phosphate, and GriH converts the resulting  $C_7$  metabolite into 3,4-AHBA. Through this two-step reaction, these two enzymes can produce an aromatic ring from  $C_4$  (L-aspartate-4-semialdehyde) and  $C_3$ (dihydroxyacetone phosphate) primary metabolites, whereas most aromatic compounds, including aromatic amino acids, are formed in a multistep reaction via the shikimate pathway [\(Liu](#page--1-0) [et al., 2013\)](#page--1-0). 3,4-AHBA serves as a precursor for polybenzoxazole, a thermostable bioplastic, and can be biosynthesized from fermentable sugars ([Suzuki et al., 2006\)](#page--1-0). To date, however, the production of 3,4-AHBA from renewable feedstocks has not been investigated.

Corynebacterium glutamicum, a nonpathogenic Gram-positive bacterium, is widely used for the industrial production of various amino acids and nucleic acids [\(Nakayama et al., 1961; Wittmann](#page--1-0) [et al., 2004\)](#page--1-0). In contrast to Escherichia coli, which lacks invertase activity to allow for sucrose utilization, C. glutamicum possesses inherent invertase activity and is therefore able to ferment the sucrose contained in sweet sorghum juice ([Wittmann et al.,](#page--1-0) [2004](#page--1-0)) and can also simultaneously consume glucose and fructose ([Dominguez et al., 1997](#page--1-0)). Due to these fermentative properties, C. glutamicum may be a suitable host for sweet sorghum juicebased bioproduction. In current industrial bioprocesses, such as amino acid fermentation, using C. glutamicum, sugar cane molasses is mainly used as a feedstock ([Xu et al., 2013](#page--1-0)). Although sweet sorghum juice is a suitable feedstock for ethanol fermentation by yeast [\(Laopaiboon et al., 2009](#page--1-0)), its compatibility for fermentation by C. glutamicum remains to be evaluated.

In the present study, we examined 3,4-AHBA production from sweet sorghum juice containing the fermentable sugars sucrose, glucose, and fructose as carbon sources, and amino acids as a source of nitrogen. Because C. glutamicum lacks the capability for 3,4-AHBA synthesis, a strain of C. glutamicum was metabolically engineered to produce 3,4-AHBA from sweet sorghum juice. In addition, the sorghum component(s) that promoted 3,4-AHBA production by the recombinant strain was examined by fractionation of the sweet sorghum juice using nanofiltration (NF) membrane separation.

#### 2. Methods

### 2.1. Materials, bacterial strains, and media

A recombinant 3,4-AHBA-producing strain of C. glutamicum (KT01) was derived from lysine-producing C. glutamicum ATCC 21799 ([Kubota et al., 1973](#page--1-0)) by transformation of ATCC 21799 with the plasmid pCACgriHI, which harbors the griH and griI genes derived from S. griseus for 3,4-AHBA biosynthesis [\(Suzuki et al.,](#page--1-0) [2006](#page--1-0)). E. coli HST02 (Takara, Shiga, Japan) was used as a host for plasmid construction and was grown aerobically at  $37^{\circ}$ C in Luria–Bertani medium ([Sambrook and Russell, 2001](#page--1-0)). For the aerobic growth of C. glutamicum, the wild-type and recombinant strains were grown at 30 $\degree$ C to late log phase in Brain Heart Infusion medium (BD Biosciences, NJ, USA), unless indicated otherwise. When appropriate, media were supplemented with 5 and 50  $\mu$ g ml<sup>-1</sup> chloramphenicol for C. glutamicum and E. coli, respectively.

Japanese sweet sorghum cultivar SIL-05 was grown at Togo Field of the Science and Education Center of Nagoya University (Aichi, Japan) in 2013. Whole plants at the heading stage were harvested and the juice was immediately extracted from stalks using a juice extractor (Okuhara Tekko, Okinawa, Japan). After removal of suspended solids by filtration with non-woven fabric (AS ONE, Osaka, Japan), the filtrate was centrifuged (8000g,  $4^{\circ}$ C, 30 min) and the obtained supernatant was then filtered aseptically through a filter membrane (500 ml Rapid-flow filter unit, 0.2-um pore size; Thermo Fischer Scientific, Waltham, MA). The filter-sterilized sweet sorghum juice was stored at  $-30$  °C before use.

For 3,4-AHBA production from either sweet sorghum juice or pure sugar, recombinant strain KT01 was aerobically cultured in a defined medium, which was based on CGXII medium [\(Keilhauer](#page--1-0) [et al., 1993](#page--1-0)) and was composed of (per liter) 5 g urea, 20  $g(NH_4)_2SO_4$ , 1 g KH<sub>2</sub>PO<sub>4</sub>, 1 g K<sub>2</sub>HPO<sub>4</sub>, 42 g 3-morpholinopropanesulfonic acid (MOPS),  $0.25 \text{ g } MgSO_4 \cdot 7H_2O$ , 10 mg CaCl<sub>2</sub>, 10 mg FeSO<sub>4</sub> $\cdot 7H_2O$ , 10 mg  $MnSO_4 \cdot H_2O$ , 1 mg  $ZnSO_4 \cdot 7H_2O$ , 0.31 mg  $CuSO_4 \cdot 5H_2O$ , 0.02 mg NiCl<sub>4</sub> $-6H<sub>2</sub>O$ , 0.2 mg biotin, 0.03 mg protocatechuic acid, and  $0.5$  g  $L$ -homoserine, and was additionally supplemented with carbon sources.

#### 2.2. DNA manipulations

Plasmid DNA was isolated from E. coli and C. glutamicum as previously described [\(Kawaguchi et al., 2008\)](#page--1-0). Chromosomal restriction endonucleases were purchased from New England Biolabs (MA, USA) and used according to the manufacturer's instructions. The PCR conditions were described previously ([Kawaguchi et al.,](#page--1-0) [2008](#page--1-0)), unless indicated otherwise. PCR fragments were purified using a QIAquick PCR Purification kit (Qiagen, CA, USA). Corynebacteria were transformed by electroporation as previously described ([Vertès et al., 1993\)](#page--1-0), whereas E. coli was transformed using the CaCl<sub>2</sub> procedure [\(Sambrook and Russell, 2001](#page--1-0)).

### 2.3. Construction of a recombinant plasmid for 3,4-AHBA production

The plasmids pCASE1, which was extracted from Corynebacterium casei JCM12072 and has been used to construct an E. coli–C. glutamicum shuttle vector ([Tsuchida et al., 2009\)](#page--1-0), and pHSG398 (Takara) were used to construct an E. coli– C. glutamicum shuttle vector to express genes for 3,4-AHBA biosynthesis. The lac promoter, multi-cloning site, and cat gene encoding chloramphenicol acetyltransferase for chloramphenicol resistance were divergently amplified by PCR using plasmid pHSG398 as the template and oligonucleotide primers (5-CCCA <u>GATCT</u>ATTCAGCTTGGCCCAGTG-3′ and 5′-CCC<u>AGATCT</u>TTTCTGCCA TTCATCCGC-3') to generate a 2227-kb DNA fragment with *Bgl*II cohesive ends. The purified PCR amplicon was digested with BglII and was then ligated in a unimolecular reaction, yielding plasmid pYTK23. In addition, a 1436-bp DNA fragment with BglII cohesive ends and containing the pCASE1 ori region was PCR amplified using pCASE1 plasmid DNA as the template and oligonucleotide primers (5'-CCCAGATCTCCTAGAACGTCCGTAGGAGC-3' and 5'-CCCAGATCT CTGACTTGGTTACGATGGAC-3<sup>'</sup>). The obtained PCR amplicon was digested with BglII and then ligated to BglII-digested pYTK23 DNA, yielding the E. coli–C. glutamicum shuttle vector pCAC.

The genes griH (1203 bp) and griI (837 bp) were individually synthesized by Eurofins Genomics (Bayern, Germany) based on the sequence of the grixazone biosynthesis gene cluster in the S. griseus chromosome [\(Suzuki et al., 2006](#page--1-0)). The synthesized genes were optimized for codon usage for expression in C. glutamicum and contained 5'-EcoRI and 3'-HindIII cohesive ends. After digestion with EcoRI and HindIII, the two DNA fragments were ligated to EcoRI- and HindIII-digested pKK223-3 (GE Healthcare, Buckinghamshire, UK) to obtain plasmids pKKgriH and pKKgriI, respectively. A 2.0-kb DNA fragment containing the tac promoter, griH Download English Version:

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