

(12) United States Patent Lee et al.

(54) 5-DEHYDRO-2-DEOXYGLUCONOKINASE VARIANT AND METHOD FOR PRODUCING 5'-INOSINIC ACID USING SAME

(71) Applicant: DAESANG CORPORATION, Seoul

(KR)

(72) Inventors: Sun Hee Lee, Seoul (KR); Tae Yeol

Choi, Seoul (KR); Hyun Ho Kim, Seoul (KR); Dong Hyun Kim, Seoul (KR); Hvun Sook Kim, Seoul (KR); Jong Hwan Shin, Seoul (KR)

(73) Assignee: DAESANG CORPORATION, Seoul

(KR)

(*) Notice: Subject to any disclaimer, the term of this

patent is extended or adjusted under 35

U.S.C. 154(b) by 0 days.

(21) Appl. No.: 18/879,995

(22) PCT Filed: Aug. 31, 2023

(86) PCT No.: PCT/KR2023/012969

§ 371 (c)(1),

Dec. 30, 2024 (2) Date:

(87) PCT Pub. No.: WO2024/210281

PCT Pub. Date: Oct. 10, 2024

(30)Foreign Application Priority Data

Apr. 6, 2023 (KR) 10-2023-0045161

(51) Int. Cl.

C12N 9/12 (2006.01)C12P 19/32 (2006.01)

(52) U.S. Cl.

CPC C12N 9/1205 (2013.01); C12P 19/32 (2013.01); C12Y 207/01092 (2013.01)

US 12,385,020 B1 (10) **Patent No.:**

(45) Date of Patent: Aug. 12, 2025

(58) Field of Classification Search

CPC C12N 9/1205 See application file for complete search history.

(56)References Cited

FOREIGN PATENT DOCUMENTS

KR	10-1166027	7/2012
KR	10-2016-0078694	7/2016
KR	10-1904675	10/2018
KR	10-1916611	11/2018
KR	10-1916622	11/2018

OTHER PUBLICATIONS

International Search Report issued Jan. 19, 2024 in International (PCT) Application No. PCT/KR2023/012969.

Zuniga-Soto, Evelyn et al., "Insights into the transcriptomic response of the plant engineering bacterium Ensifer adhaerens OV14 during transformation", Scientific Reports, 2019, vol. 9, No. 10344, pp.

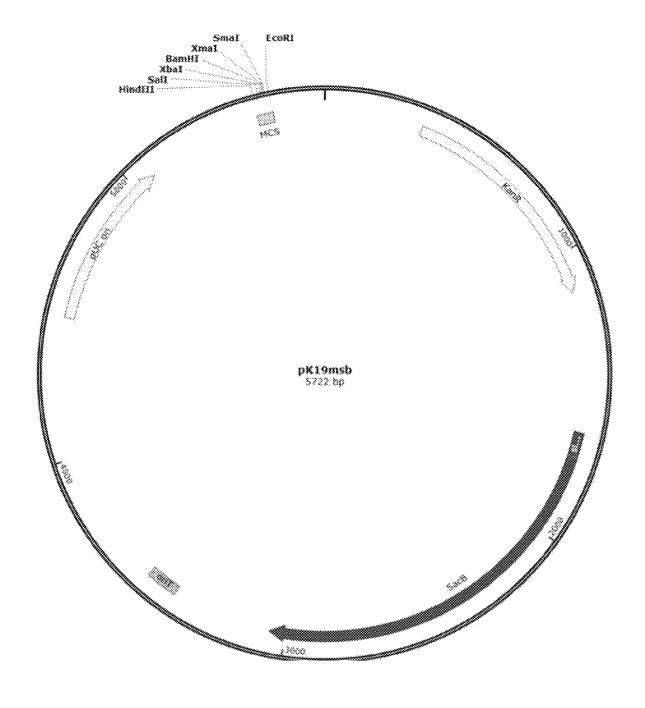
Primary Examiner — Suzanne M Noakes (74) Attorney, Agent, or Firm — Wenderoth, Lind & Ponack, L.L.P.

(57)ABSTRACT

The present invention relates to a novel 5-dehydro-2-deoxygluconokinase variant and a method of producing 5'-inosinic acid using the same. The 5-dehydro-2-deoxygluconokinase variant is obtained by substituting one or more amino acids in the amino acid sequence constituting 5-dehydro-2-deoxygluconokinase to change the activity of the protein, and a recombinant microorganism comprising the 5-dehydro-2deoxygluconokinase variant is capable of efficiently producing 5'-inosinic acid.

7 Claims, 1 Drawing Sheet

Specification includes a Sequence Listing.



5-DEHYDRO-2-DEOXYGLUCONOKINASE VARIANT AND METHOD FOR PRODUCING 5'-INOSINIC ACID USING SAME

SEQUENCE LISTING

A sequence listing in electronic (XML file) format is filed with this application and incorporated herein by reference. The name of the XML file is "Sequence_Listing-1948A.xml"; the file was created on Dec. 29, 2024: the size of the file is 17.022 bytes.

TECHNICAL FIELD

The present invention relates to a novel 5-dehydro-2-deoxygluconokinase variant and a method of producing 5'-inosinic acid using the same.

BACKGROUND ART

5'-inosinic acid (or inosine monophosphate (IMP)) is an ²⁰ intermediate in the metabolic system of nucleic acid biosynthesis, and not only plays an important physiological role in the bodies of plants and animals, but is also used in various applications, including food, medicine, and various medical applications. In particular, 5'-inosinic acid is a ²⁵ nucleic acid-based seasoning, which has drawn much attention as a savory seasoning, because it has significant synergistic effects on taste when used together with monosodium glutamate (MSG)

Methods for producing 5'-inosinic acid include a method of enzymatically degrading ribonucleic acid extracted from yeast cells, a method of chemically phosphorylating inosine produced by fermentation, etc. Recently, a method of culturing a 5'-inosinic acid-producing microorganism and recovering 5'-inosinic acid accumulated in the medium has been mainly used.

For the production of 5'-inosinic acid using microorganisms, in order to improve the efficiency of production of 5'-inosinic acid, there has been development of a variety of recombinant strains or mutant strains having excellent 5'-inosinic acid productivity by applying genetic recombination 40 technology to microorganisms such as Escherichia coli and Corynebacterium, which are widely used in the production of useful substances such as nucleic acids or L-amino acids, and methods of producing 5'-inosinic acid using the same. In particular, there have been attempts to increase the produc- 45 tion of 5'-inosinic acid by targeting genes such as enzymes, transcription factors and transport proteins, which are involved in the biosynthetic pathway of 5'-inosinic acid, or by inducing mutations in promoters that regulate the expression of these genes. However, there are dozens to hundreds of types of proteins such as enzymes, transcription factors and transport proteins, which are involved directly or indirectly in the production of 5'-inosinic acid, and thus much research is still needed on the increase in 5'-inosinic acid productivity by changes in the activity of these proteins.

PRIOR ART DOCUMENTS

Patent Documents

Korean Patent No. 10-116602

DISCLOSURE

Technical Problem

An object of present invention is to provide a novel 5-dehydro-2-deoxygluconokinase variant.

2

Another object of the present invention is to provide a polynucleotide encoding the variant.

Still another object of the present invention is to provide a transformant comprising the variant or polynucleotide.

Yet another object of the present invention is to provide a method of producing 5'-inosinic acid using the transformant.

Technical Solution

One aspect of the present invention provides a 5-dehydro-2-deoxygluconokinase variant consisting of the amino acid sequence of SEQ ID NO: 2 in which serine at position 146 in the amino acid sequence of SEQ ID NO: 4 is substituted with asparagine.

As used in the present invention, the term "5-dehydro-2-deoxygluconokinase catalyzes a reaction that produces ADP and 6-phospho-5-dehydro-2-deoxy-D-gluconate using ATP and 5-dehydro-2-deoxy-D-gluconate as substrates, and it may be a polypeptide or protein consisting of the amino acid sequence of SEQ ID NO: 4 and having 5-dehydro-2-deoxygluconokinase activity.

Information on the nucleic acid and protein sequences of the 5-dehydro-2-deoxygluconokinase is available from known sequence databases (e.g., GenBank, UniProt).

According to one embodiment of the present invention, the 5-dehydro-2-deoxygluconokinase may be encoded by the nucleotide sequence of SEQ ID NO: 3.

The amino acid sequence of the 5-dehydro-2-deoxyglu-conokinase according to the present invention or the nucleotide sequence encoding the same may include a nucleotide sequence or amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99 or 100% homology or identity to the amino acid sequence of SEQ ID NO: 4 or the nucleotide sequence of SEQ ID NO: 3. As used herein, the term "homology" or "identity" means the percentage rate of identity between two sequences, which is determined by aligning the reference nucleotide sequence or amino acid sequence and any other nucleotide sequence or amino acid sequence to correspond to each other as much as possible and analyzing the aligned sequences.

According to one embodiment of the present invention, the 5-dehydro-2-deoxygluconokinase may be derived from wild-type *Corynebacterium stationis*.

As used in the present invention, the term "variant" refers to a protein that has an amino acid sequence different from the amino acid sequence before mutation by the conservative substitution and/or modification of one or more amino acids at the N-terminus, C-terminus of and/or within the amino acid sequence, which result(s) from mutation in the nucleotide sequence of the gene encoding the protein, but retains the functions or properties of the protein before mutation. As used herein, the term "conservative substitution" means substituting one amino acid with another amino acid having similar structural and/or chemical properties. The conservative substitution may have little or no impact on the activity of the protein or polypeptide. In addition, the term "modification" refers to substitution, insertion, deletion, or the like of one or more amino acids. The amino acid is selected from among alanine (Ala, A), isoleucine (Ile, I), valine (Val, V), leucine (Leu, L), methionine (Met, M), asparagine (Asn, N), cysteine (Cys, C), glutamine (Gln, Q), serine (Ser, S), threonine (Thr, T), phenylalanine (Phe, F), tryptophan (Trp, W), tyrosine (Tyr, Y), aspartic acid (Asp, D), glutamic acid (Glu, E), arginine (Arg, R), histidine (His, 65 H), lysine (Lys, K), glycine (Gly, G), and proline (Pro, P).

In addition, some variants include those in which one or more portions, such as an N-terminal leader sequence or

transmembrane domain, have been removed, or those in which a portion has been removed from the N- and/or C-terminus of a mature protein.

The variant may have increased (enhanced), unchanged, or decreased (weakened) ability compared to that of the 5 protein before mutation. Here, the term "increased or enhanced" includes: a case in which the activity of the protein itself has increased compared to the activity of the protein before mutation; a case in which the overall activity of the protein in the cell is higher than that in the wild-type 10 strain or the strain expressing the protein before mutation due to increased expression or translation of the gene encoding the protein; and a combination thereof. In addition, the term "decreased or weakened" includes: a case in which the activity of the protein itself has decreased compared to 15 the activity of the protein before mutation; a case in which the overall activity of the protein in the cell is lower than that in the wild-type strain or the strain expressing the protein before mutation due to reduced expression or translation of the gene encoding the protein; and a combination thereof. In 20 the present invention, the term "variant" may be used interchangeably with terms such as variant type, modification, variant polypeptide, mutated protein, mutation, and the like.

The 5-dehydro-2-deoxygluconokinase variant according 25 to the present invention may comprise an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98s, 99% or 100% homology or identity to the amino acid sequence of SEQ ID NO: 2.

Another aspect of the present invention provides a polynucleotide encoding the 5-dehydro-2-deoxygluconokinase variant.

As used in the present invention, the term "polynucleotide" refers to a DNA or RNA strand having a certain length or more, which is a long-chain polymer of nucleotides 35 formed by linking nucleotide monomers via covalent bonds. More specifically, the term "polynucleotide" refers to a polynucleotide fragment encoding the variant.

According to one embodiment, the polynucleotide may comprise a nucleotide sequence encoding the amino acid 40 sequence of SEQ ID NO: 2.

More specifically, the polynucleotide may comprise the nucleotide sequence of SEQ ID NO: 1 in which nucleotide "g" at position 437 in the nucleotide sequence of SEQ ID NO: 3 encoding 5-dehydro-2-deoxygluconokinase is substituted with nucleotide "a".

Still another aspect of the present invention provides a vector comprising a polynucleotide encoding the 5-dehydro-2-deoxygluconokinase variant.

Yet another aspect of the present invention provides a 50 transformant comprising the 5-dehydro-2-deoxygluconokinase variant or the polynucleotide.

As used in the present invention, the term "vector" refers to any type of nucleic acid sequence transfer structure that is used as a means for transferring and expressing a gene of 55 interest in a host cell. Unless otherwise specified, the term "vector" may mean one allowing the nucleic acid sequence contained therein to be expressed after insertion into the host cell genome and/or one allowing the nucleic acid sequence to be expressed independently. This vector comprises essential regulatory elements operably linked so that an inserted gene can be expressed. As used herein, the term "operably linked" means that a gene of interest and regulatory sequences thereof are functionally linked together in a manner enabling gene expression, and the "regulatory elements" include a promoter for initiating transcription, any operator sequence for regulating transcription, a sequence

4

encoding suitable mRNA ribosome-binding sites, and a sequence for regulating termination of transcription and translation.

The vector in the present invention is not particularly limited as long as it may replicate in a host cell, and any vector known in the art may be used. Examples of the vector include a natural or recombinant plasmid, cosmid, virus and bacteriophage. Examples of a phage vector or cosmid vector include, but are not limited to, pWE15, M13, λMBL3, λMBL4, λIXII, λASHII, λAPII, λt10, λt11, Charon4A, and Charon21A, and examples of a plasmid vector include, but are not limited to, pBR series, pUC series, pBluescriptII series, pGEM series, pTZ series, pCL series, and pET series.

The vector may typically be constructed as a vector for cloning or as a vector for expression. The vector for expression may be a conventional vector that is used in the art to express a foreign gene or protein in a plant, animal, or microorganism, and may be constructed through various methods known in the art.

As used in the present invention, the term "recombinant vector" may be transformed into a suitable host cell, and then may replicate regardless of the genome of the host cell or may be integrated into the genome itself. In this case, the "suitable host cell" may contain a replication origin, which is a particular nucleotide sequence which enables the vector to replicate in the suitable host cell and from which replication starts. For example, when the vector used is an expression vector and uses a prokaryotic cell as a host, the vector generally comprises a strong promoter capable of promoting transcription (e.g., pL\(\lambda\) promoter, CMV promoter, trp promoter, lac promoter, tac promoter, T7 promoter, etc.), a ribosome binding site for initiation of translation, and a transcription/translation termination sequence. When a eukaryotic cell is used as a host, the vector comprises a replication origin operating in the eukaryotic cell, and examples of the replication origin include, but are not limited to, an f1 replication origin, an SV40 replication origin, a pMB1 replication origin, an adeno replication origin, an AAV replication origin, and a BBV replication origin. In addition, the recombinant vector may comprise a promoter derived from the genome of a mammalian cell (e.g., metallothionein promoter) or a promoter derived from a mammalian virus (e.g., adenovirus late promoter, vaccinia virus 7.5K promoter, SV40 promoter, cytomegalovirus promoter, HSV-tk promoter, etc.), and generally has a polyadenylation sequence as a transcription termination sequence.

The recombinant vector may comprise a selection marker. The selection marker serves to select a transformant (host cell) transformed with the vector, and since only cells expressing the selection marker can survive in the medium treated with the selection marker, it is possible to select transformed cells. Representative examples of the selection marker include, but are not limited to, kanamycin, streptomycin, and chloramphenicol.

The transformant may be produced by inserting the recombinant vector into a host cell, and the transformant may be obtained by introducing the recombinant vector into an appropriate host cell. The host cell is a cell capable of stably and continuously cloning or expressing the expression vector, and any host cell known in the art may be used.

Where the vector is transformed into prokaryotic cells to generate recombinant microorganisms, examples of host cells that may be used include, but are not limited to, *E. coli* sp. strains such as *E. coli* DH5α, *E. coli* JM109, *E. coli* BL21, *E. coli* RR1, *E. coli* LE392, *E. coli* B, *E. coli* X 1776, *E. coli* W3110, and *E. coli* XL1-Blue, *Bacillus* sp. strains such as *Bacillus subtilis* and *Bacillus thuringiensis*, *Coryne-*

bacterium sp. strains such as Corynebacterium glutamicum and Corynebacterium stationis, and various Enterobacteriaceae strains such as Salmonella typhimurium, Serratia marcescens, and Pseudomonas species.

Where the vector is transformed into eukaryotic cells to generate recombinant microorganisms, examples of host cells that may be used include, but are not limited to, yeast (e.g., *Saccharomyces cerevisiae*), insect cells, plant cells and animal cells, such as Sp2/0, CHO K1, CHO DG44, PER.C6, W138, BHK, COS7, 293, HepG2, Huh7, 3T3, RIN, and MDCK cell lines.

As used in the present invention, the term "transformation" refers to a phenomenon in which external DNA is introduced into a host cell, thereby artificially causing genetic changes, and the term "transformant" refers to a host cell into which external DNA has been introduced and in which the expression of the gene of interest is stably maintained.

The transformation may be performed using a suitable 20 vector introduction technique selected depending on the host cell, so that the gene of interest or a recombinant vector comprising the same may be expressed in the host cell. For example, introduction of the vector may be performed by electroporation, heat-shock, calcium phosphate (CaPO₄) ²⁵ precipitation, calcium chloride (CaCl₂) precipitation, microinjection, polyethylene glycol (PEG) method, DEAE-dextran method, cationic liposome method, lithium acetate-DMSO method, or any combination thereof, without being limited thereto. As long as the transformed gene may be expressed in the host cell, it may be inserted into the chromosome of the host cell, or may exist extrachromosomally, without being limited thereto.

The transformant may include a cell transfected, transformed, or infected with the recombinant vector of the present invention in vivo or in vitro, and may be used in the same sense as a recombinant host cell, a recombinant cell, or a recombinant microorganism.

Genes inserted into the recombinant vector of the present 40 invention may be introduced into a host cell such as a *Corynebacterium* sp. strain by homologous recombination crossover

According to one embodiment of the present invention, the transformant may be a *Corynebacterium* sp. microor- 45 ganism.

The Corvnebacterium sp. microorganism may be, but is not limited to, Corynebacterium glutamicum, Corynebacterium crudilactis, Corynebacterium deserti, Corynebacterium callunae, Corynebacterium suranareeae, Corynebac- 50 lubricantis, Corvnebacterium doosanense, Corynebacterium efficiens, Corynebacterium uterequi, Corynebacterium stationis, Corynebacterium pacaense, Corynebacterium singulare, Corynebacterium humireducens, Corynebacterium marinum, Corynebacterium halo- 55 tolerans, Corynebacterium spheniscorum, Corynebacterium freiburgense, Corynebacterium striatum, Corynebacterium canis, Corynebacterium ammoniagenes, Corynebacterium renale, Corynebacterium pollutisoli, Corynebacterium imitans, Corynebacterium caspium, Corynebacterium testudi- 60 noris, Corynebacaterium pseudopelargi, or Corynebacterium flavescens.

The transformant in the present invention may be a strain either comprising the above-described 5-dehydro-2-deoxygluconokinase variant or a polynucleotide encoding the 65 same or comprising the vector comprising the same, a strain expressing the 5-dehydro-2-deoxygluconokinase variant or

6

the polynucleotide, or a strain having activity for the 5-de-hydro-2-deoxygluconokinase variant, without being limited thereto.

The transformant of the present invention may comprise other protein variants or genetic mutations, in addition to the 5-dehydro-2-deoxygluconokinase variant.

According to one embodiment of the present invention, the transformant may have the ability to produce inosinic acid.

The 5'-inosinic acid is a nucleic acid-based compound that gives flavor to food, especially umami (savory) taste, and is used with the same meaning as inosine monophosphate (IMP).

The transformant may naturally have the ability to produce 5'-inosinic acid or may be one artificially endowed with the ability to produce 5'-inosinic acid.

According to one embodiment of the present invention, the transformant may have an increased ability to produce 5'-inosinic acid, due to a change in 5-dehydro-2-deoxygluconokinase activity.

As used in the present invention, the term "increased ability to produce" means that 5'-inosinic acid productivity has increased compared to that of the parent strain. As used herein, the term "parent strain" refers to a wild-type strain or mutant strain to be mutated, and includes a strain that is to be mutated directly or to be transformed with a recombinant vector or the like. In the present invention, the parent strain may be a wild-type *Corynebacterium* sp. strain or a *Corynebacterium* sp. strain mutated from the wild-type strain.

The transformant according to the present invention exhibits an increased ability to produce 5'-inosinic acid compared to the parent strain, due to the change in 5-dehydro-2-deoxygluconokinase activity caused by introduction of the 5-dehydro-2-deoxygluconokinase variant thereinto. More specifically, the amount of 5'-inosinic acid produced by the transformant may be at least 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% higher than that produced by the parent strain, or may be 1.1-fold, 1.5-fold, 2-fold, 2.5-fold, 3-fold, 3.5-fold, 4-fold, 4.5-fold, 5-fold, 5.5-fold, 6-fold, 6.5-fold, 7-fold, 7.5-fold, 8-fold, 8.5-fold, 9-fold, 9.5-fold, or 10-fold higher than that produced by the parent strain, without being limited thereto. For example, the amount of 5'-inosinic acid produced by the transformant comprising the 5-dehydro-2-deoxygluconokinase variant may be at least 5%, specifically 5 to 50% (preferably 10 to 40%) higher than that produced by the parent strain.

Still yet another aspect of the present invention provides a method for producing 5'-inosinic acid, comprising steps of: culturing the transformant in a medium; and recovering 5'-inosinic acid from the transformant or the medium in which the transformant has been cultured.

The culturing may be performed using a suitable medium and culture conditions known in the art, and any person skilled in the art may easily adjust and use the medium and the culture conditions. Specifically, the medium may be a liquid medium, without being limited thereto. Examples of the culturing method include, but are not limited to, batch culture, continuous culture, fed-batch culture, or a combination thereof.

According to one embodiment of the present invention, the medium should meet the requirements of a specific strain in a proper manner, and may be appropriately modified by a person skilled in the art. For culture media for *Escherichia* sp. strains, reference may be made to, but not limited to, a

known document (Manual of Methods for General Bacteriology, American Society for Bacteriology, Washington D.C., USA, 1981).

According to one embodiment of the present invention, the medium may contain various carbon sources, nitrogen 5 sources, and trace element components. Examples of carbon sources that may be used include: sugars and carbohydrates such as glucose, sucrose, lactose, fructose, maltose, starch, and cellulose; oils and fats such as soybean oil, sunflower oil, castor oil, and coconut oil; fatty acids such as palmitic acid, stearic acid, and linoleic acid; alcohols such as glycerol and ethanol; and organic acids such as acetic acid. These substances may be used individually or as a mixture, without being limited thereto. Examples of nitrogen sources that 15 may be used include peptone, yeast extract, meat extract, malt extract, corn steep liquor, soybean meal, urea, or inorganic compounds such as ammonium sulfate, ammonium chloride, ammonium phosphate, ammonium carbonate, and ammonium nitrate. The nitrogen sources may also 20 be used individually or as a mixture, without being limited thereto. Examples of phosphorus sources that may be used include, but are not limited to, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts. In addition, the culture medium 25 may contain, but is not limited to, metal salts such as magnesium sulfate or iron sulfate, which are required for growth. In addition, the culture medium may contain essential growth substances such as amino acids and vitamins. Moreover, suitable precursors may be used in the culture 30 medium. The medium or individual components may be added to the culture medium batchwise or in a continuous manner by a suitable method during culturing, without being limited thereto.

According to one embodiment of the present invention, 35 the pH of the culture medium may be adjusted by adding compounds such as ammonium hydroxide, potassium hydroxide, ammonia, phosphoric acid and sulfuric acid to the microorganism culture medium in an appropriate manner during the culturing. In addition, during the culturing, foaming may be suppressed using an anti-foaming agent such as a fatty acid polyglycol ester. Additionally, to keep the culture medium in an aerobic condition, oxygen or an oxygencontaining gas (for example, air) may be injected into the culture medium. The temperature of the culture medium 45 may be generally 20° C. to 45° C., for example, 25° C. to 40° C. The culturing may be continued until a desired amount of a useful substance is produced. For example, the culturing time may be 10 hours to 160 hours.

According to one embodiment of the present invention, in 50 the step of recovering 5'-inosinic acid from the cultured transformant or the medium in which the transformant has been cultured, the produced 5'-inosinic acid may be collected or recovered from the medium using a suitable method known in the art depending on the culture method. 55 Examples of a method that may be used to recover the produced 5'-inosinic acid include, but are not limited to, centrifugation, filtration, extraction, spraying, drying, evaporation, precipitation, crystallization, electrophoresis, fractional dissolution (e.g., ammonium sulfate precipitation), chromatography (e.g., ion exchange, affinity, hydrophobicity and size exclusion), and the like.

According to one embodiment of the present invention, the step of recovering 5'-inosinic acid may be performed by centrifuging the culture medium at a low speed to remove 65 biomass and separating the obtained supernatant through ion-exchange chromatography.

8

According to one embodiment of the present invention, the step of recovering 5'-inosinic acid may include a process of purifying the 5'-inosinic acid.

Advantageous Effects

The 5-dehydro-2-deoxygluconokinase variant according to the present invention is obtained by substituting one or more amino acids in the amino acid sequence constituting 5-dehydro-2-deoxygluconokinase to change the activity of the protein, and a recombinant microorganism comprising the 5-dehydro-2-deoxygluconokinase variant is capable of efficiently producing 5'-inosinic acid.

BRIEF DESCRIPTION OF DRAWINGS

FIG. 1 shows the structure of a pK19msb plasmid according to one embodiment of the present invention.

MODE FOR INVENTION

Hereinafter, the present invention will be described in more detail. However, this description is merely presented by way of example to facilitate the understanding of the present invention, and the scope of the present invention is not limited by this exemplary description.

Example 1. Construction of Strain Expressing 5-Dehydro-2-Deoxygluconokinase Variant

To evaluate the effect of a variant (SEQ ID NO: 2) having a substitution of asparagine (N) for serine (S) at position 146 in the amino acid sequence of 5-dehydro-2-deoxygluconokinase (SEQ ID NO: 4) on the production of 5'-inosinic acid, the present inventors constructed a vector for expressing the 5-dehydro-2-deoxygluconokinase variant and a strain into which the vector has been introduced.

1-1. Construction of Vector for Expression of 5-Dehydro-2-Deoxygluconokinase Variant

Using the genomic DNA of wild-type *Corynebacterium stationis* ATCC6872 as a template, PCR reactions were performed using a primer pair of primers 1 and 2 and a primer pair of primers 3 and 4, respectively. Thereafter, using the two PCR products as templates, overlapping PCR was performed using a primer pair of primers 1 and 4 to obtain a single fragment. The PCR fragment and a pK19msb plasmid (SEQ ID NO: 5) were treated with the restriction enzyme smal (NEB) and ligated together using T4 ligase. The resulting plasmid was named pK_DD.

The PCR amplification was performed using Pfu PreMix (Bioneer) under the following conditions: denaturation at 95° C. for 5 min, and then 30 cycles, each consisting of 95° C. for 30 sec, 58° C. for 30 sec, and 72° C. for 1 min and 30 sec, followed by reaction at 72° C. for 5 min.

The primer sequences used for plasmid construction are shown in Table 1 below.

TABLE 1

Primer	name	SEQ ID NO.	Primer sequence (5'→3')
Primer	1	6	AATGTGCTATTGTCAGGACATGC
Primer	2	7	GGCTCTTCGTTTAAACCGGTCA

TABLE 1-continued

Primer name	SEQ ID NO.	Primer sequence (5'→3')
Primer 3	8	TGACCGGTTTAAACGAAGAGCC
Primer 4	9	ACCTTCTGACTTAGGGCTGCTT

1-2. Construction of Mutant Strain into Which 5-Dehydro-2-Deoxygluconokinase Variant Has Been Introduced

An electrocompetent cell preparation method, a modification of the method of van der Rest et al., was used as a method for transformation of *Corynebacterium stationis* KCCM13339P.

First, Corynebacterium stationis KCCM13339P was pri- 15 marily cultured in 10 mL of 2YT medium (containing 16 g/l of tryptone, 10 g/l of yeast extract, and 5 g/l of sodium chloride) supplemented with 2% glucose, thus preparing a seed culture. Isonicotinic acid hydrazine at a concentration of 1 mg/ml and 2.5% glycine were added to 100 ml of 2YT $\,\,$ 20 medium free of glucose. Next, the seed culture was inoculated into the $2\overline{YT}$ medium to reach an OD_{610} value of 0.3, and then cultured at 30° C. and 180 rpm for 5 to 8 hours so that the OD_{610} value reached 0.6 to 0.7. The culture was kept on ice for 30 minutes, and then centrifuged at 3,500 rpm at 25 4° C. for 10 minutes. Thereafter, the supernatant was discarded and the precipitated Corvnebacterium stationis KCCM13339P was washed 4 times with a 10% glycerol solution and finally re-suspended in 0.5 ml of a 10% glycerol solution, thereby preparing competent cells. Electroporation 30 was performed using a Bio-Rad electroporator. The prepared competent cells and the constructed pK_DD vector were placed in an electroporation cuvette (0.2 mm), and then subjected to electroporation under conditions of 2.5 kV, 200Ω and 12.5 pF. Immediately after completion of the ³⁵ electroporation, 1 ml of a regeneration (RG) medium (containing 18.5 g/l brain heart infusion and 0.5 M sorbitol) was added to the cells which were then heat-treated at 46° C. for 6 minutes. Next, the cells were cooled at room temperature, transferred into a 15-ml cap tube, incubated at 30° C. for 2 40 hours, and plated on a selection medium (containing 5 g/l tryptone, 5 g/l NaCl, 2.5 g/l yeast extract, 18.5 g/l brain heart infusion powder, 15 g/l agar, 91 g/l sorbitol, and 20 pg/l kanamycin). The cells were cultured at 30° C. for 72 hours, and the generated colonies were cultured in medium until 45 the stationary phase to induce secondary recombination. Then, the cells were diluted to 10^{-5} to 10^{-7} , and plated on an antibiotic-free plate medium (containing 10% sucrose), and a strain having no kanamycin resistance and grown on the medium containing 10% sucrose was selected and named 50 IDD-1.

Experimental Example 1. Evaluation of 5'-Inosinic Acid Productivity of Strain Expressing 5-Dehydro-2-Deoxygluconokinase Variant

5'-Inosinic acid productivity was compared between the parent strain KCCM13339P and the mutant strain IDD-1 into which the 5-dehydro-2-deoxygluconokinase variant has been introduced.

10

Each strain (parent strain or mutant strain) was inoculated at 1% by volume into a 100-mL flask containing 10 mL of the medium for 5'-inosinic acid production shown in Table 2 below, and cultured with shaking at 200 rpm at 34° C. for 45 hours. After completion of the culturing, the concentration of 5'-inosinic acid in the medium was measured using HPLC (Agilent), and the results are shown in Table 3 below.

TABLE 2

Component	Content
Glucose	70 g/L
$(NH_4)_2SO_4$	2 g/L
$MgSO_4$	1 g/L
Urea	2 g/L
Yeast extract	20 g/L
KH_2PO_4	2 g/L
$FeSO_4$	10 mg/L
$MnSO_4$	10 mg/L
Thiamine_HCl	5 mg/L
biotin	20 ug/L
Cystein	20 mg/L
Bata-alanine	20 mg/L
Adenine	30 mg/L

TABLE 3

Strain	5'-inosinic acid production (g/L)
KCCM13339P	19.8
IDD-1	23.0

As shown in Table 3 above, it was confirmed that the amount of 5'-inosinic acid produced by the mutant strain into which the 5-dehydro-2-deoxygluconokinase variant has been introduced was increased by about 16% compared to that produced by the parent strain, due to substitution of serine at position 146 with asparagine. These results suggest that introduction of a point mutation into 5-dehydro-2-deoxygluconokinase provides a significant effect on 5'-inosinic acid productivity.

So far, the present invention has been described with reference to the preferred embodiments. Those of ordinary skill in the art to which the present invention pertains will appreciate that the present invention may be embodied in modified forms without departing from the essential characteristics of the present invention. Therefore, the disclosed embodiments should be considered from an illustrative point of view, not from a restrictive point of view. The scope of the present invention is defined by the claims rather than the foregoing description, and all differences within the scope equivalent thereto should be construed as being included in the present invention

Accession Number

Depository Authority: Korean Culture Center of Microorganisms (KCCM)

Accession Number: KCCM13339P Deposit Date: Mar. 29, 2023

-continued

```
FEATURE
                      Location/Qualifiers
source
                      1..957
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 1
atggcgtatt taactagcgc tcacgaagtt ctggccatcg gcaggcttgg cgtggatatc
                                                                 120
tatccactac agtccggcgt tgggctagaa gaggtatctt ctttcggcaa atacctaggc
180
tcacgagtag gcaatgaccc actgggtaag tacctgctca atgagctgga aaggctcggg
                                                                 240
gtagataatc agtacgtcgc tactgatccg acttataaaa ccccgctgac tttgtgcgaa
                                                                 300
attttcccac cagatgattt cccgctgtac ttctaccgcg agcccaaagc tccggatatg
                                                                 360
tgcatcgagt cctctgacgt caacctcgaa gatgtccgcg atgcagaaat cttgtggttt
                                                                  420
accetgaceg gtttaaacga agagecaage egeggegeac ateaggaaat cetgaacace
cgcgcccggc gcaagcacac catcttggac ttggactacc gcgacatgtt ctggaattcc
                                                                  540
aagcaggaag caacagagca ggcacagtgg gcactcgagc atgccaccgt tgcggtcggt
                                                                  600
aacaaggaag aatgcgaggt cgccatcggc gaaaccgaac cagaacgcgc cggcaaggcg
ttgttggaac atggcgtgaa gttggccatc gttaagcaag gccccaaagg cgtgctggcc
atgactgaag atgaaaccgt cgaagtgcca ccggtgtggg tcgatgttgt caacggcctc
ggegetggeg atgeettegg tggegegetg tgccaeggte tgttgteega etggeeaete
gaaaaagtcc tgcgctttgc caacgcggca ggctcggtgg ttgccggacg cttagagtgc
                                                                  900
agcaccgcca tgccaaccac tgaagaagtt gaagcagccc taagtcagaa ggtctag
SEQ ID NO: 2
                      moltype = AA length = 318
                      Location/Qualifiers
FEATURE
                      1..318
source
                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 2
MAYLTSAHEV LAIGRLGVDI YPLQSGVGLE EVSSFGKYLG GSAANVSVAA ARHGHNSALL
SRVGNDPLGK YLLNELERLG VDNQYVATDP TYKTPLTLCE IFPPDDFPLY FYREPKAPDM
                                                                 120
CIESSDVNLE DVRDAEILWF TLTGLNEEPS RGAHQEILNT RARRKHTILD LDYRDMFWNS
                                                                 180
KOEATEOAOW ALEHATVAVG NKEECEVAIG ETEPERAGKA LLEHGVKLAI VKOGPKGVLA
                                                                 240
MTEDETVEVP PVWVDVVNGL GAGDAFGGAL CHGLLSDWPL EKVLRFANAA GSVVAGRLEC
                                                                 300
STAMPTTEEV EAALSQKV
                                                                  318
                      moltype = DNA length = 957
SEQ ID NO: 3
FEATURE
                      Location/Qualifiers
                      1..957
source
                      mol_type = genomic DNA
organism = Corynebacterium stationis
SEQUENCE: 3
atggcgtatt taactagcgc tcacgaagtt ctggccatcg gcaggcttgg cgtggatatc
tatccactac agtccggcgt tgggctagaa gaggtatctt ctttcggcaa atacctaggc
                                                                 120
180
tcacgagtag gcaatgaccc actgggtaag tacctgctca atgagctgga aaggctcggg
                                                                 240
gtagataatc agtacgtcgc tactgatccg acttataaaa ccccgctgac tttgtgcgaa
                                                                 300
attttcccac cagatgattt cccgctgtac ttctaccgcg agcccaaagc tccggatatg
                                                                 360
tgcatcgagt cctctgacgt caacctcgaa gatgtccgcg atgcagaaat cttgtggttt
                                                                 420
accetgaceg gtttaagega agagecaage egeggegeae ateaggaaat eetgaacace
                                                                  480
egegeeegge geaageacae catettggae ttggaetaee gegaeatgtt etggaattee
                                                                 540
aagcaggaag caacagagca ggcacagtgg gcactcgagc atgccaccgt tgcggtcggt
                                                                  600
aacaaggaag aatgcgaggt cgccatcggc gaaaccgaac cagaacgcgc cggcaaggcg
                                                                  660
ttgttggaac atggcgtgaa gttggccatc gttaagcaag gccccaaagg cgtgctggcc
                                                                  720
atgactgaag atgaaaccgt cgaagtgcca ccggtgtggg tcgatgttgt caacggcctc
                                                                  780
ggcgctggcg atgccttcgg tggcgcgctg tgccacggtc tgttgtccga ctggccactc
                                                                  840
gaaaaagtcc tgcgctttgc caacgcggca ggctcggtgg ttgccggacg cttagagtgc
agcaccgcca tgccaaccac tgaagaagtt gaagcagccc taagtcagaa ggtctag
SEQ ID NO: 4
                      moltype = AA length = 318
FEATURE
                      Location/Qualifiers
source
                      mol type = protein
                      organism = Corynebacterium stationis
MAYLTSAHEV LAIGRLGVDI YPLQSGVGLE EVSSFGKYLG GSAANVSVAA ARHGHNSALL
SRVGNDPLGK YLLNELERLG VDNQYVATDP TYKTPLTLCE IFPPDDFPLY FYREPKAPDM 120
CIESSDVNLE DVRDAEILWF TLTGLSEEPS RGAHOEILNT RARRKHTILD LDYRDMFWNS
                                                                 180
KQEATEQAQW ALEHATVAVG NKEECEVAIG ETEPERAGKA LLEHGVKLAI VKQGPKGVLA
                                                                 240
MTEDETVEVP PVWVDVVNGL GAGDAFGGAL CHGLLSDWPL EKVLRFANAA GSVVAGRLEC
STAMPTTEEV EAALSQKV
                                                                  318
SEQ ID NO: 5
                      moltype = DNA length = 5719
FEATURE
                      Location/Qualifiers
source
                      1..5719
                      mol_type = other DNA
organism = synthetic construct
SEQUENCE: 5
tgccgcaagc actcagggcg caagggctgc taaaggaagc ggaacacgta gaaagccagt
ccgcagaaac ggtgctgacc ccggatgaat gtcagctact gggctatctg gacaagggaa 120
```

-continued

aacgcaagcg caaagagaaa gcaggtagct tgcagtgggc ttacatggcg atagctagac 180 tgggcggttt tatggacagc aagcgaaccg gaattgccag ctggggcgcc ctctggtaag 240 gttgggaagc cctgcaaagt aaactggatg gctttcttgc cgccaaggat ctgatggcgc 300 aggggatcaa gatctgatca agagacagga tgaggatcgt ttcgcatgat tgaacaagat 360 ggattgcacg caggttctcc ggccgcttgg gtggagaggc tattcggcta tgactgggca 420 caacagacaa toggotgoto tgatgoogoo gtgttooggo tgtoagogoa ggggogocog 480 gttctttttg tcaagaccga cctgtccggt gccctgaatg aactccaaga cgaggcagcg 540 cggctatcgt ggctggccac gacgggcgtt ccttgcgcag ctgtgctcga cgttgtcact 600 gaagegggaa gggactgget getattggge gaagtgeegg ggeaggatet cetgteatet 660 caccttgctc ctgccgagaa agtatccatc atggctgatg caatgcggcg gctgcatacg 720 cttgatccgg ctacctgccc attcgaccac caagcgaaac atcgcatcga gcgagcacgt 780 actoggatgg aagcoggtot tgtogatoag gatgatotgg acgaagagoa toaggggoto 840 gcgccagccg aactgttcgc caggctcaag gcgcggatgc ccgacggcga ggatctcgtc gtgacccatg gcgatgcctg cttgccgaat atcatggtgg aaaatggccg cttttctgga 960 ttcatcgact gtggccggct gggtgtggcg gaccgctatc aggacatagc gttggctacc 1020 cgtgatattg ctgaagagct tggcggcgaa tgggctgacc gcttcctcgt gctttacggt 1080 atcgccgctc ccgattcgca gcgcatcgcc ttctatcgcc ttcttgacga gttcttctga gegggactet ggggtteget agaggatega teetttttaa eecateacat atacetgeeg ttcactatta tttagtgaaa tgagatatta tgatattttc tgaattgtga ttaaaaaggc aactttatgc ccatgcaaca gaaactataa aaaatacaga gaatgaaaag aaacagatag attitttagt totttaggcc cgtagtctgc aaatcctttt atgattitct atcaaacaaa agaggaaaat agaccagttg caatccaaac gagagtctaa tagaatgagg tcgaaaagta 1440 aatcqcqcqq qtttqttact qataaaqcaq qcaaqaccta aaatqtqtaa aqqqcaaaqt 1500 gtatactttg gcgtcacccc ttacatattt taggtctttt tttattgtgc gtaactaact 1560 tgccatcttc aaacaggagg gctggaagaa gcagaccgct aacacagtac ataaaaaagg 1620 agacatgaac gatgaacatc aaaaagtttg caaaacaagc aacagtatta acctttacta 1680 ccgcactgct ggcaggaggc gcaactcaag cgtttgcgaa agaaacgaac caaaagccat 1740 ataaggaaac atacggcatt tcccatatta cacgccatga tatgctgcaa atccctgaac 1800 agcaaaaaaa tgaaaaatat caagtttctg aatttgattc gtccacaatt aaaaatatct 1860 tegeaaacta teaeggetae eacategtet tegeattage eggagateet aaaaatgegg 1920 1980 atgacacatc gatttacatg ttctatcaaa aagtcggcga aacttctatt gacagctgga aaaacgctgg ccgcgtcttt aaagacagcg acaaattcga tgcaaatgat tctatcctaa 2040 2100 aagaccaaac acaagaatgg tcaggttcag ccacatttac atctgacgga aaaatccgtttattctacac tgatttctc ggtaaacatt acggcaaaca aacactgaca actgcacaag 2160 2220 ttaacgtatc agcatcagac agctctttga acatcaacgg tgtagaggat tataaatcaa 2280 tetttgaegg tgaeggaaaa acgtateaaa atgtaeagca gtteategat gaaggeaact 2340 acageteagg egacaaceat aegetgagag atecteaeta egtagaagat aaaggeeaca 2400 aatacttagt atttgaagca aacactggaa ctgaagatgg ctaccaaggc gaagaatctt 2460 tatttaacaa agcatactat ggcaaaagca catcattctt ccgtcaagaa agtcaaaaac 2520 ttctgcaaag cgataaaaaa cgcacggctg agttagcaaa cggcgctctc ggtatgattg 2580 agctaaacga tgattacaca ctgaaaaaag tgatgaaacc gctgattgca tctaacacag 2640 taacagatga aattgaacgc gcgaacgtct ttaaaatgaa cggcaaatgg tacctgttca 2700 ctgactcccg cggatcaaaa atgacgattg acggcattac gtctaacgat atttacatgc 2760 ttggttatgt ttctaattct ttaactggcc catacaagcc gctgaacaaa actggccttg 2820 tgttaaaaat ggatcttgat cctaacgatg taacctttac ttactcacac ttcgctgtac 2880 ctcaagcgaa aggaaacaat gtcgtgatta caagctatat gacaaacaga ggattctacg 2940 cagacaaaca atcaacgttt gcgccgagct tcctgctgaa catcaaaggc aagaaaacat 3000 ctgttgtcaa agacagcatc cttgaacaag gacaattaac agttaacaaa taaaaacgca 3060 aaagaaaatg ccgatgggta ccgagcgaaa tgaccgacca agcgacgccc aacctgccat 3120 cacgagattt cgattccacc gccgccttct atgaaaggtt gggcttcgga atcgttttcc 3180 gggacgccct cgcggacgtg ctcatagtcc acgacgcccg tgattttgta gccctggccg 3240 acggccagca ggtaggccga caggctcatg ccggccgccg ccgccttttc ctcaatcgct 3300 cttcgttcgt ctggaaggca gtacaccttg ataggtgggc tgcccttcct ggttggcttg 3360 gtttcatcag ccatccgctt gccctcatct gttacgccgg cggtagccgg ccagcctcgc 3420 agagcaggat tcccgttgag caccgccagg tgcgaataag ggacagtgaa gaaggaacac 3480 ccgctcgcgg gtgggcctac ttcacctatc ctgcccggct gacgccgttg gatacaccaa 3540 ggaaagtcta cacgaaccct ttggcaaaat cctgtatatc gtgcgaaaaa ggatggatat accgaaaaaa tcgctataat gaccccgaag cagggttatg cagcggaaaa gcgctgcttc cctgctgttt tgtggaatat ctaccgactg gaaacaggca aatgcaggaa attactgaac tgaggggaca ggcgagagac gatgccaaag agctcctgaa aatctcgata actcaaaaaa tacgcccggt agtgatctta tttcattatg gtgaaagttg gaacctctta cgtgccgatc aacgtctcat tttcgccaaa agttggccca gggcttcccg gtatcaacag ggacaccagg atttatttat totgogaagt gatottoogt cacaggtatt tattoggogo aaagtgogto qqqtqatqct qccaacttac tqatttaqtq tatqatqqtq tttttqaqqt qctccaqtqq cttctqtttc tatcagctcc tgaaaatctc gataactcaa aaaatacgcc cggtagtgat 4080 cttatttcat tatggtgaaa gttggaacct cttacgtgcc gatcaacgtc tcattttcgc 4140 caaaagttgg cccagggctt cccggtatca acagggacac caggatttat ttattctgcg 4200 aagtgatctt ccgtcacagg tatttattcg gcgcaaagtg cgtcgggtga tgctgccaac ttactgattt agtgtatgat ggtgtttttg aggtgctcca gtggcttctg tttctatcag 4320 ggetggatga teeteeageg eggggatete atgetggagt tettegeeea eeccaaaagg 4380 atctaggtga agatcctttt tgataatctc atgaccaaaa tcccttaacg tgagttttcg 4440 ttccactgag cgtcagaccc cgtagaaaag atcaaaggat cttcttgaga tcctttttt 4500 ctgcgcgtaa tctgctgctt gcaaacaaaa aaaccaccgc taccagcggt ggtttgtttg ccggatcaag agctaccaac tctttttccg aaggtaactg gcttcagcag agcgcagata 4620 ccaaatactg ttcttctagt gtagccgtag ttaggccacc acttcaagaa ctctgtagca 4680 ccgcctacat acctcgctct gctaatcctg ttaccagtgg ctgctgccag tggcgataag 4740 togtgtotta cogggttgga otoaagacga tagttacogg ataaggogca goggtogggo 4800 tgaacggggg gttcgtgcac acagcccagc ttggagcgaa cgacctacac cgaactgaga

-continued

tacctacage gtgagetatg	agaaagcgcc acgcttcccg aagggagaaa ggcggacagg	4920
tatccggtaa gcggcagggt	cggaacagga gagcgcacga gggagcttcc agggggaaac	4980
gcctggtatc tttatagtcc	tgtcgggttt cgccacctct gacttgagcg tcgatttttg	5040
tgatgctcgt caggggggcg	gagcctatgg aaaaacgcca gcaacgcggc ctttttacgg	5100
tteetggeet tttgetggee	ttttgctcac atgttctttc ctgcgttatc ccctgattct	5160
gtggataacc gtattaccgc	ctttgagtga gctgataccg ctcgccgcag ccgaacgacc	5220
	cgaggaagcg gaagagcgcc caatacgcaa accgcctctc	5280
	ttaatgcagc tggcacgaca ggtttcccga ctggaaagcg	5340
	taatgtgagt tagctcactc attaggcacc ccaggcttta	5400
	tatgttgtgt ggaattgtga gcggataaca atttcacaca	5460
	tacgccaagc ttgcatgcct gcaggtcgac tctagaggat	5520
	ttcactggcc gtcgttttac aacgtcgtga ctgggaaaac	5580
	tegeettgea geacateece etttegeeag etggegtaat	5640
	tegecettee caacagttge geageetgaa tggegaatgg	5700
cgataagcta gcttcacgc		5719
SEQ ID NO: 6 FEATURE source	moltype = DNA length = 23 Location/Qualifiers 123 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 6	organism = bynonocio competado	
aatgtgctat tgtcaggaca	tac	23
	-5-	
SEQ ID NO: 7	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	122	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 7		
ggctcttcgt ttaaaccggt	ca	22
SEQ ID NO: 8	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	122	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 8		
tgaccggttt aaacgaagag	cc	22
CEO ID NO. O	moltima - DNA longth - 22	
SEQ ID NO: 9 FEATURE	moltype = DNA length = 22	
source	Location/Qualifiers 122	
Source	mol type = other DNA	
	organism = synthetic construct	
SEQUENCE: 9	organism - synthetic constituct	
accttctqac ttaqqqctqc	++	22

The invention claimed is:

- 1. A 5-dehydro-2-deoxygluconokinase variant consisting of the amino acid sequence of SEQ ID NO: 2 in which serine 45 at position 146 in the amino acid sequence of SEQ ID NO: 4 is substituted with asparagine.
 - 2. A polynucleotide encoding the variant of claim 1.
 - 3. A transformant comprising the variant of claim 1.
- **4**. The transformant of claim **3**, which is a *Corynebacterium* sp. microorganism.
- 5. The transformant of claim 3, which has ability to produce 5'-inosinic acid.
- **6**. A method for producing 5'-inosinic acid, comprising steps of:

culturing the transformant of claim 3 in a medium; and recovering 5'-inosinic acid from the transformant or the medium in which the transformant has been cultured.

 50 $\,$ 7. A transformant comprising the polynucleotide of claim $\,$ 2.

* * * * *