

PROMOTER SYSTEM INDUCING EXPRESSION BY 3-HYDROXYPROPIONIC ACID AND METHOD FOR BIOLOGICAL PRODUCTION OF 3-HYDROXYPROPIONIC ACID USING SAME

TECHNICAL FIELD

The present invention relates to a promoter system inducing expression of 3-hydroxypropionic acid (3-HP) and a method for biological production of 3-HP.

BACKGROUND ART

3-hydroxypropionic acid (3-HP) is an important synthetic immediate used in various chemical processes, and is used as a raw material for producing acrylic acid, acrylamide, 1,3-propanediol, malonic acid, and the like. 3-HP is also used for synthesis of a biodegradable polymer. Biological production of 3-HP using glycerol has been successfully accomplished through genetic engineering of key enzymes required for 3-HP production pathways in various bacteria. In detail, production of 3-HP has been confirmed in bacteria, such as *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas denitrificans*, and the like, by (over)expression of glycerol dehydratase which is a coenzyme B₁₂-dependent enzyme, DhaB reactivase which is a glycerol dehydratase reactivase, and aldehyde dehydrogenase which is a NAD⁺-dependent enzyme, and the like through genetic engineering. Some recombinant strains including *E. coli* W DUBGK were able to produce more than 40 g/L of 3-HP for 48 hours, but had a difficulty in increasing 3-HP production beyond that. It was particularly observed that, as fermentation time for the production of 3-HP continues, problems that enzymes, such as glycerol dehydratase and aldehyde dehydrogenase, become unstable or lose activity occur. In this regard, one important reason why the activity of glycerol dehydratase disappears is due to a mechanism called suicidal inactivation. In such a mechanism, coenzyme B₁₂ which is a coenzyme of glycerol dehydratase is irreversibly damaged during a dehydration reaction from glycerol to 3-hydroxypropionaldehyde (3-HPA), and such a deactivation reaction is promoted in the presence of oxygen. In recent years, to ease deactivation-based on such a mechanism above, mutant glycerol dehydratase has been developed according to site-directed mutagenesis. Several mutant enzymes have

been found to have improved enzyme stability, but enzyme activity thereof has been observed to be significantly reduced when compared to conventional enzymes.

Another reason for the problems above is due to toxicity of 3-HPA which is a highly reactive intermediate. When glycerol dehydratase or aldehyde dehydrogenase is present with 3-HPA, activity of glycerol dehydratase or aldehyde dehydrogenase decreases depending on a concentration of 3-HPA. Aldehydes are known to react with amino acid residues, such as ϵ -amino acid (NH_3^+), a sulfhydryl group ($-\text{C}-\text{SH}$), and an imidazole group that are present in lysine, cysteine, and histidine, respectively. Efforts have been made to improve the stability of many enzymes in the presence of aldehydes using site-directed mutagenesis and random mutagenesis, but have been limitedly succeeded.

An interesting alternative to solving the problems that the enzymes become unstable is continuous synthesis of new enzymes having activity during the whole period of cell culture. Theoretically, if new enzymes can be supplied as much as the enzymes that become unstable, the enzyme activity of the enzymes in cells can be kept constant. In particular, it is necessary to continuously express enzymes at the time when the growth of cells in the latter half of fermentation slows down and the total metabolic activity of the cells is decreased due to high concentrations of 3-HP.

DETAILED DESCRIPTION OF THE INVENTION

TECHNICAL PROBLEM

The present invention provides an inducible promoter for 3-hydroxypropionic acid (3-HP) or a derivative thereof, the inducible promoter including a binding site to a LysR protein that is reactive to 3-HP or a derivative thereof.

The present invention also provides a recombinant gene expression cassette reactive to 3-HP or a derivative thereof, the recombinant gene expression cassette including a lysR gene encoding a LysR protein that is reactive to 3-HP or a derivative thereof, a promoter comprising a binding site to a LysR protein, and a gene encoding a target expression protein.

TECHNICAL SOLUTION

To achieve the technical problems above, the present invention provides an inducible promoter for 3-hydroxypropionic acid (3-HP) or a derivative thereof, the inducible promoter including a binding site to a LysR protein that is reactive to 3-HP or a derivative thereof.

In addition, the present invention relates to a recombinant expression vector including the inducible promoter for 3-HP or a derivative thereof, a recombinant microorganism transformed by the recombinant expression vector, and a method of producing 3-HP, the method including culturing the recombinant microorganism.

In addition, the present invention provides a recombinant gene expression cassette reactive to 3-HP or a derivative thereof, the recombinant gene expression cassette including a *lysR* gene encoding a LysR protein that is reactive to 3-HP or a derivative thereof, a promoter including a binding site to a LysR protein, and a gene encoding a target expression protein.

In addition, the present invention provides a recombinant expression vector including the recombinant gene expression cassette that is reactive to 3-HP or a derivative thereof, a recombinant microorganism transformed with the recombinant expression vector, a recombinant microorganism including the recombinant gene expression cassette, which is reactive to 3-HP or a derivative thereof, inserted in a chromosome of a host cell, and a method of producing a target expression protein, the method including culturing the recombinant microorganism.

ADVANTAGEOUS EFFECTS OF THE INVENTION

The present invention relates to a promoter system inducing expression of 3-hydroxypropionic acid (3-HP) and a method of biologically producing 3-HP using the same. To improve production of 3-HP in a biological manner, continuous synthesis of new enzymes having enzyme activity is necessary. As a result of screening 3-HP reactive transcription regulators and 3-HP reactive promoters from several microorganisms including *Pseudomonas denitrificans*, it was confirmed that the transcriptions regulations and promoters are composed of LysR proteins and particular gene nucleotide sequences binding to the LysR proteins. Therefore, the 3-HP inducible system is expected to be effectively used to regulate 3-HP metabolic pathways.

DESCRIPTION OF THE DRAWINGS

FIG. 1 is shows production (A) of 3-hydroxypropionic acid (3-HP) in proliferating cells and degradation (B) of 3-HP. A strain for a 3-HP production test of *Pseudomonas denitrificans* was cultured in an M9 medium supplemented with 25 ± 2 mmol/L of 3-HP as a single carbon energy source and an energy source. Meanwhile, resting cells for a 3-HP degradation test of *P. denitrificans* were prepared by culturing on an M9 medium supplemented with 25 ± 2 mmol/L of 3-HP. Here, the standard deviation for 3-HP concentration measurements was calculated to be 10% or less. Symbols: closed circle, 3-HP; semi-circle left, cell mass; cross, pH.

FIG. 2 shows two metabolic pathways of 3-HP (oxidation and reduction pathways). Abbreviations: 3-HPDH, 3-hydroxypropionate dehydrogenase; 3-HIBDH, 3-hydroxyisobutyrate dehydrogenase; MMSADH, methylmalonate semialdehyde dehydrogenase; HPCS, 3-hydroxypropionyl-CoA synthetase.

FIG. 3 shows a relative mRNA expression level (A) and a fold increase in *P. denitrificans* ATCC13867 with respect to a 3-hydroxypropionate catabolite gene. FIG. 3(A) shows a result (shown in a grey bar) obtained by culturing *P. denitrificans* in an M9 medium supplemented with 25 mmol/L of 3-HP and a result (shown in a black bar) obtained by culturing *P. denitrificans* in an M9 medium not supplemented with 3-HP. FIG. 3(B) shows a result (shown in a grey bar) of a difference in mRNA expression levels depending on the 3-HP supply, wherein the result is indicated as a fold increase. Here, the standard deviation for mRNA level measurements was calculated to be 10% or less. Here, the mRNA expression levels are compared using a *rpoD* gene as a reference gene.

FIG. 4 shows expression of genes, i.e., *mmsadh* (shown in black) and *3hibdhIV* (shown in grey). In addition to 3-HP, 3-hydroxyisobutyrate (3HIB), 3-hydroxybutyrate (3-HB), L-valine, or the like also acts as an inducer.

FIG. 5 shows expression of a gene, *3hpdH*. In addition to 3-HP, 3HIB, 3-HB, L-valine, or the like also acts as an inducer.

FIG. 6 shows a promoter system gene sequence and a structure thereof, the promoter system being induced by 3-HP. FIG. 6A shows positions of genes, *mmsadh* and *3hibdh*, and a gene of a LysR protein (C4-LysR) that regulates gene transcription of *mmsadh* and *3hibdh*. FIG. 6B shows positions of a *3hpdh* gene and a gene of a LysR

protein (C3-LysR) that regulates gene transcription of *3hpdh*.

FIG. 7 shows results of analysis for an inducible promoter for a C4-LysR gene. O1 and O2 operators between the genes, such as C4-LysR (represented by *mmsR*) and *mmsadh* (represented by *mmsA*), are each present at position -58 and position -9 at positions relative to, as a standard, a transcription start site of *mmsadh*, and each include an inverted repeat sequence. As a result of the analysis of the inverted repeat sequence constituting each of O1 and O2, a T**A**C**G**T**G**T**A**A sequence was conserved.

FIG. 8 shows a regulatory mechanism of a LysR family transcriptional regulator.

FIG. 9 shows an amino acid sequence that is highly conserved in a LysR protein. Positions of the amino acid was centered on the C4-LysR protein. However, the amino acid sequence conserved in a DNA binding domain or a substrate binding domain was the same for all LysR proteins derived from a strain used in the present invention.

FIG. 10 shows SDS-PAGE results for analyzing solubility of C-his tag C4-LysR by using a chaperon plasmid: *pG-KJE8* (A), *pGro7* (B), *pKJE7* (C), *pG-Tf2* (D), and *pTf16* (E). A genetically engineered strain of *E. coli* BL21 was cultured in an LB medium at a temperature of 25°C, induced with 0.1 mM IPTG, and harvested within 4 or 12 hours. Here, the blue arrow shows the size of 34.4 kDa for the C4-LysR protein.

FIG. 11 shows SDS- and native-PAGE analysis results of the purified C4-LysR protein. FIG. 11(A) shows purification results by denaturing SDS-PAGE, wherein lane 1 shows a wild-type (crude) result; lane 2 shows a (-)IPTG result; lanes 3, 4, 5, and 7 each show cell-free, soluble, insoluble, and purified fraction results; and lane 6 shows a protein marker result. FIG. 11(B) shows native PAGE analysis results, wherein lanes 8, 10, and 12 show protein marker results, and lanes 9, 11, and 13 show purified C4-LysR protein results when loaded at a concentration of 65 nM, 220 nM, and 550 nM, respectively.

FIG. 12 shows the effect of C4-LysR concentrations and 3-HP on binding of DNA fragments between the C4-LysR protein and a promoter region thereof. FIG. 12(A) shows a DNA fragment sequence of a promoter used in the experiment, wherein F12 indicates a fragment including both O1 and O2, F12M indicates a fragment including only an O1 operator, F1M2 indicates a fragment including only an O2 operator, and F1M2M indicates a fragment from which both O1 and O2 are removed, and the DNA fragments used in the experiment had the same length of 135 bp. FIG. 12(B) shows results of electromobility shift assay (EMSA) obtained by analyzing *in vitro* binding of

DNA fragments between the C4-LysR protein and a promoter region thereof, wherein the upper panel shows the results of electrophoresis performed in the absence of 3-HP, and the lower panel shows the results of electrophoresis performed in the presence of 25 mM of 3-HP, and in lanes 1 to 9, the concentration of the C4-LysR protein was gradually increased from 0 nM to 0.36 nM, 0.73 nM, 1.45 nM, 2.9 nM, 5.8 nM, 11.6 nM, 14.5 nM and 24.2 nM, in lanes 10 to 15, the concentration of the C4-LysR protein was gradually increased from 0 nM to 2.9 nM, 5.8 nM, 11.6 nM, 14.5 nM, and 24.2 nM, and in lanes 16 to 21, the concentration of the C4-LysR protein was gradually increased from 0 nM to 2.9 nM, 11.6 nM, 24.2 nM, and 72.7 nM. FIG. 12(C) shows quantitative results of binding affinity of DNA fragments between the C4-LysR protein and a promoter region thereof, wherein affinity refers to a dissociation constant (K_D), and that is, half of the DNA fragments was represented by the concentration of a protein required to bind the C4-LysR protein.

FIG. 13 shows the structural comparison of genetic populations involved in the 3-HP degradation pathway between *P. denitrificans* ATCC13861 and various microorganisms.

FIGS. 14 and 15 show the multiple sequence arrangement of the N-terminal HTH included in a LysR region: C4-LysR (FIG. 14) and C3-LysR (FIG. 15).

FIG. 16 shows a pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH plasmid developed for the expression of glycerol dehydratase and KGSADH in *P. denitrificans*.

FIG. 17 shows results (O1 & S1) of comparing consumption of glucose and glycerol, cell growth, 3-HP production, and pH changes by a strain of Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH) (O1, O2 & O3) and a strain of Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH) (S1, S2 & S3): no glycerol; (O2 & S2), 25 mg/L of $CoCl_2 \cdot 6H_2O$ added to a culture medium; (O3 & S3), 12 μ mol/L of coenzyme B12 added to a culture medium, and 100 mM of glycerol added at 3 hours.

FIG. 18 shows results of comparing time-dependent inactivation of glycerol dehydratase and KGSADH by using cell lysates of Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH) and Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH).

FIG. 19 shows time-dependent changes in consumption of glycerol and glucose, biomass, and 3-HP production upon a fed-batch bioreactor operation: (A) recombinant

Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH) and (B) Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH).

BEST MODE

Accordingly, in terms of efficiently maintaining expression of a 3-hydroxypropionic acid (3-HP) production enzyme, the inventors of the present invention have discovered a specific gene transcription promoter system, which induces the expression of 3-HP, in various microorganisms, and then, examined genetic and biochemical characteristics of the promoter system. The promoter system is an unusual system that has never been reported in documents yet, and consists of a transcription activating protein of 3-HP and a DNA sequence specifically binding to the transcription activating protein. The inventors of the present invention developed a recombinant strain capable of producing 3-HP at a high concentration from glycerol by overexpressing DhaB, GdrAB, and KGSADH by using the promoter system, thereby completing the present invention.

The present invention provides an inducible promoter for 3-HP or a derivative thereof, the inducible promoter including a binding site to a LysR protein which is reactive to 3-HP or a derivative thereof.

In addition, the present invention provides a recombinant expression vector including the inducible promoter for 3-HP or a derivative thereof. Preferably, the recombinant expression vector may further include a gene encoding a foreign protein linked to the inducible promoter for 3-HP or a derivative thereof. More preferably, the foreign protein may be glycerol dehydratase (DhaB), DhaB reactivase (GdrAB), or α -ketoglutaric semialdehyde dehydrogenase (KGSADH), but embodiments of the present disclosure are not limited thereto.

In addition, the present invention provides a recombinant microorganism transformed with the recombinant expression vector. Preferably, the recombinant microorganism may have producibility of 3-HP. More preferably, the recombinant microorganism may be *Pseudomonas denitrificans*, and more preferably, may be a strain of *Pseudomonas denitrificans* $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhl$ from which *3hpdh*, *3hibdh*, and *mmsadh* genes relating to degradation of 3-HP are deleted in a strain of *P. denitrificans*, but embodiments of the present disclosure are not limited thereto.

In addition, the present invention provides a method of producing 3-HP, the method including culturing the recombinant microorganism.

In addition, the present invention provides a recombinant gene expression cassette reactive to 3-HP or a derivative thereof, the recombinant gene expression cassette including a lysR gene encoding a LysR protein that is reactive to 3-HP or a derivative thereof, a promoter comprising a binding site to a LysR protein, and a gene encoding a target expression protein.

In addition, the present invention provides a recombinant expression vector including the recombinant gene expression cassette that is reactive to 3-HP or a derivative thereof, and a recombinant microorganism transformed with the recombinant expression vector.

In addition, the present invention provides a recombinant microorganism including the recombinant gene expression cassette that is reactive to 3-HP or a derivative thereof inserted in a chromosome of a host cell. It will be obvious to one of ordinary skill in the art that, even if the recombinant gene expression cassette is inserted into the genome of the host cell, the same effect as the case where the recombinant vector is introduced into a host cell is made.

In the present invention, as a method of inserting the recombinant gene expression cassette to a chromosome of a host cell, any gene engineering method known in the art may be used. In one embodiment, a method using a retrovirus vector, an adenovirus vector, an adeno-associated virus vector, a herpes simplex virus vector, a poxvirus vector, a lentivirus vector, or a non-viral vector may be used.

In addition, the present invention provides a method of producing a target expression protein, the method including culturing the recombinant microorganism. Preferably, the culturing of the recombinant microorganism may further include adding for 3-HP.

Preferably, the LysR protein or the promoter may be derived from a microorganism with 3-HP degradability. More preferably, the LysR protein or the promoter may be *Achromobacter denitrificans*, *Acidovorax avenae subsp.*, *Acidovorax sp.*, *Acinetobacter baumannii*, *Aeromonas hydrophilia*, *Agrobacterium sp.*, *Alcaligenes faecalis*, *Alcanivorax hongdengensis*, *Alicyclophilus denitrificans*, *Alteromonas marina*, *Amycolatopsis sp.*, *Anaeromyxobacter dehalogenans*, *Azospirillum brasilense*, *Azotobacter vinelandii*, *Beijerinckia indica*, *Bordetella avium*, *Bradyrhizobium japonicum*,

Burkholderia ambifaria, *Catenulispora acidiphilia*, *Caulobacter* sp., *Castellaniella defragrans*, *Chromobacterium violaceum*, *Collimonas arenae*, *Comamonas testosteroni*, *Corynebacterium vitaeruminis*, *Cupriavidus necator*, *Curvibacter gracilus*, *Delftia acidovorans*, *Ferrimonas balearica*, *Glaciecola nitratireducens*, *Gordonia bronchialis*, *Hahella chijuensis*, *Halomonas elongata*, *Hirschia litorea*, *Idiomarina* sp., *Janthinobacterium lividum*, *Kitasatospora setae*, *Kutzneria albida*, *Methylobacterium* sp., *Methylocystis* sp., *Novosphingobium* sp., *Oceanimonas smirnovii*, *Paracoccus* sp., *Parvibaculum lavamentivorans*, *Phenylobacterium kunshanensis*, *Photobacterium gaetbuleda*, *Polynucleobacter necessarius asymbioticus*, *Pseudoalteromonas carrageenovora*, *Pseudogulbenkiania* sp., *Pseudomonas denitrificans* ATCC13867, *P. knackmussii*, *P. protegens*, *P. fluorescens*, *Pseudoxanthomonas spadix*, *Psychrobacter phenylpyruvicus*, *Ralstonia oxalatica*, *Rhodomicrobium vannielli*, *Segniliparus rotundus*, *Shewanella oneidensis*, *Simiduia agarovorans*, *Sinorhizobium meliloti*, *Sphingobium chlorophenolicum*, *Sphingomonas wittichii*, *Sphingopyxis alaskensis*, *Stenotrophomonas maltophilia*, *Streptomyces nodosus*, *Tatlockia micdadei*, *Thalassospira xiamenensis*, *Variovorax paradoxus*, *Verminephrobacter eiseniae*, *Vibrio furnissii*, *Xanthobacter autotrophicus*, *Xanthomonas campestris*, and *Xanthomonas oryzae*, but embodiments of the present disclosure.

Preferably, the LysR protein may have an N-terminal domain having a helix-turn-helix structure and binding to DNA, a C-terminal domain binding to 3-HP or a derivative thereof, and a C-terminal domain contributing to stabilization of a LysR protein dimer, but embodiments of the disclosure are not limited thereto.

More preferably, the N-terminal domain having a helix-turn-helix structure and binding to DNA may include an amino acid sequence represented by SEQ ID NO: 1 or 2, the C-terminal domain binding to 3-HP or a derivative thereof may include an amino acid sequence represented by SEQ ID NO: 3, and the C-terminal domain contributing to stabilization of a LysR protein dimer may include an amino acid sequence represented by SEQ ID NO: 4, but embodiments of the present disclosure are not limited thereto.

"X" or "Xaa" described in SEQ ID NOs: 1 to 4 does not refer to particular amino acid, meaning that any amino acid may be used. More preferably, the LysR protein may be a LysR protein having Genbank ID represented by Table 4 and 5, but embodiments of the disclosure are not limited thereto.

Preferably, the binding site to the LysR may include two LysR protein dimers that

are bonded to each other, and may include a base sequence selected from SEQ ID NOs: 5 to 43, wherein an inverted repeat sequence and another inverted repeat sequence paired with therewith may be repeated twice in the binding site to a LysR protein, wherein the inverted repeat sequence may consist of a base sequence represented by one selected from SEQ ID NOs: 5 to 43, but embodiments of the disclosure are not limited thereto.

More preferably, the binding site to a LysR protein may consist of a base sequence represented by SEQ ID NO: 44 or 45.

"n" described in the SEQ ID NOs: 5 to 43 does not refer to a particular base, meaning the any base may be used.

The SEQ ID NO: 44 or 45 may be a promoter base sequence derived from *Pseudomonas denitrificans* ATCC13867.

Preferably, the derivative may be 3-hydroxyisobutyrate (3HIB) or 3-hydroxybutyrate (3-HB), but embodiments of the disclosure are not limited thereto.

The term "vector" as used herein refers to a self-replicating DNA molecule that is used to carry the clone gene (or other fragments of the clone DNA).

The term "expression vector" as used herein refers to a recombinant DNA molecule including a desired coding sequence and a suitable nucleic acid sequence necessary for expressing a coding sequence operably linked to a particular host organism. The expression vector may include at least one selective marker. The marker may be a nucleic acid sequence having characteristics that can be generally selected by a chemical method, and may include all genes capable of distinguishing a transformed cell from a non-transformed cell. Examples of the marker include antibiotic resistance genes, such as ampicillin, kanamycin, G418, Bleomycin, hygromycin, and chloramphenicol, but embodiments of the present disclosure are not limited thereto. Such a marker can be appropriately selected from one of ordinary skill in the art.

Hereinafter, the present inventive concept will be described below in further detail through Examples and Comparative Examples. However, such Examples are for illustrative purposes only and do not limit the scope of the present inventive concept.

<Example 1> Identification of gene expression system by 3-HP

1. Materials

A number of strains including *Achromobacter denitrificans* and *Acinetobacter*

baumannii were obtained from the Korean Culture Center of Microorganisms (KCCM). A number of strains including *Acidovorax avenae subsp.* and *Agrobacterium sp.* were purchased from the Korean Collection for Type Cultures (KCTC). A number of strains including *Alicyclophilus denitrificans* and *Anaeromyxobacter dehalogenans* were obtained from DSM in Germany. A number of strains including *Aeromonas hydrophilia* and *Pseudomonas denitrificans* ATCC13867 purchased from ATCC in the United States. A primer was synthesized by COSMO GENETECH (Seoul, Korea). 3-HP was purchased from Tokyo Kasei Kogyo (TCI America, Portland, OR) in Japan. An enzyme extract (Cat. 212750) and tripton (Cat. 211705) were purchased from Difco (Becton Dickinson; Franklin Lakes, NJ). All chemicals and enzymes not mentioned were purchased from Sigma Aldrich (St. Louis, MO).

2. 3-HP production of proliferating cells and 3-HP degradation in dormant cells

Shake flask experiments were carried out in a 250 mL non-baffled Erlenmeyer flask in a volume of 30 mL in shaking incubator at a temperature of 37°C and a stirring speed of 200 rpm. Experiments on 3-HP production by *P. denitrificans* were performed under conditions where an M9 medium having a modified volume of 30 mL was added to a 250 mL non-baffled Erlenmeyer flask for culturing in a shaking incubator at a temperature of 37°C at a stirring speed of 200 rpm. Here, compositions of the modified M9 medium for culturing a strain included 100 mM phosphate buffer (pH 7.0), 0.25 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 1.0 g/L of NaCl, 1.0 g/L of NH_4Cl , and 3-HP 25 mM.

Experiments on the dormant cells were carried out to investigate 3-HP degradation in a total of 69 microorganisms including *P. denitrificans*, and bacteria used in the experiments are shown in Table 1. To prepare active cells, 3-HP was added to a nutrient-enriched medium specified for each strain, and then, cultured in a for 250 mL non-baffled erlenmeyer flask at a volume of 50 mL. Strain culture was performed at a temperature of 37°C, and when OD_{600} of cells reached about 1 to 1.5, cells were harvested by centrifugation at a speed of 5,000 rpm for 10 minutes. The precipitated cells were washed with 100 mM phosphate buffer (pH 7.0), and resuspended with 25 ± 2 mmol/L of 3-HP in the same buffer. The above-mentioned cell harvesting, washing and resuspending procedures were performed prior to the 3-HP degradation experiments. Samples were taken periodically to investigate the concentration of 3-HP.

[Table 1]

Strains used in the present invention

Genus No.	Strain	Medium	Culture temperature	Aerobic condition	Purchase site
1	<i>Achromobacter denitrificans</i>	Nutrient medium	26 °C	Aerobic	KCCM
2	<i>Acidovorax avenaesubsp.</i>	Nutrient medium	25 °C	Aerobic	KCTC
	<i>Acidovorax sp</i>	Tryptone soya broth	28 °C	Aerobic	DSM
3	<i>Acinetobacter baumannii</i>	Nutrient medium	30 °C	Aerobic	KCCM
4	<i>Aeromonas hydrophilia</i>	Nutrient medium	30 °C	Aerobic	ATCC
5	<i>Agrobacterium sp.</i>	Nutrient medium	30 °C	Aerobic	KCTC
6	<i>Alcaligenes faecalis</i>	Nutrient medium	30 °C	Aerobic	KCCM
7	<i>Alcanivorax hongdengensis</i>	Nutrient medium	26 °C	Aerobic	KCTC
8	<i>Alicyclophilus denitrificans</i>	Nutrient medium	26 °C	Aerobic	DSM
9	<i>Alteromonas marina</i>	Marine broth 2216 (DIFCO 0791)	30 °C	Aerobic	KCCM
10	<i>Amycolatopsis sp.</i>	Nutrient medium	30 °C	Aerobic	KCTC

11	<i>Anaeromyxobacter dehalogenans</i>	<i>R2A medium</i>	28 °C	Microaerobic	DSM
12	<i>Azospirillum brasilense</i>	<i>Azospirillum medium</i>	30 °C	Aerobic	KCCM
13	<i>Azotobacter vinelandii</i>	<i>Azotobacter medium</i>	30 °C	Aerobic	KCCM
14	<i>Beijerinckia indica</i>	<i>Beijerinckia medium</i>	30 °C	Aerobic	KCTC
15	<i>Bordetella avium</i>	<i>Trypticase soy broth</i>	37 °C	Aerobic	KCCM
16	<i>Bradyrhizobium japonicum</i>	<i>Rhizobium medium</i>	26 °C	Aerobic	KCCM
17	<i>Burkholderia ambifaria</i>	<i>Trypticase soy broth</i>	28 °C	Aerobic	KCCM
18	<i>Catenulispora acidiphilia</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
19	<i>Caulobacter sp.</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
20	<i>Castellaniella defragrans</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
21	<i>Chromobacterium violaceum</i>	<i>Nutrient medium</i>	26 °C	Aerobic	ATCC
22	<i>Collimonas arenae</i>	<i>Nutrient medium with 5g/L NaCl</i>	28 °C	Aerobic	DSM
23	<i>Comamonas testosteroni</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCCM

24	<i>Corynebacterium vitaeruminis</i>	<i>Corynebacterium broth</i>	30 °C	Aerobic	KCCM
25	<i>Cupriavidus necator</i>	<i>Nutrient medium</i>	26 °C	Aerobic	KCCM
26	<i>Curvibacter gracilis</i>	<i>Peptone, yeast extract with magnesium sulfate</i>	30 °C	Aerobic	ATCC
27	<i>Delftia acidovorans</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
28	<i>Ferrimonas balearica</i>	<i>Triple-sugar-iron medium (Difco)</i>	28 °C	Aerobic	KCTC
29	<i>Glaciecola nitratreducens</i>	<i>Broth Medium Marine Broth 2216 (BD 279110)</i>	25 °C	Aerobic	KCTC
30	<i>Gordonia bronchialis</i>	<i>Trypticase soy broth</i>	28 °C	Aerobic	KCCM
31	<i>Hahella chijuensis</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
32	<i>Halomonas elongata</i>	<i>Halomonas medium</i>	30 °C	Aerobic	KCCM
33	<i>Hirschia litorea</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
34	<i>Idiomarina sp.</i>	<i>Bactomarine broth (Difco 2216)</i>	30 °C	Aerobic	KCTC
35	<i>Janthinobacterium lividum</i>	<i>Nutrient medium</i>	25 °C	Aerobic	KCTC
36	<i>Kitasatospora setae</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
37	<i>Kutzneria albida</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC

38	<i>Methylobacterium</i> <i>sp.</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
39	<i>Methylocystis sp.</i>	<i>NMS medium for Methanotrophs with 20% methane(v/v) in the air head space</i>	28 °C	Aerobic	ATCC
40	<i>Novosphingobium</i> <i>sp.</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
41	<i>Oceanimonas</i> <i>smirnovii</i>	<i>Marine Broth 2216 (BD 279110)</i>	23 °C	Aerobic	ATCC
42	<i>Paracoccus sp.</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
43	<i>Parvibaculum</i> <i>lavamentivorans</i>	<i>Peptone 10.0 g /L; NaCl 5.0 g/L; CaCl₂H₂O 0.1 g/L; Tween 80 10.0 g/L</i>	30 °C	Aerobic	KCTC
44	<i>Phenylobacterium</i> <i>kunshanensis</i>	<i>R2A medium</i>	30 °C	Aerobic	KCTC
45	<i>Photobacterium</i> <i>gaetbuleda</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
46	<i>Polynucleobacter</i> <i>necessarius</i> <i>asymbioticus</i>	<i>R2A medium</i>	28 °C	Aerobic	DSM
47	<i>Pseudoalteromonas</i> <i>carrageenovora</i>	<i>Sea water yeast peptone broth</i>	20 °C	Aerobic	KCCM
48	<i>Pseudogulbenkiania</i> <i>sp.</i>	<i>Nutrient medium</i>	37 °C	Aerobic	DSM

49	<i>Pseudomonas denitrificans</i> ATCC13867	Minimal medium	37 °C	Aerobic	ATCC
	<i>Pseudomonas knackmussii</i>	Nutrient medium	30 °C	Aerobic	DSM
	<i>Pseudomonas protegens</i>	Nutrient medium	28 °C	Aerobic	DSM
	<i>Pseudomonas fluorescens</i>	1213 King medium B	28 °C	Aerobic	ATCC
50	<i>Pseudoxanthomonas spadix</i>	R2A medium	35 °C	Microaerobic	KCTC
51	<i>Psychrobacter phenylpyruvicus</i>	Trypticase soy broth	30 °C	Aerobic	ATCC
52	<i>Ralstonia oxalatica</i>	Nutrient medium	30 °C	Aerobic	KCCM
53	<i>Rhodococcus vannieli</i>	Nutrient medium	30 °C	Aerobic	KCTC
54	<i>Segniliparus rotundus</i>	Bacto Middlebrook 7H10 medium (Difco 262710)	28 °C	Aerobic	DSM
55	<i>Shewanella oneidensis</i>	Trypticase soy broth	30 °C	Aerobic	ATCC
56	<i>Simiduia agarovorans</i>	Nutrient medium	30 °C	Aerobic	KCTC

57	<i>Sinorhizobium meliloti</i>	<i>Rhizobium medium</i>	26 °C	Aerobic	KCCM
58	<i>Sphingobium chlorophenolicum</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
59	<i>Sphingomonas wittichii</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
60	<i>Sphingopyxis alaskensis</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
61	<i>Stenotrophomonas maltophilia</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCCM
62	<i>Streptomyces nodosus</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
63	<i>Tatlockia micdadei</i>	<i>BCYE (Buffered Charcoal Yeast Extract) medium</i>	37 °C	Microaerophilic	DSM
64	<i>Thalassospira xiamenensis</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
65	<i>Variovorax paradoxus</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCTC
66	<i>Verminephrobacter eiseniae</i>	<i>R2A medium</i>	28 °C	Aerobic	DSM
67	<i>Vibrio furnissii</i>	<i>Bactomarine broth (Difco 2216)</i>	28 °C	Aerobic	KCCM
68	<i>Xanthobacter autotrophicus</i>	<i>Nutrient medium</i>	30 °C	Aerobic	KCCM

69	<i>Xanthomonas campestris</i>	Nutrient medium	26 °C	Aerobic	KCCM
	<i>Xanthomonas oryzae</i>	IFO medium 802	30 °C	Aerobic	KCCM

3. RNA extraction and reverse transcription polymerase chain reaction

An M9 medium was used for culture of a *P. denitrificans* strain (ATCC 13567), and a nutrient medium specified for each strain was used for culture of other microorganisms shown in Table 1. Then, when examining the effect of 3-HP, 25 mM of 3-HP was added to the media provided herein. all the strains were cultured in a shaking incubator at a temperature of 37°C at a stirring speed of 200 rpm under an aerobic condition, and cells were harvested when the cultured cells reached an exponential growth phase. After the cells were harvested in an amount of about 5×10^8 , centrifugation was performed thereon at 5,000 g for 10 minutes. Then, 500 µl of RNA later solution (Ambion,, UK) was immediately added to the precipitated cells, and then, the mixed solution was resuspended. RNA was extracted by using a total RNA isolation kit (Macherey-Nagel, Germany). 1 µg of total RNA was used for synthesis of 20 µl first-strand cDNA, and a SuperScript III first-strand synthesis system provided by Invitrogen was used for synthesis of cDNA.

A reverse transcription polymerase chain reaction was performed by using a SYBR green step with a One Real Time PCR system (Applied Biosystems, USA). In a reaction solution (20 µL) for the reverse transcription polymerase chain reaction, 300 ng of cDNA, 10µL 2×Power SYBR Green PCR Master Mix (Applied Biosystems, UK), 5 pmol of forward and reverse primers, and DEPC treated water were contained. Conditions for the reverse transcription polymerase chain reaction were determined as follows: denaturation, 1 cycle of 95°C for 30 seconds; amplification, 40 cycles of 95°C for 15 seconds, 62°C for 30 sections, and 72°C for 30 seconds. Prior to performing the reverse transcription polymerase chain reaction, PCR was performed to confirm the effect of the primers used in the experiments for measurement of mRNA levels, and relative quantification for mRNA levels was calculated according to the $\Delta\Delta CT$ method.

4. Gene cloning of LysR protein, protein production, and separation-purification

In the case of *P. denitrificans*, two operons, i.e., 3HPDH (hereinafter, referred to as C3 system) and 3HIBDH-IV (hereinafter, referred to as C4 system), that are involved in the 3-HP degradation were present, as well as LysR proteins, such as C3-LysR and C4-LysR, that regulate transcription of the operons. Among the proteins, protein production was attempted for C4-LysR. *E. coli* BL21 (DE3) was used as a host and *E. coli* strain Top10 was used for cloning and maintaining of plasmids. C4 LysR genes were amplified in the *P. denitrificans* genome by PCR, cloned into a pET30b(+) plasmid, and *E. coli* strain Top10 was added thereto to confirm sequences, and then, *E. coli* BL21 (DE3) was added thereto. For protein purification, a His tag was labeled at a C-terminus site. To express the LysR protein in an active soluble form, the LysR protein was co-expressed along with several chaperone plasmids, such as pG-KJE8, pGRO7, pG-TF2, and pTF-16. For use as a medium, an LB medium appropriately supplemented with kanamycin, chloramphenicol, L-arabinose, or the like was used and cultured under aerobic conditions. When the cell concentration reached OD of 0.6, 0.1 mM of IPTG was added to induce production of the LysR protein. For water-soluble expression of the LysR protein, various culture conditions were examined, and eventually, the LysR protein was cultured at a temperature of 25°C at a speed of 150 rpm for 10 hours. The cultured cells were obtained by centrifugation, washed with 100 mM (pH 7) phosphate buffer, resuspended in binding buffer, and then, disrupted by French Press. Afterwards, the resulting cells were subjected to centrifugation again, and solid and undisrupted cells were removed while the solution was purified by using a Ni-affinity column. followed by being stored in a 20% glycerol solution at a temperature of 80°C.

5. Measurement of electrophoretic mobility shift assay (EMSA) for analyzing protein-DNA binding under *in vitro* conditions

To study binding between the separated C4-LysR gene and a promoter region thereof under *in vitro* conditions, a DNA fragment of the promoter region was synthesized (see FIG. 7). Three types of fragments were synthesized: first, a fragment (designated as F12) including both O1 and O2 operators, expecting that a transcription

regulatory protein binds to the entire DNA fragments between genes, C4-LysR and mmsadh; second, a fragment (designated as F12M) including a part of the O1 operator; third, a fragment (designated as F1M2) including a part of the O2 operator. The EMSA experiments were performed by using a molecular probes fluorescence-based mobility shift assay kit (fluorescence-EMSA) manufactured by Invitrogen Company. First, a DNA fragment of the promoter region was purified by a glass fiber column, mixed with a LysR protein purified with binding buffer, and a reaction was allowed at room temperature for 30 minutes. Afterwards, the mixture was loaded onto a 6% non-denaturing polyacrylamide gel, and developed in TBE buffer (pH 8) at 220 V for 30 minutes. Then, to confirm DNA bands after fixing the gel, SYBR Green EMSA staining was performed thereon, followed by quantification of band intensity by a gel documentation system (Bio-Rad). For observation of the proteins, the DNA-protein band was stained with SYPRO Ruby EMSA.

6. Analysis method

The cell concentration was measured by using a double beam spectrophotometer (Lambda 20, Perkin-Elmer, Norwalk, CT) with a cuvette having a length of 10 mm. The 3-HP concentration was measured by using a high performance liquid chromatography (HPLC) (Raj et al, 2008). For preparation of a sample, a sample taken for HPLC analysis was centrifuged at 10,000×g for 10 minutes to remove cell precipitates, and a tuffryn membrane filter (Acrodisc; Pall Life Sciences, Port Washington, NY). A column used for HPLC analysis had a size of 300 mm × 7.8 mm Aminex HPX-87H (Bio-Rad, USA) and 2.5 mmol/L of H₂SO₄ was used as a mobile phase at a temperature of 65°C.

7. Results

(1) Screening of 3-HP inducible promoter in *P. denitrificans*

3-HP is a carbon compound rarely present in natural environments, and there are few reports on its use as a carbon substrate or its biological degradation. However, recently, the inventors of the present invention found that *P. denitrificans* degraded 3-HP rapidly in both a growth phase and a non-growth phase. During the growth phase of the cells, *P. denitrificans* was able to use 3-HP as a sole carbon source and an energy source (FIG. 1A). During non-growth phase of the cells, *P. denitrificans* showed

characteristics of degrading 3-HP in the presence of oxygen (FIG. 1B). Biological degradation of 3-HP is known to use a reducing or oxidative pathway (FIG. 2). Through genome analysis and metabolite analysis using gas chromatography-mass spectrometry, it was estimated that the 3-HP degradation in *P. denitrificans* utilized an oxidation pathway. According to this pathway, two enzymes, presumably 3-hydroxypropionated dehydrogenase (3HPDH) and (methyl)malonate-semialdehyde dehydrogenase (MMSADH), sequentially converted 3-HP to methylmalonate semialdehyde and methylmalonate semialdehyde to acetyl-CoA (FIG. 2). In addition to 3HPDH, many 3-hydroxybutylate dehydrogenases assumed to be capable of degrading 3-HP and 3-hydroxy acid similar to 3-HP were confirmed in *P. denitrificans*. In this regard, the expression of various enzymes having activity against 3-HP may be possible induced by 3-HP. The mRNA levels of three genes (*3hpdh*, *3hibdhIV*, and *mmsadh*) assumed to be 3-HP catabolic genes were compared by RT-PCR (FIG. 3). Here, *rpoD*, which is known to encode sigma factor 70 and is known as a housekeeping gene, was used as a reference gene. As a result, it was interesting to observe that the expression of genes, assumed to be related to the 3-HP degradation, was significantly increased by 3-HP. When the cells were exposed to 3-HP, *3hpdh* showed a 46-fold increase, *3hibdhIV* showed a 146-fold increase, and *mmsadh* showed a 137-fold increase. As such, up-regulation of the genes can be explained by the nature of the promoters of genes induced by 3-HP.

The expression of the genes, i.e., *3hpdh*, *3hibdhIV*, and *mmsadh*, was similar with 3-HP in size, but the possibility of being amplified by other compounds having different structures from the genes above was also examined (FIGS. 4 and 5). The genes were all amplified by 3-HP, 3-hydroxyisobutyrate (3HIB), and 3-hydroxybutyrate (3-HB). However, the amplification of the genes was not induced by lactic acid, acetic acid, propionic acid, 1,3-propanediol, and 2,3-butandiol. In particular, the amplification of the genes was induced by L-valine, and it is assumed that the induction is due to conversion from L-valine to 3-HIB in a process of metabolism. In this regard, it is determined that the transcriptional regulatory proteins were specifically reactive to 3-HP, 3-HIB, 3-HB, or the like.

(2) Analysis of 3-HP inducible gene expression system

LysR-type transcriptional regulators (LTTRs) are known as transcriptional

activators that regulate the same catabolic pathway as the aromatic compounds. In general, genes encoding the LTTRs are located in front of a population of genes involved in degradation of aromatic compounds and regulate the compound degradation. To identify the 3-HP degradation pathway, the gene structure analysis of operons related to 3HPDH and 3HIBDH-IV of *P. denitrificans* was performed. As a result, it was confirmed that the LTTRs were located in a similar gene sequence in the front part of the 3-HP degrading genes (FIG. 6). That is, it showed possibility that the expression of the 3-HP degrading genes may be related to the LysR protein in *P. denitrificans*. In particular, the genes (i.e., *mmsadh*, *3hibdh4*, and *3hpdh*) whose transcription was regulated by a *lysR* gene and a gene binding to the LysR protein (hereinafter, LysR binding to a gene of 3-hydroxyisobutyrate dehydrogenase which is a C4 compound is designated as C4-LysR, and LysR binding to a gene of 3-HP dehydrogenase which is a C3 compound is designated as C3-LysR) were located in an opposite orientation, two specific binding sites, i.e., a regulatory binding site (RS) having a conservative T-N11-A motif and an activation binding site (AS) adjacent to a 35 RNA polymerase binding site, were confirmed (FIG. 6). In addition, it was confirmed that the RS and AS overlap over positions 10 and -35 of the genes encoding the LysR protein. In this regard, it is assumed that the expression of the *lysR* gene is suppressed by an expression product, LysR.

More detailed analysis of the C4 LysR inducible promoter present in *P. denitrificans* was performed. O1 and O2 operators between a *lysR* gene and a *mmsadh* gene were each located at positions -58 and -9 relative to a transcription start site of the *mmsadh* gene, and each had an inverted repeat (FIG. 7). The inverted repeat sequence or the palindromic structure was often found in an operator site of prokaryotes, and is known to be a binding site for the transcriptional regulatory proteins. A distance between O1 and O2 sites was about 50 bp, which corresponds to 5 turns of helical DNA, and thus, it is assumed that the LysR protein can bind in the same direction when binding to O1 and O2 sites. The O1 site dyad consists of 9 bases at an interval of 15 bp, but since there was only one mismatch, it was found that the O1 site dyad was highly symmetrical. Meanwhile, the inverted repeat sequence of the O2 site also consists of 9 bases at a relatively short interval of 11 bp. 6 out of 9 was mismatched, and that is, the symmetry of the O2 site was weak. As a result of examining homology of four palindromic fragments present in the O1 and O2 operators, TACGTGTAA was found. The bases at positions 3,

4, and 5 (bold letters) were conserved in all fragments, and the bases at positions 2 and 8 (underlined) were conserved in three fragments, suggesting that these bases play an important role in binding to the C4 LysR protein.

The effect of the O1 and O2 operators on biosynthesis of the C4-LysR protein and the *mmsadh* expression was examined by using a green fluorescent protein (GFP) as a reporter (Table 2). In Table 2, the effect of the C4-LysR protein and the O1 and O2 operators on the expression of the C4-LysR and the *mmsadh*. The relative size of the GFP was shown relative to the wild type in the absence of 3-HP. the C4-LysR protein was either not present or was produced by a constitutive promoter, and a plasmid was prepared to control the expression of the GFP upon the existing promoter having the O1 and O2 operators. Then, the experiment was carried out by inserting the prepared plasmid into a host of *P. denitrificans* from which genes between the C4-LysR and the *mmsadh* was deleted. Accordingly, the expression of the GFP was suppressed by the C4-LysR protein itself. That is, when the C4-LysR is expressed, the GFP expression was reduced by more than 10-fold. In addition, the expression regulation was also constant regardless of the presence of 3-HP. In this regard, it was confirmed that the transcription of C4-LysR mRNA was negatively regulated by the C4-LysR protein. This experiment was repeated by using a promoter that randomized the O1 and O2 operators to eliminate the symmetrical dyad. As a result, in the case where the O1 or O2 operator site was randomized, the GFP expression was not regulated by the C4-LysR protein, referring that the C4-LysR protein in the *P. denitrificans* strain was negatively regulated by the strain itself.

Meanwhile, the effect of the O1 and O2 operators on the *mmsadh* gene expression was examined in a similar manner. That is, the C4-LysR protein was constitutively expressed, and a plasmid was prepared so that GFP can be located after a promoter having O1 and O2 promoters. Here, an O1 or O2 operator was mutated so that the symmetrical dyad of an O1 or O2 site was randomized. As a result, when the O1 or O2 site was mutated, the phenomenon of up-regulation of transcription by 3-HP disappeared. That is, it means that the O1 and O2 operators are all essential sites for up-regulation of the expression by 3-HP. Thus, it has been found that the promoter of the present invention is a promoter requiring the presence of the O1 and O2 operators.

[Table 2]

Genes	3-HP	wildtype	Δ C4-LysR	O1	O2	O1 & O2
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tested ¹	addition ²			mutation ³	mutation ³	mutation ³
C4-LysR	w/o 3-HP	1	10	10	1	10
C4-LysR	w 3-HP	1	10	10	1	10
mmsadh	w/o 3-HP	1	3	3	3	3
mmsadh	w 3-HP	55	3	3	3	3

¹GFP was used as a reporter protein, and that is, a plasmid to which a GFP gene was inserted at a C4-LysR position or a mmsadh position was used.

²3-HP was added in a concentration of 25 mM.

³When O1 and O2 were randomized, C4-LysR used a promoter expressed weakly but constitutively.

Meanwhile, the LTTRs protein was known to consist of an N-terminal which is a DNA binding domain (helix-turn-helix motif), a C-terminal which is a substrate binding domain, and a linker connecting the N-terminal and the C-terminal. The LysR protein forms a homodimer to bind RS and AS, and when an effector molecule (3-HP in the case of the present invention) binds each of the LysR proteins, due to protein-protein interaction between two LTTR dimers the LTTR forms a tetramer, which in turn causes a structural change in DNA associated with the LysR protein. A derivative specifically binding to the LTTR tetramer is known to cause a structural changes of the LysR protein, and subsequently alter the structure of the promoter region DNA, thereby ultimately helping binding of a RNA polymerase to the promoter (FIG. 8).

When examining the structure of the C4-LysR protein which has been emphasized in the present invention, it was also resulted that the C4-LysR protein consists of an N-terminal which is a DNA binding domain (helix-turn-helix motif), a C-terminal which is a substrate binding domain, and a linker connecting the N-terminal and the C-terminal (FIG. 9). It was found that four amino acids, i.e., Thr-31, Arg-34, Glu-40, and Leu-47, played a key role in the DNA binding domain, and in the substrate binding domain, amino acids that are important for binding 3-HP and amino acids that play an important role in the dimer formation have been identified. Among these amino acids, amino acids that play an important role in the binding to 3-HP were Asp-159, Thr-160, Pro-237, and Phe-239, and amino acids that play an important role in the dimer

formation were Ala-60, Gly-91, Arg-94, Pro-118, and Glu-137. In particular, amino acids that play an important role in the dimer formation were all located on the protein surface, except for Pro-118.

To confirm that the LysR protein is a transcriptional regulator, genes encoding the C3 and C4 LysR proteins were removed from *P. denitrificans* chromosomes, and then, transcription induction of transcriptionally regulated genes (*mmsadh*, *3hibdhIV*, and *3hpdh*) was examined. First, when the C4 LysR gene was removed, regardless of the presence of 3-HP, the expression of the *mmsadh* and *3hibdhIV* genes was low, and addition of 3-HP did not increase the expression. When the C3 LysR gene was removed, the expression of the *3hpdh* gene was not amplified by addition of 3-HP. However, when C3 LysR or C4 LysR gene was expressed again by using a plasmid in strains from which the C3 LysR or C4 LysR gene was removed (complementation experiment), the gene expression was amplified and restored to the same level as that of the wild type strain upon 3-HP. In this regard, it was confirmed that the C3 LysR protein and the C4 LysR protein were each a transcriptional regulatory protein that regulates the expression of the *mmsadh*, *3hibdhIV*, and *3hpdh* in cells.

(3) *In vitro* examination of binding characteristics of C4-LysR protein and O1 and O2 operator sites

To examine *in vitro* characteristics of the C4-LysR protein, the C4-LysR protein having a histidine tag at the C-terminal was produced in *E. coli* and purified therefrom. First, the His tag was labeled at the C-terminal and the N-terminal, and then, the above-mentioned complementation experiment was carried out. As a result, both cases showed the same performance as the wild type LysR having no His tag. Accordingly, among two recombinant LysR proteins, only the C-His tagged LysR was subjected to biochemical experiment. The recombinant LysR was mostly expressed in an insoluble form in *E. coli*. Here, detailed optimization experiment for the expression conditions (temperature, pH, medium composition, IPTG concentration, etc) was also carried out. In addition, the influence of the various chaperon proteins also carried out. As a result, a sufficient amount of water-soluble C4-LysR was able to be produced from *E. coli* at a comparatively low temperature of 25°C under common conditions with 0.1 M IPTG, an LB medium, and GroEL-ES chaperon (FIG. 10). The purely separated proteins were identified by SDS-PAGE. Here, the size of the C4-LysR was estimated to be about 33

kDa, which was in good match with the predicted size of the gene. However, the result of native gel electrophoresis showed that a dimer was formed in a buffer solution when the protein concentration was high (FIG. 11).

The binding between the genetically recombinant C4-LysR and the promoter DNA through EMSA experiments (FIG. 12). For the EMSA experiments, three DNA fragments were synthesized. F12 (135 bp) is a DNA fragment serving as an entire promoter region between C4-Lys and *mmsadh* genes and including both O1 and O2 operators; F12M (135 bp) is a DNA fragment including only the O1 operator region; and F1M2 (135 bp) is a DNA fragment including only the O2 operator region. For use as a control group, one fragment was synthesized, wherein the one fragment had the same size as F12, but was designed not to have a palindrome structure by randomizing both O1 and O2 regions. The C4-LysR protein was reacted with the DNA fragments (F12, F12M, and F1M2) and electrophoresis was carried out thereon. As a result, it was observed that the mobility of the DNA fragments decreased (FIG. 12), meaning that the C4-LysR protein binds to the DNA fragments under *in vitro* conditions. Such a decrease in the mobility was not observed in the control fragment. That is, the binding between C4-LysR and the DNA fragment can be achieved in the presence of base sequences of the DNA fragments, and more particularly, sequences of the O1 and O2 operators. Among the three fragments, F12 showed the highest affinity to the LysR protein, followed by F12M and F1M2. The EMASA experiments were repeated in the presence of 3-HP, and the presence of 3-HP changed affinity. That is, F12 had increased affinity, F1 had barely changed affinity, and F2 had slightly decreased affinity.

When F12 had higher affinity than F12M or F1M2, it means that the binding of O1 and O2 of the LysR is cooperative. That is, when the LysR protein binds to the O1 site having high affinity, the binding to the O2 site is promoted. The results of the EMSA experiments showed that F12 always had low mobility, compared to F12M or F1M2. In addition, at a low concentration of the LysR, the band having only one shift was shown, meaning that there is always more LysR proteins bound to F12. That is, when the LysR binds to F12, it means that the LysR binds to both O1 and O2 sites. F12 having higher affinity than F12M or F1M2 and having lower mobility than F12M or F1M2 shows the fact that the binding of the LysR protein to the O1 and O2 sites in F12 was cooperative. From these results of the EMSA experiments, the important properties of the 3-HP inducible promoter can be summarized as follows: (i) the promoter is characterized by having two

or more inverted repeat sequence pairs, each consisting of 9 bases, and providing a binding site of the LysR protein; (ii) the LysR protein is able to bind to the promoter regardless of the binding with an inducer molecule, but the improvement in transcription efficiency is only shown by the LysR protein associated with an inducer molecule, wherein the inducer molecule may be 3-HP or 3-HIB and 3-HB that are structurally similar with 3-HP; (iii) the promoter provides a site where two LysR protein dimmers are bound, wherein the binding is cooperative each other; (iv) the promoter provides a structure that can interact with the LysR protein when the RNA polymerase binds thereto; and (v) the promoter includes the O1 and O2 operators, wherein each operator consists of 9 bases and has well conserved inverted repeat sequences.

(4) Virtual search of 3-HP inducible gene expression system and analysis of characteristics of the expression system

To find out a new 3-HP inducible gene expression system, putative LysR regulatory genes and *mmsadh*, *3hipdh*, *3hpdh*, and the like were screened from various microorganisms, based on the gene homology of *P. denitrificans*. The BlastP similarity search results show that similar 3-HP inducible gene expression systems are present in various microorganisms, and among well-known microorganisms, the presence of a population of genes assumed to be 3HIBDH (C4 system) and 3HPDH(C3 system) was discovered (FIG. 13 and Tables 4 and 5). As a result of structure analysis and comparison of the genes, it was confirmed that each microorganism had various genetic structures.

In a total more than 150 microorganisms, the 3-HP inducible gene expression systems were discovered, and depending on the presence of the C3-LysR and the C4-LysR and the gene arrangement characteristics, the gene expression systems were divided into a total of 16 groups. Among the groups, 9 groups had both C4 the C3 systems, and 7 groups had only the C4 system. A group having only the C3 system was not discovered. In addition, the case of the C3 system, a gene encoding the LysR protein and a gene regulating the expression thereof by the LysR protein were all characterized in that the direction of transcription was opposite. In the case of the C4 system, a gene encoding the LysR protein and a gene regulating the expression thereby of the LysR were mostly characterized in that the direction of transcription was opposite. However, in the microorganisms belonging to Groups 15 and Group 16, the direction of transcription

was the same.

The characteristics of the promoter sequences that are reactive to the C3 and C4 LysR proteins were analyzed. In the same manner as in *P. denitrificans*, two tandem operator sites (designated as O1 and O2) were present. Two operators had a dyad symmetry, wherein each of the inverted repeats consists of 9 bases. Here, the distance between the centers of the dyad symmetry was 50 bases, so that when the LysR protein binds to the O1 and O2 operator sites, the LysR protein was spaced to bind in the same direction. In addition, the 9 bases within the inverted repeat sequence was well conserved in many microorganisms.

The palindromic binding site to the LysR that is reactive to 3-HP was conserved in various microorganisms. However, depending on species, only the O1 operator, i.e., a primary/repression binding site (PBS/RBS), was conserved (Table 3). In addition, in all species, PBS including the conserved T-N_{11/12}-A motif and having high affinity was present adjacent to positions -65 and -75 relative to a transcription start site (TSS). That is, the O2 operator, i.e., a secondary/activation binding site (SBS/ABS) motif, had low sequence conservation, so that *in silico* prediction of the ABS motif is complex and difficult. The RBS and ABS sites were each reported to play a key role in autogenic inhibition and activation. Despite having a common function as proteins that are reactive to 3-HP, the 3-HP-LysR protein had low sequence similarity among other genus and had high sequence similarity within the same genus. Therefore, it is not logically wrong that the DNA sequence of the operator region to which the LysR protein binds is different among different genus. Here, transcription factors (promoters; -10 and -35 regions) were predicted by using BPROM and BDGP tools.

The 9 base sequences shown in Table 3 refer to the conserved regions corresponding to the binding sites to the LysR that is reactive to 3-HP in each genus, wherein the capital letters are bases that appear to be conserved in all target subjects.

[Table 3]

Genus	Repressive Binding Site (T-N _{11/12} -A motif)	# Representatives
<i>Achromobacter</i>	CACAcATct	4
<i>Acidovorax</i>	TcGCACAcC	3

<i>Acinetobacter</i>	<i>GTcaAaGAT</i>	7
<i>Advenella</i>	<i>TTGCAaATT</i>	4
<i>Aeromonas</i>	<i>GGGcAaaCA</i>	2
<i>Alcaligenes</i>	<i>CACaAcATct</i>	5
<i>Alcanivorax</i>	<i>AgCAGCATG</i>	2
<i>Alicyclophilus</i>	<i>TGCaAAGcc</i>	2
<i>Anaeromyxobacter</i>	<i>GGGaCGacG</i>	3
<i>Azospirillum</i>	<i>gTGCCcGCG</i>	4
<i>Azotobacter</i>	<i>gTatcGAGC</i>	4
<i>Beijerinckia</i>	<i>ATTgcCgTG</i>	3
<i>Bordetella</i>	<i>gTTtCGTtG</i>	6
<i>Bradyrhizobium</i>	<i>AtATATcaG</i>	3
<i>Brucella</i>	<i>AaaAAtGCa</i>	3
<i>Burkholderia</i>	<i>GCCTACacT</i>	16
<i>Corynebacterium</i>	<i>CACCTtTgC</i>	6
<i>Cupriavidus</i>	<i>AGTtCAgcG</i>	3
<i>Delftia</i>	<i>GCAAAAacg</i>	3
<i>Ferrimonas</i>	<i>GCGGTTTTa</i>	2
<i>Glaciecola</i>	<i>TgAaTtGAC</i>	3
<i>Gordonia</i>	<i>GAaaCCGGC</i>	2
<i>Halomonas</i>	<i>tACACacAA</i>	3
<i>Janthinobacterium</i>	<i>TtCGcATTa</i>	3
<i>Marinobacter</i>	<i>CAgaAgGcT</i>	2
<i>Methylocystis</i>	<i>CGAtCgACC</i>	2

<i>Phenylobaculum</i>	<i>GTcCCGctC</i>	2
<i>Pseudomonas</i>	<i>TTGCAcatC</i>	24
<i>Ralstonia</i>	<i>GCctACacT</i>	5
<i>Shewanella</i>	<i>gTTcGcgTA</i>	6
<i>Sinorhizobium</i>	<i>TcGgAAaTT</i>	2
<i>Sphingobium</i>	<i>CgcACaAcC</i>	2
<i>Stenotrophomonas</i>	<i>GgcCaGATT</i>	2
<i>Tistrella</i>	<i>CCGGcgGcG</i>	3
<i>Variovorax</i>	<i>gTcTATTgT</i>	2
<i>Verminephrobacter</i>	<i>CgTGgcCGA</i>	2
<i>Vibrio</i>	<i>TGcaCcgTT</i>	6
<i>Xanthobacter</i>	<i>CTgtGCACa</i>	2
<i>Xanthomonas</i>	<i>GcgGTGGgC</i>	6

Representatives: The number of species identified as having the same repressive binding site (RBS) within the genus.

[Table 4]

Comparison of enzyme protein sequence homology for C4-LysR, MMSADH, and 3HIBDH

Enzyme Source	C4-LysR		MMSADH		3HIBDH		Genbank ID
Enzyme Source	Size (AA)	Identity (%)	Size (AA)	Identity (%)	Size (AA)	Identity (%)	C4-LysR MMSADH 3HIBDH
<i>Achromobacter</i> sp.	306	47	497	67	296	56	WP_013392250.1 WP_020924676.1 WP_046807163.1

<i>Acidovorax</i> <i>avenae</i> subsp.	295	59	507	82	299	54	WP_019701544.1 WP_019701545.1 WP_019701549.1
<i>Acidovorax</i> sp.	301	60	507	82	296	55	WP_005799303.1 WP_008905850.1 WP_026437393.1
<i>Acinetobacter</i> <i>baumannii</i>	293	49	505	70	296	59	WP_005014261.1 WP_039237888.1 WP_005025914.1
<i>Aeromonas</i> <i>hydrophilia</i>	304	36	503	58	306	55	WP_029302009.1 WP_042863805.1 WP_017784754.1
<i>Agrobacterium</i> sp.	293	37	518	47	294	45	NA
<i>Alcaligenes</i> <i>faecalis</i>	297	45	497	60	298	55	WP_026483089.1 WP_045930222.1 WP_026483274.1
<i>Alcanivorax</i> <i>hongdengensis</i>	302	39	498	56	287	48	WP_008927645.1 WP_008929937.1 WP_040297229.1
<i>Alicyclophilus</i> <i>denitrificans</i>	304	58	505	81	298	53	WP_013519376.1 WP_013519377.1 WP_013519381.1
<i>Alteromonas</i> <i>marina</i>	294	35	496	48	291	62	WP_039223538.1 WP_039216373.1 WP_039223543.1

<i>Anaeromyxobacter</i> <i>dehalogenans</i>	313	31	491	53	293	29	WP_012631783.1 ABC82015.1 WP_011419642.1
<i>Azospirillum</i> <i>brasiliense</i>	291	33	499	51	296	53	EZQ04117.1 WP_014241748.1 WP_035679372.1
<i>Azotobacter</i> <i>vinelandii</i>	296	72	501	92	297	79	WP_012699721.1 WP_012699726.1 WP_012699724.1
<i>Beijerinckia</i> <i>indica</i>	301	43	509	50	295	52	WP_012383627.1 WP_012383190.1 WP_012383623.1
<i>Bordetella avium</i>	307	48	497	66	294	58	WP_012416822.1 WP_012416824.1 WP_012417430.1
<i>Bradyrhizobium</i> <i>japonicum</i>	302	42	498	49	296	50	WP_024338218.1 WP_024338217.1 WP_028153398.1
<i>Burkholderia</i> <i>ambifaria</i>	319	47	509	74	300	65	WP_012365776.1 WP_012366631.1 WP_006761413.1
<i>Catenulispora</i> <i>acidiphila</i>	296	35	504	42	301	41	NA
<i>Caulobacter sp.</i>	295	31	498	45	295	43	NA
<i>Castellaniella</i>	303	46	497	64	297	59	WP_043685951.1

<i>defragrans</i>							WP_043680927.1 WP_043682533.1
<i>Chromobacterium violaceum</i>	305	41	500	79	296	58	WP_043617011.1 WP_045051895.1 WP_043613761.1
<i>Collimonas arenae</i>	319	47	502	67	297	54	AIY40998.1 WP_038487725.1 WP_038487728.1
<i>Comamonas testosteroni</i>	300	54	507	83	298	52	WP_034389635.1 WP_003075837.1 WP_043003783.1
<i>Corynebacterium vitaeruminis</i>	304	28	504	51	291	42	WP_025251982.1 WP_025251535.1 WP_025251536.1
<i>Cupriavidus necator</i>	308	40	507	73	296	66	WP_042881289.1 WP_042878263.1 WP_042878261.1
<i>Carvibacter gracilus</i>	296	60	505	82	294	54	WP_027474562.1 WP_027474565.1 WP_027474567.1
<i>Delftia acidovorans</i>	300	54	507	82	298	53	WP_034393435.1 WP_012205523.1 WP_016453478.1
<i>Ferrimonas balearica</i>	284	25	497	55	296	51	ADN76259.1 WP_013344534.1

							WP_013344538.1
<i>Glaciecola</i> <i>nitratireducens</i>	281	28	496	56	295	47	WP_014109619.1 WP_014108982.1 WP_014108979.1
<i>Gordonia</i> <i>bronchialis</i>	298	32	513	48	289	46	WP_041920477.1 WP_012835581.1 WP_012835579.1
<i>Hahella chejuensis</i>	302	28	498	51	296	51	NA
<i>Halomonas</i> <i>elongata</i>	315	44	499	67	300	53	WP_013331269.1 WP_013331270.1 WP_013332181.1
<i>Hirschia</i> sp.	294	37	498	43	293	45	NA
<i>Idiomarina</i> sp.	312	28	499	57	297	52	WP_007420015.1 WP_034729012.1 WP_007419652.1
<i>Janthinobacterium</i> <i>lividum</i>	305	46	502	75	297	53	WP_034757572.1 WP_034778805.1 WP_034757584.1
<i>Kitasatospora</i> <i>setae</i>	304	31	508	43	298	40	NA
<i>Kutzneria albida</i>	300	35	501	45	284	44	NA
<i>Methylobacterium</i> sp.	302	41	499	47	297	47	NA
<i>Methylocystis</i> sp.	294	30	498	48	295	46	WP_036241816.1 WP_036286001.1

							WP_036289118.1
<i>Novosphingobium</i> <i>sp.</i>	316	39	499	45	289	45	NA
<i>Oceanimonas</i> <i>smirnovii</i>	288	28	497	58	297	47	WP_019933245.1 WP_019933168.1 WP_019933171.1
<i>Paracoccus sp.</i>	297	38	533	46	302	45	NA
<i>Parvibaculum</i> <i>lavamentivorans</i>	304	30	500	52	296	57	WP_041536697.1 WP_041536463.1 WP_012111823.1
<i>Phenylobacterium</i> <i>koreense</i>	282	32	498	52	298	49	WP_041374440.1 WP_012520768.1 WP_012522231.1
<i>Photobacterium</i> <i>gaetbuleda</i>	303	26	502	53	303	44	NA
<i>Polynucleobacter</i> <i>necessarius</i> <i>asymbioticus</i>	291	49	500	79	298	66	ABP34774.1 ABP34773.1 ABP34771.1
<i>Pseudoalteromona</i> <i>s carrageenovora</i>	299	29	496	55	299	52	WP_009840151.1 WP_010381506.1 WP_033103466.1
<i>Pseudogulbenkiani</i> <i>a sp.</i>	320	46	500	79	298	59	WP_008953966.1 WP_008954515.1 WP_014086932.1
<i>Pseudomonas</i>	298	100	501	100	291	100	WP_015477414.1

<i>denitrificans</i> ATCC13867							WP_015477415.1 WP_015477416.1
<i>Pseudomonas</i> <i>knackmussii</i>	298	95%	504	93	291	92	WP_043252263.1 WP_043252261.1 WP_043252259.1
<i>Pseudomonas</i> <i>protegens</i>	316	45	508	73	295	62	WP_041751937.1 WP_011059111.1 WP_015634046.1
<i>Pseudomonas</i> <i>fluorescens</i>	315	45	505	73	295	60	WP_034128788.1 WP_046055588.1 WP_034128786.1
<i>Pseudoxanthomonas</i> <i>spadix</i>	297	27	501	79	297	57	WP_014159583.1 WP_014159749.1 WP_014159753.1
<i>Psychrobacter</i> <i>phenylpyruvicus</i>	302	27	495	71	314	52	WP_028859590.1 WP_028859166.1 WP_028859170.1
<i>Ralstonia oxalatica</i>	298	30	515	73	301	65	NA
<i>Rhodocyclomicrobium</i> <i>vannielli</i>	296	30	496	48	296	48	NA
<i>Segniliparus</i> <i>rotundus</i>	300	25	509	51	300	46	WP_013137524.1 WP_013137611.1 WP_013137610.1
<i>Shewanella</i> <i>oneidensis</i>	291	24	499	55	300	51	WP_011072126.1 WP_011071828.1

							WP_011071832.1
<i>Simiduia</i> <i>agarivorans</i>	297	29	505	55	296	47	NA
<i>Sinorhizobium</i> <i>meliloti</i>	315	40	498	50	298	52	WP_018099720.1 WP_027990465.1 WP_027991426.1
<i>Sphingobium</i> <i>chlorophenolicum</i>	292	43	499	49	294	48	WP_037446180.1 WP_037456635.1 WP_037446174.1
<i>Sphingomonas</i> <i>wittichi</i>	325	43	503	44	296	46	NA
<i>Sphingopyxis</i> <i>alaskensis</i>	310	36	497	45	291	44	NA
<i>Stenotrophomonas</i> <i>maltophilia</i>	289	32	501	80	296	57	WP_044569661.1 WP_019185504.1 WP_005407687.1
<i>Tatlockia micdadei</i>	293	22	499	45	295	47	WP_045099921.1 WP_045098082.1 WP_045098081.1
<i>Thalassospira</i> <i>xiamenensis</i>	295	38	499	45	296	48	NA
<i>Variovorax</i> <i>paradoxus</i>	298	60	507	82	300	55	WP_018905631.1 WP_012748355.1 WP_012748351.1
<i>Verminephrobacter</i>	298	26	507	78	299	51	WP_011807819.1

<i>eiseniae</i>							WP_011811243.1 WP_011811250.1
<i>Vibrio furnissii</i>	304	25	520	57	300	49	WP_014257826.1 WP_041943477.1 WP_004727845.1
<i>Xanthobacter autotrophicus</i>	307	44	498	50	299	51	WP_012114222.1 WP_012114221.1 WP_041575420.1
<i>Xanthomonas campestris</i>	301	29	501	77	295	58	WP_044099340.1 WP_003488244.1 WP_003488236.1
<i>Xanthomonas oryzae</i>	304	27	501	77	300	57	WP_024711534.1 WP_044750113.1 WP_024744051.1

[Table 5]

Comparison of enzyme protein sequence homology for C3-LysR and 3HPDH

Enzyme Source	C3-LysR		3HPDH		Genbank accession no
	Size (AA)	Identity (%)	Size (AA)	Identity (%)	C3-LysR 3HPDH
<i>Achromobacter sp.</i>	306	45	547	65	WP_006223849.1 WP_006225226.1
<i>Acidovorax avenae</i>	295	45	564	59	WP_013595009.1 WP_013592873.1

<i>Acidovorax</i> sp.	301	44	556	61	WP_020229646.1 WP_020229941.1
<i>Acinetobacter baumannii</i>	293	40	534	39	WP_000861803.1 WP_032868291.1
<i>Alcaligenes faecalis</i>	297	42	555	64	WP_026483089.1 ADT64694.1
<i>Alcanivorax hongdengensis</i>	290	27	531	42	WP_008929468.1 WP_008927596.1
<i>Alicyclophilus denitrificans</i>	304	44	560	60	WP_013519376.1 WP_013721241.1
<i>Alteromonas marina</i>	294	36	550	43	WP_039223538.1 WP_039222748.1
<i>Azospirillum brasilense</i>	391	35	537	36	WP_040137273.1 WP_035676856.1
<i>Bordetella avium</i>	307	45	540	66	WP_012416822.1 WP_012415815.1
<i>Bradyrhizobium japonicum</i>	302	41	539	57	WP_024338218.1 WP_028143201.1
<i>Burkholderia ambifaria</i>	323	38	567	60	WP_006754369.1 WP_011659279.1
<i>Castellaniella defragrans</i>	303	42	537	63	WP_043685951.1 WP_043679553.1
<i>Chromobacterium violaceum</i>	305	54	556	68	WP_043617011.1 WP_043617013.1
<i>Collimonas arenae</i>	319	44	541	61	AIY40998.1

					WP_038494339.1
<i>Comamonas testosteroni</i>	300	39	555	69	WP_043003771.1 WP_012836757.1
<i>Cupriavidus necator</i>	308	38	554	61	WP_042881289.1 WP_042883575.1
<i>Carvibacter gracilis</i>	296	45	575	57	WP_027474562.1 WP_027477384.1
<i>Delftia acidovorans</i>	300	41	575	59	WP_034393435.1 WP_043780341.1
<i>Glaciecola nitratireducens</i>	310	23	533	41	WP_014110217.1 WP_014110368.1
<i>Gordonia bronchialis</i>	298	24	443	42	WP_041920477.1 WP_012835455.1
<i>Halomonas elongata</i>	315	42	551	61	WP_013331269.1 WP_013332997.1
<i>Idiomarina sp.</i>	303	25	564	37	WP_008487425.1 WP_034821838.1
<i>Janthinobacterium lividum</i>	305	44	541	62	WP_034788899.1 WP_010393822.1
<i>Parvibaculum lavamentivorans</i>	304	28	548	40	WP_041536697.1 WP_041536013.1
<i>Polynucleobacter necessarius asymbioticus</i>	291	41	539	58	ABP34774.1 ABP33573.1
<i>Pseudogulbenkiania sp.</i>	320	42	547	42	WP_014086927.1 WP_014087291.1

<i>Pseudomonas denitrificans</i> ATCC13867	304	100	554	100	WP_015478424.1 WP_015478425.1
<i>Pseudomonas knackmussii</i>	301	89	552	85	WP_043249755.1 WP_043249752.1
<i>Pseudomonas protegens</i>	297	71	548	75	WP_041117574.1 WP_011060785.1
<i>Pseudomonas fluorescens</i>	294	72	548	76	WP_046048946.1 WP_038984218.1
<i>Pseudoxanthomonas spadix</i>	307	28	545	43	WP_043290476.1 WP_014160845.1
<i>Psychrobacter</i> <i>phenylpyruvicus</i>	302	25	565	40	WP_028859810.1 WP_028859590.1
<i>Segniliparus rotundus</i>	300	26	516	37	WP_013139368.1 WP_013137524.1
<i>Sinorhizobium meliloti</i>	315	37	531	77	WP_018094277.1 WP_010970328.1
<i>Sphingobium</i> <i>chlorophenolicum</i>	292	38	544	40	WP_037446180.1 WP_037446228.1
<i>Stenotrophomonas</i> <i>maltophilia</i>	289	29	534	44	WP_037590748.1 WP_044569661.1
<i>Variovorax paradoxus</i>	298	44	544	61	WP_018905631.1 WP_042580440.1
<i>Verminephrobacter eiseniae</i>	306	28	556	59	WP_011812258.1 WP_011808703.1
<i>Vibrio furnissii</i>	295	27	573	39	WP_004729245.1

					WP_004724290.1
<i>Xanthobacter autotrophicus</i>	307	43	556	56	ABS68474.1 WP_012114222.1
<i>Xanthomonas campestris</i>	304	30	556	53	WP_033484874.1 WP_011038502.1

The analysis of the LysR protein was performed in the same manner. As a result BLAST search for the C4 LysR and C3 LysR sequences from the non-redundant NCBI database, it was confirmed that there were 126 and 132 sequences that were homologous to the DNA-binding helix-turn-helix region. FIGS. 14 and 15 show the multiple sequence alignments of these sequences. As a result of the sequence alignments, it was confirmed that a significant portion of the LysR sequences was found to be highly conserved, and that the LysR sequences were also found to be conserved at a high level in other microorganisms. That is, it is suggested that most microorganisms use LysR in cells. In addition, the helix-turn-helix region assumed to bind strongly to the inverted repeat sequences of the operator region in the 3-HP expression promoter in all C4 LysR and C3 LysR sequences was found. In this helix-turn-helix region, four residues, such as Thr-31, Arg-34, Glu-40, and Leu-47, are well conserved. The conserved amino acid residues are considered as important parts in strong interaction upon binding between the LysR protein and DNA (FIG. 9).

To further examine protein-ligand interaction between LysR and 3-HP, homology modeling and docking experiments were carried out. First, a structure available from the PDB database was used, and as a result of comparing sequence similarity of C4-LysR and C3-LysR in *P. denitrificans* using the structure, the sequence similarity of 35% or less was shown (PDB ID: 3SZP, 24 % identical). Therefore, the modeling of the C4-LysR and the C3-LysR was carried out according to a threading method using MUSTER and LOMET server. As a result, the predicted C4-LysR and C3-LysR models were purified and verified using RAMPAGE, and it was confirmed by Ramachandran plot that 98% of the amino acid residues were in the appropriate region. Then, the active sites to which 3-HP binds in C4-LysR and C3-LysR were predicted by using COACH. Here, the valid models and the residues at the predicted active sites were used to perform docking experiments in the Maestro program on SCHRODINGERTM. Target proteins (C4-LysR

and C3-LysR) and a ligand (3-HP) were each examined by using Protein Preparation Wizard and LigPrep Wizard. To produce a grid box, a receptor grid generation tool was used, and ligand docking was performed in the produced grid box by using standard precision (SP) and eXtra precision (XP) docking settings. Consequently, the excellent docking pose was shown when having a docking score of 5.01 for C4-LysR and a docking score of 3.74 for C3-LysR. It was also confirmed that C4-LysR and C3-LysR had interaction with 3-HP and several molecules. Among amino acid residues of C4-LysR, it was examined that Asp-159, Thr-160, Pro-237, and Phe-239 had hydrogen bonding with 3-HP, and ARG24 had hydrophobic interaction with 3-HP (FIG. 9). Among amino acid residues of C3-LysR, it was examined that LEU74, THR190, and THR28 had hydrogen bonding, and THR73, VAL150, PRO167, PHE127, and PHE169 had hydrophobic interaction. Unlike the prediction that there is no interaction between 3-HP and LysR, the docking results interestingly show that 3-HP had strong interaction with a substrate binding domain (ARG94, LYS96, and GLU137) and a helix-turn-helix domain (ARG24) in C4-LysR. In a similar manner, THR28 (helix-turn-helix domain) of C3-LysR was found to have strong interaction with 3-HP. In particular, in a substrate binding domain, in addition to the 3-HP bonding, amino acids that play an important role in the dimer formation have been identified, and the identified amino acids are Ala-60, Gly-91, Arg-94, Pro-118, and Glu-137. In particular, amino acids that play an important role in the dimer formation were all located on the protein surface, except for Pro-118. In this regard, when 3-HP directly affects LysR and causes dimerization of LysR, LysR undergoing dimerization binds to DNA and highly regulates transcription of the 3-HP degrading genes located below the LysR gene.

(5) 3-HP degradation and expression of 3-HP inducible genes by microorganisms having 3-HP inducible genes

According to the gene structure analysis, the 3-HP degradation pathway was found to be present in various microorganisms. To evaluate the 3-HP degradation ability of various microorganisms, cells were suspended in a 100 mM phosphate solution containing 25 mmol/L of 3-HP and allowed to degrade 3-HP for 24 hours (Table 6). As a result, there was a difference in 3-HP degrading rates depending on the microorganisms, but all of the microorganisms were found to effectively degrade 3-HP. The transcription levels of the 3-HP degrading genes (*3hpdh*, *3hibdh*, and *mmsadh*) were evaluated

depending on the presence of 3-HP (Table 7). As shown in Table 7, 3-HP increased the expression of the *3hpdh*, *3hibdh*, and *mmsadh* genes by 6-fold, 14-fold, and 16-fold, respectively in the microorganisms. Such results refer that the 3-HP inducible systems are common in various microorganisms. Meanwhile, in comparison with *P. denitrificans*, the rate of transcription increase in other microorganisms was about 10 times lower than that of *P. denitrificans*, probably due to differences in culture conditions. That is, except for *P. denitrificans*, to improve the growth of other microorganisms, the microorganisms were cultured in a medium supplemented with a large amount of complex nitrogen source, but in this case, in addition to 3-HP, amino acids included in the complex nitrogen source or degradation products of the amino acids activated the transcription of *3hpdh*, *3hibdh*, and *mmsadh* at a certain point under conditions where 3-HP was not present so that the amount of the transcription was able to be highly maintained even in the absence of 3-HP.

[Table 6]

3-HP degradation of dormant cells

Genus No.	Strains	3-HP degraded (mM) ^a
1	<i>Achromobacter denitrificans</i>	18.40
2	<i>Acidovorax avenae</i> subsp.	20.43
	<i>Acidovorax</i> sp.	16.60
3	<i>Acinetobacter baumannii</i>	18.76
4	<i>Aeromonas hydrophilia</i>	17.88
5	<i>Agrobacterium</i> sp.	20.54
6	<i>Alcaligenes faecalis</i>	19.32
7	<i>Alcanivorax hongdengensis</i>	24.51
8	<i>Alicyclophilus denitrificans</i>	20.62
9	<i>Alteromonas marina</i>	20.42
10	<i>Amycolatopsis</i> sp.	21.13

11	<i>Anaeromyxobacter dehalogenans</i>	23.14
12	<i>Azospirillum brasilense</i>	17.96
13	<i>Azotobacter vinelandii</i>	19.44
14	<i>Beijerinckia indica</i>	23.13
15	<i>Bordetella avium</i>	23.87
16	<i>Bradyrhizobium japonicum</i>	21.67
17	<i>Burkholderia ambifaria</i>	18.33
18	<i>Catenulispora acidiphilia</i>	19.45
19	<i>Caulobacter sp.</i>	22.34
20	<i>Castellaniella defragrans</i>	13.97
21	<i>Chromobacterium violaceum</i>	14.56
22	<i>Collimonas arenae</i>	16.11
23	<i>Comamonas testosteroni</i>	15.96
24	<i>Corynebacterium vitaeruminis</i>	17.35
25	<i>Cupriavidus necator</i>	18.46
26	<i>Curvibacter gracilis</i>	19.12
27	<i>Delftia acidovorans</i>	15.89
28	<i>Ferrimonas balearica</i>	17.32
29	<i>Glaciecola nitratireducens</i>	16.57
30	<i>Gordonia bronchialis</i>	18.41
31	<i>Hahella chijuensis</i>	17.59
32	<i>Halomonas elongata</i>	19.14
33	<i>Hirschia litorea</i>	18.47
34	<i>Idiomarina sp.</i>	17.86

35	<i>Janthinobacterium lividum</i>	18.02
36	<i>Kitasatospora setae</i>	19.05
37	<i>Kutzneria albida</i>	21.14
38	<i>Methylobacterium sp.</i>	23.04
39	<i>Methylocystis sp.</i>	16.97
40	<i>Novosphingobium sp.</i>	15.87
41	<i>Oceanimonas smirnovii</i>	15.91
42	<i>Paracoccus sp.</i>	17.96
43	<i>Parvibaculum lavamentivorans</i>	18.02
44	<i>Phenylobacterium kunshanensis</i>	17.56
45	<i>Photobacterium gaetbuleda</i>	19.04
46	<i>Polynucleobacter necessarius</i> <i>asymbioticus</i>	16.97
47	<i>Pseudoalteromonas carrageenovora</i>	19.03
48	<i>Pseudogulbenkiania sp.</i>	7.36
49	<i>Pseudomonas denitrificans</i> ATCC13867	20.53
	<i>Pseudomonas knackmussii</i>	7.42
	<i>Pseudomonas protegens</i>	25.24
	<i>Pseudomonas fluorescens</i>	24.41
50	<i>Pseudoxanthomonas spadix</i>	23.01
51	<i>Psychrobacter phenylpyruvicus</i>	20.17
52	<i>Ralstonia oxalatica</i>	18.09
53	<i>Rhodocrobium vannielli</i>	19.42
54	<i>Segniliparus rotundus</i>	8.96

55	<i>Shewanella oneidensis</i>	10.14
56	<i>Simiduia agarovorans</i>	23.78
57	<i>Sinorhizobium meliloti</i>	13.87
58	<i>Sphingobium chlorophenolicum</i>	14.76
59	<i>Sphingomonas wittichii</i>	21.04
60	<i>Sphingopyxis alaskensis</i>	23.56
61	<i>Stenotrophomonas maltophilia</i>	15.34
62	<i>Streptomyces nodosus</i>	21.13
63	<i>Tatlockia micdadei</i>	17.81
64	<i>Thalassospira xiamenensis</i>	18.88
65	<i>Variovorax paradoxus</i>	19.34
66	<i>Verminephrobacter eiseniae</i>	17.04
67	<i>Vibrio furnissii</i>	16.98
68	<i>Xanthobacter autotrophicus</i>	15.92
69	<i>Xanthomonas campestris</i>	14.37
	<i>Xanthomonas oryzae</i>	13.88

^a The amount of 3-HP degraded was calculated between 0 and 24h.

[Table 7]

Relative mRNA levels of 3-HP degrading genes

Genus	Strains	3hpdh		3hibdh		mmsadh	
No.							
Genus	Strains	-	+	-	+	-	+
No.		3-HP	3-HP	3-HP	3-HP	3-HP	3-HP
1	<i>Achromobacter denitrificans</i>	0.04	0.24	0.31	6.40	0.24	6.34

2	<i>Acidovorax avenae</i> subsp.	0.05	0.28	0.34	5.97	0.21	5.98
	<i>Acidovorax</i> sp.	0.02	0.31	0.33	6.76	0.36	6.04
3	<i>Acinetobacter baumannii</i>	0.01	0.19	0.35	6.02	0.27	5.76
4	<i>Aeromonas hydrophila</i>	-	-	0.37	6.17	0.32	6.14
5	<i>Agrobacterium</i> sp.	0.01	0.27	0.36	6.27	0.41	6.56
6	<i>Alcaligenes faecalis</i>	0.04	0.26	0.39	5.87	0.28	5.73
7	<i>Alcanivorax hongdengensis</i>	0.03	0.27	0.33	6.74	0.37	6.58
8	<i>Alicyclophilus denitrificans</i>	0.07	0.30	0.31	7.01	0.25	6.01
9	<i>Alteromonas marina</i>	0.06	0.34	0.34	6.09	0.22	5.73
10	<i>Amycolatopsis</i> sp.	-	-	0.32	5.96	0.24	6.05
11	<i>Anaeromyxobacter</i> <i>dehalogenans</i>	-	-	0.37	6.43	0.28	5.44
12	<i>Azospirillum brasilense</i>	0.05	0.41	0.36	6.54	0.33	6.05
13	<i>Azotobacter vinelandii</i>	-	-	0.38	6.73	0.31	5.87
14	<i>Beijerinckia indica</i>	-	-	0.34	6.59	0.29	5.01
15	<i>Bordetella avium</i>	0.08	0.45	0.31	6.04	0.24	4.98
16	<i>Bradyrhizobium japonicum</i>	0.07	0.52	0.41	7.21	0.34	5.49
17	<i>Burkholderia ambifaria</i>	0.03	0.31	0.29	5.94	0.21	5.13
18	<i>Catenulispora acidiphilia</i>	0.05	0.41	0.32	5.84	0.25	5.24
19	<i>Caulobacter</i> sp.	0.04	0.45	0.35	5.96	0.24	5.96
20	<i>Castellaniella defragrans</i>	-	-	0.45	7.43	0.37	5.98
21	<i>Chromobacterium violaceum</i>	0.02	0.25	0.38	7.02	0.32	6.31
22	<i>Collimonas arenae</i>	-	-	0.37	7.20	0.30	5.87
23	<i>Comamonas testosteroni</i>	0.04	0.24	0.28	5.88	0.21	4.96

24	<i>Corynebacterium vitaeruminis</i>	0.03	0.28	0.47	6.99	0.34	5.89
25	<i>Cupriavidus necator</i>	0.02	0.21	0.42	6.84	0.33	6.05
26	<i>Curvibacter gracilis</i>	-	-	0.29	5.76	0.19	3.99
27	<i>Delftia acidovorans</i>	-	-	0.33	6.34	0.26	4.03
28	<i>Ferrimonas balearica</i>	-	-	0.41	7.04	0.34	5.17
29	<i>Glaciecola nitratisreducens</i>	0.05	0.30	0.36	7.11	0.29	4.81
30	<i>Gordonia bronchialis</i>	0.04	0.29	0.45	6.99	0.33	5.21
31	<i>Hahella chijuensis</i>	0.03	0.28	0.42	6.81	0.34	5.97
32	<i>Halomonas elongata</i>	0.06	0.32	0.27	5.41	0.19	4.34
33	<i>Hirschia litorea</i>	0.05	0.34	0.29	6.19	0.18	4.56
34	<i>Idiomarina sp.</i>	0.08	0.42	0.47	7.21	0.32	5.43
35	<i>Janthinobacterium lividum</i>	0.03	0.33	0.41	6.98	0.29	5.01
36	<i>Kitasatospora setae</i>	0.04	0.36	0.39	6.46	0.25	5.25
37	<i>Kutzneria albida</i>	0.03	0.41	0.35	5.96	0.24	5.61
38	<i>Methylobacterium sp.</i>	0.05	0.45	0.33	6.02	0.23	5.98
39	<i>Methylocystis sp.</i>	-	-	0.32	6.51	0.21	4.91
40	<i>Novosphingobium sp.</i>	0.04	0.39	0.29	5.98	0.25	6.04
41	<i>Oceanimonas smirnovii</i>	0.02	0.24	0.36	6.44	0.28	4.88
42	<i>Paracoccus sp.</i>	0.03	0.25	0.34	6.32	0.27	4.96
43	<i>Parvibaculum lavamentivorans</i>	0.04	0.28	0.46	7.31	0.32	4.99
44	<i>Phenylobacterium kunshanensis</i>	0.06	0.33	0.41	7.43	0.33	5.02
45	<i>Photobacterium gaetbuleda</i>	-	-	0.36	7.02	0.29	5.06
46	<i>Polynucleobacter necessarius</i> <i>asymbioticus</i>	0.09	0.45	0.39	6.99	0.27	5.37

47	<i>Pseudoalteromonas carrageenovora</i>	-	-	0.29	5.76	0.21	5.03
48	<i>Pseudogulbenkiania sp.</i>	0.04	0.26	0.32	5.98	0.23	5.36
49	<i>Pseudomonas denitrificans</i> ATCC13867	0.03	0.23	0.39	6.20	0.26	5.43
	<i>Pseudomonas knackmussii</i>	0.03	0.25	0.41	6.81	0.35	5.96
	<i>Pseudomonas protegens</i>	0.02	0.19	0.28	5.62	0.21	5.01
	<i>Pseudomonas fluorescens</i>	0.04	0.27	0.26	5.81	0.18	4.70
50	<i>Pseudoxanthomonas spadix</i>	-	-	0.31	5.99	0.27	4.96
51	<i>Psychrobacter phenylpyruvicus</i>	0.08	0.37	0.43	7.04	0.31	5.03
52	<i>Ralstonia oxalatica</i>	-	-	0.40	7.21	0.34	5.21
53	<i>Rhodocrobium vannielli</i>	0.05	0.41	0.39	7.01	0.32	6.02
54	<i>Segniliparus rotundus</i>	0.07	0.27	0.25	5.81	0.19	4.32
55	<i>Shewanella oneidensis</i>	0.05	0.28	0.25	5.81	0.19	4.07
56	<i>Simiduia agarovorans</i>	0.03	0.29	0.23	5.76	0.21	4.87
57	<i>Sinorhizobium meliloti</i>	-	-	0.24	5.79	0.16	4.07
58	<i>Sphingobium chlorophenolicum</i>	0.06	0.33	0.33	5.99	0.23	4.86
59	<i>Sphingomonas wittichii</i>	0.03	0.45	0.31	7.02	0.32	6.42
60	<i>Sphingopyxis alaskensis</i>	-	-	0.35	7.00	0.35	6.94
61	<i>Stenotrophomonas maltophilia</i>	0.04	0.31	0.29	6.02	0.24	5.21
62	<i>Streptomyces nodosus</i>	0.07	0.39	0.43	6.72	0.34	5.14
63	<i>Tatlockia micdadei</i>	-	-	0.47	6.61	0.36	5.65
64	<i>Thalassospira xiamenensis</i>	-	-	0.32	7.02	0.33	6.10
65	<i>Variovorax paradoxus</i>	-	-	0.38	6.59	0.28	4.97

66	<i>Verminephrobacter eiseniae</i>	0.08	0.43	0.42	6.43	0.30	5.14
67	<i>Vibrio furnissii</i>	0.05	0.39	0.39	6.03	0.27	4.91
68	<i>Xanthobacter autotrophicus</i>	0.04	0.27	0.27	6.23	0.21	5.41
69	<i>Xanthomonas campestris</i>	0.03	0.25	0.24	5.81	0.18	5.09
	<i>Xanthomonas oryzae</i>	0.02	0.19	0.45	6.43	0.34	5.19

Analysis of 3-HP inducible promoters was performed on the microorganism above. In the same manner as in *P. denitrificans* of the previous case, all of the promoters had O1 and O2 operator sequences, and it was confirmed that these sequences had a palindromic structure consisting of 9 bases. Although no further studies on these sequences have been made yet, binding to the LysR protein was expected in the same manner as in *P. denitrificans*.

In conclusion, to improve the 3-HP production in a biological manner, it is necessary to continuously produce new enzymes with enzyme activity. In the present invention, transcriptional regulators that are reactive to 3-HP and promoters have been screened from microorganisms including *P. denitrificans*, wherein the transcriptional regulators and promoters consist of LysR proteins and specific gene sequences binding to the LysR proteins. In addition, in the presence of 3-HP, it was found that the LysR family transcriptional regulator up-regulated the expression of the corresponding genes. The molecular modeling and docking experiments showed the presence of important residues for C4-LysR (ARG94, LYS96, GLU137, and ARG24) and C3-LysR (LEU74, THR190, THR28, THR73, VAL150, PRO167, PHE127, and PHE169). Therefore, the 3-HP inducible system is expected to be effectively used to regulate the 3-HP metabolic pathway.

<Example 2> Optimization of 3-HP production pathway in *P. denitrificans*

1. Strains, plasmids, and experimental materials

Bacterial species and plasmids used in the present study were shown in Table 8. An *E. coli* strain was provided from KCTC and a *P. denitrificans* strain was provided from ATCC. *E. coli* XL1-Blue was used for plasmid cloning and maintenance. A genome DNA separation kit and a pGEM-T vector were purchased from Promega (Madison, WI, USA), a high-performance pfx polymerase was purchased from Invitrogen (Seoul, Korea), a

DNA modification enzyme was purchased from New England Bio-Labs (Beverly, MA, USA), and a Miniprep and DNA gel extraction kit was purchased from Qiagen (Mannheim, Germany). In addition, primers were purchased from Cosmogenetech Co. Ltd. (Seoul, Korea), bacto tryptone and yeast extract were purchased from Difco (Becton Dickinson; Franklin Lakes, NJ, USA), and other chemicals and enzymes were purchased from Sigma-Aldrich (St. Louis, MO, USA).

[Table 8]

Bacterial species and plasmids used in the present study

	Analysis contents	Source
Strains		
<i>E. coli</i> DH5α	Cloning host	KCTC, Korea
<i>P. denitrificans</i> wt	<i>P. denitrificans</i> ATCC13867; Source for <i>3hibdhIV</i> and <i>3hpdh</i> promoters and terminators	ATCC, America
$\Delta 3hpdh\Delta 3hibdhIV$	<i>P. dentirificans</i> ATCC13867 $\Delta 3hpdh\Delta 3hibdhIV$ double mutant strain	Zhou et al. 2014
$\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$	<i>P. dentirificans</i> ATCC13867 $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ triple mutant strain	This study
Plasmids		
pGEM-T	<i>lacZa</i> ; cloning vector; pGEM 5zf(+) derivative; 3T-overhang; Amp ^r	Promega
pUCP19	ColE1- <i>ori</i> ;pRO1614- <i>ori</i> ;broad-host-range cloning vector; Amp ^r	West et al. 1994
pUCPK/ P _{C3} -dhaB-gdrAB, P _{C4} -KGSADH	<i>KGSADH</i> gene amplified from pQKS1 were overlapped with <i>3hibdhIV</i> promoter and terminator and cloned in	This study

	pUCPK/P _{C3} -dhaB-gdrAB; Km ^r	
pUCPK/ P _{C3} -gdrAB-dhaB, P _{C4} -KGSADH	<i>gdrAB</i> and <i>dhaB</i> gene order were switched and cloned in pUCPK/P _{C4} -KGSADH, ; Km ^r	This study

2. Development of $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhI}$ deletion mutant strain of *P. denitrificans*

To understand the role of the 3-HP degrading genes, 3hibdhI was removed from the chromosome of *P. denitrificans* $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}$. A target gene was deleted therefrom based on a sacB negative counter-selection system. A sacB-Km cassette was introduced to NdeI and XbaI restriction sites of pQE-80L to prepare a pQSAK plasmid which is to be used for removal of the target gene. The genome DNA of *P. denitrificans* was used to obtain a DNA fragment including ~700 bp upstream and downstream of the target gene by PCR. After DNA sequencing thereon, the DNA fragment was cloned into a pGEM-T vector. Afterwards, sub-cloning into the pQSAK plasmid was made again, and then, a mutant strain of *P. denitrificans* was developed through two rounds of recombination. The mutant strain was re-identified by PCR and sequencing performed thereon. The mutant strains thus obtained was designated as *P. denitrificans* $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhI}$.

3. Plasmid construction

A gene encoding glycerol dehydratase and reactivation enzyme was amplified by using a pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH plasmid, and an expression cassette was constructed by cloning a C3 promoter and a C3 terminator onto promoters at the 5'-end and 3'-end of gdrAB and dhaB123 genes, respectively. The expression cassette was replicated at XbaI and SacI restriction sites of the pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH plasmid, and a resulting plasmid was designated as pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH. The pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH plasmid thus obtained was transformed with *P. denitrificans* $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhI}$, and finally, a *Pd* $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhI}$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH) plasmid was constructed (FIG. 16).

4. Determination of enzyme activity

The DhaB activity can be measured by measuring the KGSADH enzyme activity. 1 unit of the DhaB activity is defined as the amount of enzyme required to reduce 1 μmol of NAD^+ to NADH for 1 minute. Briefly, first, 20 μL of 26 U/mg NAD^+ -dependent KGSADH was cultured at a temperature of 37°C for 5 minutes in 50 mM potassium phosphate buffer (pH 8.0) (total volume of 1 mL) containing 1 mM DTT, 15 μM coenzyme B12, 3 mM MgCl_2 , and 1.5 mM ATP. Here, KGSADH contained 25% glycerol. A reaction was started by the addition of an appropriate amount of a cell extract containing 1.5 mM NAD^+ and DhaB preheated at a temperature of 37°C , and was observed through changes in absorbance of NADH. The KGSADH activity was determined according to the method reported by Dr. Raj by measuring the reduction from NAD^+ to NADH at 340. A reaction mixture including 50 mM potassium phosphate buffer (pH 8.0), 1 mM DTT, and an appropriate amount of an enzyme extract was cultured at a temperature of 37°C for 5 minutes, and a reaction was initiated by the addition of 2.0 mM 3-HPA and 2.0 mM NAD^+ . The amount of NADH was determined by using $6.22 \times 10^3 \text{ M}^{-1}\text{cm}^{-1}$ of molar extinction coefficient ($\Delta\epsilon_{340}$). 1 unit activity of KGSADH is defined as the amount of enzyme required to reduce 1 μmol of NAD^+ to NADH for 1 minute. All enzyme activities were measured by using a crude cell extract.

5. Culture medium and culture conditions

Unless otherwise stated, shaking culture was performed by using a 250 mL non-baffled Erlenmeyer flask containing 20 mL of a culture broth at a speed of 200 rpm at a temperature of 30°C . Here, an M9 culture medium supplemented with, per liter, MgSO_4 , 0.25 g; NaCl, 1.0 g; NH_4Cl , 1.0 g; yeast extract, 1 g; glycerol, 100 mmol; L-glutamate, 5 g; tryptone, 2 g; and glucose 2.5 g was used, and the medium contained 100 mM potassium phosphate buffer (pH 7.0). If necessary, 12 $\mu\text{mol/L}$ of coenzyme B12 was additionally injected, and then, the flask was sealed with an oxygen-permeable sponge plug. For the measure of cell mass, residual substrates, and metabolites, sampling was periodically done, and all shaking culture experiments were repeated three times, wherein a standard deviation of biomass and metabolites was less than 10%. The bioreactor experiments were carried out in a 1-L working volume in a 1.5-L

capacity Biotron-LiFlus GM bioreactor (Biotron, Seoul, Korea).

An M9 culture medium for the bioreactor experiments was supplemented with, per liter, $\text{MgSO}_4 \cdot \text{H}_2\text{O}$, 0.25 g; NaCl, 1.0 g; NH_4Cl , 1.0 g; yeast extract, 1 g; L-glutamate, 5 g; tryptone, 2 g; casamino acids, 2g; glucose 2.5 g, and trace element solution, 10 mL/L, and the medium contained 100 mM of potassium phosphate buffer (pH 7.0). The culturing was performed in a fed-type culturing mode at a temperature of 30°C while concentrated glycerol (10 M) and 7 mM glucose were periodically injected thereto. Here, pH was maintained to 7.0 ± 0.1 by using 5 N NaOH and 2.5 N HCl. Air was continuously supplied at an agitation speed of 650 rpm at 1 vvm. During the culturing, a medium supplemented with tryptone, 2 g/L; casamino acids, 2 g/L; L-glutamate, 5.0 g/L; and yeast extract, 1 g/L was added every 6 hours to the bioreactor. Samples thereof were regularly analyzed to measure cell mass, residual substrates, and metabolites.

6. Analysis method

The cell concentration was measured by using a spectrophotometer (Lambda 20, Perkin Elmer; Norwalk, CT, USA) with a cuvette having a length of 10 mm. 1 unit of absorbance at 600 nm (OD600) was consistent with a dry cell volume of 0.3 g per liter. The protein concentration was analyzed according to a Bradford method with a microtiter plate reader based on bovine serum albumin (1420, Wallac Victor 2; Perkin Elmer). The concentrations of glycerol, 3-HP, and other metabolites were measured by HPLC, wherein the supernatant obtained by centrifugation performed on a culturing sample for 10 minutes at $10,000 \times g$ was filtered through a tuffryn-membrane (Acrodisc, Pall Life Sciences), and then, was eluted with by 300 mm $\times$ 7.8 mm Aminex HPX-87H (Bio-Rad, USA) column using 2.5 mM H_2SO_4 as a mobile phase at a temperature of 65°C.

7. Results

(1) Shaking flask culture of recombinant Pd $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhI}$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH)

The inventors of the present invention had observed in the previous study that the DhaB activity was significantly reduced due to self-destructive catalytic reaction by DhaB when glycerol conversion occurred. Such reduction may be caused by low expression of GdrAb that reactivates DhaB. In addition, it was also expected that the

expression of GdrAB would be improved by sequentially arranging GdrAB and DhaB right below the PC3 promoter. Based on this hypothesis, a pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH plasmid was developed and introduced to a *P. denitrificans* (hereinafter, referred to as Pd) $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$ strain for the production of 3-HP. The effect of changing the arrangement order of GdrAB and DhaB regarding the 3-HP production from glycerol was measured in Pd $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH). The supplying effect of coenzyme B12 was examined by supplying 12 μM of coenzyme B12 at 0 h. Pd $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH) was used as a control group. S1~S3 in FIG. 17 shows the production of 3-HP from glycerol by recombinant Pd $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH), and O1~O3 in FIG. 17 shows the production of 3-HP from glycerol by recombinant Pd $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH). S1 and O1 in FIG. 17 show the results in the case where there was no supply of glycerol, and S2 and O2 of FIG. 17 show the results in the case where there was no supply of coenzyme B12. Meanwhile, S3 and O3 of FIG. 17 show the results obtained in associated with supply of coenzyme B12. It was confirmed that there was no significant difference in cell growth between the two strains. However, the production of 3-HP by the Pd $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH) strain supplied with cobalt and coenzyme B12 increased to 41% and 29% after 12 hours. These results indicate that the rate of DhaB reaction was affected by the amount of coenzyme or the amount of cobalt.

It was observed that the addition of cobalt led to the production of 3-HPA and 1,3-PDO at 12 h, but in a control strain, it was observed that 3-HPA (with cobalt) was not accumulated (Table 9). The yield of 3-HP from glycerol was about ~ 1, meaning that glycerol supplied thereto was completely used for the production of 3-HP, and the produced 3-HP was not degraded again.

[Table 9]

Carbon distribution in 12-h culture of recombinant *P. denitrificans* $\Delta 3\text{hpdh}\Delta 3\text{hibdhIV}\Delta 3\text{hibdhl}$

	S2	S3	O2	O3
substrates				
Glucose (mM)	0.58	0.91	0.67	0.88
Glycerol (mM)	64.13	52.15	44.92	37.45
Biomass (g/L)	1.51	1.36	1.66	1.17
Metabolites				
3-HP (mM)	64.83	49.51	45.93	38.24
3-HPA (mM)	0.78	0.52	0	0.39
1,3-PDO (mM)	3.55	4.95	1.37	1.42
Growth rate ($\mu_{\max}$, h ⁻¹)	0.56	0.54	0.54	0.53
3-HP yield on glycerol (mol/mol)	1.01	0.95	1.02	1.02
Glycerol carbon recovery (%)	1.08	1.05	1.05	1.07

(2) Enzyme activity

Time-dependent *in vitro* enzyme activity of DhaB and KGSADH was measured (FIG. 18). The DhaB enzyme activity was examined by using the KGSADH enzyme activity, and the KGSADH enzyme activity was measured by using propionaldehyde as a substrate. When the order of DhaB and GdrAB genes was changed, it was observed that the DhaB activity was reduced. Meanwhile, the addition of glycerol, cobalt, or coenzyme B12 was observed to rather cause significant reduction in the DhaB enzyme activity. In this regard, additional experiments are needed to determine whether such effects are caused by the accumulation of 3-HPA or other factors. However, one thing that is clear is that changing of the order of gdrAB and DhaB was not enough to sufficiently improve the DhaB enzyme activity. Thus, it is unclear whether the expression of gdrB is improved in the recombinant strain used herein. For the gdrB translation, RBS of *Klebsiella pneumoniae* was used, but further verification thereof is required.

(3) Bioreactor culture of DhaB, KGSADH overexpression recombinant Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ (pUCPK'/PC3- gdrAB-dhaB, PC4-KGSADH)

A fed-type glycerol-glucose bioreactor operation was performed by using Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ (pUCPK'/PC3-gdrAB-dhaB, PC4-KGSADH) and Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH) strains. In the bioreactor experiments, the concentrations of glucose and glycerol were maintained at low levels of 10 mM and 150 mM, respectively. For every 6 hours, glutamate was supplied for cell growth. As a result of the culture, similar cell growth was observed in the two bioreactors. The cell growth decreased in both cultures after 9 hours, but the cell growth continued until the end of the reaction. In bioreactor A, a Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ (pUCPK'/PC3-dhaB-gdrAB, PC4-KGSADH) strain was used (FIG. 19). Here, the production of 3-HP mostly increased up to 36 hours, resulting in an amount of more than 58 ± 2 g/L at a production rate of 1.2 g/L/h or more, and a 3-HP yield of more than 0.9 mol/mol from glycerol. The 3-HP production rate decreased after 36 hours. Between 36 hours to 48 hours, only 2 ± 0.5 g/L of the 3-HP production was maintained. Overall, for 48 hours, based on a production rate of 1.0 g/L/h and a 3-HP yield of 0.93 mol/mol from glycerol, 60 ± 2 g/L of 3-HP was produced. In comparison with previous experiments, i.e., the fermentation experiment of the strain in which 3hibdhI was not deleted, the yield of 3-HP was significantly increased, confirming that 3hibdhI had an important role in the 3-HP degradation. The influence of 3hibdhI was not observed at all in the flask experiments with short fermentation times.

In bioreactor B, the strain in which the gene order (dhaB and gdrAB) was changed was used, and as a result, the production of 3-HP was improved in the latter half of fermentation. Based on a production rate of 1.3 g/L/h and a yield of 0.95 mol/mol from glycerol, about 63 ± 2 g/L of 3-HP was produced. In comparison with bioreactor A, the 3-HP production was increased by 5%. Although the results were not seen in the enzyme activity assays or flask experiments, the degree of GdrAB expression was significantly important in terms of the 3-HP production.

In conclusion, when the 3-HP production enzymes, i.e., DhaB, GdrAB, and KGSADH, were expressed, *P. denitrificans* was able to produce 3-HP from glycerol. The recombinant plasmids were developed by using two strong inducible promoters, PC3 and PC4, and Pd $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ from which three genes were deleted was

used as a host. To alleviate the degree of inactivation of DhaB, *gdrAB* was located in front of *dhaB*, so as to enhance the expression of *gdrAB*. The enzyme activity analysis and protein expression analysis by SDS-PAGE showed that the activity of DhaB was reduced by such a positional change. However, regardless of the reduced activity of DhaB, the production of 3-HP was improved. As a result of operating the fed-type bioreactor using new recombinant strains, 3-HP was obtained in high concentrations, high production rates, and high yields.

CLAIMS

1. An inducible promoter for 3-hydroxypropionic acid (3-HP) or a derivative thereof, the inducible promoter comprising a binding site to a LysR protein which is reactive to 3-HP or a derivative thereof.
2. The inducible promoter of claim 1, wherein the promoter is derived from a microorganism having 3-HP degradability.
3. The inducible promoter of claim 2, wherein the microorganism is one selected from the group consisting of *Achromobacter denitrificans*, *Acidovorax avenae* subsp., *Acidovorax* sp., *Acinetobacter baumannii*, *Aeromonas hydrophilia*, *Agrobacterium* sp., *Alcaligenes faecalis*, *Alcanivorax hongdengensis*, *Alicyclophilus denitrificans*, *Alteromonas marina*, *Amycolatopsis* sp., *Anaeromyxobacter dehalogenans*, *Azospirillum brasilense*, *Azotobacter vinelandii*, *Beijerinckia indica*, *Bordetella avium*, *Bradyrhizobium japonicum*, *Burkholderia ambifaria*, *Catenulispora acidiphilia*, *Caulobacter* sp., *Castellaniella defragrans*, *Chromobacterium violaceum*, *Collimonas arenae*, *Comamonas testosteroni*, *Corynebacterium vitaeruminis*, *Cupriavidus necator*, *Curvibacter gracilus*, *Delftia acidovorans*, *Ferrimonas balearica*, *Glaciecola nitratireducens*, *Gordonia bronchialis*, *Hahella chijuensis*, *Halomonas elongata*, *Hirschia litorea*, *Idiomarina* sp., *Janthinobacterium lividum*, *Kitasatospora setae*, *Kutzneria albida*, *Methylobacterium* sp., *Methylocystis* sp., *Novosphingobium* sp., *Oceanimonas smirnovii*, *Paracoccus* sp., *Parvibaculum lavamentivorans*, *Phenylobacterium kunshanensis*, *Photobacterium gaetbuleda*, *Polynucleobacter necessarius asymbioticus*, *Pseudoalteromonas carrageenovora*, *Pseudogulbenkiania* sp., *Pseudomonas denitrificans* ATCC13867, *P. knackmussii*, *P. protegens*, *P. fluorescens*, *Pseudoxanthomonas spadix*, *Psychrobacter phenylpyruvicus*, *Ralstonia oxalatica*, *Rhodomicrobium vannielli*, *Segniliparus rotundus*, *Shewanella oneidensis*, *Simiduia agarovorans*, *Sinorhizobium meliloti*, *Sphingobium chlorophenolicum*, *Sphingomonas wittichii*, *Sphingopyxis alaskensis*, *Stenotrophomonas maltophilia*, *Streptomyces nodosus*, *Tatlockia micdadei*, *Thalassospira xiamenensis*, *Variovorax paradoxus*, *Verminephrobacter eiseniae*, *Vibrio furnissii*, *Xanthobacter autotrophicus*, *Xanthomonas campestris*, and *Xanthomonas oryzae*.

4. The inducible promoter of claim 1, wherein the LysR protein comprises an N-terminal domain having a helix-turn-helix structure and binding to DNA, a C-terminal domain binding to 3-HP or a derivative thereof, and a C-terminal domain contributing to stabilization of a LysR protein dimer.

5. The inducible promoter of claim 4, wherein the N-terminal domain having a helix-turn-helix structure and binding to DNA comprises an amino acid sequence represented by SEQ ID NO: 1 or 2.

6. The inducible promoter of claim 4, wherein the C-terminal domain binding to 3-HP or a derivative thereof comprises an amino acid sequence represented by SEQ ID NO: 3.

7. The inducible promoter of claim 4, wherein the C-terminal domain contributing to stabilization of a LysR protein dimer comprises an amino acid sequence represented by SEQ ID NO: 4.

8. The inducible promoter of claim 1, wherein the binding site to a LysR protein comprises two LysR protein dimers that are bonded to each other.

9. The inducible promoter of claim 1, wherein the binding site to a LysR protein comprises a base sequence selected from SEQ ID NOs: 5 to 43.

10. The inducible promoter of claim 9, wherein the binding site to a LysR protein comprises an inverted repeat sequence and another inverted repeat sequence paired with therewith are repeated twice, wherein the inverted repeat sequence comprises a base sequence selected from SEQ ID NOs: 5 to 43.

11. The inducible promoter of claim 10, wherein the binding site to a LysR protein comprises a base sequence selected from SEQ ID NOs: 44 or 45.

12. The inducible promoter of claim 1, wherein the derivative is

3-hydroxyisobutyrate (3HIB) or 3-hydroxybutyrate (3-HB).

13. A recombinant expression vector comprising the inducible promoter of any one of claims 1 to 12.

14. The recombinant expression vector of claim 13, wherein the recombinant expression vector further comprises a gene encoding a foreign protein linked to the inducible promoter for 3-hydroxypropionic acid (3-HP) or a derivative thereof.

15. The recombinant expression vector of claim 14, the foreign protein is glycerol dehydratase (DhaB), DhaB reactivase (GdrAB), or α -ketoglutaric semialdehyde dehydrogenase (KGSADH).

16. A recombinant microorganism transformed with the recombinant expression vector of claim 13.

17. The recombinant microorganism of claim 16, wherein the recombinant microorganism has producibility of 3-HP.

18. The recombinant microorganism of claim 17, wherein the recombinant microorganism is *Pseudomonas denitrificans*.

19. The recombinant microorganism of claim 17, wherein the recombinant microorganism is a strain of *Pseudomonas denitrificans* $\Delta 3hpdh\Delta 3hibdhIV\Delta 3hibdhI$ from which *3hpdh*, *3hibdh*, and *mmsadh* genes relating to degradation of 3-HP are deleted in a strain of *P. denitrificans*.

20. A method of producing 3-hydroxypropionic acid (3-HP), the method comprising:
culturing the recombinant microorganism of claim 16.

21. A recombinant gene expression cassette reactive to 3-hydroxypropionic acid (3-HP) or a derivative thereof, the recombinant gene expression cassette

comprising a lysR gene encoding a LysR protein that is reactive to 3-HP or a derivative thereof, a promoter comprising a binding site to a LysR protein, and a gene encoding a target expression protein.

22. The recombinant gene expression cassette of claim 21, wherein the LysR protein or the promoter is derived from a microorganism having degradability of 3-HP.

23. The recombinant gene expression cassette of claim 22, wherein the microorganism having degradability of 3-HP is one selected from the group consisting of *Achromobacter denitrificans*, *Acidovorax avenae* subsp., *Acidovorax* sp., *Acinetobacter baumannii*, *Aeromonas hydrophilia*, *Agrobacterium* sp., *Alcaligenes faecalis*, *Alcanivorax hongdengensis*, *Alicyclophilus denitrificans*, *Alteromonas marina*, *Amycolatopsis* sp., *Anaeromyxobacter dehalogenans*, *Azospirillum brasilense*, *Azotobacter vinelandii*, *Beijerinckia indica*, *Bordetella avium*, *Bradyrhizobium japonicum*, *Burkholderia ambifaria*, *Catenulispora acidiphilia*, *Caulobacter* sp., *Castellaniella defragrans*, *Chromobacterium violaceum*, *Collimonas arenae*, *Comamonas testosteroni*, *Corynebacterium vitaeruminis*, *Cupriavidus necator*, *Curvibacter gracilus*, *Delftia acidovorans*, *Ferrimonas balearica*, *Glaciecola nitratireducens*, *Gordonia bronchialis*, *Hahella chijuensis*, *Halomonas elongata*, *Hirschia litorea*, *Idiomarina* sp., *Janthinobacterium lividum*, *Kitasatospora setae*, *Kutzneria albida*, *Methylobacterium* sp., *Methylocystis* sp., *Novosphingobium* sp., *Oceanimonas smirnovii*, *Paracoccus* sp., *Parvibaculum lavamentivorans*, *Phenylobacterium kunshanensis*, *Photobacterium gaetbuleda*, *Polynucleobacter necessarius asymbioticus*, *Pseudoalteromonas carrageenovora*, *Pseudogulbenkiania* sp., *Pseudomonas denitrificans* ATCC13867, *P. knackmussii*, *P. protegens*, *P. fluorescens*, *Pseudoxanthomonas spadix*, *Psychrobacter phenylpyruvicus*, *Ralstonia oxalatica*, *Rhodomicrobium vannielli*, *Segniliparus rotundus*, *Shewanella oneidensis*, *Simiduia agarovorans*, *Sinorhizobium meliloti*, *Sphingobium chlorophenolicum*, *Sphingomonas wittichii*, *Sphingopyxis alaskensis*, *Stenotrophomonas maltophilia*, *Streptomyces nodosus*, *Tatlockia micdadei*, *Thalassospira xiamenensis*, *Variovorax paradoxus*, *Verminephrobacter eiseniae*, *Vibrio furnissii*, *Xanthobacter autotrophicus*, *Xanthomonas campestris*, and *Xanthomonas oryzae*.

24. The recombinant gene expression cassette of claim 21, wherein the LysR

protein comprises an N-terminal domain having a helix-turn-helix structure and binding to DNA, a C-terminal domain binding to 3-HP or a derivative thereof, and a C-terminal domain contributing to stabilization of a LysR protein dimer.

25. The recombinant gene expression cassette of claim 24, wherein the N-terminal domain having a helix-turn-helix structure and binding to DNA comprises an amino acid sequence represented by SEQ ID NO: 1 or 2.

26. The recombinant gene expression cassette of claim 24, wherein the C-terminal domain binding to 3-HP or a derivative thereof comprises an amino acid sequence represented by SEQ ID NO: 3.

27. The recombinant gene expression cassette of claim 24, wherein the C-terminal domain contributing to stabilization of a LysR protein dimer comprises an amino acid sequence represented by SEQ ID NO: 4.

28. The recombinant gene expression cassette of claim 21, wherein the binding site to a LysR protein comprises a base sequence selected from SEQ ID NOs: 5 to 43.

29. The recombinant gene expression cassette of claim 28, wherein the binding site to a LysR protein comprises an inverted repeat sequence and an inverted repeat sequence paired with therewith are repeated twice, wherein the inverted repeat sequence comprises a base sequence selected from SEQ ID NOs: 5 to 43.

30. The recombinant gene expression cassette of claim 29, wherein the binding site to a LysR protein comprises a base sequence selected from SEQ ID NOs: 44 or 45.

31. The recombinant gene expression cassette of claim 21, wherein the derivative is 3-hydroxyisobutyrate (3HIB) or 3-hydroxybutyrate (3-HB).

32. A recombinant expression vector comprising the recombinant gene

expression cassette of any one of claims 21 to 31.

33. A recombinant microorganism transformed with the recombinant expression vector of claim 32.

34. A recombinant microorganism comprising the recombinant gene expression cassette of any one of claims 21 to 31 inserted to a chromosome of a host cell.

35. A method of producing a target expression protein, the method comprising: culturing the recombinant microorganism of claim 33.

36. The method of claim 35, wherein the culturing of the recombinant microorganism further comprises adding for 3-hydroxypropionic acid (3-HP) to the culture.