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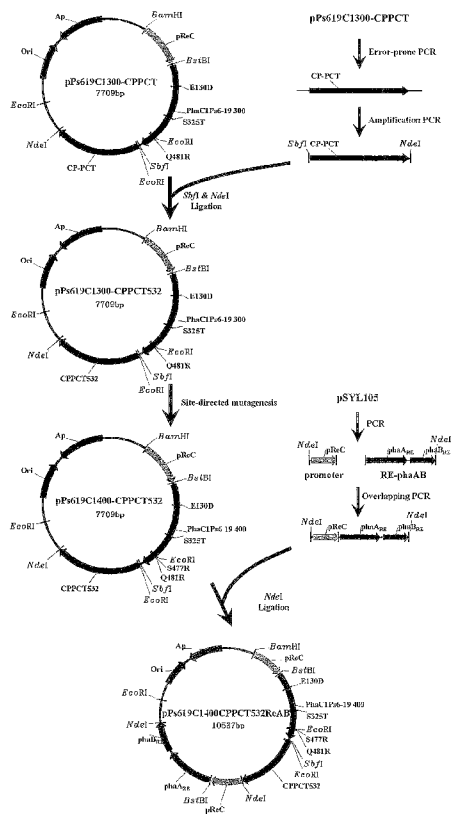
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(54) Title: RECOMBINANT MICROORGANISM CAPABLE OF PRODUCING POLYLACTATE OR POLYLACTATE COPOLYMER FROM SUCROSE AND METHOD FOR PRODUCING POLYLACTATE OR POLYLACTATE COPOLYMER FROM SUCROSE USING THE SAME

FIG. 1



(57) Abstract: Provided are a microorganism capable of producing a polylactate (PLA) or PLA copolymer from sucrose and a method of producing the PLA or PLA copolymer from sucrose using the same. A gene of an enzyme converting lactate into lactyl-CoA and a gene of a polyhydroxyalkanoate (PHA) synthase using lactyl-CoA as a substrate are introduced into a microorganism capable of using sucrose as a substrate, and the microorganism is cultured using sucrose as the substrate, thereby allowing efficient production of a PLA or PLA copolymer.

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RECOMBINANT MICROORGANISM CAPABLE OF PRODUCING POLYLACTATE
OR POLYLACTATE COPOLYMER FROM SUCROSE AND METHOD FOR
PRODUCING POLYLACTATE OR POLYLACTATE COPOLYMER FROM SUCROSE
USING THE SAME

5

【Technical Field】

The present invention relates to a recombinant microorganism capable of producing a polylactate (PLA) or PLA copolymer from sucrose and a method of producing a PLA or PLA copolymer from sucrose using the microorganism.

10

【Background Art】

Poly lactate (PLA) is a typical biodegradable polymer derived from lactate that is highly applicable commercially and biomedically. Although preparation of PLA presently involves polymerization of lactate produced by fermenting microorganisms, only PLA with a low molecular weight of about 1000 to 5000 daltons is obtained by direct
15 polymerization of lactate. In order to synthesize PLA with a molecular weight of 100,000 daltons or higher, PLA with a low molecular weight obtained by direct polymerization of lactate may be polymerized using a chain coupling agent. In this method, however, the entire process becomes complicated due to addition of an organic solvent or the chain coupling agent, which are not easy to remove. A presently commercially available process
20 of preparing high-molecular weight PLA may include converting lactate into lactide and synthesizing PLA using ring-opening polycondensation of lactide rings.

When PLA is synthesized by chemical synthesis of lactate, a PLA homopolymer is easily obtained, but a PLA copolymer composed of various types of monomers is difficult to synthesize and commercially unavailable.

5 Meanwhile, polyhydroxyalkanoate (PHA) is polyester stored by microorganisms as energy or a carbon source when there are excessive carbon sources and a lack of other nutrients such as phosphorus (P), nitrogen (N), magnesium (Mg), and oxygen (O), etc. Since PHA has similar physical properties to conventional synthetic polymers from petroleum and exhibits complete biodegradability, it is being recognized as a substitute for conventional synthetic plastics.

10 In order to produce PHAs using microorganisms, enzymes converting microbial metabolic products into a PHA monomer and a PHA synthase for synthesizing a PHA polymer using the PHA monomer are needed. When synthesizing PLA and PLA copolymer using microorganisms, the same system is required, and enzymes for providing lactyl-CoA are needed in addition to an enzyme for providing hydroxyacyl-CoA, which is
15 an original substrate of a PHA synthase.

Furthermore, it is very important to adopt a low-cost substrate in order to economically produce biodegradable polymers. In particular, it is necessary to develop a technique of producing a PLA or PLA copolymer using sucrose as a low-cost substrate.

【Disclosure】

20 【Technical Problem】

The present invention is directed to a microorganism capable of producing a polylactate (PLA) or PLA copolymer using sucrose as a substrate and a method of producing a PLA or PLA copolymer using the same.

【Technical Solution】

One aspect of the present invention provides a method of producing a polylactate (PLA) or hydroxyalkanoate-lactate copolymer from sucrose. The method includes culturing or growing a cell or plant in an environment containing lactate and sucrose or an
5 environment containing lactate, sucrose, and hydroxyalkanoate. The cell or plant contains a gene of an enzyme converting lactate into lactyl-CoA and a gene of a polyhydroxyalkanoate (PHA) synthase using lactyl-CoA as a substrate and is able to produce a PLA or hydroxyalkanoate-lactate copolymer using sucrose as a substrate. Thereafter, the PLA or hydroxyalkanoate-lactate copolymer is retrieved from the cell or
10 plant.

The present inventors successfully synthesized PLA and PLA copolymer using a propionyl-CoA transferase from *Clostridium propionicum* for providing lactyl-CoA, and a mutant of a PHA synthase from *Pseudomonas* sp. 6-19 using lactyl-CoA as a substrate, as disclosed in Korean Patent Application No. 10-2006-0116234.

15 Furthermore, the present inventors attempted to produce PLA and PLA copolymer using a low-cost substrate, sucrose, in order to economically produce biodegradable polymers. As a result, the present inventors transformed E.coli using sucrose as a low-cost substrate with a plasmid expressing a propionyl-CoA transferase from *Clostridium propionicum* and a PHA synthase from *Pseudomonas* sp. 6-19, and found that PLA and
20 PLA copolymer could be efficiently produced from sucrose using the transformed recombinant E.coli. This led them to complete the present invention.

The cell or plant capable of producing the PLA or PLA copolymer (hydroxyalkanoate-lactate copolymer) may be obtained by transforming a cell or plant that does not include at least one of: (a) the gene of the enzyme converting lactate into lactyl-

CoA and (b) the gene of the PHA synthase using lactyl-CoA as the substrate with at least one of (a) and (b). That is, the cell or plant capable of producing the PLA or hydroxyalkanoate-lactate copolymer may be obtained by transforming a cell or plant not having (a) and (b) with at least one of (a) and (b), or by transforming a cell or plant not having (a) but having (b) with (a), but the present invention is not limited thereto. For example, according to the present invention, when a cell has one of (a) and (b), the cell capable of producing the PLA or hydroxyalkanoate-lactate copolymer may be obtained by amplifying the included one of (a) and (b) and transforming the cell with the absent one of (a) and (b).

10 In the present invention, hydroxyalkanoate of the hydroxyalkanoate-lactate copolymer may be at least one selected from the group consisting of 3-hydroxybutyrate, 3-hydroxyvalerate, 4-hydroxybutyrate, medium chain-length (D)-3-hydroxycarboxylic acid with 6 to 14 carbon atoms, 2-hydroxypropionic acid, 3-hydroxypropionic acid, 3-hydroxyhexanoic acid, 3-hydroxyheptanoic acid, 3-hydroxyoctanoic acid, 3-hydroxynonanoic acid, 3-hydroxydecanoic acid, 3-hydroxyundecanoic acid, 3-hydroxydodecanoic acid, 3-hydroxytetradecanoic acid, 3-hydroxyhexadecanoic acid, 4-hydroxyvaleric acid, 4-hydroxyhexanoic acid, 4-hydroxyheptanoic acid, 4-hydroxyoctanoic acid, 4-hydroxydecanoic acid, 5-hydroxyvaleric acid, 5-hydroxyhexanoic acid, 6-hydroxydodecanoic acid, 3-hydroxy-4-pentenoic acid, 3-hydroxy-4-trans-hexenoic acid, 3-hydroxy-4-cis-hexenoic acid, 3-hydroxy-5-hexenoic acid, 3-hydroxy-6-trans-octenoic acid, 3-hydroxy-6-cis-octenoic acid, 3-hydroxy-7-octenoic acid, 3-hydroxy-8-nonenoic acid, 3-hydroxy-9-decenoic acid, 3-hydroxy-5-cis-dodecenoic acid, 3-hydroxy-6-cis-dodecenoic acid, 3-hydroxy-5-cis-tetradecenoic acid, 3-hydroxy-7-cis-tetradecenoic acid, 3-hydroxy-5,8-cis-cis-tetradecenoic acid, 3-hydroxy-4-methylvaleric acid, 3-

hydroxy-4-methylhexanoic acid, 3-hydroxy-5-methylhexanoic acid, 3-hydroxy-6-methylheptanoic acid, 3-hydroxy-4-methyloctanoic acid, 3-hydroxy-5-methyloctanoic acid, 3-hydroxy-6-methyloctanoic acid, 3-hydroxy-7-methyloctanoic acid, 3-hydroxy-6-methylnonanoic acid, 3-hydroxy-7-methylnonanoic acid, 3-hydroxy-8-methylnonanoic acid, 3-hydroxy-7-methyldecanoic acid, 3-hydroxy-9-methyldecanoic acid, 3-hydroxy-7-methyl-6-octenoic acid, malic acid, 3-hydroxysuccinic acid-methylester, 3-hydroxyadipinic acid-methylester, 3-hydroxysuberic acid-methylester, 3-hydroxyazelaic acid-methylester, 3-hydroxysebacic acid-methylester, 3-hydroxysuberic acid-ethylester, 3-hydroxysebacic acid-ethylester, 3-hydroxypimelic acid-propylester, 3-hydroxysebacic acid-benzylester, 3-hydroxy-8-acetoxyoctanoic acid, 3-hydroxy-9-acetoxynonanoic acid, phenoxy-3-hydroxybutyric acid, phenoxy-3-hydroxyvaleric acid, phenoxy-3-hydroxyheptanoic acid, phenoxy-3-hydroxyoctanoic acid, para-cyanophenoxy-3-hydroxybutyric acid, para-cyanophenoxy-3-hydroxyvaleric acid, para-cyanophenoxy-3-hydroxyhexanoic acid, para-nitrophenoxy-3-hydroxyhexanoic acid, 3-hydroxy-5-phenylvaleric acid, 3-hydroxy-5-cyclohexylbutyric acid, 3,12-dihydroxydodecanoic acid, 3,8-dihydroxy-5-cis-tetradecenoic acid, 3-hydroxy-4,5-epoxydecanoic acid, 3-hydroxy-6,7-epoxydodecanoic acid, 3-hydroxy-8,9-epoxy-5,6-cis-tetradecanoic acid, 7-cyano-3-hydroxyheptanoic acid, 9-cyano-3-hydroxynonanoic acid, 3-hydroxy-7-fluoroheptanoic acid, 3-hydroxy-9-fluorononanoic acid, 3-hydroxy-6-chlorohexanoic acid, 3-hydroxy-8-chlorooctanoic acid, 3-hydroxy-6-bromohexanoic acid, 3-hydroxy-8-bromooctanoic acid, 3-hydroxy-11-bromoundecanoic acid, 3-hydroxy-2-butenic acid, 6-hydroxy-3-dodecenoic acid, 3-hydroxy-2-methylbutyric acid, 3-hydroxy-2-methylvaleric acid, and 3-hydroxy-2,6-dimethyl-5-heptenoic acid, but the present invention is not limited thereto.

In the present invention, the gene of the enzyme converting lactate into lactyl-CoA may be a propionyl-CoA transferase (*pct*) gene. More specifically, the gene of the enzyme converting lactate into lactyl-CoA may be a *pct* gene from *Clostridium propionicum*. In a specific example of the present invention, the gene of the enzyme converting lactate into

5 lactyl-CoA may have one selected from the group consisting of: a base sequence (CpPCT) of SEQ ID NO: 1; a base sequence (CpPCT522) obtained by mutating T78C, T669C, A1125G and T1158C in the base sequence of SEQ ID NO:1; a base sequence (CpPCT512) obtained by mutating A1200G in the base sequence of SEQ ID NO:1; a base sequence (CpPCT531) obtained by mutating A1200G in the base sequence of SEQ ID NO:1 and

10 mutating Gly335Asp in an amino-acid sequence of SEQ ID NO: 2; a base sequence (CpPCT533) obtained by mutating T669C, A1125G and T1158Ca in the base sequence of SEQ ID NO:1 and mutating Asp65Gly in the amino-acid sequence of SEQ ID NO: 2; a base sequence (CpPCT535) obtained by mutating T669C, A1125G, and T1158C in the base sequence of SEQ ID NO: 1 and mutating Asp65Asn in the amino-acid sequence of

15 SEQ ID NO: 2; a base sequence (CpPCT537) obtained by mutating T669C, A1125G, and T1158C in the base sequence of SEQ ID NO: 1 and mutating Thr199Ile in the amino-acid sequence of SEQ ID NO: 2; a base sequence (CpPCT532) obtained by mutating A1200G in the base sequence of SEQ ID NO: 1 and mutating Ala243Thr in the amino-acid sequence of SEQ ID NO: 2; a base sequence (CpPCT534) obtained by mutating A1200G

20 in the base sequence of SEQ ID NO: 1 and mutating Asp257Asn in the amino-acid sequence of SEQ ID NO: 2; and a base sequence (CpPCT540) obtained by mutating T78C, T669C, A1125G and T1158C in the base sequence of SEQ ID NO: 1 and mutating Val193Ala in the amino-acid sequence of SEQ ID NO: 2.

In particular, the CpPCT532 gene may be a mutant gene of a propionyl-CoA transferase from *Clostridium propionicum* that is preferable for producing a PLA or PLA copolymer using sucrose.

The cell or plant according to the present invention may include the gene of the
5 PHA synthase using lactyl-CoA as the substrate, which is a gene of a PHA synthase from
Pseudomonas sp. 6-19. The gene of the PHA synthase using lactyl-CoA as the substrate
may be a gene having an amino-acid sequence of SEQ ID NO: 4 or a gene having a base
sequence corresponding to a mutant amino acid sequence in which at least one selected
from the group consisting of E130D, S325T, S477R, S477H, S477F, S477Y, S477G,
10 Q481M, Q481K, and Q481R is mutated in the amino-acid sequence of SEQ ID NO: 4.

In particular, the phaC1_{Ps6-19}400 gene may be the gene of a PHA synthase from
Pseudomonas sp. 6-19 that is preferable for producing the PLA or PLA copolymer using
sucrose.

Also, the cell or plant according to the present invention may further include a gene
15 of an enzyme for producing hydroxyacyl-CoA from sucrose. Since a recombinant cell or
plant further including the gene of the enzyme for producing hydroxyacyl-CoA from
sucrose can produce hydroxyacyl-CoA on its own, even if hydroxyalkanoate is not
included in a medium, hydroxyalkanoate-lactate copolymer may be produced with high
yield. In a specific example of the present invention, the enzymes for producing
20 hydroxyacyl-CoA from sucrose may be a ketothiolase and an acetoacetyl-CoA reductase,
but the present invention is not limited thereto. The ketothiolase and acetoacetyl-CoA
reductase may be derived from *Ralstonia eutropha*.

In a specific example of the present invention, the cell capable of producing the
PLA or hydroxyalkanoate-lactate copolymer may be a bacterium, particularly, *E. coli*.

The present invention provides a cell or plant that is transformed with a recombinant vector for producing a PLA or PLA copolymer containing a gene of an enzyme converting lactate into lactyl-CoA and a gene of a polyhydroxyalkanoate (PHA) synthase using lactyl-CoA as a substrate and uses sucrose as a substrate. The cell or plant
5 may further include a gene of an enzyme for producing 3-hydroxybutyl-CoA from sucrose.

A vector refers to a DNA construct containing a DNA sequence operably linked to a suitable control sequence capable of expressing DNA in an appropriate host. In the present invention, the vector may be a plasmid vector, a bacteriophage vector, a cosmid vector, or a yeast artificial chromosome (YAC) vector. For the purpose of the present
10 invention, a plasmid vector may be used. A typical plasmid vector that serves the purpose of the invention includes (a) a replication origin that allows efficient replication such that each host cell includes several hundred plasmid vectors, (b) an antibiotic-resistance gene that allows selection of a host cell transformed into a plasmid vector, and (c) a restriction enzyme cleavage site in which a foreign DNA fragment may be inserted. Even if there is
15 no appropriate restriction enzyme cleavage site, a vector may be easily ligated with foreign DNA by an ordinary method using a synthetic oligonucleotide adaptor or a linker.

After the ligation process, the vector has to be transformed into an appropriate host cell. In the present invention, the host cell may be a prokaryotic cell or a eukaryotic cell. Preferably, the host cell is a prokaryotic cell. The prokaryotic cell may be a
20 microorganism having one of the above-described three genes or a microorganism having none of the above-described three genes, for example, E.coli. The E.coli may include E.coli strain DH5a, E.coli strain JM101, E.coli K12, E.coli W3110, E.coli X1776, E.coli XL1-Blue (Stratagene), E.coli B, etc. However, E.coli strains, such as FMB101, NM522, NM538, and NM539, and other prokaryotic species and genera may be also used. In

addition to the above-described E.coli and microorganisms having genes of the PHA synthase, *Agrobacterium* sp. strains such as *Agrobacterium* A4, bacilli such as *Bacillus subtilis*, and other enterobacteria such as *Salmonella typhimurium* or *Serratia marcescens*, may be used as host cells. Known eukaryotic host cells such as yeast and mold, insect
5 cells such as *Spodoptera frugiperda* (SF9), animal cells such as Chinese hamster ovary (CHO) cells and mouse cells, and tissue-cultured human and plant cells may be used as host cells. When the vector is transformed into an appropriate host, the vector is capable of replicating or functioning irrespective of a host genome or, in some cases, being integrated with the genome itself.

10 As is known to one skilled in the art, in order to raise an expression level of a transformed gene in a host cell, the transformed gene must be operably linked to an expression control sequence that performs transcription and translation functions in a selected expression host. Preferably, the expression control sequence and the transformed gene are included in a single expression vector including both a bacterial selectable marker
15 and a replication origin. When an expression host is a eukaryotic cell, the expression vector must further include an expression marker that is useful in the eukaryotic expression host.

The term "expression control sequence" means a DNA sequence essential for expression of an operably linked coding sequence in a specific host. The control sequence
20 includes a promoter required for transcription, an arbitrary operator sequence for controlling the transcription, a sequence for encoding an appropriate mRNA ribosome binding site (RBS), and a sequence for controlling termination of transcription and translation. For example, a control sequence suitable for a prokaryote includes a promoter, a random operator sequence, and an RBS. A control sequence suitable for a eukaryotic

cell includes a promoter, a polyadenylation signal, and an enhancer. The most important factor that affects the expression amount of a gene in a plasmid is a promoter. A SR α promoter or a cytomegalovirus promoter may be used as a high-expression promoter.

In order to express a DNA sequence of the present invention, any one of various
5 expression control sequences may be used for a vector. The expression control sequence may be, for example, early and late promoters of SV40 or adenovirus, the lac system, the trp system, the tac system, the trc system, T3 and T7 promoters, the major operator and promoter regions of phage λ , the control region of fd code protein, the promoters of 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of phosphatase, for
10 example, the promoters, e.g., Pho5, the promoter of a yeast α -mating system, other sequences with configurations or derivations known to control expression of a prokaryotic or eukaryotic cell or their viruses, and various combinations thereof.

When a nucleic acid is disposed in a functional relationship with another nucleic acid sequence, it is operably linked to the nucleic acid sequence. An appropriate molecule
15 (e.g., a transcription-activating protein) may be a gene and control sequence(s) that are linked in such a manner as to enable expression of the gene when it couple with the control sequence(s). For example, DNA of a pre-sequence or a secretory leader is operably linked to DNA of polypeptide when it is expressed as a pre-protein that participates in secretion of polypeptide; a promoter or enhancer is operably linked to a coding sequence when it
20 affects transcription of the coding sequence; an RBS is operably linked to a coding sequence when it affects transcription of the coding sequence; or the RBS is operably linked to the coding sequence when it is disposed to facilitate translation. In general, “operably linked sequences” means that DNA sequences being linked are contiguous, and in case of the secretory leader contiguous and in a reading frame. However, an enhancer

does not have to contact a coding sequence. Linkage between sequences may be performed by ligation in a convenient restriction enzyme site. However, when there is no restriction enzyme site, a synthetic oligonucleotide adaptor or a linker may be used according to an ordinary method.

5 Of course, it should be understood that all vectors and expression control sequences do not equally function to express DNA sequences according to the present invention. Similarly, all hosts do not equally function with respect to the same expression system. However, one skilled in the art may appropriately select from among various vectors, expression control sequences, and hosts without either departing from the scope of the
10 present invention or bearing excessive experimental burden. For example, a vector must be selected considering a host because the vector must be replicated in the host. Specifically, the copy number and copy number control of the vector and expression of other protein (e.g., an antibiotic marker) encoded by the corresponding vector must be also considered. One skilled in the art may select an appropriate combination out of various
15 vectors, expression control sequences, and hosts within appropriate ranges of the above-described variables.

Also, the transformation of a eukaryotic cell may be easily accomplished using a calcium chloride method described in section 1.82, supra by Sambrook et al. Alternatively, electroporation may be employed for transformation of these cells (Neumann et al., EMBO
20 J., 1:841(1982)).

Meanwhile, transformation of a plant may be achieved by an ordinary method using *Agrobacterium*, a virus vector, etc. For example, a microorganism is transformed with a recombinant vector containing a gene according to the present invention, and the transformed *Agrobacterium* sp. microorganism may infect tissue of a target plant, thereby

obtaining a transformed plant. For instance, a transformed plant according to the present invention may be obtained in the same manner as or in a similar manner to a method of producing PHA using a transformed plant disclosed in WO 94/11519 or US 6,103,956. More specifically, production of a transfected plant may involve (a) pre-culturing an explant of a target plant and co-culturing the explant with transformed agrobacterium for
5 transfection of the plant; (b) culturing the transfected explant in a callus-inducing medium to obtain a callus; and (c) cleaving the callus and culturing the cleaved callus in a shoot-inducing medium to obtain a shoot.

In the present invention, the term "explant" refers to a tissue fragment cut off from a plant and includes a cotyledon or a hypocotyl. The cotyledon or hypocotyl may be used
10 as an explant of a plant used for the method of the present invention. The cotyledon, which is obtained by disinfecting and cleaning a seed of a plant and germinating the seed in a Murashige and Skoog (MS) medium, is preferably used.

In the present invention, target plants to be transformed may be tobacco, tomatoes,
15 red peppers, beans, rice plants, corn, etc, but the present invention is not limited thereto. Also, it is known to one skilled in the art that even if a plant used for transformation is sexually reproducible, it can be asexually reproduced by tissue culture, etc.

【Advantageous Effects】

As explained above, the present invention provides a cell or plant capable of
20 efficiently producing a polylactate (PLA) or PLA copolymer from sucrose and a method of producing PLA and PLA copolymer by growing or culturing the cell or plant.

【Description of Drawings】

FIG. 1 is a schematic diagram of a process of preparing a recombinant expression vector containing a mutant gene of a polyhydroxyalkanoate (PHA) synthase from *Pseudomonas* sp. 6-19, a mutant gene of a propionyl-CoA transferase from *Clostridium propionicum*, and a gene of a phaAB from *Ralstonia eutropha* according to an example of
5 the present invention.

【Modes of the Invention】

Hereinafter, examples of the present invention will be described in detail. However, the present invention is not limited to the examples disclosed below, but can be implemented in various modified forms. The present examples are provided to fully
10 enable those of ordinary skill in the art to embody and practice the invention

Example 1: Preparation of a recombinant E.coli

A recombinant E.coli W transformed with a pPs619C1400CPPCT532ReAB plasmid was prepared. The E.coli strain W (ATCC9637) according to the present Example may metabolize sucrose as a carbon source.

15 The pPs619C1400CPPCT532ReAB plasmid prepared for the present invention was constructed to express four kinds of major enzymes. The major enzymes are essential for biosynthesis of poly(3-hydroxybutyrate-co-lactate), which is a biodegradable polymer, in the E. coli. The major enzymes may be phaC_{1Ps6-19}400, which is a polymerase from *Pseudomonas* sp. 6-19 (KCTC 11027BP), a propionyl-CoA transferase from *Clostridium propionicum* (CP-PCT), which is an enzyme transferring CoA from acetyl-CoA to lactate
20 to be converted into lactyl-CoA, and a ketothiolase(phaA_{RE}) and an acetoacetyl-CoA reductase (phaB_{RE}) from *Ralstonia eutropha*, which are enzymes for synthesizing 3-hydroxybutyl-CoA from sucrose. The pPs619C1400CPPCT532ReAB plasmid includes

phaC1_{Ps6-19}400, CPPCT532, phaA_{RE} and phaB_{RE} genes respectively encoding the above major enzymes (refer to FIG. 1).

Also, the phaC1_{Ps6-19}400 and CPPCT532 genes are respectively obtained by mutating a gene of phaC1_{Ps6-19}, which is a PHA synthase from *Pseudomonas* sp. of SEQ ID NO: 3, and a gene of a CP-PCT of SEQ ID NO: 1, to be advantageous for PLA and PLA copolymer. The pPs619C1400CPPCT532ReAB plasmid is prepared to constitutively express all four genes in the recombinant *E. coli*.

Example 1-1: Preparation of a substrate-specific mutant of a PHA synthase from *Pseudomonas* sp. 6-19

Among various kinds of PHA synthases, a Type II PHA synthase is known as a medium-chain-length PHA (MCL-PHA) synthase for polymerizing a substrate having relatively many carbon atoms, and the MCL-PHA synthase is expected to be very useful in production of a PLA copolymer. Although a phaC1 synthase from *Pseudomonas* sp. 61-3, which has a high homology with the phaC1_{Ps6-19} synthase obtained according to the present invention, is the Type II synthase, it has been reported that the phaC1 synthase has a relatively wide range of substrate specificity (Matsusaki et al., *J. Bacteriol.*, 180:6459, 1998), and results of research into a mutant suitable for production of short-chain-length PHA (SCL-PHA) were reported (Takase et al., *Biomacromolecules*, 5:480, 2004). Based on the above research, the present inventors prepared mutants of a phaC1_{Ps6-19} synthase by an SDM method using amino acids affecting SCL activation, as disclosed in Korean Patent Application No. 10-2006-0116234.

More specifically, in order to separate a PHA synthase ((phaC1_{Ps6-19}) gene from *Pseudomonas* sp. 6-19(KCTC 11027BP), the total DNA of *Pseudomonas* sp. 6-19 was extracted, primers having base sequences of SEQ ID NOS: 5 and 6 were prepared based on

the phaC1_{Ps6-19} base sequence (Ae-jin Song, Master's Thesis, Department of Chemical and Biomolecular Engineering, KAIST, 2004), and polymerase chain reaction (PCR) was performed to obtain the phaC1_{Ps6-19} gene.

SEQ ID NO: 5: 5'-GAG AGA CAA TCA AAT CAT GAG TAA CAA GAG TAA
5 CG-3'

SEQ ID NO:6: 5'-CAC TCA TGC AAG CGT CAC CGT TCG TGC ACG TAC-3'

When Agarose gel electrophoresis was performed on a PCR reactant, a 1.7-kbp gene fragment corresponding to the phaC1_{Ps6-19} gene was confirmed. In order to express the phaC1_{Ps6-19} synthase, an operon-type constitutive expression system in which a monomer supplying enzyme and a synthase are expressed together was adopted.

From a pSYL105 vector (Lee et al., *Biotech. Bioeng.*, 1994, 44:1337-1347), a DNA fragment containing a PHB producing operon from *Ralstonia eutropha* H16 was cleaved with BamHI/EcoRI, and then inserted into a BamHI/EcoRI restriction site of pBluescript II (Stratagene), thereby preparing a pReCAB recombinant vector.

15 It is known that the pReCAB vector constitutively expresses a PHA synthase (phaC_{RE}) and monomer-supplying enzymes (phaA_{RE} and phaB_{RE}) by a PHB operon promoter, and also effectively operated in E.coli (Lee et al., *Biotech. Bioeng.*, 1994, 44:1337-1347). The pReCAB vector was cleaved with BstBI/SbfI to remove a R. *eutropha* H16 PHA synthase (phaC_{RE}), and the phaC1_{Ps6-19} gene was inserted into a
20 BstBI/SbfI restriction site, thereby preparing a pPs619C1-ReAB recombinant vector.

In order to prepare a phaC1_{Ps6-19} synthase gene fragment having only a BstBI/SbfI restriction site at an either end, an endogenous BstBI site was removed by site-directed mutagenesis (SDM) without changes of amino acids, and the BstBI/SbfI restriction site

was added by overlapping PCR using primers having base sequences of SEQ ID NOs: 7 and 8, 9 and 10, and 11 and 12.

SEQ ID NO: 7: 5'- atg ccc gga gcc ggt tcg aa -3'

5 SEQ ID NO: 8: 5'- CGT TAC TCT TGT TAC TCA TGA TTT GAT TGT CTC TC
-3'

SEQ ID NO: 9: 5'- GAG AGA CAA TCA AAT CAT GAG TAA CAA GAG TAA
CG -3'

SEQ ID NO: 10: 5'- CAC TCA TGC AAG CGT CAC CGT TCG TGC ACG TAC
-3'

10 SEQ ID NO: 11: 5'- GTA CGT GCA CGA ACG GTG ACG CTT GCA TGA GTG
-3'

SEQ ID NO: 12: 5'- aac ggg agg gaa cct gca gg - 3'

The sequence of the phaC1_{Ps6-19} gene of the prepared pPs619C1-ReAB recombinant vector was confirmed by sequencing and represented as SEQ ID NO: 3, and a sequence of
15 an amino acid encoded by the base sequence of SEQ ID NO: 3 was represented as SEQ ID
NO: 4.

In order to check if the phaC1_{Ps6-19} synthase produces PHB or not, the pPs619C1-ReAB recombinant vector was transformed into E.coli XL-1Blue(Stratagene), and then the transformed E.coli was grown in a PHB detection medium (Luria Bertani (LB) agar,
20 glucose 20g/L, Nile red 0.5μ g/ml). As a result, PHB production was not detected.

Three amino-acid sites affecting SCL activity were found via amino-acid sequence analysis, and mutants of a phaC1_{Ps6-19} synthase were prepared by SDM using primers of SEQ ID NOs: 13 to 18 as shown in Table 1.

[Table 1]

Recombinant vector	Nucleic acid substitution	Amino acid substitution	Primer
pPs619C1200-ReAB	AGC → ACC	S325T	SEQ ID NOs: 13/14
	CAG → ATG	Q481M	SEQ ID NOs: 15/16
pPs619C1300-ReAB	GAA → GAT	E130D	SEQ ID NOs: 17/18
	AGC → ACC	S325T	SEQ ID NOs: 13/14
	CAG → ATG	Q481M	SEQ ID NOs: 15/16

S325T

SEQ ID NO: 13: 5'- CTG ACC TTG CTG GTG ACC GTG CTT GAT ACC ACC-

3'

SEQ ID NO: 14: 5'- GGT GGT ATC AAG CAC GGT CAC CAG CAA GGT

5 CAG-3'

Q481M

SEQ ID NO: 15: 5'- CGA GCA GCG GGC ATA TC A TGA GCA TCC TGA

ACC CGC-3'

SEQ ID NO: 16: 5'- GCG GGT TCA GGA TGC TCA TGA TAT GCC CGC TGC

10 TCG-3'

E130D

SEQ ID NO: 17: 5'- atc aac ctc atg acc gat gcg atg gcg ccg acc- 3'

SEQ ID NO: 18: 5'- ggt cgg cgc cat cgc atc ggt cat gag gtt gat- 3'

The recombinant vectors were transformed into E.coli XL-1Blue and grown in a
 15 PHB detection medium (LB agar, glucose 20g/L, Nile red 0.5 μ g/ml). As a result,
 production of PHB could be confirmed in both E.coli XL-1Blue transformed with
 pPs619C1200-ReAB and E.coli XL-1Blue transformed with pPs619C1300-ReAB. That is,
 3HB-CoA was produced from glucose due to monomer-supplying enzymes, phaA_{RE} and

phaB_{RE}, and phaC1_{Ps6-19} synthase SCL mutants (phaC1_{Ps6-19}200 & phaC1_{Ps6-19}300) synthesized PHB using 3HB-CoA as a substrate.

Here, in order to construct an operon-type constitutive expression system expressing a propionyl-CoA transferase from *Clostridium propionicum* (CP-PCT) for providing lactyl-CoA functioning as a monomer required for synthesis of PLA and PLA copolymer, a *cp-pct* gene was used. For the *cp-pct* gene, a DNA fragment obtained by polymerizing chromosomal DNA of *Clostridium propionicum* was cloned by PCR using primers of SEQ ID NOs: 19 and 20. In this case, an *NdeI* site existing in a wild-type *cp-pct* gene was removed by SDM to facilitate cloning.

10 SEQ ID NO: 19: 5'-ggaattcATGAGAAAGGTTCCATTATTACCGCAGATGA

SEQ ID NO: 20: 5'-gc tctaga tta gga ctt cat ttc ctt cag acc cat taa gcc ttc tg

Also, overlapping PCR was performed using primers of SEQ ID NOs: 21 and 22 in order to add a *SbfI/NdeI* restriction site.

SEQ ID NO: 21: 5'-agg cct gca ggc gga taa caa ttt cac aca gg- 3'

15 SEQ ID NO: 22: 5'-gcc cat atg tct aga tta gga ctt cat ttc c- 3'

A pPs619C1300-ReAB vector containing phaC1_{Ps6-19}300, which is a phaC1_{Ps6-19} synthase SCL mutant, was cleaved with *SbfI/NdeI* to remove the monomer-supplying enzymes (phaA_{RE} and phaB_{RE}) from *Ralstonia eutropha* H16, and the PCR-cloned *cp-pct* gene was inserted into the *SbfI/NdeI* restriction site, thereby producing a pPs619C1300-
20 CPPCT recombinant vector.

Similarly, various PHA synthase mutants were produced using the following primers. The produced mutants were arranged in the following Tables 2 through 5.

E130D

SEQ ID NO: 17: 5'-atc aac ctc atg acc gat gcg atg gcg ccg acc- 3'

SEQ ID NO: 18: 5' -ggg cgg cgc cat cgc atc ggt cat gag gtt gat- 3'

S325T

SEQ ID NO: 13: 5'-CTG ACC TTG CTG GTG ACC GTG CTT GAT ACC ACC-

3'

5 SEQ ID NO: 14: 5'- GGT GGT ATC AAG CAC GGT CAC CAG CAA GGT

CAG- 3'

S477R

SEQ ID NO: 23: 5'-gaa ttc gtg ctg tcg agc cgc ggg cat atc- 3'

SEQ ID NO: 24: 5'-gat atg ccc gcg gct cga cag cac gaa ttc- 3'

10

S477H

SEQ ID NO: 25: 5'-gaa ttc gtg ctg tcg agc cat ggg cat atc- 3'

SEQ ID NO: 26: 5'-gat atg ccc atg gct cga cag cac gaa ttc- 3'

S477F

SEQ ID NO: 27: 5'- gaa ttc gtg ctg tcg agc ttt ggg cat atc- 3'

15

SEQ ID NO: 28: 5'- gat atg ccc aaa gct cga cag cac gaa ttc- 3'

S477Y

SEQ ID NO: 29: 5'-gaa ttc gtg ctg tcg agc tat ggg cat atc- 3'

SEQ ID NO: 30: 5'-gat atg ccc ata gct cga cag cac gaa ttc- 3'

S477G

20

SEQ ID NO: 31: 5'-gaa ttc gtg ctg tcg agc ggc ggg cat atc- 3'

SEQ ID NO: 32: 5'-gat atg ccc gcc gct cga cag cac gaa ttc- 3'

Q481K

SEQ ID NO: 33: 5'-ggg cat atc aaa agc atc ctg aac ccg c- 3'

SEQ ID NO: 34: 5'-gcg ggt tca gga tgc ttt tga tat gcc c- 3'

Q481M

SEQ ID NO: 35: 5'-ggg cat atc atg agc atc ctg aac ccg c- 3'

SEQ ID NO: 36: 5'-gcg ggt tca gga tgc tca tga tat gcc c- 3'

Q481R

5 SEQ ID NO: 37: 5'-ggg cat atc cgc agc atc ctg aac ccg c- 3'

SEQ ID NO: 38: 5'-gcg ggt tca gga tgc tgc gga tat gcc c- 3'

[Table 2]

Recombinant synthase	Nucleic acid substitution	Amino acid substitution	Primer
pPs619C1200	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1202	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1203	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1204	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1205	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	CAG → CGC	Q481R	SEQ ID NOs: 37 and 38

[Table 3]

Recombinant synthase	Nucleic acid substitution	Amino acid substitution	Primer
pPs619C1300	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1301	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1304	GAA → GAT	E130D	SEQ ID NOs: 17 and 18

	AGC → CGC	S477R	SEQ ID NOs: 23 and 24
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1305	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → CGC	S477R	SEQ ID NOs: 23 and 24
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1306	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → CGC	S477R	SEQ ID NOs: 23 and 24
	CAG → CGC	Q481R	SEQ ID NOs: 37 and 38
pPs619C1307	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → CAT	S477H	SEQ ID NOs: 25 and 26
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1308	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → CAT	S477H	SEQ ID NOs: 25 and 26
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1309	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → CAT	S477H	SEQ ID NOs: 25 and 26
	CAG → CGC	Q481R	SEQ ID NOs: 37 and 38
pPs619C1310	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → TTT	S477F	SEQ ID NOs: 27 and 28
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34

[Table 4]

Recombinant synthase	Nucleic acid substitution	Amino acid substitution	Primer
pPs619C1311	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → TTT	S477F	SEQ ID NOs: 27 and 28
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1312	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → TTT	S477F	SEQ ID NOs: 27 and 28
	CAG → CGC	Q481R	SEQ ID NOs: 37 and 38
pPs619C1313	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → TAT	S477Y	SEQ ID NOs: 29 and 30

	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1314	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → TAT	S477Y	SEQ ID NOs: 29 and 30
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1315	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → TAT	S477Y	SEQ ID NOs: 29 and 30
	CAG → CGC	Q481R	SEQ ID NOs: 37 and 38

[Table 5]

Recombinant synthase	Nucleic acid substitution	Amino acid substitution	Primer
pPs619C1400	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	AGC → CGC	S477R	SEQ ID NOs: 23 and 24
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1401	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	AGC → CGC	S477R	SEQ ID NOs: 23 and 24
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34
pPs619C1334	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	AGC → TTT	S477F	SEQ ID NOs: 27 and 28
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1336	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	AGC → GGC	S477G	SEQ ID NOs: 31 and 32
	CAG → ATG	Q481M	SEQ ID NOs: 35 and 36
pPs619C1339	GAA → GAT	E130D	SEQ ID NOs: 17 and 18
	AGC → ACC	S325T	SEQ ID NOs: 13 and 14
	AGC → TTT	S477F	SEQ ID NOs: 27 and 28
	CAG → AAA	Q481K	SEQ ID NOs: 33 and 34

Example 1-2: Preparation and screening of a library of a mutant of propionyl-CoA transferase from *Clostridium propionicum*

As is known, when CP-PCT is overexpressed in E.coli, it causes serious metabolic disorder and exhibits toxicity. In general, all recombinant E.coli were dead at the same
5 time with addition of an inducer in an isopropyl- β -D-thio-galactoside (IPTG)-inducible protein expression system using a tac promoter or T7 promoter, which is widely used to express recombinant proteins. For this reason, synthesis of PLA and PLA copolymer was succeeded using a constitutive expression system weakly but continuously expressing a gene with growth of a microorganism. In order to introduce random mutation on a *cp-pct*
10 gene, pPs619C1300-CPPCT disclosed in Korean Patent Application No. 10-2006-0116234 was used as a template, Mn^{2+} was added using primers of SEQ ID NOs: 39 and 40, and error-prone PCR was performed under conditions in which the concentrations of dNTPs varied.

SEQ ID NO: 39: 5'- cgc cgg cag gcc tgc agg -3'

15 SEQ ID NO: 40: 5'- ggc agg tca gcc cat atg tc -3'

Thereafter, in order to amplify a randomly mutated PCR fragment, PCR was performed under common conditions using the primer of SEQ ID NOs: 39 and 40. A pPs619C1300-CPPCT vector containing *phaC1*_{P86-19}300, which is a *phaC1*_{P86-19} synthase, was cleaved with *SbfI/NdeI* to remove a wild-type *cp-pct* gene, and the amplified mutated PCR
20 fragment was inserted into a *SbfI/NdeI* restriction site to produce a ligation mixture. The ligation mixture was introduced to E. coli JM109, thereby preparing a CP-PCT library with a scale of about $\sim 10^5$. The prepared CP-PCT library was incubated for 3 days in a polymer detection medium (LB agar, glucose 20g/L, 3HB 1g/L, Nile red 0.5 μ g/ml) and screened to confirm whether a polymer was produced, thereby primarily selecting up to 80

candidates. The candidates were grown for 4 days in a liquid medium (LB agar, glucose 20g/L, 3HB 1g/L, ampicillin 100mg/L, 37°C) under polymer-generating conditions and analyzed by fluorescence activated cell sorting (FACS), thereby selecting two final samples. In order to find out the positions of the prepared CP-PCT mutants, gene sequence analysis of the CP-PCT mutants was performed as shown in Table 6.

[Table 6]

Recombinant vector	Nucleic acid substitution
CP-PCT Mutant 512	A1200G
CP-PCT Mutant 522	T78C, T669C, A1125G, T1158C

Random mutagenesis was performed on the finally selected mutants 512 and 522 using the above-described error-prone PCR, thereby obtaining the following CP-PCT mutants 531-537.

10 [Table 7]

	Mutations	Silent Mutations
CpPct512		A1200G
CpPct522		T78C, T669C, A1125G, T1158C
CpPct531	Gly335Asp	A1200G
CpPct532	Ala243Thr	A1200G
CpPct533	Asp65Gly	T669C, A1125G, T1158C
CpPct534	Asp257Asn	A1200G
CpPct535	Asp65Asn	T669C, A1125G, T1158C
CpPct537	Thr199Ile	T669C, A1125G, T1158C
CpPct540	Val193Ala	T78C, T669C, A1125G, T1158C

Thereafter, in order to amplify a PCR fragment including the CpPct532 mutant, a PCR method was performed under common conditions using the primers of SEQ ID NOs: 39 and 40. The pPs619C1300-CPPCT vector was cleaved with *SbfI/NdeI* to remove a wild-type CP-PCT gene, and the amplified CpPct532 PCR fragment was inserted into a

SbfI/NdeI restriction site to produce a ligation mixture, thereby producing the pPs619C1300-CPPCT532 vector used in the following Example 1-3.

Example 1-3: Preparation of the pPs619C1300-CPPCT532 vector

A PHA synthase mutant (*phaC1_{Ps6-19}400*) from *Pseudomonas* sp. 6-19, which has
 5 an amino-acid sequence in which E130D, S325T, S477R, and Q481M were mutated, was prepared using the *phaC1_{Ps6-19}* synthase mutant (*phaC1_{Ps6-19}300*) by SDM using primers of SEQ ID NOS: 41 and 42.

SEQ ID NO: 41: 5'- ttc gtg ctg tcg agc aga ggg cat atc- 3'

SEQ ID NO: 42: 5'- gat atg ccc tct gct cga cag cac gaa- 3'

10 The resultant recombinant vector (pPs619C1400-CPPCT532) was transformed into *E.coli* JM109 and grown in a 3HB-containing polymer detection medium (LB agar, glucose 20g/L, 3HB 2g/L, Nile red 0.5 μ g/ml). As a result, polymer production was detected.

**Example 1-4: Preparation of a pPs619C1400CPPCT532ReAB plasmid and
 15 transformation of *E.coli***

In order to produce plasmids containing *phaC1_{Ps6-19}400*, CPPCT532, *phaA_{RE}*, and *phaB_{RE}* genes respectively encoding enzymes required for efficient production of PLA and PLA copolymer from sucrose, PCR cloning was performed with respect to a PHB - producing promoter pReC and *phaA_{RE}* and *phaB_{RE}* genes from *Ralstonia eutropha* H16 on
 20 a pSYL105 vector (Lee et al., Biotech. Bioeng., 1994, 44:1337-1347) using primers of SEQ ID NOS: 43 and 44 and primers of SEQ ID NOS: 45 and 46, respectively.

SEQ ID NO: 43: 5'- aga cat atg caa gta cct tgc cga cat cta tg- 3'

SEQ ID NO: 44: 5'- gat gac aac gtc agt cat gat ttg att gtc tct ctg - 3'

SEQ ID NO: 45: 5'- cag aga gac aat caa atc atg act gac gtt gtc atc - 3'

SEQ ID NO: 46: 5'- gca ggt cag ccc ata tgc ag - 3'

A PCR reactant was purified on an agarose gel, and the overlapping PCR was performed using the PCR reactant as a template and the primers of SEQ ID NOs: 43 and 46. The PCR reactant and the pPs619C1400CPPCT532 vector were cleaved with *NdeI*,
5 and the PCR reactant (pReC-phaABRE) was inserted into a *NdeI* restriction site of the pPs619C1400CPPCT532 vector, thereby completing a pPs619C1400CPPCT532ReAB vector as shown in FIG. 1. In the pPs619C1400CPPCT532ReAB vector, the PHB-producing promoter (pReC) was additionally inserted into the front portions of the phaA_{RE} and phaB_{RE} genes in order to further promote transcription of the target phaA_{RE} and
10 phaB_{RE} genes.

The recombinant vector (pPs619C1400CPPCT532ReAB) was transformed into *E.coli* JM109, and grown in a 3HB-free polymer detection medium (LB agar, glucose 20g/L, Nile red 0.5 μ g/ml). As a result, polymer production could be observed. Thus, it could be confirmed that the phaA_{RE} and phaB_{RE} genes additionally inserted into the
15 pPs619C1400CPPCT532 vector were expressed and operated normally.

Example 2: Preparation of poly(3-hydroxybutyrate-co-lactate) (P(3HB-co-LA)) from a recombinant *E.coli* using sucrose as a carbon source

A colony on an LB agar plate containing 100 mg/L of ampicillin as an antibiotic was inoculated into 3mL of a LB medium containing 100 mg/L of ampicillin and cultured
20 for 12 hours at 30°C, while being stirred at 200rpm. 1mL of the culture solution was inoculated into each of 100mL methyl red (MR) medium and 100mL LB medium, which contains 100 mg/L of ampicillin, 20 g/L of sucrose, and in some cases, 2 g/L of 3-hydroxybutyrate. Thereafter, each culture solution was cultured at about 30°C for 4 days,

while being stirred at 200 rpm. The initial pH of the MR medium was adjusted to pH 7 using 10 N NaOH. The medium samples used in the present culturing process are shown in the following Table 8.

After the culture was finished, biomasses were retrieved from the culture solutions.

- 5 The retrieved cells were cleaned 3 times with distilled water and dried for 24 hours in a dryer maintained at about 100 °C. The dried cells were partially collected and underwent gas chromatographic (GC) analysis, thereby measuring the content of P(3HB-co-LA) synthesized in cells. Standard materials used for the GC analysis were a P(3HB-co-3HV) copolymer (including about 12% by weight 3HV) and a PLA homopolymer. The GC
- 10 analysis results are shown in the following Table 9. As can be seen from Table 9, biosynthesis of a P(3HB-co-LA) copolymer was enabled in both the MR and LB media irrespective of the addition of 3HB. Also, it could be confirmed that the biosynthesis of the P(3HB-co-LA) copolymer was more efficient in the MR medium than in the LB medium. Therefore, the P(3HB-co-LA) copolymer could be produced from sucrose using
- 15 the recombinant *E. coli* according to the present invention.

[Table 8]

Component	LB medium (/L)	MR medium (/L)
Trypsin	10 g	
Yeast extract	5 g	
NaCl	10 g	
KH ₂ PO ₄	-	6.67 g
(NH ₄) ₂ HPO ₄	-	4 g
Citrate	-	0.8 g
MgSO ₄ .H ₂ O	-	0.8 g
3HB	0 g or 2 g	0 g or 2 g
Sucrose	20 g	20 g

Tracer*	-	5 mL
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*Tracer (/L): 10g of FeSO₄.H₂O ; 2.25g of ZnSO₄.H₂O; 1g of CuSO₄.H₂O; 0.5g of MnSO₄.H₂O; 2g of CaCl₂.H₂O; 0.23g of Na₂B₄O₇.H₂O; 0.1g of (NH₄)₆Mo₇O₂₄; 10mL of 35 % HCl.

[Table 9]

Medium	Initial substrate	Type of biosynthesized polymer	Polymer content (weight ratio)	Content of LA in polymer (molar ratio)
MR	Su*	P(3HB-co-LA)	13.41	12.03
MR	Su, 3HB**	P(3HB-co-LA)	21.74	9.15
LB	Su	P(3HB-co-LA)	2.68	17.49
LB	Su, 3HB	P(3HB-co-LA)	2.29	10.85

5 * Su: 20 g/L of sucrose

** 3HB: 2g/L of 3-hydroxybutyrate

While the invention has been shown and described with reference to certain examples thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims.

10

【CLAIMS】**【Claim 1】**

A method of producing a polylactate (PLA) or hydroxyalkanoate-lactate copolymer from sucrose, comprising:

5 culturing or growing a cell or plant in an environment containing lactate and sucrose or an environment containing lactate, sucrose, and hydroxyalkanoate, wherein the cell or plant comprises a gene of an enzyme converting lactate into lactyl-CoA and a gene of a polyhydroxyalkanoate (PHA) synthase using lactyl-CoA as a substrate, and is capable of producing the PLA or hydroxyalkanoate-lactate copolymer using sucrose as a substrate;

10 and

 harvesting the PLA or hydroxyalkanoate-lactate copolymer from the cell or plant.

【Claim 2】

The method according to claim 1, wherein the cell or plant is obtained by transforming a cell or plant that does not include at least one of the gene of the enzyme
15 converting lactate into lactyl-CoA and the gene of the PHA synthase using lactyl-CoA as the substrate and is capable of using sucrose as a substrate, with at least one of the gene of the enzyme converting lactate into lactyl-CoA and the gene of the PHA synthase using lactyl-CoA as the substrate.

【Claim 3】

20 The method according to claim 1, wherein hydroxyalkanoate of the hydroxyalkanoate-lactate copolymer is at least one selected from the group consisting of 3-hydroxybutyrate, 3-hydroxyvalerate, 4-hydroxybutyrate, medium chain-length (D)-3-hydroxycarboxylic acid with 6 to 14 carbon atoms, 2-hydroxypropionic acid, 3-

hydroxypropionic acid, 3-hydroxyhexanoic acid, 3-hydroxyheptanoic acid, 3-hydroxyoctanoic acid, 3-hydroxynonanoic acid, 3-hydroxydecanoic acid, 3-hydroxyundecanoic acid, 3-hydroxydodecanoic acid, 3-hydroxytetradecanoic acid, 3-hydroxyhexadecanoic acid, 4-hydroxyvaleric acid, 4-hydroxyhexanoic acid, 4-hydroxyheptanoic acid, 4-hydroxyoctanoic acid, 4-hydroxydecanoic acid, 5-hydroxyvaleric acid, 5-hydroxyhexanoic acid, 6-hydroxydodecanoic acid, 3-hydroxy-4-pentenoic acid, 3-hydroxy-4-trans-hexenoic acid, 3-hydroxy-4-cis-hexenoic acid, 3-hydroxy-5-hexenoic acid, 3-hydroxy-6-trans-octenoic acid, 3-hydroxy-6-cis-octenoic acid, 3-hydroxy-7-octenoic acid, 3-hydroxy-8-nonenoic acid, 3-hydroxy-9-decenoic acid, 3-hydroxy-5-cis-dodecenoic acid, 3-hydroxy-6-cis-dodecenoic acid, 3-hydroxy-5-cis-tetradecenoic acid, 3-hydroxy-7-cis-tetradecenoic acid, 3-hydroxy-5,8-cis-cis-tetradecenoic acid, 3-hydroxy-4-methylvaleric acid, 3-hydroxy-4-methylhexanoic acid, 3-hydroxy-5-methylhexanoic acid, 3-hydroxy-6-methylheptanoic acid, 3-hydroxy-4-methyloctanoic acid, 3-hydroxy-5-methyloctanoic acid, 3-hydroxy-6-methyloctanoic acid, 3-hydroxy-7-methyloctanoic acid, 3-hydroxy-6-methylnonanoic acid, 3-hydroxy-7-methylnonanoic acid, 3-hydroxy-8-methylnonanoic acid, 3-hydroxy-7-methyldecanoic acid, 3-hydroxy-9-methyldecanoic acid, 3-hydroxy-7-methyl-6-octenoic acid, malic acid, 3-hydroxysuccinic acid-methylester, 3-hydroxyadipinic acid-methylester, 3-hydroxysuberic acid-methylester, 3-hydroxyazelaic acid-methylester, 3-hydroxysebacic acid-methylester, 3-hydroxysuberic acid-ethylester, 3-hydroxysebacic acid-ethylester, 3-hydroxypimelic acid-propylester, 3-hydroxysebacic acid-benzylester, 3-hydroxy-8-acetoxyoctanoic acid, 3-hydroxy-9-acetoxynonanoic acid, phenoxy-3-hydroxybutyric acid, phenoxy-3-hydroxyvaleric acid, phenoxy-3-hydroxyheptanoic acid, phenoxy-3-hydroxyoctanoic acid, para-cyanophenoxy-3-hydroxybutyric acid, para-cyanophenoxy-3-hydroxyvaleric acid, para-cyanophenoxy-3-

hydroxyhexanoic acid, para-nitrophenoxy-3-hydroxyhexanoic acid, 3-hydroxy-5-phenylvaleric acid, 3-hydroxy-5-cyclohexylbutyric acid, 3,12-dihydroxydodecanoic acid, 3,8-dihydroxy-5-cis-tetradecenoic acid, 3-hydroxy-4,5-epoxydecanoic acid, 3-hydroxy-6,7-epoxydodecanoic acid, 3-hydroxy-8,9-epoxy-5,6-cis-tetradecanoic acid, 7-cyano-3-
5 hydroxyheptanoic acid, 9-cyano-3-hydroxynonanoic acid, 3-hydroxy-7-fluoroheptanoic acid, 3-hydroxy-9-fluorononanoic acid, 3-hydroxy-6-chlorohexanoic acid, 3-hydroxy-8-chlorooctanoic acid, 3-hydroxy-6-bromohexanoic acid, 3-hydroxy-8-bromooctanoic acid, 3-hydroxy-11-bromoundecanoic acid, 3-hydroxy-2-butenic acid, 6-hydroxy-3-dodecenoic acid, 3-hydroxy-2-methylbutyric acid, 3-hydroxy-2-methylvaleric acid, and 3-hydroxy-2,6-
10 dimethyl-5-heptenoic acid.

【Claim 4】

The method according to claim 1, wherein the gene of the enzyme converting lactate into lactyl-CoA is a propionyl-CoA transferase gene (*pct*).

【Claim 5】

15 The method according to claim 1, wherein the gene of the enzyme converting lactate into lactyl-CoA is a *pct* gene from *Clostridium propionicum*.

【Claim 6】

The method according to claim 1, wherein the gene of the enzyme converting lactate into lactyl-CoA has one selected from the group consisting of:

20 a base sequence of SEQ ID NO: 1;

a base sequence obtained by mutating T78C, T669C, A1125G, and T1158C in the base sequence of SEQ ID NO: 1;

a base sequence obtained by mutating A1200G in the base sequence of SEQ ID NO: 1;

a base sequence obtained by mutating A1200G in the base sequence of SEQ ID NO: 1 and mutating Gly335Asp in an amino-acid sequence of SEQ ID NO: 2;

5 a base sequence obtained by mutating T669C, A1125G, and T1158Ca in the base sequence of SEQ ID NO: 1 and mutating Asp65Gly in the amino-acid sequence of SEQ ID NO: 2;

a base sequence obtained by mutating T669C, A1125G, and T1158C in the base sequence of SEQ ID NO: 1 and mutating Asp65Asn in an amino-acid sequence with SEQ
10 ID NO: 2;

a base sequence obtained by mutating T669C, A1125G, and T1158C in the base sequence of SEQ ID NO: 1 and mutating Thr199Ile in the amino-acid sequence of SEQ ID NO: 2;

a base sequence obtained by mutating A1200G in the base sequence of SEQ ID
15 NO: 1 and mutating Ala243Thr in the amino-acid sequence of SEQ ID NO: 2;

a base sequence obtained by mutating A1200G in the base sequence of SEQ ID NO: 1 and mutating Asp257Asn in the amino-acid sequence of SEQ ID NO: 2; and

a base sequence obtained by mutating T78C, T669C, A1125G, and T1158C in the base sequence of SEQ ID NO: 1 and mutating Val193Ala in the amino-acid sequence of
20 SEQ ID NO: 2.

【Claim 7】

The method according to claim 6, wherein the gene of the enzyme converting lactate into lactyl-CoA has a base sequence obtained by mutating A1200G in the base

sequence of SEQ ID NO: 1 and mutating Ala243Thr in the amino-acid sequence of SEQ ID NO: 2.

【Claim 8】

The method according to claim 1, wherein the gene of the PHA synthase using
5 lactyl-CoA as the substrate is a gene of a PHA synthase from *pseudomonas* sp. 6-19.

【Claim 9】

The method according to claim 1, wherein the gene of the PHA synthase using
lactyl-CoA as the substrate has a base sequence corresponding to:

an amino-acid sequence of SEQ ID NO: 4; or

10 an amino-acid sequence in which at least one selected from the group consisting of
E130D, S325T, S477R, S477H, S477F, S477Y, S477G, Q481M, Q481K, and Q481R is
mutated in SEQ ID NO: 4.

【Claim 10】

The method according to claim 1, wherein the gene of the PHA synthase using
15 lactyl-CoA as the substrate has a base sequence corresponding to an amino-acid sequence
in which E130D, S325T, S477R, and Q481M are mutated in SEQ ID NO: 4.

【Claim 11】

The method according to any one of claims 1 to 3, wherein the cell or plant further
comprises a gene of an enzyme producing hydroxyacyl-CoA from sucrose.

20 **【Claim 12】**

The method according to claim 11, wherein the enzyme producing hydroxyacyl-
CoA from sucrose is a ketothiolase and an acetoacetyl-CoA reductase.

【Claim 13】

The method according to claim 12, wherein the ketothiolase and the acetoacetyl-CoA reductase are derived from *Ralstonia eutropha*.

【Claim 14】

The method according to any one of claims 1 to 9, wherein the cell is a bacterium.

5 【Claim 15】

The method according to claim 14, wherein the bacterium is an E.coli.

FIG. 1

