acids or ammonia and disposing through the ornithine cycle during the *in-vivo* metabolism of higher organisms. Ornithine is effective in muscle production and reduction of body fat, and thus it has been used as a nutrient supplement and also as a pharmaceutical drug for improving liver cirrhosis and hepatic dysfunction. Methods of producing ornithine include a method of using milk casein as a digestive enzyme and a method of using *E. coli* or a microorganism of the genus *Corynebacterium* (Korean Patent No. 10-1372635; T. Gotoh *et al.*, *Bioprocess Biosyst. Eng.*, 33: 773 - 777, 2010).

E. coli and a microorganism of the genus *Corynebacterium* are simillar in the biosynthetic pathways for producing putrescine or ornithine, but they also exhibit differences as follows. First, the microorganism of the genus *Corynebacterium* has a "cyclic pathway", in which glutamic acid is converted into N-acetyl-L-glutamic acid and N-acetyl-L-ornithine is converted into L-ornithine by argJ (bifunctional ornithine acetyltransferase/N-acetylglutamate synthase, EC 2.3.1.35). In contrast, *E. coli* is involved in the biosynthesis of putrescine or ornithine by a "linear pathway", in which argA (N-acetylglutamate synthase, EC 2.3.1.1) and argE (Acetylornithine deacetylase, EC 3.5.1.16) replace the role of the argJ in the microorganism of the genus *Corynebacterium*.

In the microorganism of the genus *Corynebacterium*, it is known that an acetyl group recycles between ornithine and glutamic acid in ArgJ. However, in *E. coli*, ArgA attaches the acetyl group of acetyl-CoA to glutamate in order to produce N-acetyl-glutamate, and ArgE N-acetyl-ornithine decomposes N-acetyl-ornithine to produce ornithine and acetate (Schneider *et al., Appl. Microbiol. Biotechnol.* 91, 17 - 30., 2011).

In particular, pta-ackA (pta, phosphotransacetylase; ackA, acetate kinase) operon and acetyl-coenzyme A synthetase (acs) are known as genes to synthesize acetyl-CoA using acetate.

SUMMARY

TECHNICAL PROBLEM

The present inventors have made many efforts to improve the ability of a microorganism of the genus *Corynebacterium* to produce ornithine and putrescine, and as a result they have discovered that the introduction of *E. coli*-derived *argA* and *argE* into a microorganism of the genus *Corynebacterium* can improve its ability to produce ornithine and putrescine, thereby completing the present invention.

TECHNICAL SOLUTION

In one aspect, the present invention refers to a modified microorganism of the genus *Corynebacterium* producing putrescine or ornithine, wherein activities of N-acetylglutamate synthase from *E. coli* and acetylornithine deacetylase from *E. coli* are introduced into a microorganism of the genus *Corynebacterium* having ornithine acetyltransferase (ArgJ) activity.

In another aspect, the present invention refers to a method for producing putrescine or ornithine comprising:

(i) culturing the modified microorganism of the genus Corynebacterium of any one of claims 1 to 15 in a medium; and

(ii) recovering putrescine or ornithine from the cultured microorganism or the medium..

ADVANTAGEOUS EFFECTS OF THE INVENTION

It was confirmed that the microorganism of the genus *Corynebacterium* of the present disclosure producing putrescine or ornithine can improve the amount of putrescine- or ornithine production when the microorganism is introduced with *E. coli*-derived *argA* and *E. coli*-derived *argE*, and also when the acetate utilization pathway is reinforced. Accordingly, the microorganism of the present disclosure can be widely used for the production of putrescine or ornithine, and also, can be widely used as an effective and desirable means to supply raw materials for the production of various polymer products, in which the putrescine or ornithine is used as a raw material, from the economic and environmental aspects.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic diagram illustrating a biosynthetic pathway (a cyclic pathway) for producing putrescine and ornithine in a microorganism of the genus *Corynebacterium* (A) and a biosynthetic pathway (a linear pathway) for producing putrescine and ornithine in *E. coli* (B).

FIG. 2 is a schematic diagram illustrating the biosynthetic pathway which has improved the ability to produce putrescine and ornithine by introducing *E. coli*-derived *argA* and *E. coli*-derived *argE* into a microorganism of the genus *Corynebacterium*, which is in a state expressing *argJ*.

BEST MODE

An aspect of the present disclosure provides a modified microorganism of the genus Corynebacterium producing putrescine or ornithine, in which activities of N-acetylglutamate synthase from *E. coli* and acetylornithine deacetylase from *E. coli* are introduced.

An exemplary embodiment of the present disclosure provides a modified microorganism of the genus *Corynebacterium* producing putrescine or ornithine, in which the *E. coli*-derived N-acetylglutamate synthase consists of an amino acid sequence of SEQ ID NO: 1.

CLAIMS

1. A modified microorganism of the genus *Corynebacterium* producing putrescine or ornithine, wherein activities of N-acetylglutamate synthase from *E. coli* and acetylornithine deacetylase from *E. coli* are introduced into a microorganism of the genus *Corynebacterium* having ornithine acetyltransferase (ArgJ) activity.

2. The modified microorganism according to claim 1, wherein the N-acetylglutamate synthase from *E. coli* consists of an amino acid sequence of SEQ ID NO: 1.

3. The modified microorganism according to claim 1, wherein the acetylornithine deacetylase from *E. coli* consists of an amino acid sequence of SEQ ID NO: 3.

4. The modified microorganism according to claim 1, wherein the microorganism of the genus *Corynebacterium* is *Corynebacterium glutamicum.*

5. The modified microorganism according to claim 1, wherein an activity of phosphotransacetylase and acetate kinase operon (*pta-ackA* operon) is further enhanced compared to its endogenous activity

6. The modified microorganism according to claim 5, wherein the phosphotransacetylase and acetate kinase operon consists of an amino acid sequence of SEQ ID NO: 5 or SEQ ID NO: 7.

7. The modified microorganism according to claim 1, wherein an activity of acetyl-CoA synthetase (acs) from *E. coli* is further introduced.

8. The modified microorganism according to claim 7, wherein the acetyl-CoA synthetase consists of an amino acid sequence of SEQ ID NO: 9.

9. The modified microorganism according to claim 1, wherein an activity of ornithine decarboxylase (ODC) is further introduced.

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Ala Asp Leu Leu Ala Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn
     50                  55                  60

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 65                  70                  75                  80

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Val Asn Asn Ala Gly Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln
            100                 105                 110

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785 790 795 800

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Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser Thr
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Thr Phe Phe Asp Ala Gln Val Ala Ala Ala Leu Gly Val Pro Val Leu
 65                  70                  75                  80

Leu Leu Val Asp Lys Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln
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Val Asn Asn Ala Gly Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln
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Glu Pro Met Pro Asp Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn
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