[CLAIMS]

[Claim 1]

A variant polypeptide having glycosyltransferase activity, comprising at least one amino acid substitution selected from the group consisting of : (i) a substitution of an amino acid residue corresponding to position 92 of SEQ ID NO: 1, with tryptophan; (ii) a substitution of an amino acid residue corresponding to position 208 of SEQ ID NO: 1, with alanine or methionine; (iii) a substitution of an amino acid residue corresponding to position 380 of SEQ ID NO: 1, with histidine, threonine, alanine, or glycine; and (iv) a substitution of an amino acid residue corresponding to position 381 of SEQ ID NO: 1, with phenylalanine, serine, alanine, or asparagine.

[Claim 2]

The variant polypeptide of claim 1, wherein the variant polypeptide comprises

(i) a substitution of the amino acid residue corresponding to position 92 of SEQ ID NO: 1 with tryptophan;

(ii) a substitution of the amino acid residue corresponding to position 208 of SEQ ID NO: 1 with alanine or methionine;

(iii) a substitution of the amino acid residue corresponding to position 380 of SEQ ID NO: 1 with histidine, threonine, or alanine;

(iv) a substitution of the amino acid residue corresponding to position 381 of SEQ ID NO: 1 with phenylalanine, serine, alanine, or asparagine; or

(v) a substitution of the amino acid residue corresponding to position 380 of SEQ ID NO: 1 with histidine, threonine, or glycine and a substitution of the amino acid residue corresponding to position 381 of SEQ ID NO: 1 with phenylalanine, serine, alanine, or asparagine.

[Claim 3]

The variant polypeptide of claim 1, wherein the variant polypeptide comprises

(i) a substitution of the amino acid residue corresponding to position 208 of SEQ ID NO: 1 with alanine, a substitution of the amino acid residue corresponding to

position 380 of SEQ ID NO: 1 with threonine or alanine, and a substitution of the amino acid residue corresponding to position 381 of SEQ ID NO: 1 with phenylalanine, serine, or alanine;

(ii) a substitution of the amino acid residue corresponding to position 92 of SEQ ID NO: 1 with tryptophan, a substitution of the amino acid residue corresponding to position 380 of SEQ ID NO: 1 with threonine or alanine, and a substitution of the amino acid residue corresponding to position 381 of SEQ ID NO: 1 with phenylalanine, serine, or alanine;

(iii) a substitution of the amino acid residue corresponding to position 92 of SEQ ID NO: 1 with tryptophan, and a substitution of the amino acid residue corresponding to position 208 of SEQ ID NO: 1 with alanine; or

(iv) a substitution of the amino acid residue corresponding to position 92 of SEQ ID NO: 1 with tryptophan, a substitution of the amino acid residue corresponding to position 208 of SEQ ID NO: 1 with alanine, a substitution of the amino acid residue corresponding to position 380 of SEQ ID NO: 1 with threonine or alanine, and a substitution of the amino acid residue corresponding to position 381 of SEQ ID NO: 1 with phenylalanine, serine, or alanine.

[Claim 4]

The variant polypeptide of claim 1, wherein the amino acid sequence of the variant polypeptide has at least 80% sequence identity to SEQ ID NO: 1.

[Claim 5]

A polynucleotide encoding the variant polypeptide of any one of claims 1 to 4.

[Claim 6]

A vector comprising the polynucleotide of claim 5.

[Claim 7]

A microorganism comprising any one or more of the variant polypeptide of any one of claims 1 to 4, a polynucleotide encoding the variant polypeptide, and a vector

comprising the polynucleotide.

[Claim 8]

The microorganism of claim 7, wherein the microorganism has an enhanced ability to produce one or both of rebaudioside D and rebaudioside M, compared to a microorganism comprising a polynucleotide encoding a polypeptide having the amino acid sequence of SEQ ID NO: 1.

[Claim 9]

The microorganism of claim 7, wherein the microorganism is a microorganism of *Corynebacterium* sp. or *Escherichia* sp.

[Claim 10]

The microorganism of claim 9, wherein the microorganism is *Corynebacterium ammoniagenes*, *Corynebacterium glutamicum*, or *Escherichia coli*.

[Claim 11]

A method of producing a steviol glycoside, the method comprising reacting rebaudioside A with a nucleotide diphosphate-linked glucose in the presence of the variant polypeptide of claim 1 or the microorganism of claim 7, thereby producing one or both of rebaudioside D and rebaudioside M.

[Claim 12]

The method of claim 11, further comprising recovering one or both of rebaudioside D and rebaudioside M.

[Claim 13]

The method of claim 11, further comprising producing rebaudioside M by reacting the rebaudioside D with nucleotide diphosphate-linked glucose in the presence of glycosyltransferase A (UGT-A); or a microorganism comprising any one or more of the glycosyltransferase A, a polynucleotide encoding the same, and a vector comprising the same.

[Claim 14]

A composition for producing rebaudioside D and/or rebaudioside M, the composition comprising one or more selected from the group consisting of: the variant polypeptide of any one of claims 1 to 4; a polynucleotide encoding the variant polypeptide; a microorganism comprising any one or more of the variant polypeptide, the polynucleotide encoding the variant polypeptide, and a vector comprising the polynucleotide; and a culture of the microorganism.

[Claim 15]

Use of a microorganism comprising any one or more of the variant polypeptide of any one of claims 1 to 4, a polynucleotide encoding the variant polypeptide, and a vector comprising the polynucleotide, for the production of rebaudioside D and/or rebaudioside M.

[Claim 16]

Use of a composition comprising one or more selected from the group consisting of the variant polypeptide of any one of claims 1 to 4, a polynucleotide encoding the variant polypeptide, a microorganism comprising any one or more of the variant polypeptide, the polynucleotide encoding the variant polypeptide, and a vector comprising the polynucleotide, and a culture of the microorganism, for the production of rebaudioside D and/or rebaudioside M.