CLAIMS

1. A uridine diphosphate-dependent glycosyltransferase (UGT) enzyme comprising an amino acid sequence that is at least 85% identical to the amino acid sequence of SEQ ID NO: 5 or SEQ ID NO: 6, wherein:

the enzyme has an insertion with respect to SEQ ID NO: 1 of a flexible and hydrophilic sequence of 6 to 12 amino acids that is predominately Glycine and Serine residues after the position corresponding to position 155 of SEQ ID NO: 5; and

the enzyme retains one or more of:

a glycine (G) at the position corresponding to position 54 of SEQ ID NO: 5;

a leucine (L) at the position corresponding to position 111 of SEQ ID NO: 5; and

a methionine (M) at the position corresponding to position 183 of SEQ ID NO: 5.

2. The enzyme of claim 1, wherein the amino acid sequence is at least 95% identical to SEQ ID NO: 5 or SEQ ID NO: 6.

3. The enzyme of claim 1, wherein the enzyme has Gly at the position corresponding to position 54 of SEQ ID NO: 5, Leu at the position corresponding to position 111 of the SEQ ID NO: 5, and a Met at the position corresponding to position 183 of SEQ ID NO: 5.

4. The enzyme of claim 1, wherein the insertion is GSGGSG (SEQ ID NO: 7) or GSGGSGGSG (SEQ ID NO: 8).

5. The enzyme of claim 1, wherein the enzyme comprises a deletion of at least three amino acids corresponding to amino acids E225 to T232 with respect to the amino acid sequence of SEQ ID NO: 6.

6. The enzyme of claim 5, wherein the enzyme comprises a deletion of the amino acids corresponding to amino acids E225 to T232 of SEQ ID NO: 6.

7. The enzyme of claim 1, wherein the enzyme comprises an amino acid substitution at one or more positions corresponding to position 72, position 305, position 345, and position 428 of SEQ ID NO: 6.

8. The enzyme of claim 7, wherein the enzyme comprises one or more amino acid substitutions selected from: a glutamine (Q) at the position corresponding to position 72 of SEQ ID NO: 6; a cysteine (C) at the position corresponding to position 305 of SEQ ID NO: 6; a phenylalanine (F) at the position corresponding to position 345 of SEQ ID NO: 6; and an isoleucine (I) at the position corresponding to position 428 of SEQ ID NO: 6.

9. A uridine diphosphate-dependent glycosyltransferase (UGT) enzyme comprising an amino acid sequence that is at least 85% identical to the amino acid sequence of SEQ ID NO: 5 or SEQ ID NO: 6, wherein the UGT enzyme comprises:

a glycine (G) at the position corresponding to position 54 of SEQ ID NO: 5;

a leucine (L) at the position corresponding to position 111 of SEQ ID NO: 5; and

a methionine (M) at the position corresponding to position 183 of SEQ ID NO: 5.

10. A uridine diphosphate-dependent glycosyltransferase (UGT) enzyme comprising an amino acid sequence that has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:1, and comprising a deletion of amino acids corresponding to E74 to T81 of SEQ ID NO: 1.

11. A uridine diphosphate-dependent glycosyltransferase (UGT) enzyme that is a circular permutant of SrUGT76G1 (SEQ ID NO: 1), and having from 1 to 20 amino acid modifications independently selected from amino acid substitutions, deletions, and insertions with respect to the corresponding position of SEQ ID NO:1, with the proviso that the circular permutant has a deletion of amino acids corresponding to amino acids E74 to T81 of SEQ ID NO: 1.

12. The enzyme of claim 5, wherein the enzyme comprises a deletion of at least five amino acids corresponding to amino acids E74 to T81 with respect to the amino acid sequence of SEQ ID NO: 6.

13. The enzyme of claim 7, wherein the enzyme comprises a substitution of glutamine (Q) or asparagine (N) at the position corresponding to position 72 of SEQ ID NO: 6.

14. The enzyme of claim 7, wherein the enzyme comprises a neutral hydrophilic amino acid selected from cysteine (C), Serine (S), or Threonine (T) at the position corresponding to position 305 of SEQ ID NO: 6.

15. The enzyme of claim 7, wherein the enzyme comprises a substitution of phenylalanine (F) or Tryptophan (W) at the position corresponding to position 345 of SEQ ID NO: 6.

16. The enzyme of claim 7, wherein the enzyme comprises a substitution of isoleucine (I), valine (V), or alanine (A) at the position corresponding to position 428 of SEQ ID NO: 6.

17. The enzyme of claim 7, wherein the enzyme comprises 2, 3, or 4 of the following substitutions with respect to SEQ ID NO: 6: S72Q, A305C, Y345F, and L428I.

18. A uridine diphosphate-dependent glycosyltransferase (UGT) enzyme comprising an amino acid sequence that is at least 85% identical to the amino acid sequence of SEQ ID NO: 5 or SEQ ID NO: 6, and comprising a deletion of at least three amino acids corresponding to amino acids E225 to T232 with respect to SEQ ID NO: 6.

19. The UGT enzyme of claim 18, wherein the enzyme comprises a deletion of at least five amino acids corresponding to amino acids E225 to T232 with respect to SEQ ID NO: 6.

20. The UGT enzyme of claim 18, wherein the enzyme comprises a deletion of the amino acids corresponding to amino acids E225 to T232 with respect to SEQ ID NO: 6.

21. The UGT enzyme of claim 18, wherein the enzyme is at least 90% identical to SEQ ID NO: 5 or SEQ ID NO: 6.

22. The UGT enzyme of claim 18, wherein the enzyme is at least 95% identical to SEQ ID NO: 5 or SEQ ID NO: 6.

23. A polynucleotide encoding the enzyme of any one of claims 1, 9, 10, 11 or 18.

24. An isolated recombinant microorganism comprising the polynucleotide of claim 23.

25. A method for transferring a monosaccharide group to a substrate comprising contacting a NDP-sugar and the substrate with the isolated recombinant microorganism of claim 24.

26. A method for transferring a glycosyl group to a substrate comprising growing the isolated recombinant microorganism of claim 24 in the presence of the substrate.