WHAT IS CLAIMED IS:

1. A method of producing a plant or plant cell with a modified cucurbitacin content, the method comprising down-regulating expression of at least one cucurbitacin biosynthetic pathway gene in the plant or plant cell, thereby modifying cucurbitacin expression in said plant or plant cell and, optionally growing said plant or plant cell with a modified cucurbitacin content.

2. A plant or plant cell modified to have reduced expression of at least one gene of the cucurbitacin biosynthetic pathway, wherein said cucurbit plant or plant cell is obtainable according to the method of claim 1, and, optionally, wherein said plant or plant cell is an elite plant or plant cell, or a hybrid plant or plant cell or an inbred plant or plant cell.

3. The plant or plant cell of claim 2, wherein said plant or plant cell comprises at least one tetracyclic triterpene capable of glucosylation by a UDP-glucoronosyltransferase (UGT).

4. The plant or plant cell of claim 3, wherein said UGT is a plant UGT characterized by at least one of the following:

i) said UGT is selected from the group consisting of S. grosvenorii UGTs selected from the group consisting of UGT74-345-2, UGT73-348-2, UGT94-289-1, UGT73-327-2, UGT73-251-5, UGT73-251-6, UGT75-281-2, UGT85-269-4, UGT85-269-1, UGT94-289-2 and UGT94-289-3;

ii) said UGT is a UGT having an amino acid sequence selected from the group consisting of SEQ ID NOs. 139, 140, 141, 142, 143, 144, 145, 146, 147, 148 and 149, and

iii) said UGT is a UGT encoded by a polynucleotide having a nucleotide sequence selected from the group consisting of SEQ ID NOs. 128, 129, 130, 131, 132, 133, 135 and 137.

5. An extract of the plant or plant cell of any one of claims 2 or 3, comprising at least one tetracyclic triterpene capable of glucosylation by a UGT.

6. The method of any one of claims 1, or plant or plant cell of any one of any one of claims 2-4, or the extract of claim 5, wherein said plant or plant cell is characterized by at least of the following:

i) said plant or plant cell is of a bitter cucurbit species;

ii) said plant or plant cell is of a species naturally expressing said at least one cucurbitacin biosynthetic pathway gene;

iii) said plant or plant cell is of a species genetically modified to express said at least one cucurbitacin biosynthetic pathway gene, and

iv) said plant or plant cell is an Iberis amara plant or plant cell.

7. The method of claim 1, or plant or plant cell of any one of any one of claims 2-4, or the extract of claim 5, wherein said plant is selected from the group consisting of cultivated bitter cucurbits and non-cultivated cucurbits, optionally, wherein said non-cultivated bitter cucurbit is selected from the group consisting of non-cultivated bitter melon, non-cultivated bitter cucumber and non-cultivated bitter watermelon, and optionally wherein said cultivated bitter cucurbit is Citrullus vulgaris (bitter Hawkesbury), Cucumis sativus or Cucurbita pepo.

8. The method or plant or plant cell of claim 6, wherein said non-cultivated bitter cucurbit is selected from the group consisting of Cucumis species, Citrullis species, Momordica species and Cucurbita species.

9. The method of claim 1, plant or plant cell of any one of any one of claims 2-4 and 7-8, or extract of claim 5, wherein said at least one cucurbitacin biosynthetic pathway gene is a gene selected from the genes of Table 2.

10. The method of claim 1, plant or plant cell of any one of any one of claims 2-4 and 7-9, or extract of claim 5, wherein said at least one cucurbitacin biosynthetic pathway gene is selected from the group consisting of:

i) a (2OG) and Fe(II)-dependent oxygenase gene, optionally wherein said (2OG) and Fe(II)-dependent oxygenase gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 64, 67 and 70 and optionally wherein said down-regulation of said (2OG) and Fe(II)-dependent oxygenase gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 66, 69 and 72;

ii) wherein said at least one cucurbitacin biosynthetic pathway gene is a cytochrome P450 gene, optionally wherein said cytochrome p450 gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58 and 61, and wherein said down-regulation of said cytochrome

p450 gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60 and 63,

or wherein said cytochrome p450 gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 7, 28, 31, 34, 37 and 49, and wherein said down-regulation of said cytochrome p450 gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 9, 30, 33, 36, 39 and 51;

iii) an FAD-binding Berberine gene, optionally wherein said FAD-binding Berberine gene has the nucleic acid sequence as set forth in SEQ ID NO: 85, and wherein said down-regulation of said FAD-binding Berberine gene is effected by targeting the nucleic acid sequence selected as set forth in SEQ ID NO: 87;

iv) an NAD(P)-binding Rossman-fold gene, optionally wherein said NAD(P)-binding Rossman-fold gene has the nucleic acid sequence as set forth in SEQ ID NO: 88 or 91 and wherein said down-regulation of said NAD(P)-binding Rossman-fold gene is effected by targeting the nucleic acid sequence selected as set forth in SEQ ID NO: 90 or 93, or

wherein said NAD(P)-binding Rossman-fold gene has the nucleic acid sequence as set forth in SEQ ID NO: 88 and wherein said down-regulation of said NAD(P)-binding Rossman-fold gene is effected by targeting the nucleic acid sequence selected as set forth in SEQ ID NO: 90;

v) an HXXXD-type acyl-transferase-like protein gene, optionally wherein said HXXXD-type acyl-transferase-like protein gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 118, 121 and 124, wherein said down-regulation of said HXXXD-type acyl-transferase-like protein gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 120, 123 and 126, or

wherein said HXXXD-type acyl-transferase-like protein gene has the nucleic acid sequence as set forth in SEQ ID NO: 124, wherein said down-regulation of said HXXXD-type acyl-transferase-like protein gene is effected by targeting a nucleic acid sequence as set forth in SEQ ID NO: 126;

vi) a polyketide cyclase/hydrase gene, optionally wherein said polyketide cyclase/hydrase gene has the nucleic acid sequence as set forth in SEQ ID NO: 109, wherein said down-regulation of said polyketide cyclase/hydrase gene is effected by targeting the nucleic acid sequence selected as set forth in SEQ ID NO: 111;

vii) a proline dehydrogenase gene, optionally wherein said proline dehydrogenase gene has the nucleic acid sequence as set forth in SEQ ID NO: 112, wherein said down-regulation of

said proline dehydrogenase gene is effected by targeting the nucleic acid sequence selected as set forth in SEQ ID NO: 114;

viii) a short-chain dehydrogenase/reductase gene, optionally wherein said short-chain dehydrogenase/reductase gene has the nucleic acid sequence as set forth in SEQ ID NO: 115, wherein said down-regulation of said short-chain dehydrogenase/reductase gene is effected by targeting the nucleic acid sequence selected as set forth in SEQ ID NO: 117;

ix) an alcohol dehydrogenase gene, optionally wherein said alcohol dehydrogenase gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 73, 76, 79 and 82, wherein said down-regulation of said alcohol dehydrogenase gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 75, 78, 81 and 84, or

wherein said alcohol dehydrogenase gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 73 and 79, wherein said down-regulation of said alcohol dehydrogenase gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 75 and 81;

x) a peroxidase gene, optionally wherein said peroxidase gene has the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 94, 97, 100, 103 and 106, wherein said down-regulation of said peroxidase gene is effected by targeting a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 96, 99, 102, 105 and 108.

11. A method of producing a glucosylated tetracylic triterpene, comprising glucosylating the at least one tetracyclic triterpene capable of glucosylation of the plant or plant cell of claim 3 by contacting said at least one tetracyclic triterpene with a UGT, thereby producing a glucosylated tetracyclic triterpene.

12. The method of claim 11, wherein said glucosylated tetracyclic triterpene is a non-bitter glucosylated tetracyclic triterpene, optionally, wherein said glucosylated tetracyclic triterpene is a mogroside.

13. The method of any one of claims 11 or 12, wherein:

i) said glucosylating is effected in a cell, optionally, wherein said cell is a plant cell, or

ii) said glucosylating is effected in a cell-free system.

14. The method of any one of claims 11-13, wherein said UGT is a plant UGT characterized by at least one of the following:

i) said UGT is selected from the group consisting of S. grosvenorii UGTs selected from the group consisting of UGT74-345-2, UGT73-348-2, UGT94-289-1, UGT73-327-2, UGT73-251-5, UGT73-251-6, UGT75-281-2, UGT85-269-4, UGT85-269-1, UGT94-289-2 and UGT94-289-3;

ii) said UGT is a UGT having an amino acid sequence selected from the group consisting of SEQ ID NOs. 139, 140, 141, 142, 143, 144, 145, 146, 147, 148 and 149;

iii) said UGT is a UGT encoded by a polynucleotide having a nucleotide sequence selected from the group consisting of SEQ ID NOs. 128, 129, 130, 131, 132, 133, 135 and 137, and

iv) said UGT is a recombinant UGT.

15. A composition comprising a plant or plant cell having modified cucurbitacin biosynthesis pathway gene expression, the plant or plant cell comprising tetracyclic triterpene capable of glucosylation by a UGT and, optionally, wherein said composition is enriched in tetracyclic triterpene glucosides.