CLAIMS

1. Grain of a rice plant, the grain comprising an aleurone, a starchy endosperm, a *ROS1a* gene encoding a ROS1a polypeptide and one or more genetic variations which each reduce the activity of at least one *ROS1a* gene in the plant when compared to a corresponding wild-type rice plant, wherein the aleurone is thickened compared to aleurone from a corresponding wild-type grain, and wherein the one or more one genetic variation(s) comprise an introduced genetic modification in the *ROS1a* gene.

2. The grain of claim 1, which is further characterised by one or more or all of:

(a) the ROS1a polypeptide has DNA glycosylase activity;

(b) the ROS1a polypeptide is different in amino acid sequence compared to the corresponding wild-type ROS1a polypeptide;

(c) the ROS1a polypeptide has a level of DNA glycosylase activity which is between 2% and 60% of the level of DNA glycosylase activity of a corresponding wild-type ROS1a polypeptide and/or of ROS1a polypeptide whose amino acids have a sequence set forth in SEQ ID NO: 2;

(d) a level of ROS1a polypeptide between 2% and 60% is present in the grain compared to the level of ROS1a polypeptide in the corresponding wild-type grain; and

(e) the thickened aleurone comprises at least two, at least three, at least four or at least five layers of cells, about 3, about 4, about 5 or about 6 layers of cells, or 2-8, 2-7, 2-6 or 2-5 layers of cells.

3. The grain of claim 1 or claim 2, wherein the one or more genetic variations are each, independently:

(a) a *ROS1a* gene encoding a mutant ROS1a polypeptide with reduced DNA glycosylase activity relative to the wild-type ROS1a polypeptide (SEQ ID NO:2);

(b) a *ROS1a* gene which when expressed produces a reduced level of a wild-type ROS1a polypeptide, for example which comprises a splice-site mutation that results in a reduced level of expression of the *ROS1a* gene, relative to the wild-type *ROS1a* gene whose cDNA sequence is provided as SEQ ID NO:8, or which *ROS1a* gene comprises a mutation in its promoter which results in reduced expression of the *ROS1a* gene relative to the wild-type *ROS1a* gene; and

(c) a *ROS1a* gene comprising a premature translational stop codon in its protein coding region such that the gene encodes a truncated polypeptide relative to a wild-type ROS1a polypeptide.

4. The grain according to any one of claims 1 to 3, wherein the rice plant is characterised by one or more or all of:

(a) the rice plant has a level of DNA glycosylase activity in its developing grain which is between 2% and 60% of the level of DNA glycosylase activity in a corresponding wild-type developing grain;

(b) the activity of at least one *ROS1a* gene in the rice plant is reduced in one or more or all of aleurone, pericarp, nucellar projection, ovary, testa and starchy endosperm of the developing grain;

(c) the activity of a *ROS1a* gene is reduced at least at a time point between the time of anthesis and 7 days post-anthesis, and/or in the egg cell prior to anthesis;

(d) the rice plant is male and female fertile; and

(e) the rice plant exhibits delayed grain maturation.

5. The grain according to any one or more of claims 1 to 4, which is further characterised by one or more of:

(a) the grain comprises, when compared to a corresponding wild-type grain, one or more or all of the following, each on a weight basis,

i) a higher mineral content, wherein the mineral content is the content of one or more or all of zinc, iron potassium, magnesium, phosphorus and sulphur, a higher antioxidant content,

ii) a higher phytate content,

iii) a higher content of one or more or all of vitamins B3, B6 and B9,

iv) a higher dietary fibre content and/or insoluble fibre content,

v) a starch content which is between 90% and 100% by weight relative to the starch content of the corresponding wild-type grain;

vi) a higher sucrose content,

vii) a higher monosaccharide content, and

ix) a lipid content of at least 90% or at least 100% relative to the

lipid content of the corresponding wild-type grain,

(b) the grain comprises an embryo;

(c) the grain is whole grain or cracked grain;

(d) the grain has been processed so that it is no longer able to germinate,

(e) the grain has a germination rate which is between 70 and 100% relative to the germination rate of a corresponding wild-type grain;

(f) the grain comprises an increased proportion of amylose in its total starch content compared to the corresponding wild-type grain; and

(g) the grain comprises an increased proportion of oleic acid and/or a decreased proportion of palmitic acid in its total fatty acid content compared to the corresponding wild- type grain.

6. The grain according to any one or more of claims 1 to 5, which is characterised by one or more or all of:

(a) the grain comprises a *ROS1a* gene which encodes a ROS1a polypeptide which has DNA glycosylase activity, wherein the ROS1a polypeptide which has DNA glycosylase activity is a mutant ROS1a polypeptide;

(b) the grain comprises a mutant ROS1a polypeptide having decreased DNA glycosylase activity when expressed in the rice plant compared to a corresponding wild-type ROS1a polypeptide; and

(c) the grain has a reduced total amount of ROS1a polypeptide compared to a corresponding wild-type grain provided that the grain comprises at least one *ROS1a* gene which encodes a ROS1a polypeptide which has DNA glycosylase activity.

7. A recombinant cell comprising an exogenous polynucleotide encoding a ROS1a polypeptide whose amino acid sequence is different to the amino acid sequence of a corresponding wild-type ROS1a polypeptide and which has reduced DNA glycosylase activity when compared to the corresponding wild-type ROS1a polypeptide, wherein a rice plant comprising a *ROS1a* gene encoding said ROS1a polypeptide produces grain having a thickened aleurone compared to the aleurone from a corresponding wild-type grain.

8. A cell of a rice plant comprising a *ROS1a* gene encoding a ROS1a polypeptide and a genetic variation which reduces the activity of at least one *ROS1a* gene in the cell when compared to a corresponding wild-type cell, wherein grain of the rice plant has a thickened

aleurone compared to aleurone from a corresponding wild-type grain, and wherein the genetic variation comprises an introduced genetic modification in the *ROS1a* gene.

9. A rice plant which produces grain according to any one of claims 1 to 6 and/or which comprises a cell of claim 7 or claim 8.

10. A method of producing the cell of claim 7, the method comprising a step of introducing an exogenous polynucleotide encoding a ROS1a polypeptide whose amino acid sequence is different to the amino acid sequence of a corresponding wild-type ROS1a polypeptide and which has reduced DNA glycosylase activity when compared to the corresponding wild-type ROS1a polypeptide, into a cell, wherein a rice plant comprising a *ROS1a* gene encoding said ROS1a polypeptide produces grain having a thickened aleurone compared to the aleurone from a corresponding wild-type grain.

11. A method of producing a rice plant of claim 9 or grain therefrom, the method comprising the steps of

i) introducing into a rice cell, a mutation of an endogenous *ROS1a* gene such that the mutated *ROS1a* gene encodes a ROS1a polypeptide whose amino acid sequence is different to the amino acid sequence of a corresponding wild-type ROS1a polypeptide and which has reduced DNA glycosylase activity when compared to the corresponding wild-type ROS1a polypeptide,

ii) obtaining a rice plant from a cell obtained from step i), the rice plant comprising the mutation of the endogenous *ROS1a* gene, and

iii) optionally harvesting grain from the plant of step ii), the grain comprising the mutation of the endogenous *ROS1a* gene, and

iv) optionally producing one or more generations of progeny plants from the grain, the progeny plants comprising the mutation of the endogenous *ROS1a* gene,

thereby producing the rice plant or grain.

12. A method of selecting a rice plant of claim 9 or rice grain according to any one of claims 1 to 6, the method comprising the steps of

i) screening a population of rice plants or grain each of which were obtained from a mutagenic treatment of progenitor rice cells, grain or plants, for the production of grain according to any one of claims 1 to 6 or for the presence of a mutation in a *ROS1a*

gene, or the presence of rice grain according to any one of claims 1 to 6, and

ii) selecting from the population of step (i) a rice plant which produces grain according to any one of claims 1 to 6, or rice grain of step (i) which is rice grain according to any one of claims 1 to 6,

thereby selecting the rice plant or grain.

13. A method of selecting a rice plant of claim 9, the method comprising the steps of

i) producing one or more progeny plants from rice grain, the rice grain having been derived from a cross of two parental rice plants,

ii) screening the one or more progeny plants of step i) for the production of grain according to any one of claims 1 to 6, and

iii) selecting a progeny plant which produces the grain, thereby selecting the rice plant.

14. A method for identifying a rice plant which produces grain according to any one of claims 1 to 6, the method comprising the steps of

A) i) obtaining a nucleic acid sample from a rice plant, and

ii) screening the sample for the presence or absence of a genetic variation which reduces the activity of a *ROS1a* gene in the plant when compared to a corresponding wild-type rice plant, or,

B) i) obtaining grain from a rice plant, and

ii) screening the grain or a portion thereof for one or both of

a) the amount of ROS1a polypeptide and/or activity in the grain, and

b) the amount of mRNA encoded by *ROS1a* genes in the grain.

15. A method of producing a rice plant part, the method comprising,

a) growing a rice plant, or at least 100 such rice plants in a field, of claim 9, and

b) harvesting the rice plant part from the rice plant or rice plants.

16. A method of producing rice flour, bran, wholemeal, malt, starch or oil obtained from grain, the method comprising;

a) obtaining grain according to any one of claims 1 to 6, and

b) processing the grain to produce the flour, bran, wholemeal, malt starch or oil.

17. A product produced from grain according to any one of claims 1 to 6, or a rice plant of claim 9, or from a part of said grain or rice plant, wherein the product comprises one or more or all of the *ROS1a* gene, the genetic variation, the exogenous polynucleotide and the thickened aleurone, and wherein the product is a food ingredient, beverage ingredient, food product or beverage product.

18. The product of claim 17, wherein

i) the food ingredient or beverage ingredient is selected from the group consisting of wholemeal, flour, bran, starch, malt and oil,

ii) the food product is selected from the group consisting of: leavened or unleavened breads, pasta, noodles, animal fodder, breakfast cereals, snack foods, cakes, pastries and foods containing a flour-based sauce, or

iii) the beverage product is a packaged beverage or a beverage comprising ethanol.

19. A method of preparing a food or beverage ingredient of claim 17 or claim 18, the method comprising

A) processing grain according to any one of claims 1 to 6, or bran, flour, wholemeal, malt, starch or oil from the grain, to produce the food or beverage ingredient, or

B) mixing grain according to any one of claims 1 to 6, or bran, flour, wholemeal, malt, starch or oil from the grain, with another food or beverage ingredient.

20. Use of grain according to any one of claims 1 to 6 or part thereof, or a rice plant of claim 9 or part thereof, as animal feed or food, or to produce feed for animal consumption or food for human consumption.