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(54) Title: PLANTS HAVING INCREASED YIELD AND A METHOD FOR MAKING THE SAME

(57) Abstract: The present invention concerns a method for increasing plant yield by modulating expression in a plant of a nucleic acid encoding a synovial sarcoma translocation (SYT) polypeptide or a homologue thereof. One such method comprises introducing into a plant a SYT nucleic acid or variant thereof. The invention also relates to transgenic plants having introduced therein a SYT nucleic acid or variant thereof, which plants have increased yield relative to corresponding wild type plants. The present invention also concerns constructs useful in the methods of the invention.

Plants having increased yield and a method for making the same

The present invention relates generally to the field of molecular biology and concerns a method for increasing plant yield relative to corresponding wild type plants. More specifically, the present invention concerns a method for increasing plant yield comprising modulating expression in a plant of a nucleic acid encoding a synovial sarcoma translocation (SYT) polypeptide or a homologue thereof. The present invention also concerns plants having modulated expression of a nucleic acid encoding a SYT polypeptide or a homologue thereof, which plants have increased yield relative to corresponding wild type plants. The invention also provides constructs useful in the methods of the invention.

The ever-increasing world population and the dwindling supply of arable land available for agriculture fuels research towards improving the efficiency of agriculture. Conventional means for crop and horticultural improvements utilise selective breeding techniques to identify plants having desirable characteristics. However, such selective breeding techniques have several drawbacks, namely that these techniques are typically labour intensive and result in plants that often contain heterogeneous genetic components that may not always result in the desirable trait being passed on from parent plants. Advances in molecular biology have allowed mankind to modify the germplasm of animals and plants. Genetic engineering of plants entails the isolation and manipulation of genetic material (typically in the form of DNA or RNA) and the subsequent introduction of that genetic material into a plant. Such technology has the capacity to deliver crops or plants having various improved economic, agronomic or horticultural traits.

A trait of particular economic interest is yield, and in the case of many plants seed yield. Yield is normally defined as the measurable produce of economic value from a crop. This may be defined in terms of quantity and/or quality. Plant seeds are an important source of human and animal nutrition. Crops such as, corn, rice, wheat, canola and soybean account for over half of total human caloric intake, whether through direct consumption of the seeds themselves or through consumption of meat products raised on processed seeds. They are also a source of sugars, oils and many kinds of metabolites used in industrial processes. Seeds contain an embryo, the source of new shoots and roots after germination, and an endosperm, the source of nutrients for embryo growth, during germination and early growth of seedlings. The development of a seed involves many genes, and requires the transfer of metabolites from roots, leaves and stems into the growing seed. The endosperm, in particular, assimilates the metabolic precursors of carbohydrate polymers, oil and proteins and synthesizes them into storage

macromolecules to fill out the grain. The ability to increase plant seed yield, whether through seed number, seed biomass, seed development, seed filling or any other seed-related trait would have many applications in agriculture, and even many non-agricultural uses such as in the biotechnological production of substances such as pharmaceuticals, antibodies or vaccines.

Yield may also depend on factors, such as the number and size of organs, plant architecture (for example, the number of branches), seed production and more. Root development, nutrient uptake and stress tolerance may also be important factors in determining yield. Optimizing these factors may therefore also contribute to increasing crop yield.

It has now been found that modulating expression in a plant of a nucleic acid encoding a SYT polypeptide or a homologue thereof gives plants having increased yield relative to corresponding wild type plants.

SYT is a transcriptional co-activator which, in plants, forms a functional complex with transcription activators of the GRF (growth-regulating factor) family of proteins (Kim HJ, Kende H (2004) Proc Nat Acad Sc 101: 13374-9). SYT is also called GIF for GRF-interacting factor. The GRF transcription activators share structural domains (in the N-terminal region) with the SWI/SNF proteins of the chromatin-remodelling complexes in yeast (van der Knaap E *et al.,* (2000) Plant Phys 122: 695-704). Transcriptional co-activators of these complexes are proposed to be involved in recruiting SWI/SNF complexes to enhancer and promoter regions to effect local chromatin remodelling (review Näär AM *et al.*, (2001) Annu Rev Biochem 70: 475-501). The alteration in local chromatin structure modulates transcriptional activation. More precisely, SYT is proposed to interact with plant SWI/SNF complex to affect transcriptional activation of GRF target gene(s) (Kim HJ, Kende H (2004) Proc Nat Acad Sc 101: 13374-9).

SYT belongs to a gene family of three members in *Arabidopsis*. The SYT polypeptide shares homology with the human SYT. The human SYT polypeptide was shown to be a transcriptional co-activator (Thaete *et al.* (1999) Hum Molec Genet 8: 585-591). Three domains characterize the mammalian SYT polypeptide:

(i) the N-terminal SNH (SYT N-terminal homology) domain, conserved in mammals, plants, nematodes and fish;

(ii) the C-terminal QPGY-rich domain, composed predominantly of glycine, proline, glutamine and tyrosine, occurring at variable intervals;

(iii) a methionine-rich (Met-rich) domain located between the two previous domains.

In plant SYT polypeptides, the SNH domain is well conserved. The C-terminal domain is rich in glycine and glutamine, but not in proline or tyrosine. It has therefore been named the QG-rich domain in contrast to the QPGY domain of mammals. As with mammalian SYT, a Met-rich domain may be identified N-terminally of the QG domain. The QG-rich domain may be taken to be substantially the C-terminal remainder of the protein (minus the SHN domain); the Met-rich domain is typically comprised within the first half of the QG-rich (from the N-terminus to the C-terminus). A second Met-rich domain may precede the SNH domain in plant SYT polypeptides (see Fig 1).

A SYT loss-of function mutant and transgenic plants with reduced expression of SYT was reported to develop small and narrow leaves and petals, which have fewer cells (Kim HJ, Kende H (2004) Proc Nat Acad Sc 101: 13374-9).

According to the present invention, there is provided a method for increasing plant yield, comprising modulating expression in a plant of a nucleic acid encoding a SYT polypeptide or a homologue thereof.

Reference herein to "corresponding wild type plants" is taken to mean any suitable control plant or plants, the choice of which would be well within the capabilities of a person skilled in the art and may include, for example, corresponding wild type plants or corresponding plants without the gene of interest. A "control plant" as used herein refers not only to whole plants, but also to plant parts, including seeds and seed parts.

Advantageously, performance of the methods according to the present invention results in plants having increased yield, particularly seed yield, relative to corresponding wild type plants.

The term "increased yield" as defined herein is taken to mean an increase in any one or more of the following, each relative to corresponding wild type plants: (i) increased biomass (weight) of one or more parts of a plant, particularly aboveground (harvestable) parts, increased root biomass or increased biomass of any other harvestable part (such as fruits, nuts and pulses); (ii) increased total seed yield, which includes an increase in seed biomass (seed weight) and which may be an increase in the seed weight per plant or on an individual seed basis; (iii) increased number of (filled) seeds; (iv) increased seed size, which may also influence the composition of seeds; (v) increased seed volume, which may also influence

the composition of seeds (including oil, protein and carbohydrate total content and composition); (vi) increased individual seed area; (vii) increased individual seed length or width; (viii) increased harvest index, which is expressed as a ratio of the yield of harvestable parts, such as seeds, over the total biomass; and (ix) increased thousand kernel weight (TKW), which is extrapolated from the number of filled seeds counted and their total weight. An increased TKW may result from an increased seed size and/or seed weight. An increased TKW may result from an increase in embryo size and/or endosperm size. An increase in seed size, seed volume, seed area, seed perimeter, seed width and seed length may be due to an increase in specific parts of a seed, for example due to an increase in the size of the embryo and/or endosperm and/or aleurone and/or scutellum, or other parts of a seed.

Taking corn as an example, a yield increase may be manifested as one or more of the following: increase in the number of plants per hectare or acre, an increase in the number of ears per plant, an increase in the number of rows, number of kernels per row, kernel weight, thousand kernel weight, ear length/diameter, increase in the seed filling rate (which is the number of filled seeds divided by the total number of seeds and multiplied by 100), among others. Taking rice as an example, a yield increase may be manifested by an increase in one or more of the following: number of plants per hectare or acre, number of panicles per plant, number of spikelets per panicle, number of flowers (florets) per panicle (which is expressed as a ratio of the number of filled seeds over the number of primary panicles), increase in the seed filling rate (which is the number of filled seeds divided by the total number of seeds and multiplied by 100), increase in thousand kernel weight, among others.

An increase in yield may also result in modified architecture, or may occur as a result of modified architecture.

According to a preferred feature, performance of the methods of the invention result in plants having increased seed yield. Therefore, according to the present invention, there is provided a method for increasing seed yield in a plant, which method comprises modulating expression in a plant of a nucleic acid encoding a SYT polypeptide or a homologue thereof.

Since the transgenic plants according to the present invention have increased yield, it is likely that these plants exhibit an increased growth rate (during at least part of their life cycle), relative to the growth rate of corresponding wild type plants at a corresponding stage in their life cycle. The increased growth rate may be specific to one or more parts of a plant (including seeds), or may be throughout substantially the whole plant. A plant having an

increased growth rate may even exhibit early flowering. The increase in growth rate may take place at one or more stages in the life cycle of a plant or during substantially the whole plant life cycle. Increased growth rate during the early stages in the life cycle of a plant may reflect enhanced vigour. The increase in growth rate may alter the harvest cycle of a plant allowing plants to be sown later and/or harvested sooner than would otherwise be possible. If the growth rate is sufficiently increased, it may allow for the further sowing of seeds of the same plant species (for example sowing and harvesting of rice plants followed by sowing and harvesting of further rice plants all within one conventional growing period). Similarly, if the growth rate is sufficiently increased, it may allow for the further sowing of seeds of different plants species (for example the sowing and harvesting of rice plants followed by, for example, the sowing and optional harvesting of soybean, potato or any other suitable plant). Harvesting additional times from the same rootstock in the case of some crop plants may also be possible. Altering the harvest cycle of a plant may lead to an increase in annual biomass production per acre (due to an increase in the number of times (say in a year) that any particular plant may be grown and harvested). An increase in growth rate may also allow for the cultivation of transgenic plants in a wider geographical area than their wild-type counterparts, since the territorial limitations for growing a crop are often determined by adverse environmental conditions either at the time of planting (early season) or at the time of harvesting (late season). Such adverse conditions may be avoided if the harvest cycle is shortened. The growth rate may be determined by deriving various parameters from growth curves, such parameters may be: T-Mid (the time taken for plants to reach 50% of their maximal size) and T-90 (time taken for plants to reach 90% of their maximal size), amongst others.

Performance of the methods of the invention gives plants having an increased growth rate relative to corresponding wild type plants. Therefore, according to the present invention, there is provided a method for increasing growth rate in plants, which method comprises modulating expression in a plant of a nucleic acid encoding a SYT polypeptide or a homologue thereof.

An increase in (seed) yield and/or growth rate occurs whether the plant is under non-stress conditions or whether the plant is exposed to various stresses compared to suitable control plants. Plants typically respond to exposure to stress by growing more slowly. In conditions of severe stress, the plant may even stop growing altogether. Mild stress on the other hand is defined herein as being any stress to which a plant is exposed which does not result in the plant ceasing to grow altogether without the capacity to resume growth. Due to advances in agricultural practices (irrigation, fertilization, pesticide treatments) severe

stresses are not often encountered in cultivated crop plants. As a consequence, the compromised growth induced by mild stress is often an undesirable feature for agriculture. Mild stresses are the typical stresses to which a plant may be exposed. These stresses may be the everyday biotic and/or abiotic (environmental) stresses to which a plant is exposed. Typical abiotic or environmental stresses include temperature stresses caused by atypical hot or cold/freezing temperatures; salt stress; water stress (drought or excess water). Chemicals may also cause abiotic stresses. Biotic stresses are typically those stresses caused by pathogens, such as bacteria, viruses, fungi and insects.

Advantageously, yield may be modified in any plant.

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, leaves, roots (including tubers), flowers, and tissues and organs, wherein each of the aforementioned comprise the transgene of interest. The term "plant" also encompasses plant cells, suspension cultures, callus tissue, embryos, meristematic regions, gametophytes, sporophytes, pollen and microspores, again wherein each of the aforementioned comprise the transgene.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs selected from the list comprising *Acacia* spp.,*Acer* spp., *Actinidia* spp., *Aesculus* spp., *Agathis australis, Albizia amara, Alsophila tricolor, Andropogon* spp., *Arachis* spp, *Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula* spp., *Brassica* spp., *Bruguiera gymnorrhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra* spp, *Camellia sinensis, Canna indica, Capsicum* spp., *Cassia* spp., *Centroema pubescens, Chaenomeles* spp., *Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coronillia varia, Cotoneaster serotina, Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon* spp., *Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium* spp., *Dicksonia squarosa, Diheteropogon amplectens, Dioclea* spp, *Dolichos* spp., *Dorycnium rectum, Echinochloa pyramidalis, Ehrartia* spp., *Eleusine coracana, Eragrestis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperi, Eulalia villosa, Fagopyrum* spp., *Feijoa sellowiana, Fragaria* spp., *Flemingia* spp, *Freycinetia banksii, Geranium thunbergii, Ginkgo biloba, Glycine javanica, Gliricidia* spp, *Gossypium hirsutum, Grevillea* spp., *Guibourtia coleosperma, Hedysarum* spp., *Hemarthia altissima, Heteropogon contortus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hyperthelia dissoluta, Indigo incarnata, Iris*

spp., *Leptarrhena pyrolifolia, Lespediza* spp., *Lettuca* spp., *Leucaena leucocephala, Loudetia simplex, Lotonus bainesii, Lotus* spp., *Macrotyloma axillare, Malus* spp., *Manihot esculenta, Medicago sativa, Metasequoia glyptostroboides, Musa sapientum, Nicotianum* spp., *Onobrychis* spp., *Ornithopus* spp., *Oryza* spp., *Peltophorum africanum, Pennisetum* spp., *Persea gratissima, Petunia* spp., *Phaseolus* spp., *Phoenix canariensis, Phormium cookianum, Photinia* spp., *Picea glauca, Pinus* spp., *Pisum sativum, Podocarpus totara, Pogonarthria fleckii, Pogonarthria squarrosa, Populus* spp., *Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus* spp., *Rhaphiolepsis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes* spp., *Robinia pseudoacacia, Rosa* spp., *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum, Sciadopitys verticillata, Sequoia sempervirens, Sequoiadendron giganteum, Sorghum bicolor, Spinacia* spp., *Sporobolus fimbriatus, Stiburus alopecuroides, Stylosanthos humilis, Tadehagi* spp, *Taxodium distichum, Themeda triandra, Trifolium* spp., *Triticum* spp., *Tsuga heterophylla, Vaccinium* spp., *Vicia* spp., *Vitis vinifera, Watsonia pyramidata, Zantedeschia aethiopica, Zea mays*, amaranth, artichoke, asparagus, broccoli, Brussels sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, strawberry, sugar beet, sugar cane, sunflower, tomato, squash, tea and algae, amongst others. According to a preferred embodiment of the present invention, the plant is a crop plant. Examples of crop plants include amongst others soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco. *Arabidopsis thaliana* is generally not considered as a crop plant. Further preferably, the plant is a monocotyledonous plant, such as sugarcane. More preferably the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum or oats.

The term "SYT polypeptide or homologue thereof" as defined herein refers to a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having in increasing order of preference at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain.

Preferably, SNH domain having at least 40% identity to the SNH domain of SEQ ID NO: 2 comprises the residues shown in black in Figure 2. Further preferably, the SNH domain is represented by SEQ ID NO: 1.

Additionally, the SYT polypeptide or a homologue thereof may comprise one or more of the following: (a) SEQ ID NO: 90; (b) SEQ ID NO: 91; and (c) a Met-rich domain at the N-terminal preceding the SNH domain.

A SYT polypeptide or a homologue thereof typically interacts with GRF (growth-regulating factor) polypeptides in yeast two-hybrid systems. Yeast two-hybrid interaction assays are well known in the art (see Field *et al.* (1989) Nature 340(6230): 245-246). For example, the SYT polypeptide as represented by SEQ ID NO: 4 is capable of interacting with AtGRF5 and with AtGRF9. SYT polypeptide and homologues thereof have been demonstrated by the inventors to increase yield, particularly seed yield, in plants.

A SYT polypeptide or homologue thereof is encoded by a SYT nucleic acid/gene. Therefore the term "SYT nucleic acid/gene" as defined herein is any nucleic acid/gene encoding a SYT polypeptide or a homologue thereof as defined hereinabove.

SYT polypeptides or homologues thereof may readily be identified using routine techniques well known in the art, such as by sequence alignment. Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch ((1970) J Mol Biol 48: 443-453) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. The BLAST algorithm (Altschul *et al.* (1990) J Mol Biol 215: 403-10) calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information. Homologues of SYT comprising an SNH domain having at least 40% sequence identity to the SNH domain of SEQ ID NO: 2 and/or comprising SEQ ID NO: 90 and/or SEQ ID NO: 91, may readily be identified using, for example, the ClustalW multiple sequence alignment algorithm (version 1.83) available at http://clustalw.genome.jp/sit-bin/nph-clustalw, with the default pairwise alignment parameters, and a scoring method in percentage. A sequence having a 40% identity to the SNH domain of SEQ ID NO: 2 is sufficient to identify a sequence as being a SYT.

Furthermore, the presence of a Met-rich domain or a QG-rich domain may also readily be identified. As shown in Figure 3, the Met-rich domain and QG-rich domain follows the SNH domain. The QG-rich domain may be taken to be substantially the C-terminal remainder of the protein (minus the SHN domain); the Met-rich domain is typically comprised within the first half of the QG-rich (from the N-term to the C-term). Primary amino acid composition (in %) to determine if a polypeptide domain is rich in specific amino acids may be calculated using software programs from the ExPASy server (Gasteiger E et al. (2003) ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Res 31:3784-3788), in particular the ProtParam tool. The composition of the protein of interest may then

be compared to the average amino acid composition (in %) in the Swiss-Prot Protein Sequence data bank. Within this databank, the average Met (M) content is of 2.37%, the average Gln (Q) content is of 3.93% and the average Gly (G) content is of 6.93%. As defined herein, a Met-rich domain or a QG-rich domain has Met content (in %) or a Gln and Gly content (in %) above the average amino acid composition (in %) in the Swiss-Prot Protein Sequence data bank.

Examples of SYT polypeptide or homologues thereof include (encoded by polynucleotide sequence accession number in parenthesis; see also Table 1): *Arabidopsis thaliana* Arath_SYT1 (AY102639.1) SEQ ID NO: 4, *Arabidopsis thaliana* Arath_SYT2 (AY102640.1) SEQ ID NO: 6, *Arabidopsis thaliana* Arath_SYT3 (AY102641.1) SEQ ID NO: 8, *Aspergillus officinalis* Aspof_SYT (CV287542) SEQ ID NO: 10, *Brassica napus* Brana_SYT (CD823592) SEQ ID NO: 12, *Citrus sinensis* Citsi_SYT (CB290588) SEQ ID NO: 14, *Gossypium arboreum* Gosar_SYT (BM359324) SEQ ID NO: 16, *Medicago trunculata* Medtr_SYT (CA858507.1) SEQ ID NO: 18, *Oryza sativa* Orysa_SYT1 (AK058575) SEQ ID NO: 20, *Oryza sativa* Orysa_SYT2 (AK105366) SEQ ID NO: 22, *Oryza sativa* Orysa_SYT3 (BP185008) SEQ ID NO: 24, *Solanum tuberosum* Soltu_SYT (BG590990) SEQ ID NO: 26, *Zea mays* Zeama_SYT1 (BG874129.1, CA409022.1) SEQ ID NO: 28, *Zea mays* Zeama_SYT2 (AY106697) SEQ ID NO: 30, *Homo sapiens* Homsa_SYT (CAG46900) SEQ ID NO: 32, *Allium cepa* Allce_SYT2 (CF437485) SEQ ID NO: 34, *Aquilegia formosa x Aquilegia pubescens* Aqufo_SYT1 (DT758802) SEQ ID NO: 36, *Brachypodium distachyon* Bradi_SYT3 (DV480064) SEQ ID NO: 38, *Brassica napus* Brana_SYT2 (CN732814) SEQ ID NO: 40, *Citrus sinensis* Citsi_SYT2 (CV717501) SEQ ID NO: 42, *Euphorbia esula* Eupes_SYT2 (DV144834) SEQ ID NO: 44, *Glycine max* Glyma_SYT2 (BQ612648) SEQ ID NO: 46, *Glycine soya* Glyso_SYT2 (CA799921) SEQ ID NO: 48, *Gossypium hirsutum* Goshi_SYT1 (DT558852) SEQ ID NO: 50, *Gossypium hirsutum* Goshi_SYT2 (DT563805) SEQ ID NO: 52, *Hordeum vulgare* Horvu_SYT2 (CA032350) SEQ ID NO: 54, *Lactuca serriola* Lacse_SYT2 (DW110765) SEQ ID NO: 56, *Lycopersicon esculentum* Lyces_SYT1 (AW934450, BP893155) SEQ ID NO: 58, *Malus domestica* Maldo_SYT2 (CV084230, DR997566) SEQ ID NO: 60, *Medicago trunculata* Medtr_SYT2 (CA858743, BI310799, AL382135) SEQ ID NO: 62, *Panicum virgatum* Panvi_SYT3 (DN152517) SEQ ID NO: 64, *Picea sitchensis* Picsi_SYT1 (DR484100, DR478464) SEQ ID NO: 66, *Pinus taeda* Pinta_SYT1 (DT625916) SEQ ID NO: 68, *Populus tremula* Poptr_SYT1 (DT476906) SEQ ID NO: 70, *Saccharum officinarum* Sacof_SYT1 (CA078249, CA078630, CA082679, CA234526, CA239244, CA083312) SEQ ID NO: 72, *Saccharum officinarum*. Sacof_SYT2 (CA110367) SEQ ID NO: 74, *Saccharum officinarum* Sacof_SYT3 (CA161933, CA265085) SEQ ID NO: 76, *Solanum tuberosum* Soltu_SYT1 (CK265597) SEQ ID NO: 78, *Sorghum*

bicolor Sorbi_SYT3 (CX611128) SEQ ID NO: 80, *Triticum aestivum* Triae_SYT2 (CD901951) SEQ ID NO: 82, *Triticum aestivum* Triae_SYT3 (BJ246754, BJ252709) SEQ ID NO: 84, *Vitis vinifera* Vitvi_SYT1 (DV219834) SEQ ID NO: 86, *Zea mays* Zeama_SYT3 (CO468901) SEQ ID NO: 88.

Table 1: Examples of SYT homologues

Name	NCBI nucleotide accession number	Nucleotide SEQ ID NO	Translated polypeptide SEQ ID NO	Source
Arath_SYT1	AY102639.1	3	4	*Arabidopsis thaliana*
Arath_SYT2	AY102640.1	5	6	*Arabidopsis thaliana*
Arath_SYT3	AY102641.1	7	8	*Arabidopsis thaliana*
Aspof_SYT1	CV287542	9	10	*Aspergillus officinalis*
Brana_SYT1	CD823592	11	12	*Brassica napus*
Citsi_SYT1	CB290588	13	14	*Citrus sinensis*
Gosar_SYT1	BM359324	15	16	*Gossypium arboreum*
Medtr_SYT1	CA858507.1	17	18	*Medicago trunculata*
Orysa_SYT1	AK058575	19	20	*Oryza sativa*
Orysa_SYT2	AK105366	21	22	*Oryza sativa*
Orysa_SYT3	BP185008	23	24	*Oryza sativa*
Soltu_SYT2	BG590990	25	26	*Solanum tuberosum*
Zeama_SYT1	BG874129.1 CA409022.1*	27	28	*Zea mays*
Zeama_SYT2	AY106697	29	30	*Zea mays*
Homsa_SYT	CR542103	31	32	*Homo sapiens*
Allce_SYT2	CF437485	33	34	*Allium cepa*
Aqufo_SYT1	DT758802.1	35	36	*Aquilegia formosa x Aquilegia pubescens*
Bradi_SYT3	DV480064.1	37	38	*Brachypodium distachyon*
Brana_SYT2	CN732814	39	40	*Brassica napa*
Citsi_SYT2	CV717501	41	42	*Citrus sinensis*
Eupes_SYT2	DV144834	43	44	*Euphorbia esula*
Glyma_SYT2	BQ612648	45	46	*Glycine max*
Glyso_SYT2	CA799921	47	48	*Glycine soya*
Goshi_SYT1	DT558852	49	50	*Gossypium hirsutum*
Goshi_SYT2	DT563805	51	52	*Gossypium hirsutum*
Horvu_SYT2	CA032350	53	54	*Hordeum vulgare*
Lacse_SYT2	DW110765	55	56	*Lactuca serriola*
Lyces_SYT1	AW934450.1 BP893155.1*	57	58	*Lycopersicon esculentum*
Maldo_SYT2	CV084230 DR997566*	59	60	*Malus domestica*
Medtr_SYT2	CA858743 BI310799.1 AL382135.1*	61	62	*Medicago trunculata*

Panvi_SYT3	DN152517	63	64	*Panicum virgatum*
Picsi_SYT1	DR484100 DR478464.1	65	66	*Picea sitchensis*
Pinta_SYT1	DT625916	67	68	*Pinus taeda*
Poptr_SYT1	DT476906	69	70	*Populus tremula*
Sacof_SYT1	CA078249.1 CA078630 CA082679 CA234526 CA239244 CA083312*	71	72	*Saccharum officinarum*
Sacof_SYT2	CA110367	73	74	*Saccharum officinarum*
Sacof_SYT3	CA161933.1 CA265085*	75	76	*Saccharum officinarum*
Soltu_SYT1	CK265597	77	78	*Solanum tuberosum*
Sorbi_SYT3	CX611128	79	80	*Sorghum bicolor*
Triae_SYT2	CD901951	81	82	*Triticum aestivum*
Triae_SYT3	BJ246754 BJ252709*	83	84	*Triticum aestivum*
Vitvi_SYT1	DV219834	85	86	*Vitis vinifera*
Zeama_SYT3	CO468901	87	88	*Zea mays*

*Compiled from cited accessions

It is to be understood that sequences falling under the definition of "SYT polypeptide or homologue thereof" are not to be limited to the sequences represented by SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, but that any polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having at least 40% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain may be suitable in performing the methods of the invention.

Examples of SYT nucleic acids include but are not limited to those represented by any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45,

SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87. SYT nucleic acids/genes and variants thereof may be suitable in practising the methods of the invention. Variant SYT nucleic acid/genes typically are those having the same function as a naturally occurring SYT nucleic acid/genes, which can be the same biological function or the function of increasing yield when expression of the nucleic acids/genes is modulated in a plant. Such variants include portions of a SYT nucleic acid/gene and/or nucleic acids capable of hybridising with a SYT nucleic acid/gene as defined below.

The term portion as defined herein refers to a piece of DNA encoding a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having in increasing order of preference at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the SNH domain of SEQ ID NO: 2 and (ii) a Met-rich domain; and (iii) a QG-rich domain. A portion may be prepared, for example, by making one or more deletions to a SYT nucleic acid. The portions may be used in isolated form or they may be fused to other coding (or non coding) sequences in order to, for example, produce a protein that combines several activities. When fused to other coding sequences, the resulting polypeptide produced upon translation may be bigger than that predicted for the SYT fragment. Preferably, the portion is a portion of a nucleic acid as represented by any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87. Most preferably the portion of a nucleic acid is as represented by SEQ ID NO: 3 SEQ ID NO: 5 or SED IQ NO: 7.

Another variant of a SYT nucleic acid/gene is a nucleic acid capable of hybridising under reduced stringency conditions, preferably under stringent conditions, with a SYT nucleic acid/gene as hereinbefore defined, which hybridising sequence encodes a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having in increasing order of preference at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the SNH domain of SEQ ID NO: 2 and (ii) a Met-rich domain; and (iii) a QG-rich domain. Preferably, the hybridising sequence is one that is capable of hybridising to a nucleic acid as represented by any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87 or to a portion of any of the aforementioned sequences as defined hereinabove. Most preferably the hybridizing sequence of a nucleic acid is as represented by SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7.

The term "hybridisation" as defined herein is a process wherein substantially homologous complementary nucleotide sequences anneal to each other. The hybridisation process can occur entirely in solution, i.e. both complementary nucleic acids are in solution. The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitro-cellulose or nylon membrane or immobilised by e.g. photolithography to, for example, a siliceous glass support (the latter known as nucleic acid arrays or microarrays or as nucleic acid chips). In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration, ionic strength and hybridisation buffer composition.

“Stringent hybridisation conditions” and “stringent hybridisation wash conditions” in the context of nucleic acid hybridisation experiments such as Southern and Northern hybridisations are sequence dependent and are different under different environmental parameters. The skilled artisan is aware of various parameters which may be altered during hybridisation and washing and which will either maintain or change the stringency conditions.

The T_m is the temperature under defined ionic strength and pH, at which 50% of the target sequence hybridises to a perfectly matched probe. The T_m is dependent upon the solution conditions and the base composition and length of the probe. For example, longer sequences hybridise specifically at higher temperatures. The maximum rate of hybridisation is obtained from about 16°C up to 32°C below T_m. The presence of monovalent cations in the hybridisation solution reduce the electrostatic repulsion between the two nucleic acid strands thereby promoting hybrid formation; this effect is visible for sodium concentrations of up to 0.4M. Formamide reduces the melting temperature of DNA-DNA and DNA-RNA duplexes with 0.6 to 0.7°C for each percent formamide, and addition of 50% formamide allows hybridisation to be performed at 30 to 45°C, though the rate of hybridisation will be lowered. Base pair mismatches reduce the hybridisation rate and the thermal stability of the duplexes. On average and for large probes, the T_m decreases about 1°C per % base mismatch. The T_m may be calculated using the following equations, depending on the types of hybrids:

1. DNA-DNA hybrids (Meinkoth and Wahl, Anal. Biochem., 138: 267-284, 1984):
   $T_m = 81.5°C + 16.6 \times \log[Na^+]^a + 0.41 \times \%[G/C^b] - 500 \times [L^c]^{-1} - 0.61 \times \%$ formamide
2. DNA-RNA or RNA-RNA hybrids:
   $T_m = 79.8 + 18.5 (\log_{10}[Na^+]^a) + 0.58 (\%G/C^b) + 11.8 (\%G/C^b)^2 - 820/L^c$
3. oligo-DNA or oligo-RNA[d] hybrids:
   For <20 nucleotides: $T_m = 2 (l_n)$
   For 20–35 nucleotides: $T_m = 22 + 1.46 (l_n)$

[a] or for other monovalent cation, but only accurate in the 0.01–0.4 M range.

[b] only accurate for %GC in the 30% to 75% range.

[c] L = length of duplex in base pairs.

[d] Oligo, oligonucleotide; l_n, effective length of primer = 2×(no. of G/C)+(no. of A/T).

Note: for each 1% formamide, the T_m is reduced by about 0.6 to 0.7°C, while the presence of 6 M urea reduces the T_m by about 30°C

Specificity of hybridisation is typically the function of post-hybridisation washes. To remove background resulting from non-specific hybridisation, samples are washed with dilute salt solutions. Critical factors of such washes include the ionic strength and temperature of the final wash solution: the lower the salt concentration and the higher the wash temperature, the higher the stringency of the wash. Wash conditions are typically performed at or below hybridisation stringency. Generally, suitable stringent conditions for nucleic acid

hybridisation assays or gene amplification detection procedures are as set forth above. Conditions of greater or less stringency may also be selected. Generally, low stringency conditions are selected to be about 50°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. Medium stringency conditions are when the temperature is 20°C below T_m, and high stringency conditions are when the temperature is 10°C below T_m. For example, stringent conditions are those that are at least as stringent as, for example, conditions A-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R. Non-specific binding may be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein containing solutions, additions of heterologous RNA, DNA, and SDS to the hybridisation buffer, and treatment with RNase. Examples of hybridisation and wash conditions are listed in Table 2 below.

Table 2: Examples of hybridisation and wash conditions

Stringency Condition	Polynucleotide Hybrid ‡	Hybrid Length (bp) ‡	Hybridization Temperature and Buffer †	Wash Temperature and Buffer†
A	DNA:DNA	> or equal to 50	65°C 1×SSC; or 42°C, 1×SSC and 50% formamide	65°C; 0.3×SSC
B	DNA:DNA	<50	Tb*; 1×SSC	Tb*; 1×SSC
C	DNA:RNA	> or equal to 50	67°C 1×SSC; or 45°C, 1×SSC and 50% formamide	67°C; 0.3×SSC
D	DNA:RNA	<50	Td*; 1×SSC	Td*; 1×SSC
E	RNA:RNA	> or equal to 50	70°C 1×SSC; or 50°C, 1×SSC and 50% formamide	70°C; 0.3×SSC
F	RNA:RNA	<50	Tf*; 1×SSC	Tf*; 1×SSC
G	DNA:DNA	> or equal to 50	65°C 4×SSC; or 45°C, 4×SSC and 50% formamide	65°C; 1×SSC
H	DNA:DNA	<50	Th*; 4 ×SSC	Th*; 4×SSC
I	DNA:RNA	> or equal to 50	67°C 4×SSC; or 45°C, 4×SSC and 50% formamide	67°C; 1×SSC
J	DNA:RNA	<50	Tj*; 4 ×SSC	Tj*; 4 ×SSC

K	RNA:RNA	> or equal to 50	70°C 4×SSC; or 40°C, 6×SSC and 50% formamide	67°C; 1×SSC
L	RNA:RNA	<50	Tl*; 2 ×SSC	Tl*; 2×SSC
M	DNA:DNA	> or equal to 50	50°C 4×SSC; or 40°C, 6×SSC and 50% formamide	50°C; 2×SSC
N	DNA:DNA	<50	Tn*; 6 ×SSC	Tn*; 6×SSC
O	DNA:RNA	> or equal to 50	55°C 4×SSC; or 42°C, 6×SSC and 50% formamide	55°C; 2×SSC
P	DNA:RNA	<50	Tp*; 6 ×SSC	Tp*; 6×SSC
Q	RNA:RNA	> or equal to 50	60°C 4×SSC; or 45°C, 6×SSC and 50% formamide	60°C.; 2×SSC
R	RNA:RNA	<50	Tr*; 4 ×SSC	Tr*; 4×SSC

‡ The "hybrid length" is the anticipated length for the hybridising nucleic acid. When nucleic acids of known sequence are hybridised, the hybrid length may be determined by aligning the sequences and identifying the conserved regions described herein.

† SSPE (1×SSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH7.4) may be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridisation and wash buffers; washes are performed for 15 minutes after hybridisation is complete. The hybridisations and washes may additionally include 5 × Denhardt's reagent, 0.5-1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.5% sodium pyrophosphate, and up to 50% formamide.

* Tb-Tr: The hybridisation temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature T_m of the hybrids; the T_m is determined according to the above-mentioned equations.

‡ The present invention also encompasses the substitution of any one, or more DNA or RNA hybrid partners with either a PNA, or a modified nucleic acid.

For the purposes of defining the level of stringency, reference can be made to Sambrook *et al.* (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor

Laboratory Press, CSH, New York or to Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989).

The SYT nucleic acid or variant thereof may be derived from any artificial source or natural source, such as plant, algae or animal. This nucleic acid may be modified from its native form in composition and/or genomic environment through deliberate human manipulation. The nucleic acid is preferably of plant origin, whether from the same plant species (for example to the one in which it is to be introduced) or whether from a different plant species. Preferably the nucleic acid of plant origin encodes a SYT1. Alternatively, the nucleic acid may encode a SYT2 or SYT3, which are closely related to one another on a polypeptide level. The nucleic acid may be isolated from a dicotyledonous species, preferably from the family Brassicaceae, further preferably from *Arabidopsis thaliana*. More preferably, the three SYT nucleic acids isolated from *Arabidopsis thaliana* are represented by SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7, and the three SYT amino acid sequences are as represented by SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 8.

The expression of a nucleic acid encoding a SYT polypeptide or a homologue thereof may be modulated by introducing a genetic modification (preferably in the locus of a SYT gene). The locus of a gene as defined herein is taken to mean a genomic region, which includes the gene of interest and 10 kb up- or downstream of the coding region.

The genetic modification may be introduced, for example, by any one (or more) of the following methods: T-DNA activation, TILLING, site-directed mutagenesis, directed evolution and homologous recombination, or by introducing and expressing in a plant a nucleic acid encoding a SYT polypeptide or a homologue thereof. Following introduction of the genetic modification, there follows a step of selecting for modulated expression of a nucleic acid encoding a SYT polypeptide or a homologue thereof, which modulated expression gives plants having increased yield, particularly increased seed yield.

T-DNA activation tagging (Hayashi *et al.* Science (1992) 1350-1353) involves insertion of T-DNA, usually containing a promoter (may also be a translation enhancer or an intron), in the genomic region of the gene of interest or 10 kb up- or downstream of the coding region of a gene in a configuration such that the promoter directs expression of the targeted gene. Typically, regulation of expression of the targeted gene by its natural promoter is disrupted and the gene falls under the control of the newly introduced promoter. The promoter is typically embedded in a T-DNA. This T-DNA is randomly inserted into the plant genome, for example, through *Agrobacterium* infection and leads to overexpression of genes near the

inserted T-DNA. The resulting transgenic plants show dominant phenotypes due to overexpression of genes close to the introduced promoter. The promoter to be introduced may be any promoter capable of directing expression of a gene in the desired organism, in this case a plant. For example, constitutive, tissue-preferred, cell type-preferred and inducible promoters are all suitable for use in T-DNA activation.

A genetic modification may also be introduced in the locus of a SYT gene using the technique of TILLING (Targeted Induced Local Lesions In Genomes). This is a mutagenesis technology useful to generate and/or identify, and to eventually isolate mutagenised variants of a SYT nucleic acid encoding a protein with enhanced SYT activity. TILLING also allows selection of plants carrying such mutant variants. These mutant variants may even exhibit higher SYT activity than that exhibited by the gene in its natural form. TILLNG combines high-density mutagenesis with high-throughput screening methods. The steps typically followed in TILLING are: (a) EMS mutagenesis (Redei GP and Koncz C (1992) *In* Methods in Arabidopsis Research, Koncz C, Chua NH, Schell J, eds. Singapore, World Scientific Publishing Co, pp. 16–82; Feldmann *et al.*, (1994) *In* Meyerowitz EM, Somerville CR, eds, Arabidopsis. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp 137-172; Lightner J and Caspar T (1998) *In* J Martinez-Zapater, J Salinas, eds, Methods on Molecular Biology, Vol. 82. Humana Press, Totowa, NJ, pp 91-104); (b) DNA preparation and pooling of individuals; (c) PCR amplification of a region of interest; (d) denaturation and annealing to allow formation of heteroduplexes; (e) DHPLC, where the presence of a heteroduplex in a pool is detected as an extra peak in the chromatogram; (f) identification of the mutant individual; and (g) sequencing of the mutant PCR product. Methods for TILLING are well known in the art (McCallum *et al.*, (2000) Nat Biotechnol 18: 455-457; reviewed by Stemple (2004) Nat Rev Genet 5(2): 145-50).

Site-directed mutagenesis may be used to generate variants of SYT nucleic acids. Several methods are available to achieve site-directed mutagenesis, the most common being PCR based methods (current protocols in molecular biology. Wiley Eds. http://www.4ulr.com/products/currentprotocols/index.html).

Directed evolution may also be used to generate variants of SYT nucleic acids. This consists of iterations of DNA shuffling followed by appropriate screening and/or selection to generate variants of SYT nucleic acids or portions thereof encoding SYT polypeptides or homologues or portions thereof having an modified biological activity (Castle *et al.,* (2004) Science 304(5674): 1151-4; US patents 5,811,238 and 6,395,547).

T-DNA activation, TILLING, site-directed mutagenesis and directed evolution are examples of technologies that enable the generation of novel SYT alleles and variants.

Homologous recombination allows introduction in a genome of a selected nucleic acid at a defined selected position. Homologous recombination is a standard technology used routinely in biological sciences for lower organisms such as yeast or the moss *Physcomitrella*. Methods for performing homologous recombination in plants have been described not only for model plants (Offringa *et al.* (1990) EMBO J 9(10): 3077-84) but also for crop plants, for example rice (Terada *et al.* (2002) Nat Biotech 20(10): 1030-4; Iida and Terada (2004) Curr Opin Biotech 15(2): 132-8). The nucleic acid to be targeted (which may be a SYT nucleic acid or variant thereof as hereinbefore defined) is targeted to the locus of a SYT gene. The nucleic acid to be targeted may be an improved allele used to replace the endogenous gene or may be introduced in addition to the endogenous gene.

A preferred method for introducing a genetic modification (which in this case need not be in the locus of a SYT gene) is to introduce and express in a plant a nucleic acid encoding a SYT polypeptide or a homologue thereof. A SYT polypeptide or a homologue thereof is defined as a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having in increasing order of preference at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain.

Preferably, SNH domain having at least 40% identity to the SNH domain of SEQ ID NO: 2 comprises the residues shown in black in Figure 2. Further preferably, the SNH domain is represented by SEQ ID NO: 1.

The nucleic acid to be introduced into a plant may be a full-length nucleic acid or may be a portion or a hybridizing sequence as hereinbefore defined.

"Homologues" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived. To produce such homologues, amino acids of the protein may be replaced by other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α-helical structures or β-sheet structures). Conservative substitution tables are well known in the art

(see for example Creighton (1984) Proteins. W.H. Freeman and Company and Table 3 below).

Homologues include orthologues and paralogues, which encompass evolutionary concepts used to describe ancestral relationships of genes. Paralogues are genes within the same species that have originated through duplication of an ancestral gene and orthologues are genes from different organisms that have originated through speciation.

Orthologues in, for example, monocot plant species may easily be found by performing a so-called reciprocal blast search. This may be done by a first blast involving blasting a query sequence (for example, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7 or SEQ ID NO: 8) against any sequence database, such as the publicly available NCBI database which may be found at: http://www.ncbi.nlm.nih.gov. BLASTN or TBLASTX (using standard default values) may be used when starting from a nucleotide sequence and BLASTP or TBLASTN (using standard default values) may be used when starting from a protein sequence. The BLAST results may optionally be filtered. The full-length sequences of either the filtered results or non-filtered results are then BLASTed back (second BLAST) against sequences from the organism from which the query sequence is derived (where the query sequence is SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7 or SEQ ID NO: 8 the second blast would therefore be against *Arabidopsis* sequences). The results of the first and second BLASTs are then compared. A paralogue is identified if a high-ranking hit from the second blast is from the same species as from which the query sequence is derived; an orthologue is identified if a high-ranking hit is not from the same species as from which the query sequence is derived. High-ranking hits are those having a low E-value. The lower the E-value, the more significant the score (or in other words the lower the chance that the hit was found by chance). Computation of the E-value is well known in the art. In the case of large families, ClustalW may be used, followed by a neighbour joining tree, to help visualize clustering of related genes and to identify orthologues and paralogues.

A homologue may be in the form of a "substitutional variant" of a protein, i.e. where at least one residue in an amino acid sequence has been removed and a different residue inserted in its place. Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide; insertions will usually be of the order of about 1 to 10 amino acid residues. Preferably, amino acid substitutions comprise conservative amino acid substitutions. Conservative substitution tables are readily available in the art. The table below gives examples of conserved amino acid substitutions.

Table 3: Examples of conserved amino acid substitutions

Residue	Conservative Substitutions	Residue	Conservative Substitutions
Ala	Ser	Leu	Ile; Val
Arg	Lys	Lys	Arg; Gln
Asn	Gln; His	Met	Leu; Ile
Asp	Glu	Phe	Met; Leu; Tyr
Gln	Asn	Ser	Thr; Gly
Cys	Ser	Thr	Ser; Val
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp; Phe
His	Asn; Gln	Val	Ile; Leu
Ile	Leu, Val		

A homologue may also be in the form of an "insertional variant" of a protein, i.e. where one or more amino acid residues are introduced into a predetermined site in a protein. Insertions may comprise N-terminal and/or C-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than N- or C-terminal fusions, of the order of about 1 to 10 residues. Examples of N- or C-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, (histidine)-6-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag·100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

Homologues in the form of "deletion variants" of a protein are characterised by the removal of one or more amino acids from a protein.

Amino acid variants of a protein may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulations. Methods for the manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art. For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen *in vitro* mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene,

San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

The SYT polypeptide or homologue thereof may be a derivative. "Derivatives" include peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise substitutions, deletions or additions of non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the protein, for example, as presented in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86 and SEQ ID NO: 88.

"Derivatives" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise naturally occurring altered, glycosylated, acylated, prenylated or non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents compared to the amino acid sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence, such as a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein.

The SYT polypeptide or homologue thereof may be encoded by an alternative splice variant of a SYT nucleic acid/gene. The term "alternative splice variant" as used herein encompasses variants of a nucleic acid sequence in which selected introns and/or exons have been excised, replaced or added, or in which introns have been shortened or lengthened. Such variants will be ones in which the biological activity of the protein is retained, which may be achieved by selectively retaining functional segments of the protein. Such splice variants may be found in nature or may be manmade. Methods for making such splice variants are well known in the art. Preferred splice variants are splice variants of the nucleic acid encoding a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having in increasing order of preference at least 40%, 45%, 50%, 55%, 60%,

65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain. Preferably, SNH domain having at least 40% identity to the SNH domain of SEQ ID NO: 2 comprises the residues shown in black in Figure 2. Further preferably, the SNH domain is represented by SEQ ID NO: 1.

Additionally, the SYT polypeptide or a homologue thereof may comprise one or more of the following: (i) SEQ ID NO: 90; and/or (ii) SEQ ID NO: 91; and/or (iii) a Met-rich domain at the N-terminal preceding the SNH domain.

Further preferred are splice variants of nucleic acids represented by SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85 and SEQ ID NO: 87 . Most preferred are splice variants of a SYT nucleic acid/gene represented by SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7.

The homologue may also be encoded by an allelic variant of a nucleic acid encoding a SYT polypeptide or a homologue thereof, preferably an allelic variant of the nucleic acid encoding a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having in increasing order of preference at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain. Preferably, SNH domain having at least 40% identity to the SNH domain of SEQ ID NO: 2 comprises the residues shown in black in Figure 2. Further preferably, the SNH domain is represented by SEQ ID NO: 1. Additionally, the SYT polypeptide or a homologue thereof may comprise one or more of the following: (i) SEQ ID NO: 90; and/or (ii) SEQ ID NO: 91; and/or (iii) a Met-rich domain at the N-terminal preceding the SNH domain.

Further preferably, the allelic variant is an allelic variant of a nucleic acid as represented by any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID

NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85 and SEQ ID NO: 87. Most preferably, the allelic variant is an allelic variant of a nucleic acid as represented by any one of SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7.

Allelic variants exist in nature, and encompassed within the methods of the present invention is the use of these natural alleles. Allelic variants encompass Single Nucleotide Polymorphisms (SNPs), as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms.

According to a preferred aspect of the present invention, the modulated expression of a SYT nucleic acid or variant thereof is increased expression. The increase in expression may lead to raised SYT mRNA or polypeptide levels, which could equate to raised activity of the SYT polypeptide; or the activity may also be raised when there is no change in polypeptide levels, or even when there is a reduction in polypeptide levels. This may occur when the intrinsic properties of the polypeptide are altered, for example, by making mutant versions that are more active that the wild type polypeptide. Methods for increasing expression of genes or gene products are well documented in the art and include, for example, overexpression driven by appropriate promoters, the use of transcription enhancers or translation enhancers. Isolated nucleic acids which serve as promoter or enhancer elements may be introduced in an appropriate position (typically upstream) of a non-heterologous form of a polynucleotide so as to upregulate expression of a SYT nucleic acid or variant thereof. For example, endogenous promoters may be altered *in vivo* by mutation, deletion, and/or substitution (see, Kmiec, US 5,565,350; Zarling *et al.*, PCT/US93/03868), or isolated promoters may be introduced into a plant cell in the proper orientation and distance from a gene of the present invention so as to control the expression of the gene. Methods for reducing the expression of genes or gene products are well documented in the art.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or

octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence may also be added to the 5' untranslated region or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold, Buchman and Berg, Mol. Cell biol. 8:4395-4405 (1988); Callis *et al.*, Genes Dev. 1:1183-1200 (1987). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of the maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. See generally, The Maize Handbook, Chapter 116, Freeling and Walbot, Eds., Springer, N.Y. (1994).

The invention also provides genetic constructs and vectors to facilitate introduction and/or expression of the nucleotide sequences useful in the methods according to the invention.

Therefore, there is provided a gene construct comprising:

(i) Any SYT nucleic acid or variant thereof, as defined hereinabove;

(ii) One or more control sequences capable of driving expression of the nucleic acid sequence of (i); and optionally

(iii) A transcription termination sequence.

A preferred construct is one whether the control sequence is a promoter derived from a plant, preferably from a monocotyledonous plant.

Constructs useful in the methods according to the present invention may be constructed using recombinant DNA technology well known to persons skilled in the art. The gene constructs may be inserted into vectors, which may be commercially available, suitable for transforming into plants and suitable for expression of the gene of interest in the transformed cells.

Plants are transformed with a vector comprising the sequence of interest (i.e., a nucleic acid encoding a SYT polypeptide or homologue thereof). The sequence of interest is operably linked to one or more control sequences (at least to a promoter). The terms "regulatory element", "control sequence" and "promoter" are all used interchangeably herein and are to be taken in a broad context to refer to regulatory nucleic acid sequences capable of

effecting expression of the sequences to which they are ligated. Encompassed by the aforementioned terms are transcriptional regulatory sequences derived from a classical eukaryotic genomic gene (including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence) and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or external stimuli, or in a tissue-specific manner. Also included within the term is a transcriptional regulatory sequence of a classical prokaryotic gene, in which case it may include a –35 box sequence and/or –10 box transcriptional regulatory sequences. The term "regulatory element" also encompasses a synthetic fusion molecule or derivative that confers, activates or enhances expression of a nucleic acid molecule in a cell, tissue or organ. The term "operably linked" as used herein refers to a functional linkage between the promoter sequence and the gene of interest, such that the promoter sequence is able to initiate transcription of the gene of interest.

Advantageously, any type of promoter may be used to drive expression of the nucleic acid sequence. The promoter may be an inducible promoter, i.e. having induced or increased transcription initiation in response to a developmental, chemical, environmental or physical stimulus. An example of an inducible promoter being a stress-inducible promoter, i.e. a promoter activated when a plant is exposed to various stress conditions. Additionally or alternatively, the promoter may be a tissue-preferred promoter, i.e. one that is capable of preferentially initiating transcription in certain tissues, such as the leaves, roots, seed tissue etc. Promoters able to initiate transcription in certain tissues only are referred to herein as "tissue-specific".

Preferably, the SYT nucleic acid or variant thereof is operably linked to a constitutive promoter. A constitutive promoter is transcriptionally active during most, but not necessarily all, phases of its growth and development and is substantially ubiquitously expressed. Preferably the promoter is derived from a plant, further preferably a monocotyledonous plant. Most preferred is use of a GOS2 promoter (from rice) (SEQ ID NO: 89). It should be clear that the applicability of the present invention is not restricted to the SYT nucleic acid represented by SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, nor is the applicability of the invention restricted to expression of a SYT nucleic acid when driven by a GOS2 promoter. Examples of other constitutive promoters which may also be used to drive expression of a SYT nucleic acid are shown in Table 4 below.

Table 4: Examples of constitutive promoters

Gene Source	Expression Pattern	Reference
Actin	Constitutive	McElroy *et al,* Plant Cell, 2: 163-171, 1990
CAMV 35S	Constitutive	Odell *et al,* Nature, 313: 810-812, 1985
CaMV 19S	Constitutive	Nilsson *et al., Physiol. Plant. 100*:456-462, 1997
GOS2	Constitutive	de Pater *et al,* Plant J Nov;2(6):837-44, 1992
Ubiquitin	Constitutive	Christensen *et al,* Plant Mol. Biol. 18: 675-689, 1992
Rice cyclophilin	Constitutive	Buchholz *et al,* Plant Mol Biol. 25(5): 837-43, 1994
Maize H3 histone	Constitutive	Lepetit *et al,* Mol. Gen. Genet. 231:276-285, 1992
Actin 2	Constitutive	An *et al,* Plant J. 10(1); 107-121, 1996

Optionally, one or more terminator sequences may also be used in the construct introduced into a plant. The term "terminator" encompasses a control sequence which is a DNA sequence at the end of a transcriptional unit which signals 3' processing and polyadenylation of a primary transcript and termination of transcription. Additional regulatory elements may include transcriptional as well as translational enhancers. Those skilled in the art will be aware of terminator and enhancer sequences that may be suitable for use in performing the invention. Such sequences would be known or may readily be obtained by a person skilled in the art.

The genetic constructs of the invention may further include an origin of replication sequence that is required for maintenance and/or replication in a specific cell type. One example is when a genetic construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule). Preferred origins of replication include, but are not limited to, the f1-ori and colE1.

The genetic construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene that confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells that are transfected or transformed with a nucleic acid construct of the invention. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance, that introduce a new metabolic trait or that allow visual selection. Examples of selectable marker genes include genes conferring resistance to antibiotics (such as nptII that phosphorylates neomycin and kanamycin, or hpt, phosphorylating hygromycin), to herbicides (for example bar which provides resistance to Basta; aroA or gox providing resistance against glyphosate), or genes that provide a metabolic trait (such as manA that allows plants to use mannose as sole carbon source). Visual marker genes result in the formation of colour (for example β-glucuronidase, GUS), luminescence (such as luciferase) or fluorescence (Green Fluorescent Protein, GFP, and derivatives thereof).

The present invention also encompasses plants obtainable by the methods according to the present invention. The present invention therefore provides plants, plant parts and plant cells obtainable by the methods according to the present invention, which plants have introduced therein a SYT nucleic acid or variant thereof and which plants, plant parts and plant cells are preferably from a crop plant, further preferably from a monocotyledonous plant.

The invention also provides a method for the production of transgenic plants having increased yield, comprising introduction and expression in a plant of a SYT nucleic acid or a variant thereof.

More specifically, the present invention provides a method for the production of transgenic plants, preferably monocotyledonous plants, having increased yield, which method comprises:

(i) introducing and expressing in a plant or plant cell a SYT nucleic acid or variant thereof; and

(ii) cultivating the plant cell under conditions promoting plant growth and development.

Subsequent generations of the plants obtained from cultivating step (ii) may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous

second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.

The nucleic acid may be introduced directly into a plant cell or into the plant itself (including introduction into a tissue, organ or any other part of a plant). According to a preferred feature of the present invention, the nucleic acid is introduced into a plant by transformation.

The term "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant regenerated from there. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

Transformation of plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. *et al.*, (1982) Nature 296, 72-74; Negrutiu I *et al.* (1987) Plant Mol Biol 8: 363-373); electroporation of protoplasts (Shillito R.D. et al., 1985 Bio/Technol 3, 1099-1102); microinjection into plant material (Crossway A *et al.,* (1986) Mol. Gen Genet 202: 179-185); DNA or RNA-coated particle bombardment (Klein TM *et al.*, (1987) Nature 327: 70) infection with (non-integrative) viruses and the like. Transgenic rice plants expressing a SYT nucleic acid/gene are preferably produced via *Agrobacterium*-mediated transformation using any of the well known methods for rice transformation, such as described in any of the following: published European patent application EP 1198985 A1, Aldemita and Hodges (Planta 199: 612-617, 1996); Chan *et al.* (Plant Mol Biol 22 (3): 491-

506, 1993), Hiei *et al.* (Plant J 6 (2): 271-282, 1994), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida *et al.* (Nat. Biotechnol 14(6): 745-50, 1996) or Frame *et al.* (Plant Physiol 129(1): 13-22, 2002), which disclosures are incorporated by reference herein as if fully set forth.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant.

Following DNA transfer and regeneration, putatively transformed plants may be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, quantitative PCR, such techniques being well known to persons having ordinary skill in the art.

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.

The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

The present invention clearly extends to any plant cell or plant produced by any of the methods described herein, and to all plant parts and propagules thereof. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced by the parent in the methods according to the invention. The invention also includes host cells containing an isolated SYT nucleic acid or variant thereof. Preferred host cells according to the invention are plant cells. The invention also extends to harvestable parts of a plant such as, but not limited to seeds, leaves, fruits, flowers, stem cultures, rhizomes, tubers and bulbs. The invention furthermore

relates to products derived, preferably directly derived, from a harvestable part of such a plant, such as dry pellets or powders, meal, oil, fat and fatty acids, starch or proteins.

The present invention also encompasses use of SYT nucleic acids or variants thereof and use of SYT polypeptides or homologues thereof and to use of a construct as defined hereinabove in increasing plant yield, especially seed yield. The seed yield is as defined above and preferably includes increased total seed yield or increased TKW.

SYT nucleic acids or variants thereof, or SYT polypeptides or homologues thereof may find use in breeding programmes in which a DNA marker is identified which may be genetically linked to a SYT gene or variant thereof. The SYT nucleic acids/ genes or variants thereof, or SYT polypeptides or homologues thereof may be used to define a molecular marker. This DNA or protein marker may then be used in breeding programmes to select plants having increased yield. The SYT gene or variant thereof may, for example, be a nucleic acid as represented by any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85 and SEQ ID NO: 87.

Allelic variants of a SYT nucleic acid/gene may also find use in marker-assisted breeding programmes. Such breeding programmes sometimes require introduction of allelic variation by mutagenic treatment of the plants, using for example EMS mutagenesis; alternatively, the programme may start with a collection of allelic variants of so called “natural” origin caused unintentionally. Identification of allelic variants then takes place, for example, by PCR. This is followed by a step for selection of superior allelic variants of the sequence in question and which give increased yield. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question, for example, different allelic variants of any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49,

SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85 and SEQ ID NO: 87. Growth performance may be monitored in a greenhouse or in the field. Further optional steps include crossing plants, in which the superior allelic variant was identified, with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

A SYT nucleic acid or variant thereof may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. Such use of SYT nucleic acids or variants thereof requires only a nucleic acid sequence of at least 15 nucleotides in length. The SYT nucleic acids or variants thereof may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Sambrook J, Fritsch EF and Maniatis T (1989) Molecular Cloning, A Laboratory Manual) of restriction-digested plant genomic DNA may be probed with the SYT nucleic acids or variants thereof. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander *et al.* (1987) Genomics 1: 174-181) in order to construct a genetic map. In addition, the nucleic acids may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the SYT nucleic acid or variant thereof in the genetic map previously obtained using this population (Botstein *et al.* (1980) Am. J. Hum. Genet. 32:314-331).

The production and use of plant gene-derived probes for use in genetic mapping is described in Bematzky and Tanksley (1986) Plant Mol. Biol. Reporter 4: 37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

The nucleic acid probes may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel *et al. In*: Non-mammalian Genomic Analysis: A Practical Guide, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, the nucleic acid probes may be used in direct fluorescence *in situ*

hybridization (FISH) mapping (Trask (1991) Trends Genet. 7:149-154). Although current methods of FISH mapping favor use of large clones (several kb to several hundred kb; see Laan *et al.* (1995) Genome Res. 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

A variety of nucleic acid amplification-based methods for genetic and physical mapping may be carried out using the nucleic acids. Examples include allele-specific amplification (Kazazian (1989) J. Lab. Clin. Med 11:95-96), polymorphism of PCR-amplified fragments (CAPS; Sheffield *et al.* (1993) Genomics 16:325-332), allele-specific ligation (Landegren *et al.* (1988) Science 241:1077-1080), nucleotide extension reactions (Sokolov (1990) Nucleic Acid Res. 18:3671), Radiation Hybrid Mapping (Walter *et al.* (1997) Nat. Genet. 7:22-28) and Happy Mapping (Dear and Cook (1989) Nucleic Acid Res. 17:6795-6807). For these methods, the sequence of a nucleic acid is used to design and produce primer pairs for use in the amplification reaction or in primer extension reactions. The design of such primers is well known to those skilled in the art. In methods employing PCR-based genetic mapping, it may be necessary to identify DNA sequence differences between the parents of the mapping cross in the region corresponding to the instant nucleic acid sequence. This, however, is generally not necessary for mapping methods.

The methods according to the present invention result in plants having increased yield, as described hereinbefore. These yield-enhancing traits may also be combined with other economically advantageous traits, such as further yield-enhancing traits, tolerance to various stresses, traits modifying various architectural features and/or biochemical and/or physiological features.

Description of figures

The present invention will now be described with reference to the following figures in which:

Fig. 1 shows the typical domain structure of SYT polypeptides from plants and mammals. The conserved SNH domain is located at the N-terminal end of the protein. The C-terminal remainder of the protein domain consists of a QG-rich domain in plant SYT polypeptides, and of a QPGY-rich domain in mammalian SYT polypeptides. A Met-rich domain is typically comprised within the first half of the QG-rich (from the N-term to the C-term) in plants or QPGY-rich in mammals. A second Met-rich domain may precede the SNH domain in plant SYT polypeptides

Fig. 2 shows a multiple alignment of the N-terminal end of several SYT polypeptides, using VNTI AlignX multiple alignment program, based on a modified ClustalW algorithm (InforMax, Bethesda, MD, http://www.informaxinc.com), with default settings for gap opening penalty of 10 and a gap extension of 0.05). The SNH domain is boxed across the plant and human SYT polypeptides. The last line in the alignment consists of a consensus sequence derived from the aligned sequences.

Fig.3 shows a multiple alignment of several plant SYT polypeptides, using VNTI AlignX multiple alignment program, based on a modified ClustalW algorithm (InforMax, Bethesda, MD, http://www.informaxinc.com), with default settings for gap opening penalty of 10 and a gap extension of 0.05). The two main domains, from N-terminal to C-terminal, are boxed and identified as SNH domain and the Met-rich/QG-rich domain. Additionally, the N-terminal Met-rich domain is also boxed, and the positions of SEQ ID NO: 90 and SEQ ID NO 91 are underlined in bold.

Fig. 4 shows a Neighbour joining tree resulting from the alignment of multiple SYT polypeptides using CLUSTALW 1.83 (http://align.genome.jp/sit-bin/clustalw). The SYT1 and SYT2/SYT3 clades are identified with brackets.

Fig. 5 shows a binary vector p0523, for expression in *Oryza sativa* of an *Arabidopsis thaliana* AtSYT1 under the control of a GOS2 promoter (internal reference PRO0129).

Fig. 6 shows a binary vector p0524, for expression in *Oryza sativa* of an *Arabidopsis thaliana* AtSYT2 under the control of a GOS2 promoter (internal reference PRO0129).

Fig. 7 shows a binary vector p0767, for expression in *Oryza sativa* of an *Arabidopsis thaliana* AtSYT3 under the control of a GOS2 promoter (internal reference PRO0129).

Fig. 8 details examples of sequences useful in performing the methods according to the present invention. SYT nucleic acid sequences are presented from start to stop. The majority of these sequences are derived from EST sequencing, which is of lower quality. Therefore, nucleic acid substitutions may be encountered.

Examples

The present invention will now be described with reference to the following examples, which are by way of illustration alone.

DNA manipulation: unless otherwise stated, recombinant DNA techniques are performed according to standard protocols described in (Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York) or in Volumes 1 and 2 of Ausubel *et al.* (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfase (1993) by R.D.D. Croy, published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

Example 1: Gene Cloning of AtSYT1, AtSYT2 and AtSYT3

The *Arabidopsis thaliana* AtSYT1 gene was amplified by PCR using as template an *Arabidopsis thaliana* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.5 kb and the original number of clones was of the order of 1.59 x 10^7 cfu. Original titer was determined to be 9.6 x 10^5 cfu/ml after first amplification of 6x10^{11} cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 µl PCR mix. Primers prm06681 (SEQ ID NO: 92; sense, start codon in bold, AttB1 site in italic: 5'-*GGGGACAAGTTTGTACAAAAAAGCAGG*CTTAAACA**ATG**CAACAGCACCTGATG -3') and prm06682 (SEQ ID NO: 93; reverse, complementary, AttB2 site in italic: 5'-*GGGGACCACTTTGTACAAGAAAGCTGGGT*CATCATTAAGATTCCTTGTGC-3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 727 bp (including attB sites) was amplified and purified also using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombines *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone", p07466. Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.

The *Arabidopsis thaliana* AtSYT2 gene was amplified by PCR using the same method as the *Arabidopsis thaliana* AtSYT1 gene. Primers prm06685 (SEQ ID NO: 94; sense, start codon in bold, AttB1 site in italic: 5'-*GGGGACAAGTTTGTACAAAAAAGCAGG* CTTAAACA**ATG**CAGCAGCAGCAGTCT 3') and prm06686 (SEQ ID NO: 95); reverse, stop codon in bold, complementary, AttB2 site in italic: 5' *GGGGACCACTTTGTACAAGAAAG CTGGGT*TCTTTGGATCCTTTT**TCA**CTTG 3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 666 bp (including attB sites) was amplified and purified as above. The entry clone was numbered p07467.

The *Arabidopsis thaliana* AtSYT3 gene was amplified by PCR using the same method as the *Arabidopsis thaliana* AtSYT1 and AtSYT2 genes. Primers prm06683 (SEQ ID NO: 96; sense, start codon in bold, AttB1 site in italic: 5' *GGGGACAAGTTTGTACAAAAAAG CAGG*CTTAAACA**ATG**CAGCAATCTCCACAGAT 3') and prm06684 (SEQ ID NO: 97; reverse, stop codon in bold, complementary, AttB2 site in italic: 5' *GGGGACCACTTTGTAC AAGAAAGCTGGGT*TCCTCTATTTCATTTTCCTTCAG 3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 745 bp (including attB sites) was amplified and purified as above. The entry clone was numbered p07604.

Example 2: Vector Construction

The entry clones p07466, p07467 and p07604 were subsequently used in an LR reaction with p00640, a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already cloned in the entry clone. A rice GOS2 promoter (SEQ ID NO: 89) for constitutive expression (PRO0129) was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vectors, respectively p0523 for AtSYT1, p0524 for AtSYT2 and p0767 for AtSYT3 (Figures 5 to 7) were transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described in Example 3.

Example 3: Evaluation and Results of AtSYT1, AtSYT2 and AtSYT3 under the control of the rice GOS2 promoter

Approximately 15 to 20 independent T0 rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T1 seed. Six events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homo-zygotes) and approximately 10 T1 seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression.

Statistical analysis: F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the presence or position of the gene that is causing the differences in phenotype.

Seed-related parameter measurements

The mature primary panicles were harvested, bagged, barcode-labeled and then dried for three days in an oven at 37°C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. The total seed yield was measured by weighing all filled husks harvested from a plant. Total seed number per plant was measured by counting the number of husks harvested from a plant. Thousand Kernel Weight (TKW) is extrapolated from the number of filled seeds counted and their total weight.

Individual seed parameters (including width, length, area, weight) were measured using a custom-made device consisting of two main components, a weighing and imaging device, coupled to software for image analysis.

3.1 Total seed yield and TKW measurement results for transgenic plants grown in the greenhouse

The total seed yield and TKW measurement results for AtSYT1, AtSYT2 and AtSYT3 transgenic plants for the T1 generation are shown in Tables 5 to 7, respectively. The number of lines with an increase in either parameter is indicated. The percentage difference between the transgenics and the corresponding nullizygotes is also shown, as well as the P values from the F test.

Both the total seed yield and TKW are significantly increased in the T1 generation for AtSYT1, AtSYT2 and ATSYT3 transgenic plants (Tables 5 to 7, respectively).

Table 5: Results of total seed yield and TKW measurements in the T1 generation of AtSYT1 transgenic plants.

	Number of events showing an increase	**% Difference**	**P value of F test**
Total seed yield	5 out of 6	19	0.005
TKW	6 out of 6	11	<0.0001

Table 6: Results of total seed yield and TKW measurements in the T1 generation of AtSYT2 transgenic plants.

	Number of events showing an increase	**% Difference**	**P value of F test**
Total seed yield	4 out of 6	37	0.05
TKW	6 out of 6	5	<0.0001

Table 7: Results of total seed yield and TKW measurements in the T1 generation of AtSYT3 transgenic plants.

	Number of events showing an increase	**% Difference**	**P value of F test**
Total seed yield	5 out of 6	22	0.0074
TKW	5 out of 6	7	<0.0001

3.2 Seed size measurements results of seeds from T2 generation AtSYT1 transgenic plants

Individual seed parameters (width, length and area) were measured on the seeds from the T2 plants, using a custom-made device consisting of two main components, a weighing and an imaging device, coupled to software for image analysis. Measurements were performed on both husked and dehusked seeds.

The average individual seed area, length and width measurement results of the T3 seeds (harvested from the T2 plants) for the *Oryza sativa* AtSYT1 transgenic plants are shown in Table 8. The percentage difference between the transgenics and the corresponding nullizygotes is shown, as well as the number of events with an increase in a given parameter and the p values from the F test.

The average individual seed area, length and width of the T3 husked and dehusked seeds (harvested from the T2 transgenic *Oryza sativa* AtSYT1 plants) were all significantly increased compared to their null counterparts (Table 8).

Table 8: Individual seed area, length and width measurements of the T3 husked and dehusked seeds (harvested from the T2 plants) of the *Oryza sativa* AtSYT1 transgenic plants compared to their null counterparts.

	Number of events showing an increase	**% Difference**	**P value of F test**
Average seed area	6 out of 6	11 %	<0.0001
Average dehusked seed area	6 out of 6	10 %	<0.0001
Average seed length	6 out of 6	6 %	<0.0001
Average dehusked seed length	6 out of 6	5 %	<0.0001
Average seed width	6 out of 6	5 %	<0.0001
Average dehusked seed width	6 out of 6	4 %	<0.0001

3.3 Embryo and endosperm size measurement results of seeds from T2 generation AtSYT1 transgenic plants

Embryo and endosperm size were also measured by longitudinally cutting in half dehusked seeds and staining the seed halves for 2 to 3 hours at 35°C with colouring agent, 2,3,5-triphenyltetrazolium chloride. Following staining, the two halves were placed on agarose gel in a Petri dish ready for imaging. Three independent events were taken, and from each event 120 seeds homozygous for the transgene and 120 seeds without the transgene were analysed. Digital photographs of the seeds were taken and the images analysed with ImagePro software. The results for the three events are given below.

For all three events, embryos of seeds homozygous for the transgene were bigger than the embryos of seeds without the transgene. There was a significant increase in the average area of the embryo for the seeds of each of the three events, with p values from the t-test of 0.0325, <0.0001 and <0.0001. Similarly, there was a significant increase in the average perimeter of the embryo for the seeds of each of the three events, with p values from the t-test of 0.0176, <0.0001 and <0.0001. Furthermore, there was a significant increase in the average area and perimeter of the endosperm for the seeds of each of the three events, all giving p values of <0.0001.

3.4 TKW measurement results for AtSYT1 transgenic plants grown in the field

The AtSYT1 homozygous transgenic plants and their corresponding controls were transplanted into the field in September and harvested in December. Four repetitions were planted for each entry (four events) with 104 plants per repeat. The spacing between plants was of 20 by 20 cm. The field was flooded and irrigated. After seed harvest, the seeds were measured for TKW as described above. Results of these measurements are presented in Table 9.

Table 9: Results of TKW measurements in the T3 generation of AtSYT1 transgenic plants grown in the field.

Event	Percentage increase (%) in TKW
Event 1	8
Event 2	6
Event 3	5
Event 4	10

The TKW is increased in all the transgenic events evaluated in the field.

Claims

1. Method for increasing plant yield relative to corresponding wild type plants, comprising modulating expression in a plant of a nucleic acid encoding a synovial sarcoma translocation (SYT) polypeptide or homologue thereof, and optionally selecting for plants having increased yield, wherein said SYT polypeptide or homologue comprises from N-terminal to C-terminal: (i) an SNH domain having at least 40% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain.

2. Method according to claim 1, wherein said SNH domain comprises the residues shown in black in Figure 2.

3. Method according to claim 1, wherein said SNH domain is represented by SEQ ID NO: 1.

4. Method according to any one of claims 1 to 3, wherein said SYT polypeptide or homologue thereof further comprises one or more of the following: (i) SEQ ID NO: 90; (ii) SEQ ID NO: 91; (iii) a Met-rich domain at the N-terminus preceding the SNH domain.

5. Method according to any one of claims 1 to 4, wherein said modulated expression is effected by introducing a genetic modification, preferably in the locus of a gene encoding a SYT polypeptide or a homologue thereof.

6. Method according to claim 5, wherein said genetic modification is effected by one of: T-DNA activation, TILLING, site-directed mutagenesis or directed evolution.

7. Method for increasing yield, particularly seed yield, relative to that of corresponding wild type plants, comprising introducing and expressing in a plant, plant part or plant cell a SYT nucleic acid or a variant thereof.

8. Method according to claim 7, wherein said variant is a portion of a SYT nucleic acid or a sequence capable of hybridising to a SYT nucleic acid, which portion or hybridising sequence encodes a polypeptide comprising from N-terminal to C-terminal: (i) an SNH domain having at least 40% sequence identity to the SNH domain of SEQ ID NO: 2; and (ii) a Met-rich domain; and (iii) a QG-rich domain.

9. Method according to claim 7, wherein said SNH domain comprises the residues shown in black in Figure 2.

10. Method according to claim 7, wherein said SNH domain is represented by SEQ ID NO: 1.

11. Method according to any one of claims 7 to 10, wherein said SYT polypeptide or homologue thereof further comprises one or more of the following: (i) SEQ ID NO: 90; (ii) SEQ ID NO: 91; (iii) a Met-rich domain at the N-terminus preceding the SNH domain.

12. Method according to any one of claims 7 to 11, wherein said SYT nucleic acid or variant thereof is overexpressed in a plant.

13. Method according to any one of claims 7 to 12, wherein said SYT nucleic acid or variant thereof is of plant origin, preferably from a dicotyledonous plant, further preferably from the family Brassicaceae, more preferably the nucleic acid is from *Arabidopsis thaliana*.

14. Method according to any one of claims 7 to 13, wherein said variant encodes an orthologue or paralogue of the SYT protein of SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 8.

15. Method according to any one of claims 7 to 14, wherein said SYT nucleic acid or variant thereof is operably linked to a constitutive promoter.

16. Method according to claim 15, wherein said constitutive promoter is plant-derived, preferably from a monocotyledonous plant.

17. Method according to claim 15 or 16, wherein said constitutive promoter is a GOS2 promoter.

18. Method according to any one of claims 1 to 17, wherein said increased yield is increased seed yield.

19. Method according to any one of claims 1 to 18, wherein said increased yield is increased total seed yield and/or increased TKW.

20. Plant, plant part or plant cell obtainable by a method according to any one of claims 1 to 19.

21. Construct comprising:
    (i) a SYT nucleic acid or variant thereof;
    (ii) one or more control sequences capable of driving expression of the nucleic acid sequence of (a); and optionally
    (iii) a transcription termination sequence.

22. Construct according to claim 21, wherein said control sequence is a constitutive promoter derived from a monocot plant.

23. Construct according to claim 22, wherein said constitutive promoter is a GOS2 promoter.

24. Construct according to claim 23, wherein said GOS2 promoter is as represented by SEQ ID NO: 89.

25. Plant, plant part or plant cell transformed with a construct according to any one of claims 21 to 24.

26. Method for the production of a transgenic plant, preferably a monocotyledonous plant, having increased yield, particularly increased seed yield, which method comprises:
    (i) introducing and expressing in a plant or plant cell a SYT nucleic acid or variant thereof;
    (ii) cultivating the plant cell under conditions promoting plant growth and development.

27. Method according to claim 26, comprising generating one or more subsequent generations of plants and parts thereof including seeds by crossing plants obtained by said cultivating step (ii).

28. Transgenic plant or part thereof having increased yield, particularly increased seed yield, resulting from a SYT nucleic acid or a variant thereof introduced into said plant or plant part, said increased yield being relative to corresponding wild type plants.

29. Transgenic plant according to claim 20, 25 or 28, wherein said plant is a monocotyledonous plant, such as sugar cane or wherein the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, oats or sorghum.

30. Harvestable parts of a plant according to any one of claims 20, 25, 28 or 29.

31. Harvestable parts of a plant according to claim 30 wherein said harvestable parts are seeds.

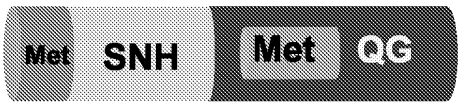
32. Products derived, preferably directly derived, from a plant according to claim 29 and/or from harvestable parts of a plant according to claims 30 or 31.

33. Use of a SYT nucleic acid/gene or variant thereof, or use of a SYT polypeptide or homologue thereof, or use of a construct according to any one of claims 21 to 24, in improving yield, especially seed yield, relative to corresponding wild type plants.

34. Use according to claim 33, wherein said seed yield is increased total seed yield and increased TKW.

35. Use of a SYT nucleic acid/gene or variant thereof, or use of a SYT polypeptide or homologue thereof, as a molecular marker.

Plant SYT-like polypeptide structure



Mammalian SYT-like polypeptide structure

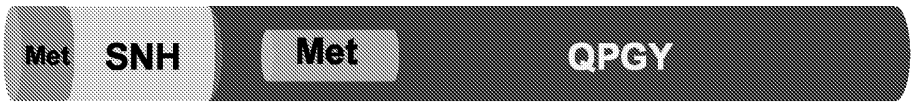


FIGURE 1

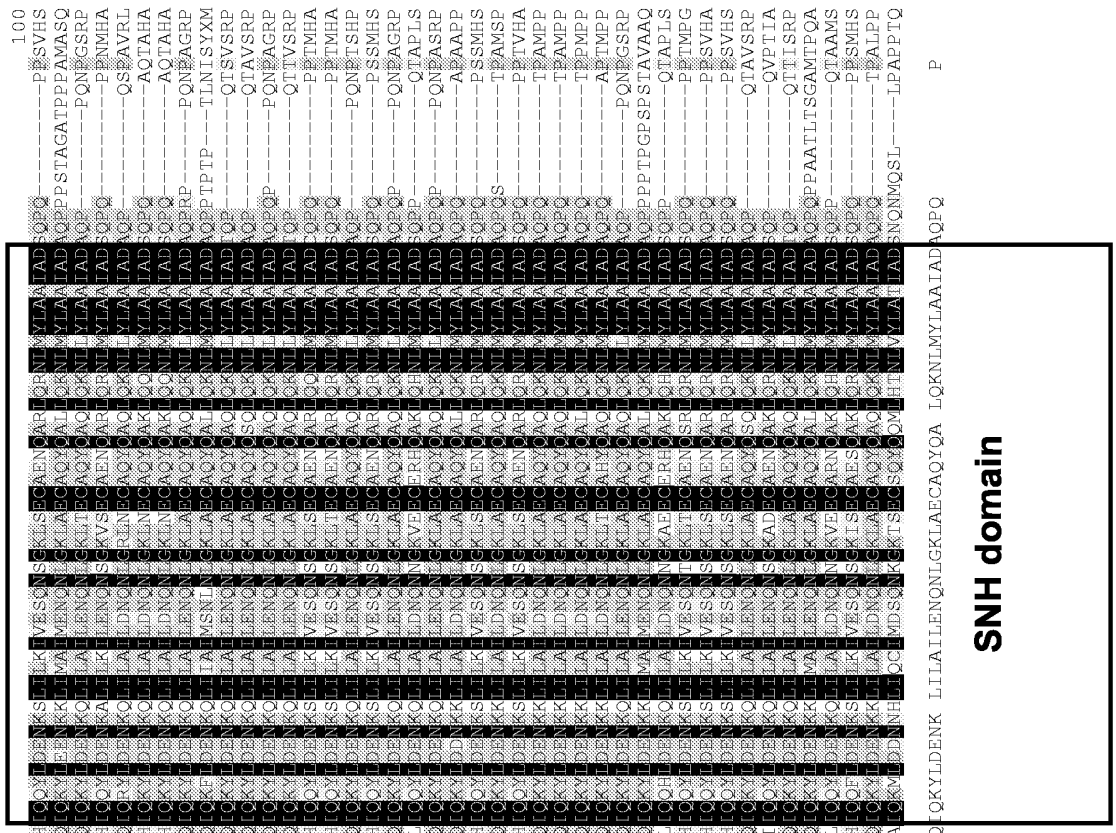


FIGURE 2

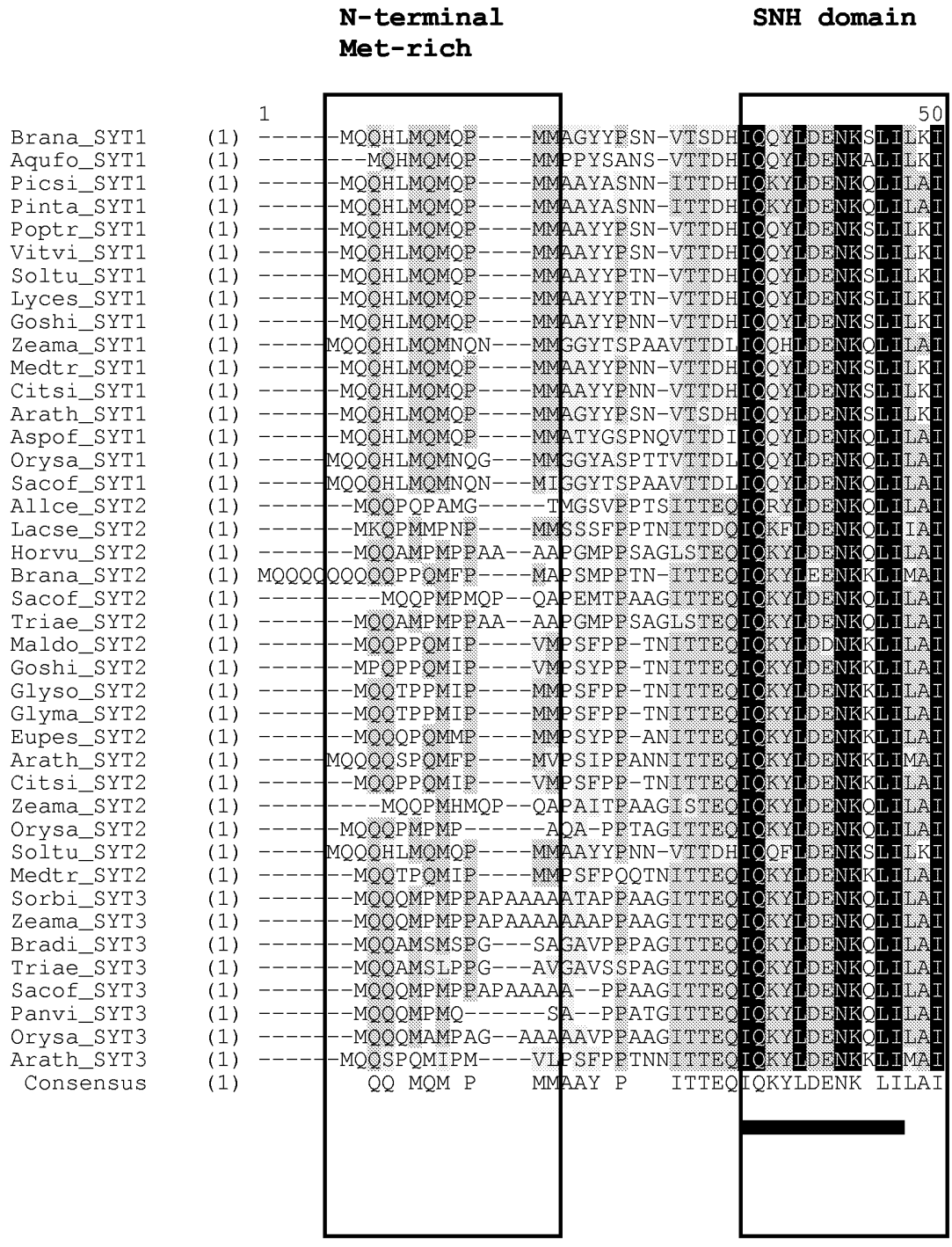

N-terminal
Met-rich
SNH domain
1
50
Brana_SYT1 (1) -----MQQHLMQMQP----MMAGYYPSN-VTSDHIQQYLDENKSLILKI
Aqufo_SYT1 (1) -----MQHMQMQP----MMPPYSANS-VTTDHIQQYLDENKALILKI
Picsi_SYT1 (1) -----MQQHLMQMQP----MMAAYASNN-ITTDHIQKYLDENKQLILAI
Pinta_SYT1 (1) -----MQQHLMQMQP----MMAAYASNN-ITTDHIQKYLDENKQLILAI
Poptr_SYT1 (1) -----MQQHLMQMQP----MMAAYYPSN-VTTDHIQQYLDENKSLILKI
Vitvi_SYT1 (1) -----MQQHLMQMQP----MMAAYYPSN-VTTDHIQQYLDENKSLILKI
Soltu_SYT1 (1) -----MQQHLMQMQP----MMAAYYPTN-VTTDHIQQYLDENKSLILKI
Lyces_SYT1 (1) -----MQQHLMQMQP----MMAAYYPTN-VTTDHIQQYLDENKSLILKI
Goshi_SYT1 (1) -----MQQHLMQMQP----MMAAYYPNN-VTTDHIQQYLDENKSLILKI
Zeama_SYT1 (1) -----MQQQHLMQMNQN---MMGGYTSPAAVTTDLIQQHLDENKQLILAI
Medtr_SYT1 (1) -----MQQHLMQMQP----MMAAYYPNN-VTTDHIQQYLDENKSLILKI
Citsi_SYT1 (1) -----MQQHLMQMQP----MMAAYYPNN-VTTDHIQQYLDENKSLILKI
Arath_SYT1 (1) -----MQQHLMQMQP----MMAGYYPSN-VTSDHIQQYLDENKSLILKI
Aspof_SYT1 (1) -----MQQHLMQMQP----MMATYGSPNQVTTDIIQQYLDENKQLILAI
Orysa_SYT1 (1) -----MQQQHLMQMNQG---MMGGYASPTTVTTDLIQQYLDENKQLILAI
Sacof_SYT1 (1) -----MQQQHLMQMNQN---MIGGYTSPAAVTTDLIQQYLDENKQLILAI
Allce_SYT2 (1) -----MQQPQPAMG-----TMGSVPPTSITTEQIQRYLDENKQLILAI
Lacse_SYT2 (1) -----MKQPMMPNP----MMSSSFPPTNITTDQIQKFLDENKQLIIAI
Horvu_SYT2 (1) -----MQQAMPMPPAA--AAPGMPPSAGLSTEQIQKYLDENKQLILAI
Brana_SYT2 (1) MQQQQQQQQQPPQMFP----MAPSMPPTN-ITTEQIQKYLEENKKLIMAI
Sacof_SYT2 (1) ----------MQQPMPMQP--QAPEMTPAAGITTEQIQKYLDENKQLILAI
Triae_SYT2 (1) -----MQQAMPMPPAA--AAPGMPPSAGLSTEQIQKYLDENKQLILAI
Maldo_SYT2 (1) -----MQQPPQMIP----VMPSFPP-TNITTEQIQKYLDDNKKLILAI
Goshi_SYT2 (1) -----MPQPPQMIP----VMPSYPP-TNITTEQIQKYLDENKKLILAI
Glyso_SYT2 (1) -----MQQTPPMIP----MMPSFPP-TNITTEQIQKYLDENKKLILAI
Glyma_SYT2 (1) -----MQQTPPMIP----MMPSFPP-TNITTEQIQKYLDENKKLILAI
Eupes_SYT2 (1) -----MQQQPQMMP----MMPSYPP-ANITTEQIQKYLDENKKLILAI
Arath_SYT2 (1) -----MQQQQSPQMFP----MVPSIPPANNITTEQIQKYLDENKKLIMAI
Citsi_SYT2 (1) -----MQQPPQMIP----VMPSFPP-TNITTEQIQKYLDENKKLILAI
Zeama_SYT2 (1) ----------MQQPMHMQP--QAPAITPAAGISTEQIQKYLDENKQLILAI
Orysa_SYT2 (1) -----MQQQPMPMP------AQA-PPTAGITTEQIQKYLDENKQLILAI
Soltu_SYT2 (1) -----MQQQHLMQMQP----MMAAYYPNN-VTTDHIQQFLDENKSLILKI
Medtr_SYT2 (1) -----MQQTPQMIP----MMPSFPQQTNITTEQIQKYLDENKKLILAI
Sorbi_SYT3 (1) -----MQQQMPMPPAPAAAAATAPPAAGITTEQIQKYLDENKQLILAI
Zeama_SYT3 (1) -----MQQQMPMPPAPAAAAAAAPPAAGITTEQIQKYLDENKQLILAI
Bradi_SYT3 (1) -----MQQAMSMSPG---SAGAVPPPAGITTEQIQKYLDENKQLILAI
Triae_SYT3 (1) -----MQQAMSLPPG---AVGAVSSPAGITTEQIQKYLDENKQLILAI
Sacof_SYT3 (1) -----MQQQMPMPPAPAAAAA--PPAAGITTEQIQKYLDENKQLILAI
Panvi_SYT3 (1) -----MQQQMPMQ------SA--PPATGITTEQIQKYLDENKQLILAI
Orysa_SYT3 (1) -----MQQQMAMPAG--AAAAAVPPAAGITTEQIQKYLDENKQLILAI
Arath_SYT3 (1) -----MQQSPQMIPM----VLPSFPPTNNITTEQIQKYLDENKKLIMAI
Consensus (1) QQ MQM P MMAAY P ITTEQIQKYLDENK LILAI

FIGURE 3

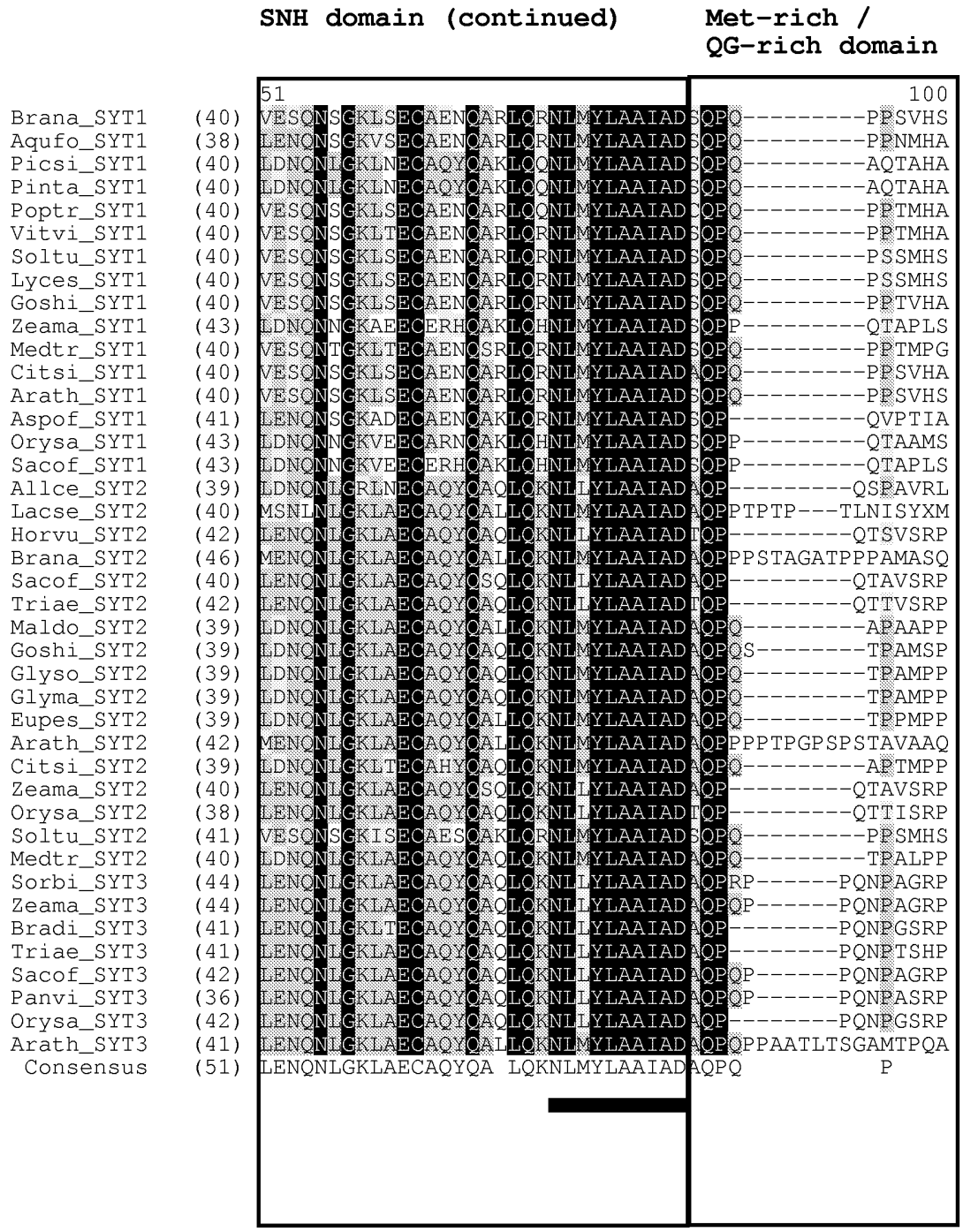


FIGURE 3 (continued)

Met-rich / QG-rich domain (continued)

```
                  101                                                 150
Brana_SYT1   (81) QYGSAGGGLIQGEGAS----HYLQQQQATQQ-----------------QQ
Aqufo_SYT1   (79) QYSNAG-----IPPGA----HYLQHQQAQQ-------------------
Picsi_SYT1   (81) QIPPNA----VMQSGG----HYMQHQQAQQQ------------------
Pinta_SYT1   (81) QIPPNA----VMQSGG----HYMQHQQAQQQ------------------
Poptr_SYT1   (81) QFPSSG---IMQPGA-----HYMQHQQAQQ-------------------
Vitvi_SYT1   (81) QFPPSG---IVQPGA-----HYMQHQQAQQ-------------------
Soltu_SYT1   (81) QFSSGG----MMQPGT----HSYLQQQQQQQQ---------------AQQ
Lyces_SYT1   (81) QFSSGG----MMQPGT----HSYLQQQQQQQQ---------------AQQ
Goshi_SYT1   (81) QFPSGG---IMQPGAG----HYMQHQQAQQ-------------------
Zeama_SYT1   (84) QYPSN----LMMQPGP----RYMPP-QSGQ-------------------M
Medtr_SYT1   (81) QYPSSG---MMQQGG-----HYMQAQQAQQ-------------------
Citsi_SYT1   (81) QFSSGG---IMQPGA-----HYMQHQQSQP-------------------
Arath_SYT1   (81) QYGSAGGGMIQGEGGS----HYLQQQQATQQ-----------------QQ
Aspof_SYT1   (81) QYPPNA--VAAMQSSA----RYMQQHQAAQ-------------------Q
Orysa_SYT1   (84) QYPSN----LMMQSGA----RYMPQ-QSAQ-------------------M
Sacof_SYT1   (84) QYPSN----LMMQPGP----RYMPP-QSGQ-------------------M
Allce_SYT2   (80) QMMPQG---AAATPQAGNQFMQQQSPNFPPKTG---------------MQ
Lacse_SYT2   (87) GPVPHP---GMPQQGG--FYMAQQHPQAAVMTAQP-------------PS
Horvu_SYT2   (83) QMAPPA---ASPGAG----HYMSQVPMFPPRT-----------------P
Brana_SYT2   (96) MGAPHP---GMQPP-----SYFMQHPQASGMAQQA-PPAGIFPPRGPLQF
Sacof_SYT2   (81) QMAPPG---ALPGVG----QYMSQVPMFPPRT-----------------P
Triae_SYT2   (83) QMAPPS---ASPGAG----HYMSQVPMFPPRT-----------------P
Maldo_SYT2   (80) QMAPHP---AMQQA-----GYYMQHPQAAAMAQQQ----GIFSPKMPMQF
Goshi_SYT2   (81) QMAPHP---AMQPG-----GYFMQHPQAAAMSQQP----GMYPQKVPLQF
Glyso_SYT2   (80) QMAPHP---AMQP------GFYMQHPQAAAAAMAQQQQQGMFPQKMPLQF
Glyma_SYT2   (80) QMAPHP---AMQP------GFYMQHPQAAAAAMAQQQQ-GMFPQKMPLQF
Eupes_SYT2   (80) QMSPHP---AMQQG-----AYYMQHPQAAAAAMAHQSG-IFPPKMSPLQF
Arath_SYT2   (92) MATPHS---GMQPP-----SYFMQHPQAS--------PAGIFAPRGPLQF
Citsi_SYT2   (80) QMAPHP---AMQAS-----GYYMQHPQAAAMAQQQ----GIFPQKMPLQF
Zeama_SYT2   (81) QMAPPG---GSPGVG----QYMSQVPMFPPRT-----------------P
Orysa_SYT2   (79) QMVPHG---ASPGLGG---QYMSQVPMFPPRT-----------------P
Soltu_SYT2   (82) QLASGG----MMQGGA----HYMQQQQ--------------------AQQ
Medtr_SYT2   (81) QMAPHP---AMQQ------GFYMQHPQAAAMAQQQ----GMFPQKMPMQF
Sorbi_SYT3   (88) QMMQPG---IVPGAG----HYMSQVPMFPPRT-----------------P
Zeama_SYT3   (88) QMMQPG---IVPGAG----HYMSQVPMFPPRT-----------------P
Bradi_SYT3   (83) QMVQPG---GMPGAG----HYMSQVPMFPPRT-----------------P
Triae_SYT3   (83) QMVQPG---SMQGAG----HYMSQVPMFPPRT-----------------P
Sacof_SYT3   (86) QMMQPG---IVPGAG----HYMSQVPMFPPRT-----------------P
Panvi_SYT3   (80) QMMQPG---MVPGAG----HYMSQVPMFPPRT-----------------P
Orysa_SYT3   (84) QMMQPG---ATPGAG----HYMSQVPMFPPRT-----------------P
Arath_SYT3   (91) MAPNPS---SMQPPP----SYFMQQHQAVG-MAQQ-IPPGIFPPRGPLQF
 Consensus  (101) QM   G    M   G     YYMQ PQA
```

FIGURE 3 (continued)

Met-rich / QG-rich domain (continued)

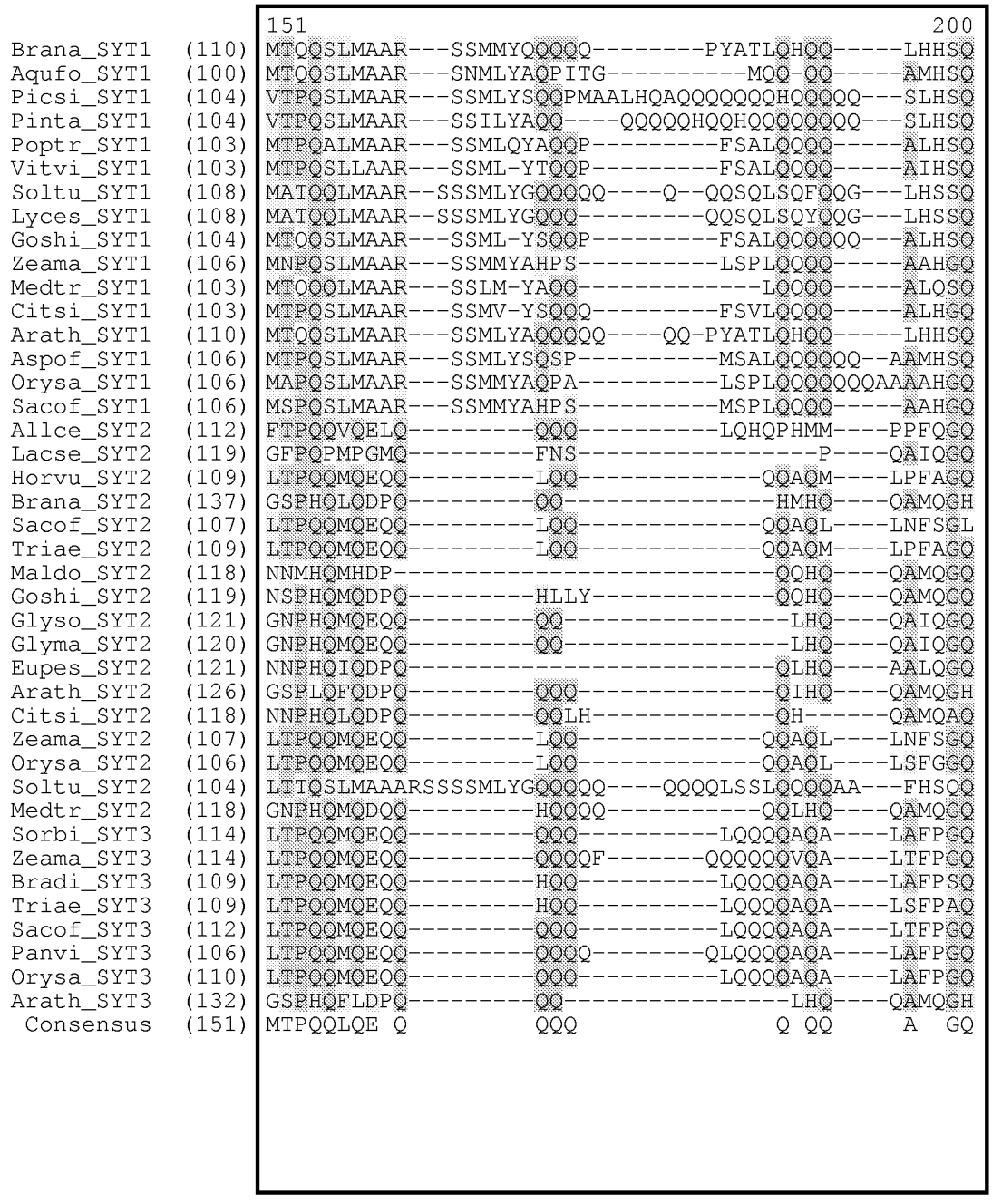


FIGURE 3 (continued)

Met-rich / QG-rich domain (continued)

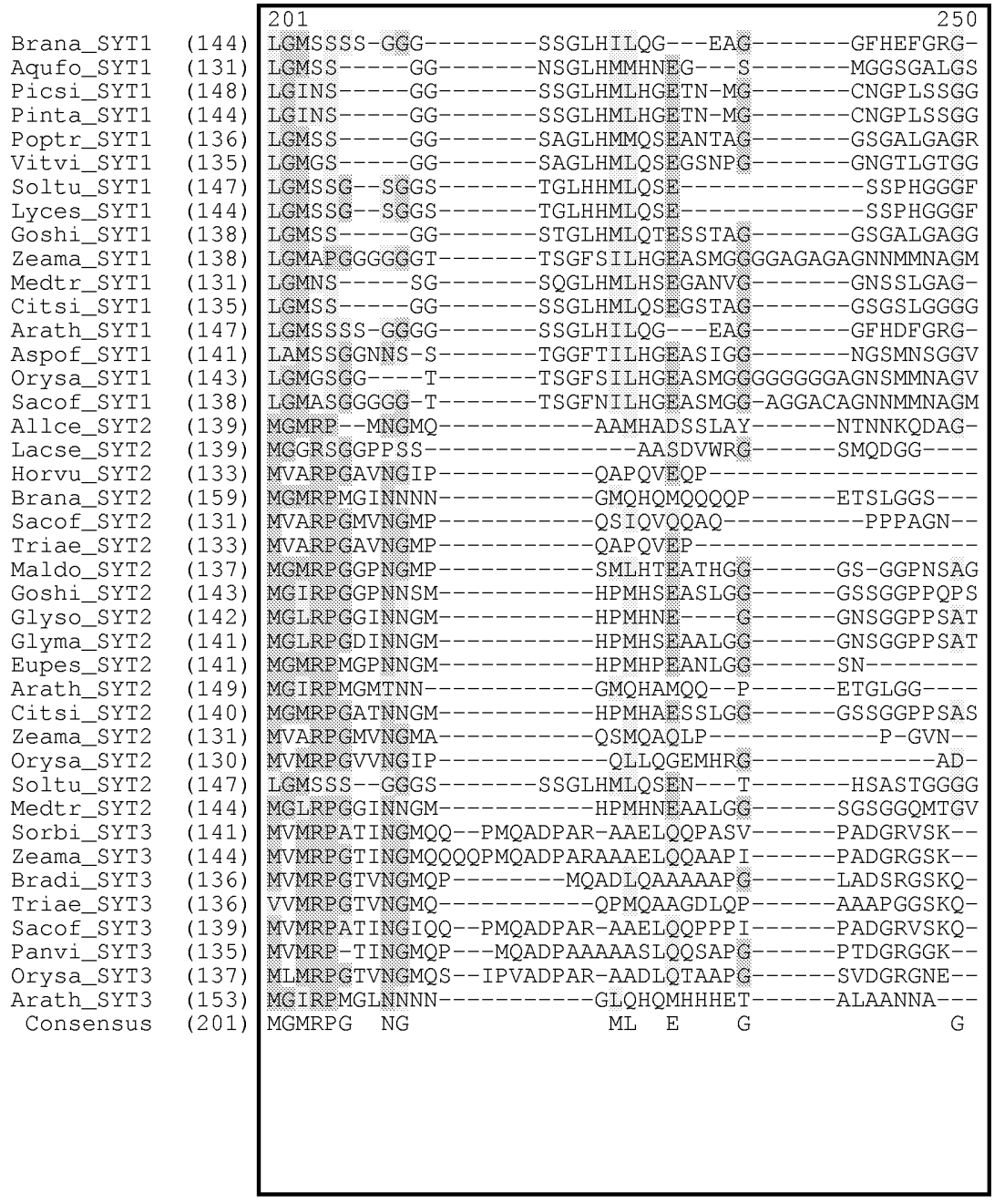


FIGURE 3 (continued)

Met-rich / QG-rich domain (continued)

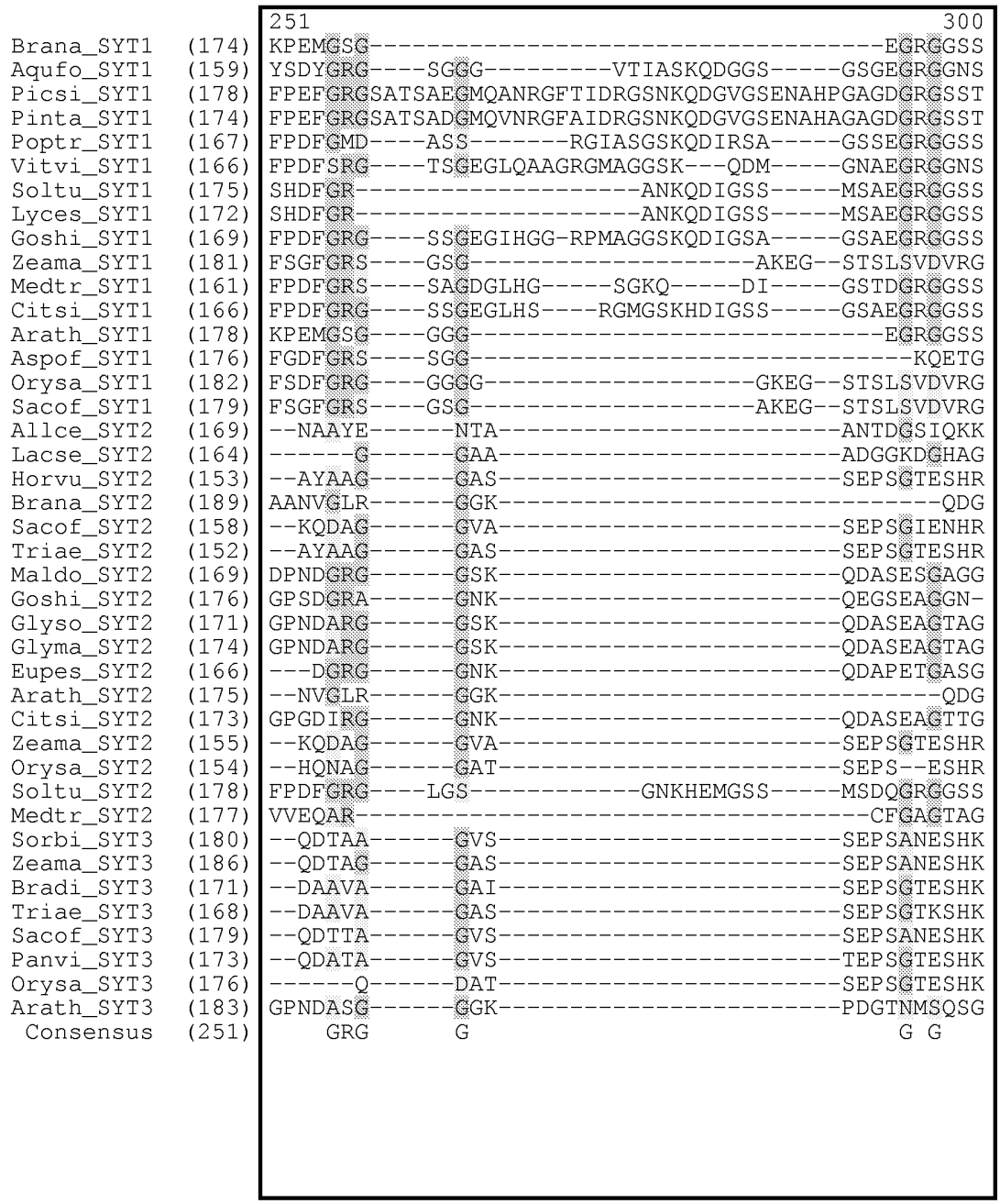


FIGURE 3 (continued)

Met-rich / QG-rich domain (continued)

```
                    301                 324
Brana_SYT1  (188)   G-----DGGETLYLKS--SDDGN-
Aqufo_SYT1  (191)   GGQS-ADGGESLYLKN--SDEGN-
Picsi_SYT1  (228)   GGQN-ADESEPSYLKA--SEE---
Pinta_SYT1  (224)   GGQN-ADESEPSYLKA--SEEEGN
Poptr_SYT1  (201)   GGQGG-DGGETLYLKS--ADDGN-
Vitvi_SYT1  (204)   GGQGG-DGGETLYLKA--AEDGN-
Soltu_SYT1  (200)   ---GG-DGGENLYLKA--SED---
Lyces_SYT1  (197)   ---G---G-ENLYLKA--SED---
Goshi_SYT1  (209)   GGQGGGDGGETLYLKA--ADDGN-
Zeama_SYT1  (205)   GTSSGAQSGDGEYLKVGTEEEGS-
Medtr_SYT1  (192)   SGHSG-DGGETLYLKS--SGDGN-
Citsi_SYT1  (203)   GSQ---DGGETLYLKG--ADDGN-
Arath_SYT1  (195)   G-----DGGETLYLKS--SDDGN-
Aspof_SYT1  (191)   --SEGHGTETPMYLKG-SEEEGN-
Orysa_SYT1  (207)   -ANSGAQSGDGEYLKG-TEEEGS-
Sacof_SYT1  (203)   GTSSGAQSGDGEYLKAGTEEEGS-
Allce_SYT2  (187)   TANDDLDPSAANPRRSEDAKSS--
Lacse_SYT2  (178)   G----------------GPEEAK-
Horvu_SYT2  (171)   S------TGADNDGGSGLADQS--
Brana_SYT2  (202)   ADGQG-------------KDDGK-
Sacof_SYT2  (176)   S------TGGDNDGGSD-------
Triae_SYT2  (170)   S------TGADNDGGSGWADQS--
Maldo_SYT2  (189)   -DGQG--TSAGGRGTG-DGEDGK-
Goshi_SYT2  (195)   --GQG--STTGGHGGGDGADEAK-
Glyso_SYT2  (191)   GDGQG--SSAAAHNSGDG-EEAK-
Glyma_SYT2  (194)   GDGQG--SSAAAHNSGDG-EEAK-
Eupes_SYT2  (183)   GDGQG-------NSGGDGAEDGK-
Arath_SYT2  (186)   ADGQG-------------KDDGK-
Citsi_SYT2  (193)   ADGQG--SSAGGHGG--DGEEAK-
Zeama_SYT2  (173)   S------TGGD-DGGSD-------
Orysa_SYT2  (170)   S------TGTENDGGSDFGDQS--
Soltu_SYT2  (207)   SGHGG-DGGENLYLKS--SEDGN-
Medtr_SYT2  (191)   GDGQGT-SAAAAHNSGDASEEGK-
Sorbi_SYT3  (198)   TT-----TGADSEAGGDVAEKS--
Zeama_SYT3  (204)   SA-----TGADTEAGGDVAEKS--
Bradi_SYT3  (189)   S------TGADHEAGGDVAEQS--
Triae_SYT3  (186)   N------AGAEEVG-ADVAEQS--
Sacof_SYT3  (197)   TT-----TGADSEAGGDVAEKS--
Panvi_SYT3  (191)   ST-----TAADHDVGTDVAEKS--
Orysa_SYT3  (190)   S------AGADNDAGGDIAEKS--
Arath_SYT3  (203)   ADGQGG-S-AARHGGGDAKTEGK-
 Consensus  (301)          TG   Y  G  AEDG
```

FIGURE 3 (continued)

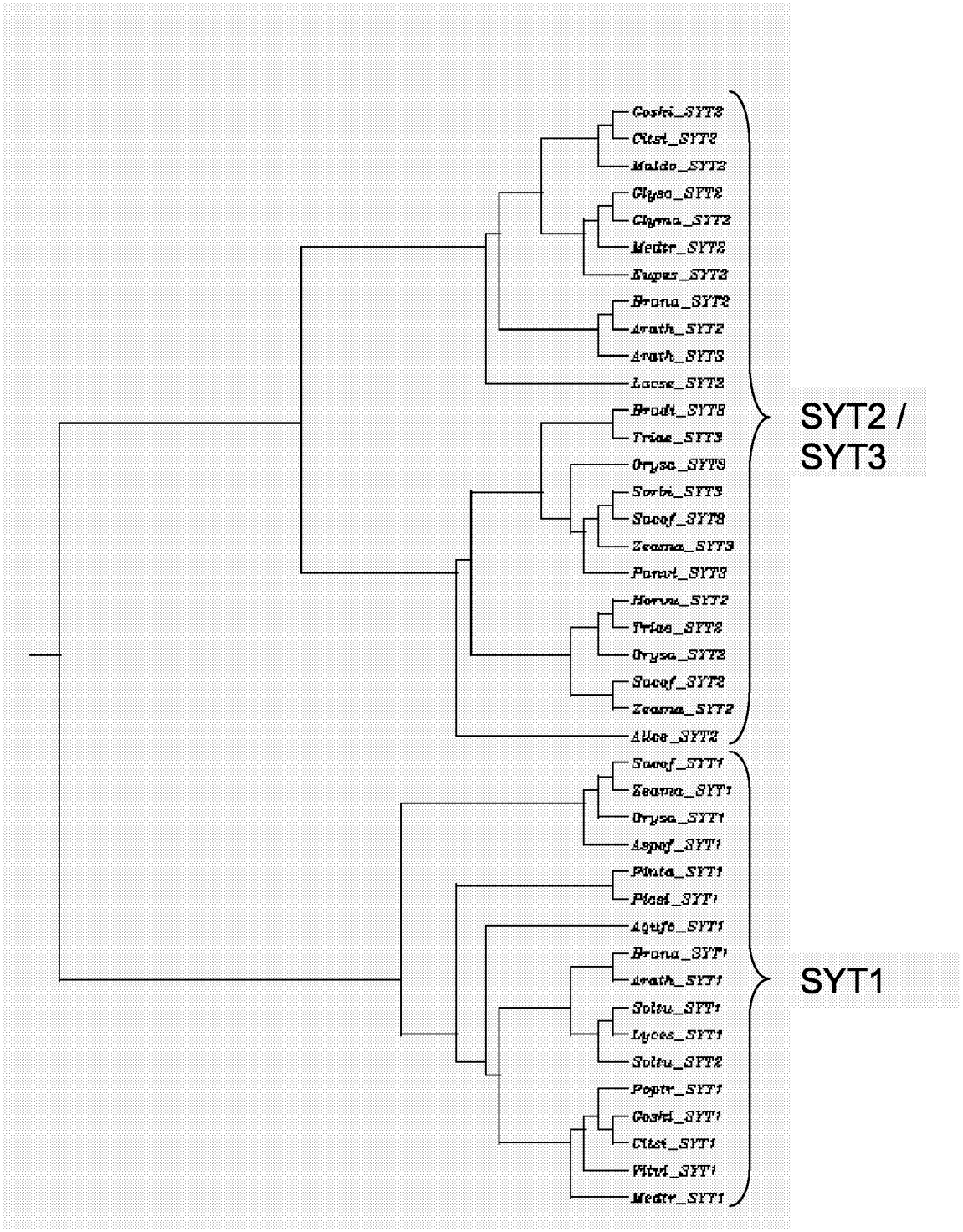

Gosti_SYT2
Citsi_SYT2
Maldo_SYT2
Glyso_SYT2
Glyma_SYT2
Medtr_SYT2
Lupan_SYT2
Brona_SYT2
Arath_SYT2
Arath_SYT3
Lacsa_SYT2
Brodt_SYT3
Triae_SYT3
Orysa_SYT3
Sorbi_SYT3
Saces_SYT3
Zeama_SYT3
Panvi_SYT3
Horvu_SYT2
Triae_SYT2
Orysa_SYT2
Saces_SYT2
Zeama_SYT2
Allce_SYT2
Saces_SYT1
Zeama_SYT1
Orysa_SYT1
Aspsp_SYT1
Phyta_SYT1
Phsi_SYT1
Aqufo_SYT1
Brona_SYT1
Arath_SYT1
Soltu_SYT1
Lyces_SYT1
Soltu_SYT2
Poptr_SYT1
Gosti_SYT1
Citsi_SYT1
Vitvi_SYT1
Medtr_SYT1
SYT2 / SYT3
SYT1

FIGURE 4

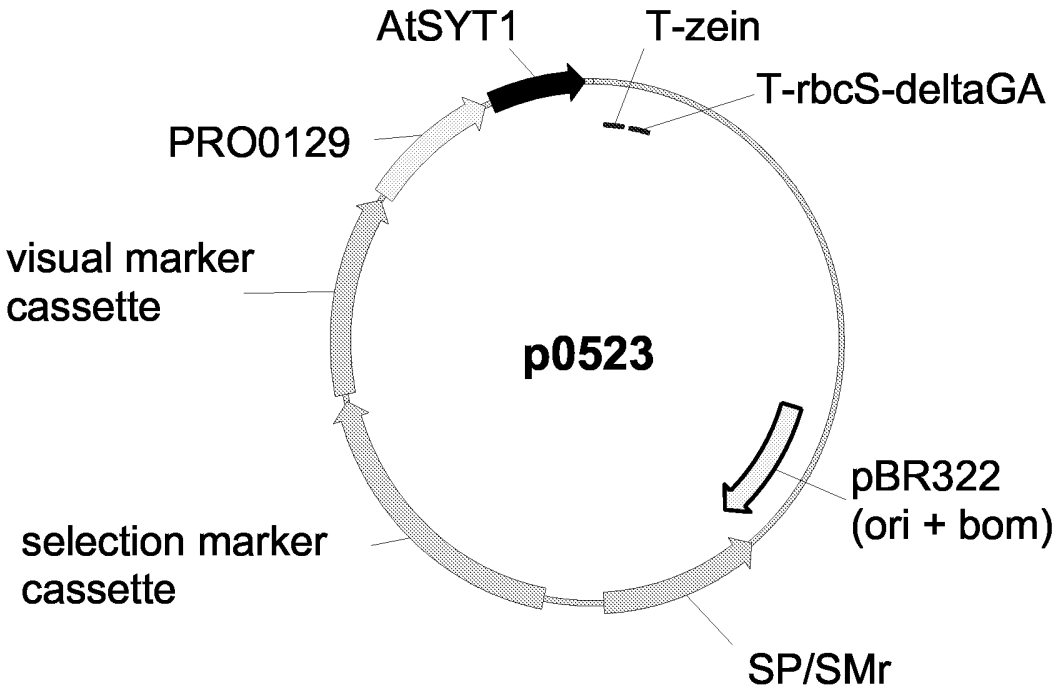

AtSYT1
T-zein
T-rbcS-deltaGA
PRO0129
visual marker cassette
p0523
pBR322 (ori + bom)
selection marker cassette
SP/SMr

FIGURE 5

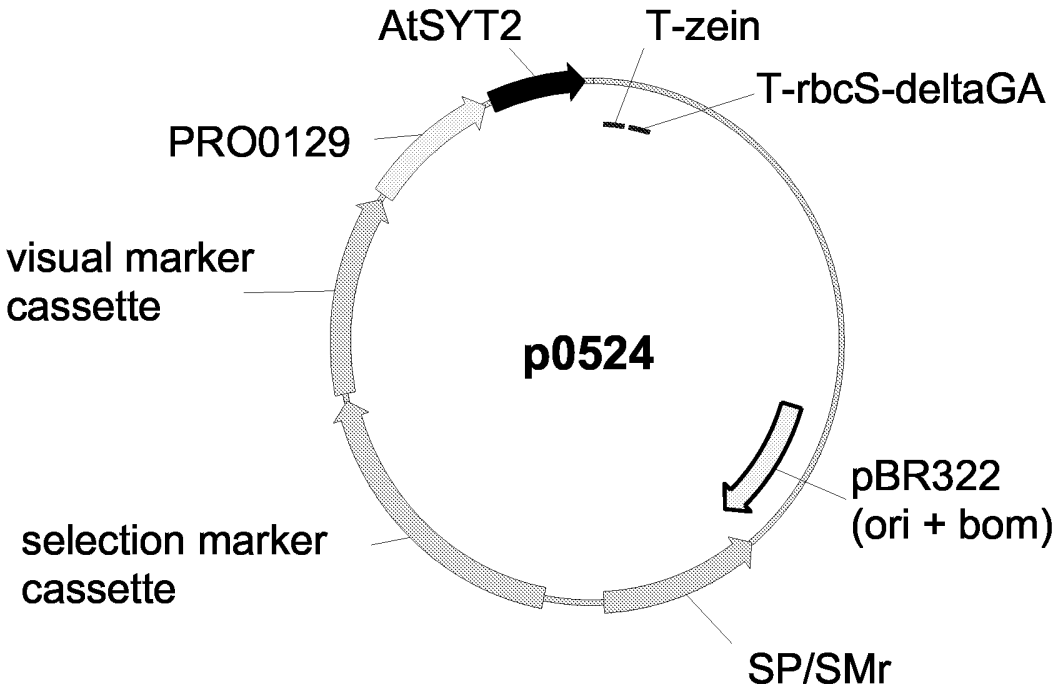

AtSYT2
T-zein
T-rbcS-deltaGA
PRO0129
visual marker cassette
p0524
pBR322 (ori + bom)
selection marker cassette
SP/SMr

FIGURE 6

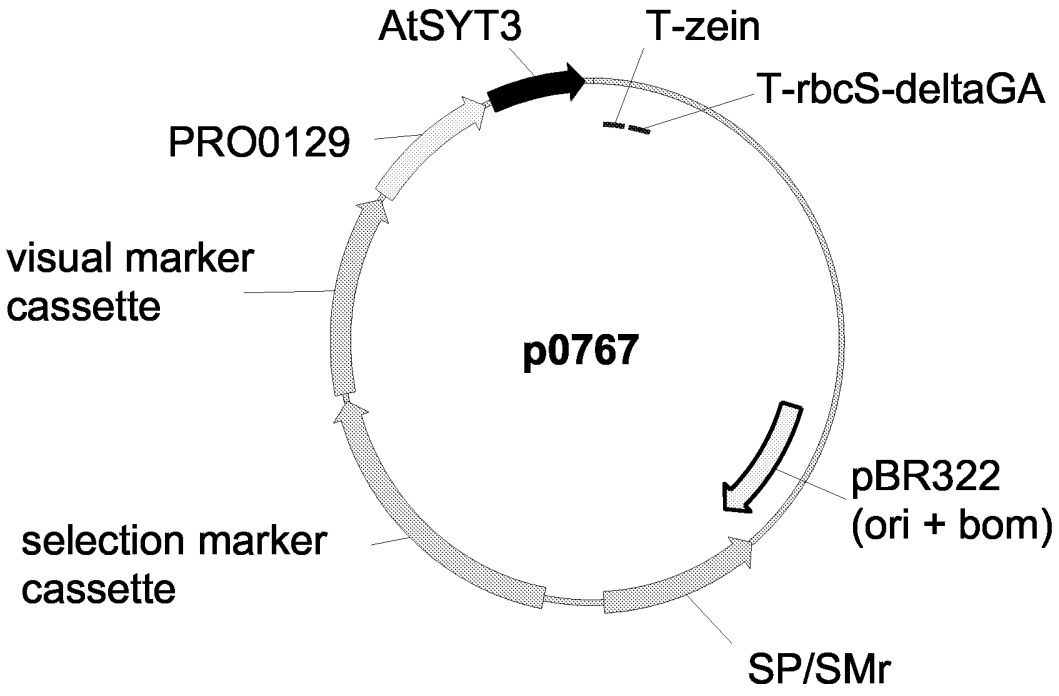

AtSYT3
T-zein
T-rbcS-deltaGA
PRO0129
visual marker cassette
p0767
pBR322 (ori + bom)
selection marker cassette
SP/SMr

FIGURE 7

SEQ ID NO : 01 SNH domain from SYT-like polypeptides

IQ(Q/K)XL(D/E)(E/D)N(K/N)XLIX(C/A/K)I(L/V/M)(E/D/S)(S/N)(Q/L)N
XG(K/R)XXEC(A/E/S)XXQ(A/S/Q)XL(Q/H)XNL(M/L/V)YLA(A/T)IAD

Where X is any amino acid

SEQ ID NO : 02 *Arabidopsis thaliana* AtSYT1 SNH domain

IQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNLMYLAAIAD

SEQ ID NO : 03 *Arabidopsis thaliana* AtSYT1 cDNA (AY102639)

ATGCAACAGCACCTGATGCAGATGCAGCCCATGATGGCTGGTTACTACCCCAGCAATGTTAC
CTCTGATCATATCCAACAGTACTTGGACGAAAACAAATCGTTGATTCTGAAGATTGTTGAGT
CTCAAAACTCTGGAAAGCTTAGCGAATGCGCCGAGAATCAAGCAAGGCTTCAACGCAACCTA
ATGTACCTAGCTGCAATAGCAGATTCTCAGCCTCAGCCACCAAGTGTGCATAGCCAGTATGG
ATCTGCTGGTGGTGGGATGATTCAGGGAGAAGGAGGGTCACACTATTTGCAGCAGCAACAAG
CGACTCAACAGCAACAGATGACTCAGCAGTCTCTAATGGCGGCTCGATCTTCAATGTTGTAT
GCTCAGCAACAGCAGCAGCAGCAGCCTTACGCGACGCTTCAGCATCAGCAATTGCACCATAG
CCAGCTTGGAATGAGCTCGAGCAGCGGAGGAGGAGGAAGCAGTGGTCTCCATATCCTTCAGG
GAGAGGCTGGTGGGTTTCATGATTTTGGCCGTGGGAAGCCGGAAATGGGAAGTGGTGGTGGC
GGTGAAGGCAGAGGAGGAAGTTCAGGGGATGGTGGAGAAACCCTTTACTTGAAATCATCAGA
TGATGGGAATTGA

SEQ ID NO : 04 Arabidopsis thaliana AtSYT1 protein

MQQHLMQMQPMMAGYYPSNVTSDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPPSVHSQYGSAGGGMIQGEGGSHYLQQQQATQQQQMTQQSLMAARSSMLY
AQQQQQQQPYATLQHQQLHHSQLGMSSSSGGGGSSGLHILQGEAGGFHDFGRGKPEMGSGGG
GEGRGGSSGDGGETLYLKSSDDGN

SEQ ID NO : 05 *Arabidopsis thaliana* AtSYT2 cDNA (AY102640)

ATGCAGCAGCAGCAGTCTCCGCAAATGTTTCCGATGGTTCCGTCGATTCCCCCTGCTAACAA
CATCACTACCGAACAGATCCAAAAGTACCTTGATGAGAACAAGAAGCTGATTATGGCCATCA
TGGAAAACCAGAATCTCGGTAAACTTGCTGAGTGCGCCCAGTACCAAGCTCTTCTCCAGAAG
AACTTGATGTATCTTGCTGCAATTGCTGATGCTCAACCCCCACCACCTACGCCAGGACCTTC
ACCATCTACAGCTGTCGCTGCCCAGATGGCAACACCGCATTCTGGGATGCAACCACCTAGCT
ACTTCATGCAACACCCACAAGCATCCCCTGCAGGGATTTTCGCTCCAAGGGGTCCTTTACAG
TTTGGTAGCCCACTCCAGTTTCAGGATCCGCAACAGCAGCAGCAGATACATCAGCAAGCTAT
GCAAGGACACATGGGGATTAGACCAATGGGTATGACCAACAACGGGATGCAGCATGCGATGC
AACAACCAGAAACCGGTCTTGGAGGAAACGTGGGGCTTAGAGGAGGAAAGCAAGATGGAGCA
GATGGACAAGGAAAAGATGATGGCAAGTGA

FIGURE 8

SEQ ID NO : 06 *Arabidopsis thaliana* AtSYT2 protein

MQQQQSPQMFPMVPSIPPANNITTEQIQKYLDENKKLIMAIMENQNLGKLAECAQYQALLQK
NLMYLAAIADAQPPPPTPGPSPSTAVAAQMATPHSGMQPPSYFMQHPQASPAGIFAPRGPLQ
FGSPLQFQDPQQQQQIHQQAMQGHMGIRPMGMTNNGMQHAMQQPETGLGGNVGLRGGKQDGA
DGQGKDDGK

SEQ ID NO : 07 *Arabidopsis thaliana* AtSYT3 cDNA (AY102641)

ATGCAGCAATCTCCACAGATGATTCCGATGGTTCTTCCTTCATTTCCGCCCACCAATAATAT
CACCACCGAACAGATCCAAAAGTATCTTGATGAGAACAAGAAGCTGATAATGGCGATCTTGG
AAAATCAGAACCTCGGTAAACTTGCAGAATGTGCTCAGTATCAAGCTCTTCTCCAGAAGAAT
TTGATGTATCTCGCTGCAATTGCGGATGCTCAACCTCAGCCACCAGCAGCTACACTAACATC
AGGAGCCATGACTCCCCAAGCAATGGCTCCTAATCCGTCATCAATGCAGCCACCACCAAGCT
ACTTCATGCAGCAACATCAAGCTGTGGGAATGGCTCAACAAATACCTCCTGGGATTTTCCCT
CCTAGAGGTCCATTGCAATTTGGTAGCCCGCATCAGTTTCTGGATCCGCAGCAACAGTTACA
TCAACAAGCTATGCAAGGGCACATGGGGATTAGACCAATGGGTTTGAATAATAACAACGGAC
TGCAACATCAAATGCACCACCATGAAACTGCTCTTGCCGCAAACAATGCGGGTCCTAACGAT
GCTAGTGGAGGAGGTAAACCGGATGGGACCAATATGAGCCAGAGTGGAGCTGATGGGCAAGG
TGGCTCAGCCGCTAGACATGGCGGTGGTGATGCAAAAACTGAAGGAAAATGA

SEQ ID NO : 08 *Arabidopsis thaliana* AtSYT3 protein

MQQSPQMIPMVLPSFPPTNNITTEQIQKYLDENKKLIMAILENQNLGKLAECAQYQALLQKN
LMYLAAIADAQPQPPAATLTSGAMTPQAMAPNPSSMQPPPSYFMQQHQAVGMAQQIPPGIFP
PRGPLQFGSPHQFLDPQQQLHQQAMQGHMGIRPMGLNNNNGLQHQMHHHETALAANNAGPND
ASGGGKPDGTNMSQSGADGQGGSAARHGGGDAKTEGK

SEQ ID NO : 09 *Aspergillus officinalis* SYT cDNA (CV287542)

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAACCTACGGTTCACCGAATCAGGT
CACCACCGATATCATTCAGCAGTATCTGGACGAGAACAAGCAGTTGATTCTGGCTATTCTTG
AAAACCAAAATTCAGGAAAAGCTGATGAATGTGCTGAGAATCAGGCTAAGCTTCAGAGGAAT
CTGATGTATCTTGCAGCCATTGCGGATAGCCAGCCCCAAGTTCCTACCATTGCTCAGTATCC
TCCCAACGCTGTTGCTGCTATGCAATCGAGTGCTCGCTACATGCAACAACACCAAGCAGCTC
AACAGATGACCCCTCAATCTCTCATGGCTGCTCGCTCCTCAATGCTCTACTCACAGTCCCCA
ATGTCTGCACTCCAGCAGCAACAGCAGCAAGCAGCAATGCATAGCCAGCTCGCCATGAGCTC
CGGAGGCAACAACAGCAGCACCGGAGGATTCACCATTCTTCATGGTGAAGCTAGCATAGGAG
GCAATGGCTCAATGAATTCTGGTGGAGTCTTTGGAGATTTTGGACGGAGCAGCGGTGGGAAG
CAAGAGACTGGGAGCGAAGGGCACGGGACAGAGACTCCTATGTACCTGAAAGGCTCTGAAGA
AGAAGGAAACTGA

FIGURE 8 (continued)

SEQ ID NO : 10 *Aspergillus officinalis* SYT protein

MQQHLMQMQPMMATYGSPNQVTTDIIQQYLDENKQLILAILENQNSGKADECAENQAKLQRN
LMYLAAIADSQPQVPTIAQYPPNAVAAMQSSARYMQQHQAAQQMTPQSLMAARSSMLYSQSP
MSALQQQQQQAAMHSQLAMSSGGNNSSTGGFTILHGEASIGGNGSMNSGGVFGDFGRSSGGK
QETGSEGHGTETPMYLKGSEEEGN

SEQ ID NO : 11 *Brassica napus* SYT cDNA (CD823592)

ATGCAGCCCATGATGGCTGGTTACTACCCCAGCAATGTCACCTCTGATCATATCCAGCAGTA
CTTGGATGAGAACAAGTCTTTGATTCTGAAGATAGTTGAGTCTCAAAACTCAGGAAAGCTCA
GCGAGTGTGCCGAGAATCAGGCAAGGCTTCAACGCAACCTCATGTACTTGGCTGCAATAGCA
GATTCTCAGCCTCAACCTCCAAGCGTGCATAGCCAGTATGGATCTGCTGGTGGTGGGTTGAT
TCAGGGAGAAGGAGCGTCACACTATTTGCAGCAGCAACAGGCGACTCAACAGCAGCAGATGA
CTCAGCAGTCTCTTATGGCAGCTCGTTCTTCAATGATGTATCAGCAGCAGCAACAGCCTTAT
GCAACGCTTCAGCATCAGCAGTTGCACCATAGCCAGCTTGGGATGAGCTCTAGCAGCGGAGG
AGGAAGCAGTGGTCTCCATATCCTTCAGGGAGAGGCTGGTGGGTTTCATGAATTTGGCCGTG
GGAAGCCGGAGATGGGAAGTGGTGAAGGCAGGGGTGGAAGCTCAGGGGATGGTGGAGAAACA
CTCTACTTGAAGTCATCAGATGATGGGAACTGA

SEQ ID NO : 12 *Brassica napus* SYT protein

MQQHLMQMQPMMAGYYPSNVTSDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPPSVHSQYGSAGGGLIQGEGASHYLQQQQATQQQQMTQQSLMAARSSMMY
QQQQQPYATLQHQQLHHSQLGMSSSSGGGSSGLHILQGEAGGFHEFGRGKPEMGSGEGRGGS
SGDGGETLYLKSSDDGN

SEQ ID NO : 13 *Citrus sinensis* SYT cDNA (CB290588)

ATGCAACAGCACCTGATGCAGATGCAGCCCATGATGGCAGCTTATTATCCCAACAACGTCAC
TACTGACCACATTCAACAGTATCTAGATGAGAACAAATCATTGATTTTGAAGATTGTTGAGA
GCCAGAATTCAGGGAAACTGAGCGAGTGTGCAGAGAACCAGGCAAGATTGCAGCGGAATCTC
ATGTACCTGGCTGCTATTGCTGATGCTCAACCCCAACCACCTAGCGTTCATGCCCAGTTCTC
TTCTGGTGGCATTATGCAGCCAGGAGCTCACTATATGCAACACCAGCAATCTCAGCCAATGA
CACCACAGTCACTTATGGCTGCACGCTCATCCATGGTGTACTCTCAACAGCAATTTTCAGTG
CTTCAGCAACAGCAAGCCTTGCATGGTCAGCTTGGCATGAGCTCTGGTGGTAGCTCAGGACT
TCACATGCTGCAAAGTGAGGGTAGTACTGCAGGAGGTAGTGGTTCACTTGGGGGTGGGGGAT
TCCCTGATTTTGGCCGTGGCTCATCTGGTGAAGGCTTGCACTCAAGGGGAATGGGGAGCAAG
CATGATATAGGCAGTTCTGGATCTGCTGAAGGACGAGGAGGGAGCTCAGGAAGCCAAGATGG
AGGCGAAACTCTCTACTTGAAAGGGGCTGATGATGGAAATTAA

SEQ ID NO : 14 *Citrus sinensis* SYT protein

MQQHLMQMQPMMAAYYPNNVTTDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADAQPQPPSVHAQFSSGGIMQPGAHYMQHQQSQPMTPQSLMAARSSMVYSQQQFSV
LQQQQALHGQLGMSSGGSSGLHMLQSEGSTAGGSGSLGGGGFPDFGRGSSGEGLHSRGMGSK
HDIGSSGSAEGRGGSSGSQDGGETLYLKGADDG

FIGURE 8 (continued)

SEQ ID NO : 15 *Gossypium arboreum* SYT cDNA (BM359324)

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCTTATTATCCCAACAACGTCAC
TACTGATCATATTCAACAGTATCTCGATGAGAACAAGTCATTGATCTTAAAGATTGTTGAGA
GCCAGAATTCTGGGAAATTGAGTGAATGTGCTGAGAACCAAGCAAGGCTGCAGCGAAACCTC
ATGTACCTGGCTGCCATTGCGGATTCTCAACCCCAACCACCCACCGTGCATGCACAGTTTCC
ATCTGGTGGTATCATGCAGCAAGGAGCTGGGCACTACATGCAGCACCAACAAGCTCAACANA
TGACACAACAGTCGCTTATGGCTGCTCGGTCCTCAATGTTGTATTCTCAGCAACCATTTTCT
GCACTGCAACAACAACAACAACAAGGCTTTGCACAGTCAGCTTGGCATGAGCTCTGGCGGGA
GCACAGGCCTTTCATATGCTGCAAACTGAATCTAGTACTGCAGGGGGCAGTGAGACACCTTG
GGCCCGAGGGTTGTCCTGATTTGGACGGGGGTCTTTTGGAGAGGCATCCCTGGTGGCAGGCC
AATGGCCGGGGGAACAACCAAAAATCCGGGGAGGCCGGCTCACCTAAGGGCCGGGAGGAGCC
CTTGGGGCAGGGGGGGGTGATGGGGGGAACCTCTTCTTAA

SEQ ID NO : 16 *Gossypium arboreum* SYT protein

MQQHLMQMQPMMAAYYPNNVTTDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPPTVHAQFPSGGIMQQGAGHYMQHQQAQXMTQQSLMAARSSMLYSQQPFS
ALQQQQQQGFAQSAWHELWREHRPFICCKLNLVLQGAVRHLGPEGCPDLDGGLLERHPWWQA
NGRGNNQKSGEAGSPKGREEPLGQGGVMGGTSS

SEQ ID NO : 17 *Medicago trunculata* SYT cDNA (CA858507)

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCTTACTATCCTAACAACGTCAC
TACTGATCATATTCAACAGTATCTTGATGAGAACAAGTCCTTGATTCTCAAGATTGTTGAAA
GCCAGAACACTGGCAAGCTCACCGAGTGTGCTGAGAACCAATCAAGGCTTCAGAGAAATCTC
ATGTACCTAGCTGCAATAGCTGATTCTCAACCCCAACCACCTACTATGCCTGGCCAGTACCC
TTCAAGTGGAATGATGCAGCAGGGAGGACACTACATGCAGGCTCAACAAGCTCAGCAGATGA
CACAACAACAATTAATGGCTGCACGTTCCTCTCTTATGTATGCTCAACAGCTTCAACAGCAG
CAAGCCTTGCAAAGCCAACTTGGTATGAATTCCAGTGGAAGTCAAGGCCTTCACATGTTGCA
TAGTGAAGGGGCTAATGTTGGAGGCAATTCATCTCTAGGGGCTGGTTTTCCTGATTTTGGCC
GTAGCTCAGCCGGTGATGGTTTGCACGGCAGTGGTAAGCAAGACATTGGAAGCACTGATGGC
CGCGGTGGAAGCTCTAGTGGTCACTCTGGTGATGGCGGCGAAACACTTTACCTGAAATCTTC
TGGTGATGGGAATTAG

SEQ ID NO : 18 *Medicago trunculata* SYT protein

MQQHLMQMQPMMAAYYPNNVTTDHIQQYLDENKSLILKIVESQNTGKLTECAENQSRLQRNL
MYLAAIADSQPQPPTMPGQYPSSGMMQQGGHYMQAQQAQQMTQQQLMAARSSLMYAQQLQQQ
QALQSQLGMNSSGSQGLHMLHSEGANVGGNSSLGAGFPDFGRSSAGDGLHGSGKQDIGSTDG
RGGSSSGHSGDGGETLYLKSSGDGN

FIGURE 8 (continued)

SEQ ID NO : 19 *Oryza sativa* SYT1 cDNA (AK058575)

ATGCAGCAGCAACACCTGATGCAGATGAACCAGGGCATGATGGGGGGATATGCTTCCCCTAC
CACCGTCACCACTGATCTCATTCAGCAGTATCTGGATGAGAACAAGCAGCTGATCCTGGCCA
TCCTTGACAACCAGAACAATGGGAAGGTGGAAGAGTGCGCTCGGAACCAAGCTAAGCTCCAG
CACAATCTCATGTACCTCGCCGCCATCGCCGACAGCCAGCCGCCGCAGACGGCCGCCATGTC
CCAGTATCCGTCGAACCTGATGATGCAGTCCGGGGCGAGGTACATGCCGCAGCAGTCGGCGC
AGATGATGGCGCCGCAGTCGCTGATGGCGGCGAGGTCTTCGATGATGTACGCGCAGCCGGCG
CTGTCGCCGCTCCAGCAGCAGCAGCAGCAGCAGGCGGCGGCGGCGCACGGGCAGCTGGGCAT
GGGCTCGGGGGGCACCACCAGCGGGTTCAGCATCCTCCACGGCGAGGCCAGCATGGGCGGCG
GCGGCGGCGGCGGTGGCGCCGGTAACAGCATGATGAACGCCGGCGTGTTCTCCGACTTCGGA
CGCGGCGGCGGCGGCGGCGGCAAGGAGGGGTCCACCTCGCTGTCCGTCGACGTCCGGGGCGC
CAACTCCGGCGCCCAGAGCGGCGACGGGGAGTACCTCAAGGGCACCGAGGAGGAAGGCAGCT
AG

SEQ ID NO : 20 *Oryza sativa* SYT1 protein

MQQQHLMQMNQGMMGGYASPTTVTTDLIQQYLDENKQLILAILDNQNNGKVEECARNQAKLQ
HNLMYLAAIADSQPPQTAAMSQYPSNLMMQSGARYMPQQSAQMMAPQSLMAARSSMMYAQPA
LSPLQQQQQQQAAAAHGQLGMGSGGTTSGFSILHGEASMGGGGGGGGAGNSMMNAGVFSDFG
RGGGGGGKEGSTSLSVDVRGANSGAQSGDGEYLKGTEEEGS

SEQ ID NO : 21 *Oryza sativa* SYT2 cDNA (AK105366)

ATGCAGCAGCAGCCGATGCCGATGCCCGCGCAGGCGCCGCCGACGGCCGGAATCACCACCGA
GCAGATCCAAAAGTATCTGGATGAAAACAAGCAGCTTATTTTGGCTATTTTGGAAAATCAGA
ATCTGGGAAAGTTGGCAGAATGTGCTCAGTATCAAGCGCAGCTTCAGAAGAATCTCTTGTAC
TTGGCTGCAATTGCTGATACTCAACCGCAGACCACTATAAGCCGTCCCCAGATGGTGCCGCA
TGGTGCATCGCCGGGGTTAGGGGGGCAATACATGTCGCAGGTGCCAATGTTCCCCCCCAGGA
CCCCTCTAACGCCCCAGCAGATGCAGGAGCAGCAGCTGCAGCAACAGCAAGCCCAGCTGCTC
TCGTTCGGCGGTCAGATGGTTATGAGGCCTGGCGTTGTGAATGGCATTCCTCAGCTTCTGCA
AGGCGAAATGCACCGCGGAGCAGATCACCAGAACGCTGGCGGGGCCACCTCGGAGCCTTCCG
AGAGCCACAGGAGCACCGGCACCGAAAATGACGGTGGAAGCGACTTCGGCGATCAATCCTAA

SEQ ID NO : 22 *Oryza sativa* SYT2 protein

MQQQPMPMPAQAPPTAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQKNLLY
LAAIADTQPQTTISRPQMVPHGASPGLGGQYMSQVPMFPPRTPLTPQQMQEQQLQQQQAQLL
SFGGQMVMRPGVVNGIPQLLQGEMHRGADHQNAGGATSEPSESHRSTGTENDGGSDFGDQS

FIGURE 8 (continued)

SEQ ID NO : 23 *Oryza sativa* SYT3 cDNA (BP185008)

ATGCAGCAGCAGATGGCCATGCCGGCGGGGGCCGCCGCCGCCGCGGTGCCGCCGGCGGCCGG
CATCACCACCGAGCAGATCCAAAAGTATTTGGATGAAAATAAACAGCTAATTTTGGCCATCC
TGGAAAATCAAAACCTAGGGAAGTTGGCTGAATGTGCTCAGTACCAAGCTCAGCTTCAAAAG
AATCTCTTGTATCTGGCTGCCATTGCAGATGCCCAACCACCTCAGAATCCAGGAAGTCGCCC
TCAGATGATGCAGCCTGGTGCTACCCCAGGTGCTGGGCATTACATGTCCCAAGTACCGATGT
TCCCTCCAAGAACTCCCTTAACCCCACAACAGATGCAAGAGCAGCAGCAGCAGCAACTCCAG
CAACAGCAAGCTCAGGCTCTAGCCTTCCCCGGCCAGATGCTAATGAGACCAGGTACTGTCAA
TGGCATGCAATCTATCCCAGTTGCTGACCCTGCTCGCGCAGCCGATCTTCAGACGGCAGCAC
CGGGCTCGGTAGATGGCCGAGGAAACAAGCAGGATGCAACCTCGGAGCCTTCCGGGACCGAG
AGCCACAAGAGTGCGGGAGCAGATAACGACGCAGGCGGTGACATAGCGGAGAAGTCCTGA

SEQ ID NO : 24 *Oryza sativa* SYT3 protein

MQQQMAMPAGAAAAAVPPAAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQK
NLLYLAAIADAQPPQNPGSRPQMMQPGATPGAGHYMSQVPMFPPRTPLTPQQMQEQQQQQLQ
QQQAQALAFPGQMLMRPGTVNGMQSIPVADPARAADLQTAAPGSVDGRGNKQDATSEPSGTE
SHKSAGADNDAGGDIAEKS

SEQ ID NO : 25 *Solanum tuberosum* SYT cDNA (BG590990)

ATGCAGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCCTATTATCCCAACAATGT
CACTACTGATCATATTCAACAGTTCCTGGATGAGAACAAATCACTTATTCTGAAGATTGTTG
AGAGCCAGAACTCTGGGAAAATAAGTGAATGTGCAGAGTCCCAAGCTAAACTTCAGAGAAAT
CTTATGTACCTTGCAGCTATTGCTGATTCACAGCCCCAGCCTCCTAGTATGCATTCACAGTT
AGCTTCTGGTGGGATGATGCAGGGAGGGGCACATTATATGCAGCAACAACAAGCTCAACAAC
TCACAACGCAATCGCTTATGGCTGCAGCAAGATCCTCCTCCTCAATGCTCTATGGACAACAA
CAACAACAACAACAACAACAACTATCATCATTGCAACAACAGCAAGCAGCCTTTCATAGCCA
GCAACTCGGAATGAGCAGCTCTGGTGGAGGAAGCAGTAGTGGACTTCACATGCTACAAAGCG
AAAACACTCATAGTGCTAGCACTGGTGGTGGGTGGTTTCCCTGA

SEQ ID NO : 26 *Solanum tuberosum* SYT protein

MQQQHLMQMQPMMAAYYPNNVTTDHIQQFLDENKSLILKIVESQNSGKISECAESQAKLQRN
LMYLAAIADSQPQPPSMHSQLASGGMMQGGAHYMQQQQAQQLTTQSLMAAARSSSSMLYGQQ
QQQQQQQLSSLQQQQAAFHSQQLGMSSSGGGSSSGLHMLQSENTHSASTGGGWFP

FIGURE 8 (continued)

SEQ ID NO : 27 *Zea mays* SYT1 cDNA (BG874129.1, CA409022.1; compiled)

ATGCAGCAGCAACACCTGATGCAGATGAACCAGAACATGATGGGGGGCTACACCTCTCCTGC
CGCCGTGACCACCGATCTCATCCAGCAGCACCTGGACGAGAACAAGCAGCTGATCCTGGCCA
TCCTCGACAACCAGAACAATGGCAAGGCGGAGGAGTGCGAACGGCACCAAGCTAAGCTCCAG
CACAACCTCATGTACCTGGCCGCCATCGCTGACAGCCAGCCGCCACAGACCGCGCCACTATC
ACAGTACCCGTCCAACCTGATGATGCAGCCGGGCCCTCGGTACATGCCACCGCAGTCCGGGC
AGATGATGAACCCGCAGTCGCTGATGGCGGCGCGGTCCTCCATGATGTACGCGCACCCGTCC
CTGTCGCCACTCCAGCAGCAGCAGGCGGCGCACGGACAGCTGGGTATGGCTCCAGGGGGCGG
CGGTGGCGGCACGACCAGCGGGTTCAGCATCCTCCACGGCGAGGCCAGCATGGGCGGTGGTG
GTGCTGGCGCAGGCGCCGGCAACAACATGATGAACGCCGGCATGTTCTCGGGCTTTGGCCGC
AGCGGCAGTGGCGCCAAGGAAGGGTCGACCTCTCTGTCGGTTGACGTCCGGGGTGGAACCAG
CTCCGGCGCGCAGAGCGGGGACGGCGAGTACCTCAAAGTCGGCACCGAGGAAGAAGGCAGTT
AG

SEQ ID NO : 28 *Zea mays* SYT1 protein

MQQQHLMQMNQNMMGGYTSPAAVTTDLIQQHLDENKQLILAILDNQNNGKAEECERHQAKLQ
HNLMYLAAIADSQPPQTAPLSQYPSNLMMQPGPRYMPPQSGQMMNPQSLMAARSSMMYAHPS
LSPLQQQQAAHGQLGMAPGGGGGGTTSGFSILHGEASMGGGGAGAGAGNNMMNAGMFSGFGR
SGSGAKEGSTSLSVDVRGGTSSGAQSGDGEYLKVGTEEEGS

SEQ ID NO : 29 *Zea mays* SYT2 cDNA (AY106697)

ATGCAGCAGCCGATGCACATGCAGCCACAGGCGCCGGCGATAACCCCAGCTGCCGGAATCAG
CACGGAGCAGATCCAAAAGTATCTGGATGAGAATAAGCAGCTTATTTTGGCTATTTTGGAAA
ATCAGAACCTAGGAAAATTGGCAGAATGTGCTCAGTATCAATCACAACTTCAGAAGAACCTC
TTGTATCTCGCTGCAATCGCAGATGCTCAACCGCAGACTGCTGTAAGCCGCCCTCAGATGGC
GCCGCCTGGTGGATCGCCTGGAGTAGGGCAGTACATGTCACAGGTGCCTATGTTCCCACCGA
GGACACCTCTTACACCCCAGCAGATGCAGGAGCAGCAGCTTCAGCAGCAGCAGGCTCAGTTG
CTAAACTTCAGTGGCCAAATGGTTGCTAGACCAGGCATGGTCAACGGCATGGCTCAGTCCAT
GCAAGCTCAGCTACCACCGGGTGTGAACAAGCAGGATGCTGGTGGGGTCGCCTCTGAGCCCT
CGGGCACCGAGAGCCACAGGAGCACTGGTGGTGACGATGGTGGAAGCGACTAG

SEQ ID NO : 30 *Zea mays* SYT2 protein

MQQPMHMQPQAPAITPAAGISTEQIQKYLDENKQLILAILENQNLGKLAECAQYQSQLQKNL
LYLAAIADAQPQTAVSRPQMAPPGGSPGVGQYMSQVPMFPPRTPLTPQQMQEQQLQQQQAQL
LNFSGQMVARPGMVNGMAQSMQAQLPPGVNKQDAGGVASEPSGTESHRSTGGDDGGSD

FIGURE 8 (continued)

SEQ ID NO : 31 *Homo sapiens* cDNA (CR542103)

ATGGGCGGCAACATGTCTGTGGCTTTCGCGGCCCCGAGGCAGCGAGGCAAGGGGGAGATCAC
TCCCGCTGCGATTCAGAAGATGTTGGATGACAATAACCATCTTATTCAGTGTATAATGGACT
CTCAGAATAAAGGAAAGACCTCAGAGTGTTCTCAGTATCAGCAGATGTTGCACACAAACTTG
GTATACCTTGCTACAATAGCAGATTCTAATCAAAATATGCAGTCTCTTTTACCAGCACCACC
CACACAGAATATGCCTATGGGTCCTGGAGGGATGAATCAGAGCGGCCCTCCCCCACCTCCAC
GCTCTCACAACATGCCTTCAGATGGAATGGTAGGTGGGGGTCCTCCTGCACCGCACATGCAG
AACCAGATGAACGGCCAGATGCCTGGGCCTAACCATATGCCTATGCAGGGACCTGGACCCAA
TCAACTCAATATGACAAACAGTTCCATGAATATGCCTTCAAGTAGCCATGGATCCATGGGAG
GTTACAACCATTCTGTGCCATCATCACAGAGCATGCCAGTACAGAATCAGATGACAATGAGT
CAGGGACAACCAATGGGAAACTATGGTCCCAGACCAAATATGAGTATGCAGCCAAACCAAGG
TCCAATGATGCATCAGCAGCCTCCTTCTCAGCAATACAATATGCCACAGGGAGGCGGACAGC
ATTACCAAGGACAGCAGCCACCTATGGGAATGATGGGTCAAGTTAACCAAGGCAATCATATG
ATGGGTCAGAGACAGATTCCTCCCTATAGACCTCCTCAACAGGGCCCACCACAGCAGTACTC
AGGCCAGGAAGACTATTACGGGGACCAATACAGTCATGGTGGACAAGGTCCTCCAGAAGGCA
TGAACCAGCAATATTACCCTGATGGAAATTCACAGTATGGCCAACAGCAAGATGCATACCAG
GGACCACCTCCACAACAGGGATATCCACCCCAGCAGCAGCAGTACCCAGGGCAGCAAGGTTA
CCCAGGACAGCAGCAGGGCTACGGTCCTTCACAGGGTGGTCCAGGTCCTCAGTATCCTAACT
ACCCACAGGGACAAGGTCAGCAGTATGGAGGATATAGACCAACACAGCCTGGACCACCACAG
CCACCCCAGCAGAGGCCTTATGGATATGACCAGGGACAGTATGGAAATTACCAGCAG

SEQ ID NO : 32 *Homo sapiens* SYT protein (CAG46900.1)

MGGNMSVAFAAPRQRGKGEITPAAIQKMLDDNNHLIQCIMDSQNKGKTSECSQYQQMLHTNL
VYLATIADSNQNMQSLLPAPPTQNMPMGPGGMNQSGPPPPPRSHNMPSDGMVGGGPPAPHMQ
NQMNGQMPGPNHMPMQGPGPNQLNMTNSSMNMPSSSHGSMGGYNHSVPSSQSMPVQNQMTMS
QGQPMGNYGPRPNMSMQPNQGPMMHQQPPSQQYNMPQGGGQHYQGQQPPMGMMGQVNQGNHM
MGQRQIPPYRPPQQGPPQQYSGQEDYYGDQYSHGGQGPPEGMNQQYYPDGNSQYGQQQDAYQ
GPPPQQGYPPQQQQYPGQQGYPGQQQGYGPSQGGPGPQYPNYPQGQGQQYGGYRPTQPGPPQ
PPQQRPYGYDQGQYGNYQQ

SEQ ID NO : 33 *Allium cepa* SYT2 cDNA CF437485

ATGCAGCAGCCGCAGCCAGCGATGGGAACCATGGGCTCGGTGCCACCTACTAGCATCACCAC
CGAACAGATTCAAAGGTACTTGGATGAGAACAAACAGTTAATATTGGCAATTTTGGATAATC
AAAATTTAGGAAGACTGAATGAGTGTGCTCAATATCAAGCTCAGCTTCAAAAGAATCTGCTT
TACCTGGCAGCAATAGCTGATGCTCAGCCTCAGTCTCCTGCGGTGCGTCTGCAGATGATGCC
TCAAGGTGCAGCTGCCACGCCTCAAGCTGGAAACCAATTTATGCAGCAGCAGAGCCCTAATT
TCCCTCCCAAAACAGGAATGCAATTTACTCCTCAACAAGTACAAGAATTGCAGCAGCAACAG
CTACAACATCAGCCACATATGATGCCTCCATTTCAAGGTCAAATGGGTATGAGACCTATGAA
TGGAATGCAGGCAGCAATGCATGCAGATTCATCTCTTGCTTATAACACTAACAATAAGCAAG
ATGCAGGAAACGCAGCTTATGAAAATACTGCTGCCAACACAGATGGTTCCATTCAAAAGAAA
ACAGCAAATGATGATTTAGACCCTTCTGCAGCAAACCCTAGAAGGTCTGAAGATGCCAAATC
ATCATGA

FIGURE 8 (continued)

SEQ ID NO : 34 *Allium cepa* SYT2 translated amino acid sequence

MQQPQPAMGTMGSVPPTSITTEQIQRYLDENKQLILAILDNQNLGRLNECAQYQAQLQKNLL
YLAAIADAQPQSPAVRLQMMPQGAAATPQAGNQFMQQQSPNFPPKTGMQFTPQQVQELQQQQ
LQHQPHMMPPFQGQMGMRPMNGMQAAMHADSSLAYNTNNKQDAGNAAYENTAANTDGSIQKK
TANDDLDPSAANPRRSEDAKSS

SEQ ID NO : 35 *Aquilegia formosa* x *Aquilegia pubescens* SYT1 cDNA DT758802.1

ATGCAACACATGCAGATGCAGCCCATGATGCCACCTTATAGTGCCAACAGCGTCACTACTGA
TCATATCCAACAGTACTTGGATGAAAATAAGGCGTTGATTCTGAAGATACTTGAGAACCAAA
ATTCGGGAAAAGTTAGTGAATGTGCAGAGAACCAAGCAAGACTTCAACGAAATCTTATGTAT
CTGGCTGCAATTGCTGATTCTCAACCACAGCCTCCCAATATGCATGCTCAGTACTCTAATGC
GGGTATACCACCTGGTGCACATTACCTACAACACCAACAGGCCCAACAGATGACACAACAGT
CGCTCATGGCTGCTCGATCAAATATGCTGTATGCTCAGCCAATCACAGGAATGCAGCAACAG
CAAGCAATGCATAGCCAGCTTGGCATGAGCTCTGGTGGTAACAGTGGACTCCACATGATGCA
CAATGAGGGCAGCATGGGAGGTAGTGGGGCACTTGGAAGCTATTCTGATTATGGCCGTGGCA
GTGGTGGTGGAGTAACTATCGCTAGCAAACAAGATGGTGGAAGTGGTTCTGGTGAAGGACGA
GGTGGAAACTCTGGAGGCCAAAGTGCAGATGGAGGTGAATCTCTTTACCTGAAAAACAGTGA
CGAAGGGAACTAA

SEQ ID NO : 36 *Aquilegia formosa* x *Aquilegia pubescens* SYT1 translated amino acid sequence

MQHMQMQPMMPPYSANSVTTDHIQQYLDENKALILKILENQNSGKVSECAENQARLQRNLMY
LAAIADSQPQPPNMHAQYSNAGIPPGAHYLQHQQAQQMTQQSLMAARSNMLYAQPITGMQQQ
QAMHSQLGMSSGGNSGLHMMHNEGSMGGSGALGSYSDYGRGSGGGVTIASKQDGGSGSGEGR
GGNSGGQSADGGESLYLKNSDEGN

SEQ ID NO : 37 *Brachypodium distachyon* SYT23 cDNA DV480064.1

ATGCAGCAGGCGATGTCCATGTCCCCGGGGTCGGCCGGCGCGGTGCCGCCTCCGGCCGGCAT
CACCACAGAGCAGATCCAAAAGTATTTGGATGAAAATAAGCAACTTATTTTGGCCATCCTGG
AAAATCAGAACCTAGGAAAGTTGACTGAATGTGCTCAGTATCAAGCTCAACTTCAGAAGAAT
CTCTTGTATCTGGCTGCCATTGCGGATGCCCAACCACCACAGAACCCTGGAAGTCGCCCCCA
GATGGTGCAGCCTGGTGGTATGCCAGGTGCAGGGCATTACATGTCGCAAGTACCAATGTTCC
CTCCAAGAACCCCTTTAACCCCACAACAGATGCAAGAGCAACAGCACCAGCAGCTTCAGCAG
CAGCAAGCACAGGCTCTTGCTTTCCCCAGCCAGATGGTCATGAGACCAGGTACTGTGAACGG
CATGCAGCCTATGCAAGCTGATCTCCAAGCAGCAGCAGCAGCACCTGGCCTGGCAGACAGCC
GAGGAAGTAAGCAGGACGCAGCGGTAGCTGGGGCCATCTCGGAACCTTCTGGCACCGAGAGT
CACAAGAGTACAGGAGCGGATCATGAGGCAGGTGGCGATGTAGCTGAGCAATCCTAA

FIGURE 8 (continued)

SEQ ID NO : 38 *Brachypodium distachyon* SYT3 translated amino acid sequence

MQQAMSMSPGSAGAVPPPAGITTEQIQKYLDENKQLILAILENQNLGKLTECAQYQAQLQKN
LLYLAAIADAQPPQNPGSRPQMVQPGGMPGAGHYMSQVPMFPPRTPLTPQQMQEQQHQQLQQ
QQAQALAFPSQMVMRPGTVNGMQPMQADLQAAAAAPGLADSRGSKQDAAVAGAISEPSGTES
HKSTGADHEAGGDVAEQS

SEQ ID NO : 39 *Brassica napus* SYT2 cDNA CN732814

ATGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCTCCGCAAATGTTTCCGATGGCTCCTTCGAT
GCCGCCAACTAACATCACCACCGAACAGATCCAAAAGTACCTTGAGGAGAACAAGAAGCTGA
TAATGGCAATCATGGAAAATCAGAATCTTGGCAAGCTTGCAGAGTGTGCACAGTACCAAGCT
CTTCTCCAGAAGAACTTAATGTACCTCGCTGCTATTGCTGATGCTCAACCTCCTCCATCTAC
CGCTGGAGCTACACCACCACCAGCTATGGCTTCCCAGATGGGGGCACCGCATCCTGGGATGC
AACCGCCGAGCTACTTTATGCAACACCCACAAGCTTCAGGGATGGCTCAACAAGCACCACCC
GCTGGTATCTTCCCTCCGAGAGGTCCTTTGCAGTTTGGTAGCCCACACCAGCTTCAGGATCC
GCAACAGCAGCATATGCATCAACAGGCTATGCAAGGACACATGGGGATGCGACCAATGGGTA
TCAACAACAACAATGGGATGCAGCATCAGATGCAGCAACAACAACCAGAAACCTCTCTTGGA
GGAAGCGCTGCAAACGTGGGGCTTAGAGGTGGAAAGCAAGATGGAGCAGATGGACAAGGAAA
AGATGATGGCAAATGA

SEQ ID NO : 40 *Brassica napus* SYT2 translated amino acid sequence

MQQHLMQMQPMMAGYYPSNVTSDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPPSVHSQYGSAGGGLIQGEGASHYLQQQQATQQQQMTQQSLMAARSSMMY
QQQQQPYATLQHQQLHHSQLGMSSSSGGGSSGLHILQGEAGGFHEFGRGKPEMGSGEGRGGS
SGDGGETLYLKSSDDGN

SEQ ID NO : 41 *Citrus sinensis* SYT2 cDNA CV717501

ATGCAGCAGCCACCGCAAATGATCCCTGTTATGCCTTCATTTCCACCCACCAACATCACCAC
AGAGCAGATTCAAAAGTACCTTGATGAGAACAAAAAGTTGATTTTGGCAATTTTGGACAATC
AAAATCTTGGAAAGCTTACAGAATGTGCCCACTATCAAGCTCAGCTTCAAAAGAATTTAATG
TATTTAGCTGCAATTGCTGATGCACAACCACAAGCACCAACAATGCCTCCTCAGATGGCTCC
ACATCCTGCAATGCAAGCTAGTGGGTATTACATGCAACATCCTCAGGCGGCAGCAATGGCTC
AGCAACAAGGAATCTTTCCCCAAAAGATGCCATTACAATTCAATAACCCTCATCAACTACAG
GATCCTCAACAGCAGCTACACCAACATCAAGCCATGCAAGCACAAATGGGAATGAGACCGGG
TGCCACTAACAATGGTATGCATCCCATGCATGCTGAAAGCTCTCTTGGAGGTGGCAGCAGTG
GAGGACCCCCTTCAGCATCAGGCCCAGGTGACATACGTGGTGGAAATAAGCAAGATGCCTCG
GAGGCTGGGACTACTGGTGCTGATGGCCAGGGCAGTTCGGCTGGTGGGCATGGTGGGGATGG
AGAGGAGGCAAAGTGA

FIGURE 8 (continued)

SEQ ID NO : 42 *Citrus sinensis* SYT2 translated amino acid sequence

MQQPPQMIPVMPSFPPTNITTEQIQKYLDENKKLILAILDNQNLGKLTECAHYQAQLQKNLM
YLAAIADAQPQAPTMPPQMAPHPAMQASGYYMQHPQAAAMAQQQGIFPQKMPLQFNNPHQLQ
DPQQQLHQHQAMQAQMGMRPGATNNGMHPMHAESSLGGGSSGGPPSASGPGDIRGGNKQDAS
EAGTTGADGQGSSAGGHGGDGEEAK

SEQ ID NO : 43 *Euphorbia esula* SYT2 cDNA DV144834

ATGCAGCAGCAACCGCAGATGATGCCTATGATGCCTTCATATCCACCAGCAAACATTACCAC
GGAGCAAATCCAAAAGTATCTTGATGAAAATAAAAAATTGATTTTGGCGATCTTGGATAATC
AAAATCTTGGAAAACTCGCTGAGTGTGCACAGTATCAAGCCCTGCTGCAAAAAAATCTGATG
TATTTAGCCGCAATTGCTGATGCACAACCCCAGACCCCACCCATGCCACCTCAGATGTCCCC
ACATCCGGCTATGCAACAAGGAGCATATTACATGCAACATCCTCAGGCTGCAGCAGCAGCAA
TGGCTCATCAGTCGGGTATTTTCCCACCAAAGATGTCTCCGTTACAATTCAATAATCCTCAT
CAAATACAGGACCCCCAGCAGTTACATCAAGCAGCCCTCCAAGGGCAAATGGGAATGAGGCC
CATGGGGCCCAATAACGGGATGCATCCGATGCACCCCGAGGCAAATCTTGGAGGATCTAATG
ATGGTCGTGGAGGAAACAAACAGGATGCTCCGGAGACGGGAGCATCGGGAGGTGATGGGCAA
GGCAATTCTGGTGGTGATGGGGCTGAAGATGGGAAATGA

SEQ ID NO : 44 *Euphorbia esula* SYT2 translated amino acid sequence

MQQQPQMMPMMPSYPPANITTEQIQKYLDENKKLILAILDNQNLGKLAECAQYQALLQKNLM
YLAAIADAQPQTPPMPPQMSPHPAMQQGAYYMQHPQAAAAAMAHQSGIFPPKMSPLQFNNPH
QIQDPQQLHQAALQGQMGMRPMGPNNGMHPMHPEANLGGSNDGRGGNKQDAPETGASGGDGQ
GNSGGDGAEDGK

SEQ ID NO : 45 *Glycine max* SYT2 cDNA BQ612648

ATGCAGCAGACACCGCCAATGATTCCTATGATGCCTTCTTTCCCACCTACGAACATAACCAC
CGAGCAGATTCAAAAATACCTTGATGAGAACAAGAAGCTGATTCTGGCAATATTGGACAATC
AAAATCTTGGAAAACTTGCAGAATGTGCCCAGTACCAAGCTCAGCTTCAAAAGAATTTGATG
TATTTAGCTGCAATTGCTGATGCCCAGCCTCAAACCCCGGCCATGCCTCCGCAGATGGCACC
GCACCCTGCCATGCAACCAGGATTCTATATGCAACATCCTCAGGCTGCTGCAGCAGCAATGG
CTCAGCAGCAGCAAGGAATGTTCCCCCAGAAAATGCCATTGCAATTTGGCAATCCACATCAA
ATGCAGGAACAACAACAGCAGCTACACCAGCAGGCCATCCAAGGTCAAATGGGACTTAGACC
TGGAGATATAAATAATGGCATGCATCCAATGCACAGTGAGGCTGCTCTTGGAGGTGGAAACA
GCGGTGGTCCACCTTCGGCTACTGGTCCAAACGATGCACGTGGTGGAAGCAAGCAAGATGCC
TCTGAGGCTGGAACAGCTGGTGGAGACGGCCAAGGCAGCTCCGCGGCTGCTCATAACAGTGG
AGATGGTGAAGAGGCAAAGTGA

FIGURE 8 (continued)

SEQ ID NO : 46 *Glycine max* SYT2 translated amino acid sequence

MQQTPPMIPMMPSFPPTNITTEQIQKYLDENKKLILAILDNQNLGKLAECAQYQAQLQKNLM
YLAAIADAQPQTPAMPPQMAPHPAMQPGFYMQHPQAAAAAMAQQQQGMFPQKMPLQFGNPHQ
MQEQQQQLHQQAIQGQMGLRPGDINNGMHPMHSEAALGGGNSGGPPSATGPNDARGGSKQDA
SEAGTAGGDGQGSSAAAHNSGDGEEAK

SEQ ID NO : 47 *Glycine soya* SYT2 cDNA CA799921

ATGCAGCAGACACCGCCTATGATTCCTATGATGCCTTCGTTCCCACCTACGAACATAACCAC
CGAGCAGATTCAAAAATACCTTGATGAGAACAAGAAGCTGATTCTGGCAATATTGGACAATC
AAAATCTTGGAAAACTTGCAGAATGTGCCCAGTACCAAGCTCAGCTTCAAAAGAATTTGATG
TATTTAGCTGCAATTGCTGATGCCCAGCCTCAAACACCAGCCATGCCTCCACAGATGGCACC
ACACCCTGCCATGCAACCAGGATTCTATATGCAACATCCTCAGGCTGCAGCAGCAGCAATGG
CTCAGCAGCAGCAGCAAGGAATGTTCCCCCAGAAAATGCCATTGCAATTTGGCAATCCACAT
CAAATGCAGGAACAACAGCAGCAGCTACACCAGCAAGCCATCCAAGGTCAAATGGGACTGAG
ACCTGGAGGAATAAATAATGGCATGCATCCAATGCACAATGAGGGCGGCAACAGCGGTGGTC
CACCCTCGGCTACCGGTCCGAACGACGCACGTGGTGGAAGCAAGCAAGATGCTTCTGAGGCT
GGAACAGCTGGTGGAGATGGCCAAGGCAGCTCTGCAGCTGCTCATAACAGTGGAGATGGTGA
AGAGGCAAAGTGA

SEQ ID NO : 48 *Glycine soya* SYT2 translated amino acid sequence

MQQTPPMIPMMPSFPPTNITTEQIQKYLDENKKLILAILDNQNLGKLAECAQYQAQLQKNLM
YLAAIADAQPQTPAMPPQMAPHPAMQPGFYMQHPQAAAAAMAQQQQQGMFPQKMPLQFGNPH
QMQEQQQQLHQQAIQGQMGLRPGGINNGMHPMHNEGGNSGGPPSATGPNDARGGSKQDASEA
GTAGGDGQGSSAAAHNSGDGEEAK

SEQ ID NO : 49 *Gossypium hirsutum* SYT1 cDNA DT558852

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCTTATTATCCCAACAACGTCAC
TACTGATCATATTCAACAGTATCTCGATGAGAACAAGTCATTGATCTTAAAGATTGTTGAGA
GCCAGAATTCTGGGAAATTGAGTGAATGTGCTGAGAACCAAGCAAGGCTGCAGCGAAACCTC
ATGTACCTGGCTGCCATTGCGGATTCTCAACCCCAACCACCCACCGTGCATGCACAGTTTCC
ATCTGGTGGTATCATGCAGCCAGGAGCTGGGCACTACATGCAGCACCAACAAGCTCAACAAA
TGACACAACAGTCGCTTATGGCTGCTCGGTCCTCAATGTTGTATTCTCAGCAACCATTTTCT
GCACTGCAACAACAACAGCAGCAAGCTTTGCACAGTCAGCTTGGCATGAGCTCTGGCGGAAG
CACAGGCCTTCATATGCTGCAAACTGAATCTAGTACTGCAGGTGGCAGTGGAGCACTTGGGG
CCGGAGGGTTTCCTGATTTTGGACGTGGTTCTTCTGGAGAAGGCATCCATGGTGGCAGGCCA
ATGGCAGGTGGAAGCAAGCAAGATATCGGGAGTGCCGGCTCAGCTGAAGGTCGTGGAGGAAG
CTCTGGTGGTCAGGGTGGTGGTGATGGGGGTGAAACCCTTTACTTAAAAGCAGCCGATGATG
GGAACTGA

FIGURE 8 (continued)

SEQ ID NO : 50 *Gossypium hirsutum* SYT1 translated amino acid sequence

MQQHLMQMQPMMAAYYPNNVTTDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPPTVHAQFPSGGIMQPGAGHYMQHQQAQQMTQQSLMAARSSMLYSQQPFS
ALQQQQQQALHSQLGMSSGGSTGLHMLQTESSTAGGSGALGAGGFPDFGRGSSGEGIHGGRP
MAGGSKQDIGSAGSAEGRGGSSGGQGGGDGGETLYLKAADDGN

SEQ ID NO : 51 *Gossypium hirsutum* SYT2 cDNA DT563805

ATGCCGCAGCCACCGCAAATGATTCCTGTGATGCCTTCATATCCACCTACTAATATCACTAC
TGAACAGATTCAGAAGTACCTTGATGAGAATAAGAAGTTGATTTTGGCAATTTTGGACAATC
AGAATCTTGGAAAACTCGCTGAATGCGCCCAGTATCAAGCTCAGCTGCAAAAGAATTTGATG
TATTTAGCTGCAATTGCGGATGCTCAACCTCAATCAACGCCAGCAATGTCGCCTCAGATGGC
ACCGCATCCAGCAATGCAACCCGGAGGATATTTTATGCAACATCCTCAAGCTGCTGCAATGT
CACAGCAACCTGGCATGTACCCTCAAAAGGTGCCATTGCAATTCAATAGTCCGCATCAAATG
CAGGACCCTCAGCACCTCCTATATCAGCAGCATCAACAAGCAATGCAAGGTCAAATGGGAAT
CAGGCCTGGGGGACCCAATAATAGCATGCATCCCATGCATTCAGAGGCTAGCCTTGGAGGCG
GCAGCAGTGGTGGTCCCCCTCAACCTTCAGGCCCAAGTGATGGACGTGCTGGAAACAAGCAA
GAGGGCTCCGAAGCTGGTGGTAATGGGCAGGGCAGCACAACTGGTGGGCATGGTGGCGGTGA
TGGAGCGGATGAGGCAAAGTGA

SEQ ID NO : 52 *Gossypium hirsutum* SYT2 translated amino acid sequence

MPQPPQMIPVMPSYPPTNITTEQIQKYLDENKKLILAILDNQNLGKLAECAQYQAQLQKNLM
YLAAIADAQPQSTPAMSPQMAPHPAMQPGGYFMQHPQAAAMSQQPGMYPQKVPLQFNSPHQM
QDPQHLLYQQHQQAMQGQMGIRPGGPNNSMHPMHSEASLGGGSSGGPPQPSGPSDGRAGNKQ
EGSEAGGNGQGSTTGGHGGGDGADEAK

SEQ ID NO : 53 *Hordeum vulgare* SYT2 cDNA CA032350

ATGCAGCAAGCGATGCCCATGCCGCCGGCGGCGGCGGCGCCTGGGATGCCTCCTTCTGCCGG
CCTCAGCACCGAGCAGATCCAAAAGTACCTGGATGAAAATAAACAACTAATTTTGGCTATCT
TGGAAAATCAGAACCTGGGAAAGTTGGCGGAATGTGCTCAGTATCAAGCTCAGCTTCAGAAG
AATCTTTTGTATTTGGCTGCGATTGCTGATACTCAGCCACAGACCTCTGTAAGCCGTCCTCA
GATGGCACCACCTGCTGCATCCCCAGGGGCAGGGCATTACATGTCACAGGTGCCAATGTTCC
CTCCGAGGACCCCTCTAACGCCTCAGCAGATGCAGGAGCAGCAACTACAGCAACAACAGGCT
CAGATGCTTCCGTTTGCTGGTCAAATGGTTGCGAGACCCGGGGCTGTCAATGGCATTCCCCA
GGCCCCTCAAGTTGAACAACCAGCCTATGCAGCAGGTGGGGCCAGTTCCGAGCCTTCTGGCA
CCGAGAGCCACAGGAGCACTGGCGCCGATAACGATGGTGGGAGCGGCTTGGCTGACCAGTCC
TAA

FIGURE 8 (continued)

SEQ ID NO : 54 *Hordeum vulgare* SYT2 translated amino acid sequence

MQQAMPMPPAAAAPGMPPSAGLSTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQK
NLLYLAAIADTQPQTSVSRPQMAPPAASPGAGHYMSQVPMFPPRTPLTPQQMQEQQLQQQQA
QMLPFAGQMVARPGAVNGIPQAPQVEQPAYAAGGASSEPSGTESHRSTGADNDGGSGLADQS

SEQ ID NO : 55 *Lactuca serriola* SYT1 cDNA DW110765

ATGAAGCAGCCGATGATGCCGAATCCAATGATGTCTTCTTCGTTTCCTCCTACAAACATCAC
CACCGATCAGATCCAAAAGTTCCTTGATGAAAACAAGCAACTAATTATAGCAATAATGAGCA
ACCTAAATCTTGGAAAGCTTGCTGAATGTGCCCAGTACCAAGCTCTACTCCAAAAAAATTTG
ATGTATCTAGCAGCCATTGCAGATGCTCAACCACCTACACCTACACCAACACTAAATATCTC
TTATNAGATGGGCCCGGTTCCACATCCAGGGATGCCACAGCAAGGTGGATTTTACATGGCGC
AGCAGCACCCTCAGGCGGCTGTAATGACGGCTCAGCCACCTTCTGGTTTTCCACAACCGATG
CCTGGTATGCAATTTAACAGCCCACAGGCTATTCAAGGGCAGATGGGCGGGAGGTCCGGTGG
GCCGCCAAGCTCAGCCGCTAGTGATGTCTGGAGAGGAAGCATGCAAGATGGTGGTGGTGGTG
CTGCTGCTGATGGTGGTAAGGATGGTCATGCTGGCGGTGGACCTGAGGAAGCAAAGTAA

SEQ ID NO : 56 *Lactuca serriola* SYT1 translated amino acid sequence

MKQPMMPNPMMSSSFPPTNITTDQIQKFLDENKQLIIAIMSNLNLGKLAECAQYQALLQKNL
MYLAAIADAQPPTPTPTLNISYXMGPVPHPGMPQQGGFYMAQQHPQAAVMTAQPPSGFPQPM
PGMQFNSPQAIQGQMGGRSGGPPSSAASDVWRGSMQDGGGGAAADGGKDGHAGGGPEEAK

SEQ ID NO : 57 *Lycopersicon esculentum* SYT1 cDNA AW934450.1 BP893155.1

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCTTACTATCCAACGAACGTCAC
TACTGACCATATTCAACAGTATTTGGATGAAAACAAATCACTCATTCTGAAGATTGTTGAGA
GCCAGAACTCTGGGAAACTCAGTGAATGTGCGGAGAACCAAGCTAGGCTTCAGAGGAATCTG
ATGTACCTTGCTGCGATTGCTGATTCACAACCTCAACCTTCTAGCATGCATTCTCAGTTCTC
TTCTGGTGGGATGATGCAGCCAGGGACACACAGTTACTTGCAGCAGCAGCAGCAGCAACAAC
AAGCGCAACAAATGGCAACACAACAACTCATGGCTGCAAGATCCTCGTCGATGCTCTATGGA
CAACAGCAGCAGCAATCTCAGTTATCGCAATATCAACAAGGCTTGCATAGTAGCCAACTCGG
CATGAGTTCTGGCAGTGGCGGAAGCACTGGACTTCATCACATGCTTCAAAGTGAATCATCAC
CTCATGGTGGTGGTTTCTCTCATGACTTCGGCCGCGCAAATAAGCAAGACATTGGGAGTAGT
ATGTCTGCTGAAGGGCGCGGCGGAAGTTCAGGTGGTGAGAATCTTTATCTGAAAGCTTCTGA
GGATTGA

SEQ ID NO : 58 *Lycopersicon esculentum* SYT1 translated amino acid sequence

MQQHLMQMQPMMAAYYPTNVTTDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPSSMHSQFSSGGMMQPGTHSYLQQQQQQQQAQQMATQQLMAARSSSMLYG
QQQQQSQLSQYQQGLHSSQLGMSSGSGGSTGLHHMLQSESSPHGGGFSHDFGRANKQDIGSS
MSAEGRGGSSGGENLYLKASED

FIGURE 8 (continued)

SEQ ID NO : 59 *Malus domestica* SYT2 CV084230 DR997566

ATGCAGCAGCCACCACAAATGATCCCCGTCATGCCTTCATTTCCTCCCACCAACATCACCAC
CGAACAAATTCAGAAGTACCTTGATGACAACAAAAAGTTGATTCTGGCAATATTGGATAATC
AAAATCTTGGAAAACTTGCTGAGTGTGCTCAGTACCAGGCTCTGCTTCAAAAGAATCTGATG
TATTTAGCAGCAATTGCCGATGCGCAACCACAGGCACCAGCTGCCCCTCCCCAGATGGCCCC
ACATCCTGCTATGCAACAGGCAGGATATTACATGCAACATCCTCAGGCAGCAGCAATGGCTC
AGCAACAGGGTATTTTCTCCCCAAAGATGCCGATGCAATTCAATAACATGCATCAAATGCAC
GATCCACAGCAGCACCAACAAGCCATGCAAGGGCAAATGGGAATGAGACCTGGAGGGCCTAA
CGGCATGCCTTCCATGCTTCATACTGAGGCCACACATGGTGGTGGTAGTGGCGGCCCAAATT
CAGCTGGAGACCCAAATGATGGGCGTGGAGGAAGCAAGCAAGACGCCTCTGAGTCTGGGGCA
GGTGGTGATGGCCAGGGGACCTCAGCCGGCGGGCGTGGAACTGGTGATGGAGAGGACGGCAA
GTGA

SEQ ID NO : 60 *Malus domestica* SYT2 translated amino acid sequence

MQQPPQMIPVMPSFPPTNITTEQIQKYLDDNKKLILAILDNQNLGKLAECAQYQALLQKNLM
YLAAIADAQPQAPAAPPQMAPHPAMQQAGYYMQHPQAAAMAQQQGIFSPKMPMQFNNMHQMH
DPQQHQQAMQGQMGMRPGGPNGMPSMLHTEATHGGGSGGPNSAGDPNDGRGGSKQDASESGA
GGDGQGTSAGGRGTGDGEDGK

SEQ ID NO : 61 *Medicago trunculata* SYT2 cDNA CA858743 BI310799.1 AL382135.1

ATGCAGCAGACACCTCAAATGATTCCTATGATGCCTTCATTCCCACAACAAACAAACATAAC
CACTGAGCAGATTCAAAAATATCTTGATGAGAACAAGAAGCTGATCCTGGCAATATTGGACA
ATCAAAATCTTGGAAAACTTGCAGAATGTGCCCAGTACCAAGCTCAGCTTCAGAAGAATTTG
ATGTATTTAGCTGCAATTGCTGACGCGCAGCCACAAACACCGGCCTTGCCTCCACAGATGGC
CCCGCACCCTGCGATGCAACAAGGATTCTATATGCAACATCCTCAGGCTGCAGCAATGGCTC
AGCAACAAGGAATGTTCCCCCAAAAAATGCCAATGCAGTTCGGTAATCCGCATCAAATGCAG
GATCAGCAGCATCAGCAGCAACAACAGCAGCTACATCAGCAAGCTATGCAAGGTCAAATGGG
ACTTAGACCTGGAGGGATAAATAACGGCATGCATCCAATGCACAACGAGGCTGCTCTCGGAG
GTAGCGGCAGTGGTGGTCAAATGACGGGCGTGGTGGTGGAGCAAGCAAGATGCTTCGGAGCT
GGGACAGCCGGCGGTGATGGTCAAGGAACCTCTGCCGCAGCTGCGCACAACAGTGGAGATGC
TTCAGAAGAAGGAAAGTAA

SEQ ID NO : *62 Medicago truncula*ta SYT2 translated amino acid sequence

MQQTPQMIPMMPSFPQQTNITTEQIQKYLDENKKLILAILDNQNLGKLAECAQYQAQLQKNL
MYLAAIADAQPQTPALPPQMAPHPAMQQGFYMQHPQAAAMAQQQGMFPQKMPMQFGNPHQMQ
DQQHQQQQQQLHQQAMQGQMGLRPGGINNGMHPMHNEAALGGSGSGGPNDGRGGGSKQDASE
AGTAGGDGQGTSAAAAHNSGDASEEGK

FIGURE 8 (continued)

SEQ ID NO : 63 *Panicum virgatum* SYT3 cDNA DN152517

ATGCAGCAGCAGATGCCCATGCAGTCGGCGCCCCCGGCGACCGGCATCACCACCGAGCAGAT
CCAAAAGTATTTGGATGAAAATAAGCAGCTTATTTTGGCCATCCTGGAAAATCAGAACTTAG
GAAAGTTGGCTGAATGTGCTCAGTATCAAGCTCAGCTTCAAAAGAATCTCTTGTACCTGGCT
GCGATTGCAGATGCCCAACCCCAACCACCACAGAACCCTGCAAGTCGCCCACAGATGATGCA
ACCTGGCATGGTACCAGGTGCAGGGCATTACATGTCCCAAGTACCAATGTTCCCGCCAAGAA
CACCATTAACCCCGCAACAGATGCAAGAACAGCAGCAGCAGCAGCAGCAGCTTCAACAGCAG
CAAGCACAGGCTCTTGCTTTCCCGGGACAGATGGTCATGAGACCTACCATTAATGGCATGCA
GCCTATGCAAGCCGACCCTGCTGCCGCCGCCGCCAGCCTACAGCAGTCAGCACCTGGCCCTA
CTGATGGGCGAGGAGGCAAGCAAGATGCAACTGCTGGGGTGAGCACAGAGCCTTCTGGCACC
GAGAGCCACAAGAGCACAACCGCAGCAGATCACGATGTGGGCACTGATGTCGCGGAGAAATC
CTAA

SEQ ID NO : 64 *Panicum virgatum* SYT3 translated amino acid sequence

MQQQMPMQSAPPATGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQKNLLYLA
AIADAQPQPPQNPASRPQMMQPGMVPGAGHYMSQVPMFPPRTPLTPQQMQEQQQQQQQLQQQ
QAQALAFPGQMVMRPTINGMQPMQADPAAAAASLQQSAPGPTDGRGGKQDATAGVSTEPSGT
ESHKSTTAADHDVGTDVAEKS

SEQ ID NO : 65 *Picea sitchensis* SYT1 cDNA DR484100 DR478464.1

ATGCAGCAGCATCTCATGCAAATGCAGCCCATGATGGCGGCATACGCCTCCAACAACATCAC
CACTGATCACATCCAGAAGTACCTGGATGAGAACAAGCAGTTGATTCTGGCAATTCTGGACA
ACCAAAATCTTGGAAAGCTCAATGAGTGTGCTCAGTACCAAGCAAAACTTCAGCAGAATTTG
ATGTATCTGGCTGCGATTGCTGATTCTCAACCACAAGCACAAACTGCACATGCTCAGATTCC
TCCTAATGCAGTGATGCAGTCTGGTGGGCATTACATGCAGCACCAGCAGGCACAGCAACAAG
TGACTCCTCAGTCTCTGATGGCAGCTAGATCTTCCATGCTGTATTCTCAGCAGCCGATGGCT
GCTTTGCATCAAGCTCAGCAACAACAGCAGCAGCAGCATCAGCAGCAACAACAATCTCTTCA
CAGCCAGCTTGGCATAAATTCTGGAGGAAGCAGTGGATTGCATATGTTGCATGGTGAGACAA
ACATGGGATGTAATGGGCCTCTCTCATCTGGGGGCTTCCCTGAATTTGGGCGTGGGTCTGCT
ACCTCTGCTGAAGGTATGCAGGCCAACAGGGGCTTCACTATAGATCGTGGTTCAAATAAGCA
GGATGGAGTAGGATCAGAGAATGCCCATCCAGGTGCTGGTGATGGAAGAGGGAGTTCAACTG
GAGGGCAGAATGCAGATGAGTCAGAACCATCATACCTGAAAGCCTCCGAAGAAGAAGGAAAC
TAG

SEQ ID NO : 66 *Picea sitchensis* SYT1 translated amino acid sequence

MQQHLMQMQPMMAAYASNNITTDHIQKYLDENKQLILAILDNQNLGKLNECAQYQAKLQQNL
MYLAAIADSQPQAQTAHAQIPPNAVMQSGGHYMQHQQAQQQVTPQSLMAARSSMLYSQQPMA
ALHQAQQQQQQQHQQQQQSLHSQLGINSGGSSGLHMLHGETNMGCNGPLSSGGFPEFGRGSA
TSAEGMQANRGFTIDRGSNKQDGVGSENAHPGAGDGRGSSTGGQNADESEPSYLKASEEEGN

FIGURE 8 (continued)

SEQ ID NO : 67 *Pinus taeda* SYT1 cDNA DT625916

ATGCAGCAGCACCTCATGCAAATGCAGCCCATGATGGCGGCCTACGCCTCCAACAATATCAC
CACTGATCACATCCAGAAGTACCTGGATGAGAACAAGCAGTTGATTCTGGCAATTTTGGACA
ACCAAAATCTCGGAAAGCTCAATGAGTGTGCTCAATACCAAGCAAAACTTCAGCAGAATTTG
ATGTATCTGGCTGCTATTGCTGATTCTCAACCTCAAGCACAAACTGCACATGCTCAGATTCC
TCCAAATGCGGTGATGCAGTCTGGTGGGCATTACATGCAGCATCAACAGGCACAGCAACAAG
TTACTCCTCAGTCTCTGATGGCAGCTAGATCTTCCATACTGTATGCTCAGCAACAACAGCAG
CAGCAGCATCAGCAGCATCAGCAGCAACAGCAGCAACAACAGTCTCTTCACAGCCAGCTTGG
CATAAATTCTGGAGGAAGCAGCGGTTTGCATATGTTGCATGGTGAGACAAACATGGGATGTA
ATGGGCCTCTGTCATCTGGGGGATTCCCTGAATTTGGGCGTGGGTCTGCTACCTCTGCTGAT
GGTATGCAGGTGAACAGGGGCTTTGCTATAGATCGTGGTTCAAACAAGCAGGATGGAGTTGG
ATCAGAGAATGCCCATGCTGGTGCTGGTGATGGAAGAGGGAGTTCAACTGGAGGGCAGAATG
CAGATGAGTCAGAACCATCATACCTGAAGGCCTCCGAGGAAGAAGGAAACTAG

SEQ ID NO : 68 *Pinus taeda* SYT1 translated amino acid sequence

MQQHLMQMQPMMAAYASNNITTDHIQKYLDENKQLILAILDNQNLGKLNECAQYQAKLQQNL
MYLAAIADSQPQAQTAHAQIPPNAVMQSGGHYMQHQQAQQQVTPQSLMAARSSILYAQQQQQ
QQHQQHQQQQQQQQSLHSQLGINSGGSSGLHMLHGETNMGCNGPLSSGGFPEFGRGSATSAD
GMQVNRGFAIDRGSNKQDGVGSENAHAGAGDGRGSSTGGQNADESEPSYLKASEEEGN

SEQ ID NO : 69 *Populus tremula* SYT1 cDNA DT476906

ATGCAACAGCACCTGATGCAGATGCAGCCCATGATGGCAGCCTATTACCCCAGCAACGTCAC
TACTGATCATATTCAACAGTATCTGGACGAAAACAAGTCATTGATTTTGAAGATTGTTGAGA
GCCAGAATTCAGGGAAACTCAGTGAGTGTGCAGAGAACCAAGCAAGACTGCAACAAAATCTC
ATGTACTTGGCTGCAATTGCTGATTGTCAGCCCCAACCACCTACCATGCATGCCCAGTTCCC
TTCCAGCGGCATTATGCAGCCAGGAGCACATTACATGCAGCATCAACAAGCTCAACAGATGA
CACCACAAGCCCTTATGGCTGCACGCTCTTCTATGCTGCAGTATGCTCAACAGCCATTCTCA
GCGCTTCAACAACAGCAAGCCTTACACAGCCAGCTCGGCATGAGCTCTGGTGGAAGCGCAGG
ACTTCATATGATGCAAAGCGAGGCTAACACTGCAGGAGGCAGTGGAGCTCTTGGTGCTGGAC
GATTTCCTGATTTTGGCATGGATGCCTCCAGTAGAGGAATCGCAAGTGGGAGCAAGCAAGAT
ATTCGGAGTGCAGGGTCTAGTGAAGGGCGAGGAGGAAGCTCTGGAGGCCAGGGTGGTGATGG
AGGTGAAACCCTTTACTTGAAATCTGCTGATGATGGGAACTGA

SEQ ID NO : 70 *Populus tremula* translated amino acid sequence

MQQHLMQMQPMMAAYYPSNVTTDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQQNL
MYLAAIADCQPQPPTMHAQFPSSGIMQPGAHYMQHQQAQQMTPQALMAARSSMLQYAQQPFS
ALQQQQALHSQLGMSSGGSAGLHMMQSEANTAGGSGALGAGRFPDFGMDASSRGIASGSKQD
IRSAGSSEGRGGSSGGQGGDGGETLYLKSADDGN

FIGURE 8 (continued)

SEQ ID NO : 71 *Saccharum officinarum* SYT1 cDNA CA078249.1 CA078630 CA082679 CA234526 CA239244 CA083312

ATGCAGCAGCAACACCTGATGCAGATGAACCAGAACATGATTGGGGGCTACACCTCTCCTGC
CGCTGTGACAACCGATCTCATCCAGCAGTACCTGGATGAGAACAAGCAGCTGATCCTGGCCA
TCCTCGACAACCAGAACAATGGCAAGGTGGAGGAGTGCGAACGGCACCAAGCTAAGCTCCAG
CACAACCTCATGTACCTGGCCGCCATCGCCGACAGCCAGCCACCACAGACTGCACCACTATC
ACAATACCCGTCCAACCTGATGATGCAGCCGGGCCCTCGGTACATGCCACCGCAGTCCGGGC
AGATGATGAGCCCGCAGTCGCTAATGGCGGCGCGGTCCTCCATGATGTACGCGCACCCGTCC
ATGTCACCACTCCAGCAGCAGCAGGCAGCGCACGGGCAGCTGGGCATGGCTTCAGGGGGCGG
CGGTGGCACGACCAGTGGGTTCAACATCCTCCATGGCGAGGCCAGTATGGGCGGTGCTGGTG
GCGCTTGTGCCGGCAACAACATGATGAACGCCGGCATGTTCTCAGGCTTTGGCCGCAGCGGC
AGTGGCGCCAAGGAGGGATCGACCTCGCTGTCGGTTGACGTCCGTGGTGGCACCAGCTCCGG
CGCGCAAAGCGGGGACGGCGAGTACCTGAAAGCAGGCACCGAGGAAGAAGGCAGTTAA

SEQ ID NO : 72 *Saccharum officinarum* SYT1 translated amino acid sequence

MQQQHLMQMNQNMIGGYTSPAAVTTDLIQQYLDENKQLILAILDNQNNGKVEECERHQAKLQ
HNLMYLAAIADSQPPQTAPLSQYPSNLMMQPGPRYMPPQSGQMMSPQSLMAARSSMMYAHPS
MSPLQQQQAAHGQLGMASGGGGGTTSGFNILHGEASMGGAGGACAGNNMMNAGMFSGFGRSG
SGAKEGSTSLSVDVRGGTSSGAQSGDGEYLKAGTEEEGS

SEQ ID NO : 73 *Saccharum officinarum* SYT2 cDNA CA110367

ATGCAGCAGCCGATGCCCATGCAGCCGCAGGCGCCGGAGATGACCCCGGCCGCCGGAATCAC
CACGGAGCAGATCCAAAAGTATCTGGATGAGAATAAGCAGCTTATTTTGGCTATTTTGGAAA
ATCAGAACCTAGGAAAATTGGCAGAATGTGCTCAGTATCAATCACAACTTCAGAAGAACCTC
TTGTATCTCGCTGCAATCGCAGATGCCCAACCACAGACTGCTGTAAGCCGCCCTCAGATGGC
GCCGCCTGGTGCATTGCCTGGAGTAGGGCAGTACATGTCACAGGTGCCTATGTTCCCACCGA
GGACACCTCTAACACCCCAGCAGATGCAGGAGCAGCAACTTCAGCAGCAGCAGGCTCAGCTG
CTAAATTTCAGTGGCCTAATGGTTGCTAGACCTGGCATGGTCAACGGCATGCCTCAGTCCAT
TCAAGTTCAGCAAGCTCAGCCACCACCAGCAGGGAACAAACAGGATGCTGGTGGGGTCGCCT
CGGAGCCCTCGGGCATTGAGAACCACAGGAGCACTGGTGGTGATAATGATGGTGGAAGCGAC
TAG

SEQ ID NO : 74 *Saccharum officinarum* SYT2 translated amino acid sequence

MQQPMPMQPQAPEMTPAAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQSQLQKNL
LYLAAIADAQPQTAVSRPQMAPPGALPGVGQYMSQVPMFPPRTPLTPQQMQEQQLQQQQAQL
LNFSGLMVARPGMVNGMPQSIQVQQAQPPPAGNKQDAGGVASEPSGIENHRSTGGDNDGGSD

FIGURE 8 (continued)

SEQ ID NO : 75 *Saccharum officinarum* SYT3 cDNA CA161933.1 CA265085

ATGCAGCAGCAGATGCCCATGCCGCCGGCGCCCGCTGCGGCGGCGGCGCCCCCGGCGGCCGG
CATCACCACCGAGCAGATCCAAAAGTATTTGGACGAAAATAAGCAACTTATTTTGGCCATCC
TGGAAAATCAGAACTTAGGAAAGTTGGCTGAATGTGCTCAGTATCAAGCTCAACTTCAAAAG
AACCTCTTGTACCTGGCTGCGATTGCTGATGCCCAACCCCAGCCACCACAAAACCCTGCAGG
TCGCCCTCAGATGATGCAACCTGGTATAGTGCCAGGTGCGGGGCATTACATGTCACAAGTAC
CAATGTTCCCTCCAAGAACTCCATTAACCCCACAGCAGATGCAAGAGCAGCAGCAGCAACAG
CTTCAGCAGCAGCAAGCGCAGGCTCTTACATTCCCTGGACAGATGGTCATGAGACCAGCTAC
CATCAACGGCATACAGCAGCCTATGCAAGCTGACCCTGCCCGGGCAGCGGAGCTGCAACAAC
CACCACCTATCCCAGCTGACGGGCGAGTAAGCAAGCAGCAGGACACAACGGCTGGCGTGAGC
TCAGAGCCTTCTGCCAATGAGAGCCACAAGACCACAACTGGAGCAGATAGTGAGGCAGGTGG
TGACGTGGCGGAGAAATCCTAA

SEQ ID NO : 76 *Saccharum officinarum* SYT3 translated amino acid sequence

MQQQMPMPPAPAAAAAPPAAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQK
NLLYLAAIADAQPQPPQNPAGRPQMMQPGIVPGAGHYMSQVPMFPPRTPLTPQQMQEQQQQQ
LQQQQAQALTFPGQMVMRPATINGIQQPMQADPARAAELQQPPPIPADGRVSKQQDTTAGVS
SEPSANESHKTTTGADSEAGGDVAEKS

SEQ ID NO : 77 *Solanum tuberosum* SYT1 cDNA CK265597

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCTTACTATCCAACGAACGTCAC
TACTGACCATATTCAACAGTATTTGGATGAGAACAAATCACTCATTCTGAAAATTGTTGAGA
GCCAAAACTCGGGAAAACTCAGTGAATGTGCAGAGAACCAAGCTAGGCTTCAGAGGAATCTG
ATGTACCTTGCTGCTATTGCTGATTCACAACCTCAGCCTTCTAGCATGCATTCTCAGTTCTC
TTCTGGTGGGATGATGCAGCCAGGGACACACAGTTACCTGCAGCAGCAGCAGCAGCAACAAC
AAGCGCAACAAATGGCAACACAACAACTCATGGCTGCAAGATCCTCATCAATGCTCTATGGA
CAACAACAGCAGCAGCAGCAGCAGTCTCAGTTATCACAATTTCAACAAGGCTTGCATAGTAG
CCAACTTGGCATGAGTTCTGGCAGTGGTGGAAGCACTGGACTTCATCACATGCTTCAAAGTG
AATCATCACCTCATGGTGGTGGTTTCTCTCATGACTTCGGCCGTGCAAATAAGCAAGACATT
GGGAGTAGTATGTCTGCTGAAGGGCGCGGCGGAAGCTCAGGTGGTGATGGTGGTGAGAATCT
TTATCTGAAAGCTTCTGAGGATTGA

SEQ ID NO : 78 *Solanum tuberosum* SYT1 translated amino acid sequence

MQQHLMQMQPMMAAYYPTNVTTDHIQQYLDENKSLILKIVESQNSGKLSECAENQARLQRNL
MYLAAIADSQPQPSSMHSQFSSGGMMQPGTHSYLQQQQQQQQAQQMATQQLMAARSSSMLYG
QQQQQQQQSQLSQFQQGLHSSQLGMSSGSGGSTGLHHMLQSESSPHGGGFSHDFGRANKQDI
GSSMSAEGRGGSSGGDGGENLYLKASED

FIGURE 8 (continued)

SEQ ID NO : 79 *Sorghum bicolor* SYT3 cDNA CX611128

ATGCAGCAGCAGATGCCCATGCCGCCGGCGCCCGCTGCGGCGGCGGCGACGGCGCCCCCGGC
GGCCGGCATCACCACCGAGCAGATCCAGAAGTATTTGGACGAAAATAAGCAACTTATTTTGG
CCATCCTAGAAAATCAGAACTTAGGAAAGTTGGCTGAATGTGCTCAGTATCAAGCTCAACTT
CAAAAGAACCTCTTGTACCTGGCTGCGATTGCTGATGCCCAACCCCGACCACCGCAAAACCC
TGCAGGTCGCCCTCAGATGATGCAACCTGGTATAGTGCCAGGTGCAGGGCATTACATGTCAC
AAGTACCAATGTTCCCTCCAAGAACTCCATTAACCCCACAGCAAATGCAAGAGCAGCAGCAG
CAACAGCTTCAGCAGCAGCAAGCGCAGGCTCTTGCATTCCCTGGGCAGATGGTCATGAGACC
AGCTACCATCAACGGCATGCAGCAGCCTATGCAGGCTGACCCTGCCCGGGCAGCGGAGCTGC
AACAGCCAGCATCTGTCCCAGCCGACGGGCGAGTAAGCAAGCAGGACACAGCGGCTGGGGTG
AGCTCAGAGCCTTCTGCCAATGAGAGCCACAAGACCACAACCGGAGCAGATAGTGAGGCAGG
TGGAGACGTGGCGGAGAAATCCTAA

SEQ ID NO : 80 *Sorghum bicolor* SYT3 translated amino acid sequence

MQQQMPMPPAPAAAAATAPPAAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQL
QKNLLYLAAIADAQPRPPQNPAGRPQMMQPGIVPGAGHYMSQVPMFPPRTPLTPQQMQEQQQ
QQLQQQQAQALAFPGQMVMRPATINGMQQPMQADPARAAELQQPASVPADGRVSKQDTAAGV
SSEPSANESHKTTTGADSEAGGDVAEKS

SEQ ID NO : 81 *Triticum aestivum* SYT2 cDNA CD901951

ATGCAGCAAGCGATGCCCATGCCGCCGGCGGCGGCGGCGCCGGGGATGCCTCCGTCTGCTGG
CCTCAGCACCGAGCAGATCCAAAAGTACCTGGATGAAAATAAGCAACTAATTTTGGCTATCT
TGGAAAATCAGAACCTGGGAAAGTTGGCGGAATGTGCTCAGTATCAAGCTCAGCTTCAGAAG
AATCTTTTGTATTTGGCTGCAATCGCTGATACTCAGCCACAGACCACTGTAAGCCGTCCTCA
GATGGCACCACCTAGTGCATCCCCAGGGGCAGGGCATTACATGTCACAGGTGCCAATGTTCC
CTCCGAGGACCCCTCTAACGCCTCAGCAGATGCAGGAGCAGCAACTACAGCAGCAACAGGCT
CAGATGCTTCCGTTTGCTGGTCAAATGGTTGCGAGACCTGGGGCTGTCAATGGCATGCCTCA
GGCCCCTCAAGTTGAACCAGCCTATGCAGCAGGTGGGGCCAGTTCTGAGCCTTCTGGCACTG
AGAGCCACAGGAGCACTGGTGCCGATAATGACGGGGGGAGCGGCTGGGCTGATCAGTCCTAA

SEQ ID NO : 82 *Triticum aestivum* SYT2 translated amino acid sequence

MQQAMPMPPAAAAPGMPPSAGLSTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQK
NLLYLAAIADTQPQTTVSRPQMAPPSASPGAGHYMSQVPMFPPRTPLTPQQMQEQQLQQQQA
QMLPFAGQMVARPGAVNGMPQAPQVEPAYAAGGASSEPSGTESHRSTGADNDGGSGWADQS

FIGURE 8 (continued)

SEQ ID NO : 83 *Triticum aestivum* SYT3 cDNA BJ246754 BJ252709

ATGCAGCAGGCGATGTCCTTGCCCCCGGGAGCGGTCGGCGCGGTGTCCTCGCCGGCCGGCAT
CACCACCGAGCAGATCCAAAAGTATTTGGATGAAAATAAGCAACTTATTTTGGCCATCCTTG
AAAATCAGAACCTAGGAAAGTTGGCTGAATGTGCTCAGTATCAAGCTCAACTCCAAAAGAAT
CTCTTGTATCTAGCTGCTATCGCGGATGCCCAACCACCACAGAACCCTACAAGTCACCCTCA
GATGGTGCAGCCTGGTAGTATGCAAGGTGCAGGGCATTACATGTCACAAGTACCAATGTTCC
CTCCAAGAACGCCTTTAACCCCACAGCAGATGCAAGAGCAGCAGCACCAGCAGCTTCAGCAG
CAGCAAGCCCAGGCCCTTTCTTTCCCCGCCCAGGTGGTCATGAGACCAGGCACCGTCAACGG
CATGCAGCAGCCTATGCAAGCAGCCGGCGACCTCCAGCCAGCAGCAGCACCTGGAGGGAGCA
AGCAGGACGCCGCAGTGGCTGGGGCCAGCTCGGAACCATCTGGCACCAAGAGCCACAAGAAC
GCGGGAGCAGAGGAGGTGGGCGCTGATGTAGCAGAACAATCCTAA

SEQ ID NO : 84 *Triticum aestivum* SYT3 translated amino acid sequence

MQQAMSLPPGAVGAVSSPAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQLQKN
LLYLAAIADAQPPQNPTSHPQMVQPGSMQGAGHYMSQVPMFPPRTPLTPQQMQEQQHQQLQQ
QQAQALSFPAQVVMRPGTVNGMQQPMQAAGDLQPAAAPGGSKQDAAVAGASSEPSGTKSHKN
AGAEEVGADVAEQS

SEQ ID NO : 85 *Vitis vinifera* SYT1 cDNA DV219834

ATGCAGCAGCACCTGATGCAGATGCAGCCCATGATGGCAGCCTATTACCCCAGCAACGTCAC
CACTGATCACATTCAGCAGTATCTTGATGAAAACAAGTCATTGATTCTGAAGATTGTTGAGA
GCCAGAATTCAGGAAAATTGACTGAATGTGCAGAGAACCAGGCAAGACTACAGAGAAACCTC
ATGTACCTGGCTGCAATTGCTGATTCTCAACCCCAACCACCCACCATGCATGCTCAGTTCCC
TCCTAGTGGCATTGTTCAGCCAGGAGCTCACTACATGCAACACCAACAAGCTCAACAAATGA
CACCACAGTCGCTCCTGGCTGCACGCTCCTCCATGCTGTACACCCAACAACCATTTTCGGCC
CTGCAACAACAACAAGCCATCCATAGCCAGCTTGGCATGGGCTCTGGTGGAAGTGCAGGACT
TCACATGCTGCAAAGCGAGGGGAGTAATCCAGGAGGCAATGGAACACTGGGGACTGGTGGGT
TTCCTGATTTCAGCCGTGGAACTTCTGGAGAAGGCCTGCAGGCTGCAGGCAGGGGAATGGCT
GGTGGGAGCAAGCAAGATATGGGAAATGCAGAAGGGCGAGGAGGGAACTCAGGAGGTCAGGG
TGGGGATGGAGGTGAGACTCTTTACTTGAAAGCTGCTGAAGATGGGAATTGA

SEQ ID NO : 86 *Vitis vinifera* SYT1 translated amino acid sequence

MQQHLMQMQPMMAAYYPSNVTTDHIQQYLDENKSLILKIVESQNSGKLTECAENQARLQRNL
MYLAAIADSQPQPPTMHAQFPPSGIVQPGAHYMQHQQAQQMTPQSLLAARSSMLYTQQPFSA
LQQQQAIHSQLGMGSGGSAGLHMLQSEGSNPGGNGTLGTGGFPDFSRGTSGEGLQAAGRGMA
GGSKQDMGNAEGRGGNSGGQGGDGGETLYLKAAEDGN

FIGURE 8 (continued)

SEQ ID NO : 87 *Zea mays* SYT3 cDNA CO468901

ATGCAGCAGCAGATGCCCATGCCGCCGGCGCCCGCTGCCGCCGCGGCGGCGGCGCCCCCGGC
GGCAGGCATCACTACCGAGCAGATCCAGAAGTATTTGGACGAAAATAAGCAACTTATTTTGG
CCATCCTGGAAAATCAGAACTTAGGGAAGTTGGCTGAATGTGCTCAGTATCAAGCTCAACTT
CAAAAGAACCTCTTGTACCTGGCTGCGATTGCTGATGCCCAACCCCAGCCTCCGCAAAACCC
TGCAGGTCGCCCTCAGATGATGCAGCCTGGTATAGTGCCAGGTGCGGGGCATTACATGTCAC
AAGTACCAATGTTCCCTCCAAGAACCCCATTAACCCCACAGCAGATGCAGGAGCAGCAGCAA
CAACAACAGTTTCAGCAGCAGCAGCAGCAAGTGCAGGCTCTTACATTTCCTGGACAGATGGT
CATGAGACCAGGCACCATCAACGGCATGCAGCAGCAGCAGCCTATGCAGGCTGACCCTGCCC
GGGCAGCAGCGGAGCTGCAGCAGGCAGCACCTATCCCAGCTGACGGGCGAGGAAGCAAGCAG
GACACCGCGGGTGGGGCGAGCTCAGAGCCTTCTGCCAATGAGAGCCACAAGAGCGCCACCGG
AGCAGATACCGAGGCAGGTGGCGACGTGGCCGAGAAATCCTAA

SEQ ID NO : 88 *Zea mays* SYT3 translated amino acid sequence

MQQQMPMPPAPAAAAAAAPPAAGITTEQIQKYLDENKQLILAILENQNLGKLAECAQYQAQL
QKNLLYLAAIADAQPQPPQNPAGRPQMMQPGIVPGAGHYMSQVPMFPPRTPLTPQQMQEQQQ
QQQFQQQQQQVQALTFPGQMVMRPGTINGMQQQQPMQADPARAAAELQQAAPIPADGRGSKQ
DTAGGASSEPSANESHKSATGADTEAGGDVAEKS

SEQ ID NO : 89 *Oryza sativa* GOS2 promoter PRO0129

AATCCGAAAAGTTTCTGCACCGTTTTCACCCCCTAACTAACAATATAGGGAACGTGTGCTAA
ATATAAAATGAGACCTTATATATGTAGCGCTGATAACTAGAACTATGCAAGAAAAACTCATC
CACCTACTTTAGTGGCAATCGGGCTAAATAAAAAAGAGTCGCTACACTAGTTTCGTTTTCCT
TAGTAATTAAGTGGGAAAATGAAATCATTATTGCTTAGAATATACGTTCACATCTCTGTCAT
GAAGTTAAATTATTCGAGGTAGCCATAATTGTCATCAAACTCTTCTTGAATAAAAAAATCTT
TCTAGCTGAACTCAATGGGTAAAGAGAGAGATTTTTTTTAAAAAAATAGAATGAAGATATTC
TGAACGTATTGGCAAAGATTTAAACATATAATTATATAATTTTATAGTTTGTGCATTCGTCA
TATCGCACATCATTAAGGACATGTCTTACTCCATCCCAATTTTTATTTAGTAATTAAAGACA
ATTGACTTATTTTTATTATTTATCTTTTTTCGATTAGATGCAAGGTACTTACGCACACACTT
TGTGCTCATGTGCATGTGTGAGTGCACCTCCTCAATACACGTTCAACTAGCAACACATCTCT
AATATCACTCGCCTATTTAATACATTTAGGTAGCAATATCTGAATTCAAGCACTCCACCATC
ACCAGACCACTTTTAATAATATCTAAAATACAAAAAATAATTTTACAGAATAGCATGAAAAG
TATGAAACGAACTATTTAGGTTTTTCACATACAAAAAAAAAAAGAATTTTGCTCGTGCGCGA
GCGCCAATCTCCCATATTGGGCACACAGGCAACAACAGAGTGGCTGCCCACAGAACAACCCA
CAAAAAACGATGATCTAACGGAGGACAGCAAGTCCGCAACAACCTTTTAACAGCAGGCTTTG
CGGCCAGGAGAGAGGAGGAGAGGCAAAGAAAACCAAGCATCCTCCTCCTCCCATCTATAAAT
TCCTCCCCCCTTTTCCCCTCTCTATATAGGAGGCATCCAAGCCAAGAAGAGGGAGAGCACCA
AGGACACGCGACTAGCAGAAGCCGAGCGACCGCCTTCTTCGATCCATATCTTCCGGTCGAGT
TCTTGGTCGATCTCTTCCCTCCTCCACCTCCTCCTCACAGGGTATGTGCCCTTCGGTTGTTC
TTGGATTTATTGTTCTAGGTTGTGTAGTACGGGCGTTGATGTTAGGAAAGGGGATCTGTATC
TGTGATGATTCCTGTTCTTGGATTTGGGATAGAGGGGTTCTTGATGTTGCATGTTATCGGTT
CGGTTTGATTAGTAGTATGGTTTTCAATCGTCTGGAGAGCTCTATGGAAATGAAATGGTTTA
GGGTACGGAATCTTGCGATTTTGTGAGTACCTTTTGTTTGAGGTAAAATCAGAGCACCGGTG

FIGURE 8 (continued)

ATTTTGCTTGGTGTAATAAAAGTACGGTTGTTTGGTCCTCGATTCTGGTAGTGATGCTTCTC
GATTTGACGAAGCTATCCTTTGTTTATTCCCTATTGAACAAAAATAATCCAACTTTGAAGAC
GGTCCCGTTGATGAGATTGAATGATTGATTCTTAAGCCTGTCCAAAATTTCGCAGCTGGCTT
GTTTAGATACAGTAGTCCCCATCACGAAATTCATGGAAACAGTTATAATCCTCAGGAACAGG
GGATTCCCTGTTCTTCCGATTTGCTTTAGTCCCAGAATTTTTTTTCCCAAATATCTTAAAAA
GTCACTTTCTGGTTCAGTTCAATGAATTGATTGCTACAAATAATGCTTTTATAGCGTTATCC
TAGCTGTAGTTCAGTTAATAGGTAATACCCCTATAGTTTAGTCAGGAGAAGAACTTATCCGA
TTTCTGATCTCCATTTTTAATTATATGAAATGAACTGTAGCATAAGCAGTATTCATTTGGAT
TATTTTTTTTATTAGCTCTCACCCCTTCATTATTCTGAGCTGAAAGTCTGGCATGAACTGTC
CTCAATTTTGTTTTCAAATTCACATCGATTATCTATGCATTATCCTCTTGTATCTACCTGTA
GAAGTTTCTTTTTGGTTATTCCTTGACTGCTTGATTACAGAAAGAAATTTATGAAGCTGTAA
TCGGGATAGTTATACTGCTTGTTCTTATGATTCATTTCCTTTGTGCAGTTCTTGGTGTAGCT
TGCCACTTTCACCAGCAAAGTTC

SEQ ID NO : 90 Box I

IQ(Q/K)(Y/M/F/H)L(D/E)(E/D)N(K/N)XLI

Where X is any amino acid

SEQ ID NO : 91 Box II

NL(M/L/V)YLA(A/T)IAD

SEQ ID NO : 92 prm06681

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGCAACAGCACCTGATG

SEQ ID NO : 93 Prm06682

GGGGACCACTTTGTACAAGAAAGCTGGGTCATCATTAAGATTCCTTGTGC

SEQ ID NO : 94 prm06685

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGCAGCAGCAGCAGTCT

SEQ ID NO : 95 prm06686

GGGGACCACTTTGTACAAGAAAGCTGGGTTCTTTGGATCCTTTTCACTTG

SEQ ID NO : 96 prm06683

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGCAGCAATCTCCACAGAT

SEQ ID NO : 97 prm06684

GGGGACCACTTTGTACAAGAAAGCTGGGTTCCTCTATTTCATTTTCCTTCAG

FIGURE 8 (continued)