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(54) Titre : UTILISATION DE LA TREHALOSE-6-PHOSPHATE SYNTHASE POUR MODULER LA CROISSANCE
VEGETALE

(54) Title: USE OF TREHALOSE-6-PHOSPHATE SYNTHASE TO MODULATE PLANT GROWTH

(57) Abrégé/Abstract:

The present invention relates to the use of trehalose-6-phosphate synthase to modulate plant growth. More specifically, it relates to the use of a class II trehalose-6-phosphate synthase, comprising both a synthase and a phosphatase-like part to modulate plant growth. Preferably, the activity of trehalose-6-phosphate synthase is downregulated to obtain an increased plant biomass yield.



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(54) **Title:** USE OF TREHALOSE-6-PHOSPHATE SYNTHASE TO MODULATE PLANT GROWTH

(57) **Abstract:** The present invention relates to the use of trehalose-6-phosphate synthase to modulate plant growth. More specifically, it relates to the use of a class II trehalose-6-phosphate synthase, comprising both a synthase and a phosphatase-like part to modulate plant growth. Preferably, the activity of trehalose-6-phosphate synthase is downregulated to obtain an increased plant biomass yield.

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Use of trehalose-6-phosphate synthase to modulate plant growth

The present invention relates to the use of a plant trehalose-6-phosphate synthase class II to modulate plant growth. More specifically, it relates to the use of a class II trehalose-6-phosphate synthase, comprising both a synthase-like and a phosphatase-like part to modulate plant growth. Preferably, the activity of the class II trehalose-6-phosphate synthase is downregulated to obtain an increased plant biomass yield.

Trehalose is a widespread disaccharide, occurring in bacteria, fungi, insects and plants. In microbes, trehalose accumulation is generally associated with stress resistance, not at least with desiccation and osmotic stress resistance. In plants, however, except for some resurrection plants such as *Selaginella lepidophylla*, the role of trehalose is less clear.

In most cases, trehalose synthesis is a two-step process in which trehalose-6-phosphate synthase (TPS) synthesizes trehalose-6-phosphate (T6P), followed by a dephosphorylation to trehalose by T6P phosphatase (TPP). Although in most plants trehalose is hardly detectable, multiple homologues of both TPS and TPP genes are present, e.g. in *Arabidopsis* (Vogel *et al.*, 2001; Leyman *et al.*, 2001; Eastmond *et al.*, 2003). Trehalose accumulation obtained in transgenic plants, transformed with heterologues trehalose biosynthesis genes leads to an improved abiotic stress tolerance (Garg *et al.*, 2002; Jang *et al.*, 2003). However, the absence of significant trehalose accumulation in most plants, in spite of the presence of multiple trehalose biosynthesis genes argues for a regulatory role of the gene products, rather than for a role of trehalose as stress protectant. Indeed, several authors suggest a regulatory role for TPS (Avonce *et al.* 2004) and its gene product T6P in sugar metabolism (Eastmond *et al.*, 2003) and starch synthesis (Kolbe *et al.*, 2005). T6P is indispensable for carbohydrate utilization and growth (Schluepmann *et al.*, 2003), but accumulation of T6P seems to cause growth inhibition in seedlings (Schluepmann *et al.*, 2004). The present data are sometimes conflicting and the role of the trehalose biosynthesis genes is still far from clear. None of these publications makes a link with a possible role of plant TPS, in particular class II plant TPS in plant growth and yield.

EP0901527 discloses the regulation of plant metabolism by modifying the level of T6P. More specifically, they claim an increase in the yield of plants by increasing the intracellular availability of trehalose-6-phosphate. However, rather conflicting, they claim also the stimulation of growth of a plant cell or tissue by decreasing the intracellular availability of trehalose-6-phosphate. Again, as shown in the recent literature, this is indicating that the T6P balance is very delicate and far from straightforward. The inventors realized the modulation of the T6P content by expressing heterologous TPS and TPP genes in the plant. Although the patent mentions that similar results can be obtained by up or down regulation of the endogenous genes, one would expect that, due to the large number of plant genes, the

deletion or overexpression of one of those genes has only a limited effect on the T6P concentration, if any effect at all. This is especially true for the class II TPS genes, where both a synthase-like domain and a phosphatase-like domain are present. If both domains are active, trehalose, rather than T6P would be the end product. Moreover, for at least two
5 *Arabidopsis* class II TPS genes, AtTPS7 and AtTPS8, no synthase nor phosphatase activity could be detected (Vogel *et al.*, 2001; Eastmond *et al.*, 2003), implying that a manipulations of these genes would not affect the T6P content of the plant at all.

Surprisingly, we found that a plant class II TPS can be used to modulate plant growth and biomass yield. Indeed, contrary to what would be expected on the base of the literature,
10 inactivation of plant TPS activity leads to increased stem and root growth, and increased plant biomass.

A first aspect of the invention is the use of a plant class II TPS for the modulation of plant growth. 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),
15 flowers, and tissues and organs, wherein each of the aforementioned comprise the gene/nucleic acid 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 comprises the gene/nucleic acid of interest. Plants that are particularly useful in the methods of the invention include all plants
20 which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants. As a non limiting example, it may be a crop used for food or fodder, whereby increase of roots, leaves, stem or seed biomass is increasing the crop yield. Alternatively, the crop may be used for ornamental or industrial purposes, such as starch production, or it may be used as raw material for biofuel production. Crops known for biofuel
25 are known to the person skilled in the art and include, but are not limited to food crops such as corn, soybean, flaxseed, rapeseed, sugar cane, industrial crops such as hemp and switchgrass but also woody biomass such as poplar and willow.

TPS as used here, refers to the structural homology of the gene and protein with other members of the trehalose-6-phosphate family, but does not imply that the protein has an
30 effective trehalose-6-phosphate synthesizing activity. Preferably, said TPS has a domain homologous to the glycosyltransferase 20 (pfam00982.12). The term "domain" refers to a set of amino acids conserved at specific positions along an alignment of sequences of evolutionarily related proteins. While amino acids at other positions can vary between homologues, amino acids that are highly conserved at specific positions indicate amino acids
35 that are likely essential in the structure, stability or activity of a protein. Identified by their high degree of conservation in aligned sequences of a family of protein homologues, they can be used as identifiers to determine if any polypeptide in question belongs to a previously identified

polypeptide family. As a non-limiting example, due to its structure, TPS as used here may have a T6P phosphatase activity, or a combination of synthase and phosphatase activity. The use of TPS, as mentioned here, covers the use of the gene, the use of the protein, as well as the use of compounds increasing or decreasing the activity of the protein. As a non-limiting example, a compound decreasing the activity of the TPS may be an inactivating TPS antibody.

Preferably, said TPS is a class II TPS, according to the classification in *Arabidopsis thaliana*. A class II TPS comprises both a trehalose-6-phosphate synthase like domain, as well as a trehalose-6-phosphate phosphatase like domain (Leyman *et al*, 2001, Vogel *et al.*, 2001), preferably said class II TPS comprises a trehalose-6-phosphate synthase like domain, as well as a trehalose-6-phosphate phosphatase like domain comprising a phosphatase box with the sequence LDYD (G/D) T and/or a phosphatase box with the sequence GDD(R/Q)SD, more preferably said class II TPS comprises both a trehalose-6-phosphate synthase like domain, as well as a trehalose-6-phosphate phosphatase like domain comprising at least one, preferably two phosphatase boxes as described by Leyman *et al.* (2001),. Even more preferably, said TPS is selected from the group consisting of SEQ ID N° 1-15 (AtTPS5-11, rice orthologue, poplar orthologues), or homologues, orthologues or paralogues thereof. "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. A deletion refers to removal of one or more amino acids from a protein. An insertion refers to one or more amino acid residues being 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. A substitution refers to replacement of amino acids of the protein with other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α -helical structures or β -sheet structures). 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. The amino acid substitutions are preferably conservative amino acid substitutions. Conservative substitution tables are well known in the art.

"Orthologues" and "paralogues" encompass evolutionary concepts used to describe the 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 and paralogues may easily be found by performing a so-called reciprocal blast search. Typically, this involves a first BLAST involving BLASTing SEQ ID N° 1 or SEQ ID N° 4 as query sequence, using BLASTP or TBLASTN (using standard default values). 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 corresponds to AtTPS8 or AtTPS5, the second BLAST would therefore be against *Arabidopsis thaliana* sequences). The results of the first and second BLASTs are then compared. A paralogue is identified if a high-ranking hit from the first blast is from the same species as from which the query sequence is derived, a BLAST back then ideally results in the query sequence amongst the highest hit; an orthologue is identified if a high-ranking hit in the first BLAST is not from the same species as from which the query sequence is derived, and preferably results upon BLAST back in the query sequence being among the highest hits. 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 addition to E-values, comparisons are also scored by percentage identity. Percentage identity refers to the number of identical amino acids between the two compared polypeptide sequences over a particular length. 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. Alternatively, homologues, orthologues and paralogues may be identified by domain searches for a trehalose synthase domain, and for one of the phosphatase domains. The full length protein sequence is then compared with SEQ ID N° 4, using bl2seq (Tatusova and Madden, 1999). Using this alignment, an orthologue or paralogue has at least 50% identities, preferably 55% identities, more preferably 60% identities. As a non-limiting examples, AtTPS8 orthologues are present in *Oryza sativa* (Genpept accession numbers ABF94728, BAF06162 and BAF11342), *Brassica oleracea* (Genpepts accession number ABD65165), *Medicago trunculata* (Genpept accession number ABE86430), *Cypripedium parviflorum* (genpept accession number AAN86570) and *Ginlo biloba* (genbank accession number AAX16015). In one preferred embodiment, said TPS is AtTPS8 (SEQ ID N° 4). In another preferred embodiment, said TPS is AtTPS5 (SEQ ID N° 1).

Preferably, said use is an inactivation of the TPS activity, and said modulation is an increase in plant biomass and/or plant yield. Methods to inactivate the TPS activity are known to the person skilled in the art and include, but are not limited to the knock out of the gene, the use of RNAi, gene silencing, knock out of the TPS promoter, inactivating mutations in the TPS promoter or in the coding region, or the synthesis by the plant of inactivating antibodies against TPS. Preferably, increase of plant biomass and/or plant yield is realized by increased root growth, increased stem thickness, increased leave number and/or increased seed size. One preferred embodiment is the use of TPS to modulate plant growth, whereby said modulation is obtained in absence of light. The term "yield" in general means a measurable produce of

economic value, typically related to a specified crop, to an area, and to a period of time. Individual plant parts directly contribute to yield based on their number, size and/or weight, or the actual yield is the yield per acre for a crop and year, which is determined by dividing total production (includes both harvested and appraised production) by planted acres. The terms

5 "increase", "improve" or "enhance" are interchangeable and shall mean in the sense of the application at least a 5%, 6%, 7%, 8%, 9% or 10%, preferably at least 15% or 20%, more preferably 25%, 30%, 35% or 40% more yield and/or growth in comparison to control plants as defined herein. Increased seed yield may manifest itself as one or more of the following: a) an increase in seed biomass (total seed weight) which may be on an individual seed basis and/or

10 per plant and/or per hectare or acre; b) increased number of flowers per plant; c) increased number of (filled) seeds; d) increased seed filling rate (which is expressed as the ratio between the number of filled seeds divided by the total number of seeds); e) increased harvest index, which is expressed as a ratio of the yield of harvestable parts, such as seeds, divided by the total biomass; and f) increased thousand kernel weight (TKW), which is extrapolated from the

15 number of filled seeds counted and their total weight. An increased TKW may result from an increased seed size and/or seed weight, and may also result from an increase in embryo and/or endosperm size.

Another aspect of the invention is the use of a plant class II TPS, as defined above, for the

20 modulation of starch synthesis. Preferably, said use is the inactivation of TPS activity, and said modulation is an increase in starch synthesis. Preferably, said TPS is a class II TPS, according to the classification in *Arabidopsis thaliana*. A class II TPS comprises both a trehalose-6-phosphate synthase like domain, as well as a trehalose-6-phosphate phosphatase like domain (Leyman *et al*, 2001, Vogel *et al.*, 2001). Even more preferably, said TPS is selected from the

25 group consisting of SEQ ID N° 1-15 (TPS5-11, rice orthologue, poplar orthologue). In one preferred embodiment, said TPS is *AtTPS8* (SEQ ID N° 4). In another preferred embodiment, said TPS is *AtTPS5* (SEQ ID N° 1)

Still another aspect of the invention is a method for improving various yield-related traits in

30 plants relative to control plants, comprising modulating expression and/or translation in a plant of a Class II TPS nucleic acid and/or a Class II TPS polypeptide, wherein said modulated expression consists of a reduction or substantial elimination of expression and/or translation of an endogenous Class II TPS gene in a plant. As a non limiting example, said reduction or substantial elimination may be obtained by RNA-mediated silencing of gene expression, by co-

35 expression, by the use of antisense class II TPS nucleic acid sequences or by the use of inverted repeats of class II TPS nucleic acids, preferably inverted repeats forming a hairpin structure.

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Still another aspect of the invention is the method for the production of a transgenic plant having increased yield relative to control plants, which method comprises:

(i) introducing and expressing in a plant a genetic construct comprising one or more control sequences for reducing expression and/or translation in a plant
5 of an endogenous Class II TPS gene; and

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

Control sequences, as used here, are sequences that influence the expression and/or translation of the class II TPS gene are known to the person skilled in the art
10 and include but are not limited to sequences causing co-expression, sequences encoding antisense RNA, and RNAi.

Still another aspect of the invention is a plant, obtainable according to the method of the invention, whereby said plant has reduced expression of an endogenous Class II TPS gene due introduction into a plant of a Class II TPS control nucleic acid
15 sequence. Reduced expression, as used here, is an expression that is substantially decreased when the expression is compared with a non transformed control plant, grown under the same conditions. Methods to measure expression are known to the person skilled in the art; a substantial reduction is a reduction with preferably 10%, more preferably 20%, even more preferably 30%.

20 Specific aspects of the invention include:

- use of inactivation of the activity of a plant class II trehalose-6-phosphate synthase to increase plant growth;
- use of inactivation of the activity of a class II plant trehalose-6-phosphate synthase to increase starch synthesis;
- 25 - a method for increasing growth of a plant, comprising the step of inactivating class II trehalose-6-phosphate synthase (class II TPS) activity in the plant; and

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- a method for increasing starch synthesis of a plant, comprising the step of inactivating class II trehalose-6-phosphate synthase (class II TPS) activity in the plant.

Brief description of the figures

5 Figure 1: Root length of *AtTPS8* KO on MS medium, with and without sucrose, in light and in the dark. GT2, GT4 and GT6 are different KO lines of *AtTPS8*.

Figure 2: Expression levels of *AtCYCD3* and *ApL3* in the *AtTPS8* KO background.

Figure 3: Phenotypic characterization of the adult *AtTPS8* KO compared to WT plants.

10 Figure 4: SALK_144791 *AtTPS5* expression data.

Figure 5: root length measurements of SALK_144791 line.

Figure 6: Phenotype of the SALK_144791 *AtTPS5* KO line, in comparison with WT (Columbia), on 1xMS, 1% sucrose medium.

Figure 7: Phenotype of the SALK_144791 *AtTPS5* KO line, in comparison with WT
15 (Columbia), on 1xMS, 1% sucrose medium: test on agravitrophic effect.

Figure 8: GT12622 *AtTPS5* expression data.

Figure 9: Phenotype of Genetrap GT12622 *AtTPS5* KO line, in comparison with WT (Landsberg erecta), on 1xMS, 1% sucrose medium.

Figure 10: Phenotype of Genetrap GT12622 *AtTPS5* KO line, in comparison with WT
20 (Landsberg erecta), on 1xMS, 1% sucrose medium: test on agravitrophic effect.

Examples

Materials and Methods to the examples

5

Plant material for AtTPS8

Wild type *Arabidopsis* plants (Columbia) were transformed with silencing and overexpression constructs (see further). In addition, a Gene Trap line (GT13138, Landsberg erecta) was obtained through Martienssen's lab at Cold Spring Harbor Laboratory. To study the phenotype of these plants, homozygous lines were obtained. Seeds were surface sterilized and germinated in vertically oriented Petri dishes on 1x Murashige and Skoog medium (Duchefa) solidified with purified agar (Duchefa), with 1% sucrose or without sucrose (as indicated in the figures), in a daily cycle of 12h at 22°C and 12h of darkness at 18°C. Ten days after germination, root length of plants was measured. Plants grown in dark conditions were kept in dark over the whole period of time.

15

Constructs

For the silencing of *AtTPS8* (At1g70290) in *Arabidopsis*, the Gateway vectors, pDONR207 and pK7GWIWG2 (Karimi *et al*, 2002) were used. 149bp of an *AtTPS8* specific sequence was amplified with two primers containing the recombination sites *AttB1* and *AttB2*. Forward primer, GGGGACAAGTTTGTACAAAAAAGCAGGC-TCCGAAGTAACTTCTACCTCC; Reverse primer, GGGGACCACTTTGTACAAG-AAAGCTGGGTCCCATCTCTAAGTTGTAAGT. The construct was transformed in competent *Agrobacterium* cells (strain C58C1), and transformed in WT *Arabidopsis* plants using the flower dip method (Clough, 2005). T0 seeds were selected on kanamycin and transferred to soil to set seeds. These T1 seeds were again selected on kanamycin and screened for homozygous T2 lines.

25

The overexpression construct of *AtTPS8* was made using a PCB302 plant vector. Full length *AtTPS8* was amplified from protoplast cDNA with the following primers: forward primer, CGGGATCCATGGTGTCAAGATCTTGTGCTAA; reverse primer, AAGGCC-TAACGATGCTTTCAAATGCAACTT. The construct was transformed in *Agrobacterium* and plants as described above.

30

Gene trap line

The gene trap line (GT13138, Landsberg erecta) was obtained from Martienssen's lab at Cold Spring Harbor Laboratory. A pWS32 vector containing a *Ds* transposable element with the β -glucuronidase (GUS) gene as a reporter and the Neomycin phosphotransferase (NPTII) gene as a selectable marker, was transformed in *Arabidopsis*, where it randomly inserted into the

35

genome. Glucuronidase assays revealed insertions into exons of different genes. Insertion sites were then amplified by TAIL PCR (Liu *et al*, 1995) and sequenced. These sequences were validated and annotated according to the sequence of the *Arabidopsis* genome.

5 Plant material for AtTPS5

SALK line 'SALK 144791' (*Arabidopsis thaliana*, ecotype *Colombia*) was available from the Alonso/Crosby/Ecker Agrobacterium T-DNA transformed plant collection and was ordered at NASC/ABRC. The T-DNA flanking DNA sequence was recovered and sequenced by the Salk Institute Genomic analysis Laboratory (SIGnAL), USA and was predicted to be in the first exon
10 of the *AtTPS5* gene (At4g17770). The ordered sequence-indexed lines were segregating T3 lines. With the *NPTII* marker (kanamycin resistance) and PCR, homozygous plants were selected, hereinafter referred to as line 070(2) (forward primer: 5'TCCTGCTTATATCCCACCTGAGC3'; and reverse primer: 5'GCGCCGCTTAAAGAAGGAGAA3'). Sequences were obtained with the left border T-DNA
15 primer (Lba1: 5'TGGTTCACGTAGTGGGCCATCG3'), and the T-DNA was found at position 923 relative to the START codon in the cDNA of *AtTPS5*.

Genetrap line GT12622 (*Arabidopsis thaliana*, ecotype *Landsberg erecta*) was ordered from the collection of transposon insertion lines produced at the Martienssen lab of Cold Spring
20 Harbor Laboratory, USA (Sundaresan *et al.*, 1995; Martienssen, 1998). The line was generated using the *Dissociation* transposons (*Ds*) from maize, engineered to carry a *uidA* (β -glucuronidase (GUS)) reporter gene and an *NPTII* (neomycin phosphotransferase) kanamycin resistance gene. Gene trap reporter genes have no promoter, so that GUS expression can occur only when the reporter inserts within a transcribed chromosomal gene, creating a
25 transcriptional fusion. These elements simultaneously monitor gene expression and disrupt endogenous gene function. The gene trap construct has a multiple splice acceptor fused to the GUS gene. Based on the flanking sequences of the insertion site obtained by TAIL-PCR, line GT12622 was predicted by CSHL to carry a unique insertion of a genetrap transposable DS element somewhere at the end of the first exon of the *AtTPS5* gene (At4g17770). The
30 delivered sequence-indexed lines were F3 seeds. With the kanamycin marker and PCR, homozygous *AtTPS5* knock-out lines (F5) were obtained, hereinafter referred to as line GT4.1 and GT6.2. Gene-specific primers (forward primer: 5'TTGGGCGCGTAGCTTTATAC3' and reverse primer: 5'CAAGAAGATATGAAAACAGCCTCA3') were designed, together with primers at the borders of the gene trap construct, to amplify specific flanking sequences of the
35 insertion site. The accurate insertion place is at position 1930 (in the first exon) in the cDNA sequence of *AtTPS5*.

Example 1: *TPS8* knock out lines show enhanced growth under different growth conditions

In the yeast *Saccharomyces cerevisiae*, trehalose is synthesized in two reactions from UDP-glucose and glucose-6-phosphate by trehalose-6-phosphate synthase (encoded by *TPS1*) and trehalose-6-phosphate phosphatase (encoded by *TPS2*). In the *Arabidopsis thaliana* genome, 11 TPS-like genes have been detected. Those genes can be grouped in two subfamilies, displaying most similarity either to yeast *TPS1* (encoding TPS in yeast; class I) or *TPS2* (encoding TPP in yeast; class II)(Leyman *et al.* 2001). Almost nothing is known about the TPP like class II genes in *Arabidopsis*. To study the effect of these genes, knock out lines (KO), RNAi lines and overexpression lines were constructed and studied as described in materials and methods.

The lines were tested on 1x Murashige and Skoog medium (Duchefa) solidified with purified agar (Duchefa) (MS), with or without addition of sucrose. Representative knock out lines were analyzed after 10 days of germination. The results for the *AtTPS8* KO are summarized in Figure 1. Independent of the growth conditions, the KO line showed always a significant increase in root length, although the effect is slightly more pronounced when sucrose was present in the medium.

Example 2: *TPS8* inactivation promotes *CYCD3* and *ApL3* expression

To analyze the underlying mechanism of the increase in growth, the effect of the *AtTPS8* KO on the expression of the cell cycle gene *AtCYCD3*, and on the starch biosynthesis gene *ApL3* was studied by real time PCR. Compared to wild type (wt), the expression of both *ApL3* and *AtCYCD3* was significantly higher. The results are shown in Figure 2. Especially the *ApL3* result is unexpected, as Kolbe *et al.* (2005) recently have shown that T6P is inducing starch synthesis, whereas one would rather expect that the concentration of T6P is lower in the *AtTPS8* KO.

Example 3: *TPS8* inactivation results in higher biomass and bigger plants

Wild type and *AtTPS8* KO seedlings were put in soil, and were grown for 30 days, to compare the phenotypes of the adult plants. Adult *AtTPS8* KO seedlings grow faster in soil, they have more but smaller rosette leaves and the inflorescence stem is twice as thick and the one in wild type. The KO has approximately two times as much siliques as wt. The cauline leaves of the KO are much larger and look more like rosette leaves (Figure 3). This leads to a higher seed yield and a higher overall biomass yield of the plant.

Example 4: *TPS5* inactivation promotes root growth

To test the expression of *AtTPS5* in the homozygous SALK_144791 line, RNA was isolated from 50 seedlings of line 070(2). RT-PCR experiments (Forward primer: 5'GCACTCCTCAACGCTGATTT3' and Reverse primer: 5'AAGCCCTATGGTTCCACGTT3') on
5 cDNA demonstrated dramatic downregulation of *AtTPS5* expression (figure 4). For the phenotypic characterization, seeds of line 070(2) were damp-sterilized (100 ml bleach + 3 ml HCL 37%) for 4-6 hours and imbibed/stratified for two days in constant light at 4°C. After two days, seeds were put on sterile plant medium plates (1x MS medium pH 5.7 (KOH), 1% sucrose) and incubated vertically in a growth chamber with 12hr-12hr light-dark cycle, 70
10 microE, 22°C day, 18°C night. After 7 days of germination, root lengths of 18 seedlings were measured. The SALK lines showed a significant increase in root length (figure 5). This result was confirmed in a second experiment, pictures of the seedlings were taken after 13 days of germination (see figure 6). The seedlings appeared to have somewhat longer roots. However, this needs to be confirmed. Some plates were turned 90°C to check possible gravitrophic
15 effects. After 4 days, no agravitrophic effect was detected (figure 7).

Example 4: *Genetrap TPS5* inactivation promotes root and hypocotyls growth

To test the expression of *AtTPS5* in the homozygous *TPS5* Genetrap lines, RNA was isolated from 50 seedlings of two GT knock-out lines. RT-PCR (Forward primer:
20 5'GCACTCCTCAACGCTGATTT3' and Reverse primer: 5'AAGCCCTATGGTTCCACGTT3') demonstrated dramatic down-regulation of *AtTPS5* expression (figure 8). Seeds were damp-sterilized (100 ml bleach + 3 ml HCL 37%) for 4-6 hours and imbibed/stratified for two days in constant light at 4°C. After two days, seeds were put on sterile plant medium plates (1x MS medium pH 5.7 (KOH), 1% sucrose) and incubated vertically in a growth chamber with 12hr-
25 12hr light-dark cycle, 70 microE, 22°C day, 18°C night. Ten days after germination, pictures were taken of seedlings (figure 9). The seedlings appeared to have significantly longer roots, and longer hypocotyls. Several days after turning the plates 90°C, and contrary to what was seen in Columbia, seedlings showed agravitrophic effects (figure 10).

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SEQUENCE LISTING IN ELECTRONIC FORM

In accordance with Section 111(1) of the Patent Rules, this description contains a sequence listing in electronic form in ASCII text format (file: 29775-76 Seq 16-07-08 v1.txt).

A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

The sequences in the sequence listing in electronic form are reproduced in the following table.

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Asp	Val	Glu	Glu	Ala	Lys	Arg	Glu	Thr	Tyr	Glu	Thr	Ala	Arg	Arg	Ile
		355					360					365			
Asn	Glu	Arg	Tyr	Gly	Thr	Ser	Asp	Tyr	Lys	Pro	Ile	Val	Leu	Ile	Asp
	370					375					380				
Arg	Leu	Val	Pro	Arg	Ser	Glu	Lys	Thr	Ala	Tyr	Tyr	Ala	Ala	Ala	Asp
385					390					395					400
Cys	Cys	Leu	Val	Asn	Ala	Val	Arg	Asp	Gly	Met	Asn	Leu	Val	Pro	Tyr
				405					410					415	
Lys	Tyr	Ile	Val	Cys	Arg	Gln	Gly	Thr	Arg	Ser	Asn	Lys	Ala	Val	Val
			420					425					430		
Asp	Ser	Ser	Pro	Arg	Thr	Ser	Thr	Leu	Val	Val	Ser	Glu	Phe	Ile	Gly
		435					440					445			
Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala	Ile	Arg	Val	Asn	Pro	Trp	Asp	Val
	450					455					460				

Asp	Ala	Val	Ala	Glu	Ala	Val	Asn	Ser	Ala	Leu	Lys	Met	Ser	Glu	Thr	465	470	475	480
Glu	Lys	Gln	Leu	Arg	His	Glu	Lys	His	Tyr	His	Tyr	Ile	Ser	Thr	His	485	490	495	
Asp	Val	Gly	Tyr	Trp	Ala	Lys	Ser	Phe	Met	Gln	Asp	Leu	Glu	Arg	Ala	500	505	510	
Cys	Arg	Asp	His	Tyr	Ser	Lys	Arg	Cys	Trp	Gly	Ile	Gly	Phe	Gly	Leu	515	520	525	
Gly	Phe	Arg	Val	Leu	Ser	Leu	Ser	Pro	Ser	Phe	Arg	Lys	Leu	Ser	Val	530	535	540	
Glu	His	Ile	Val	Pro	Val	Tyr	Arg	Lys	Thr	Gln	Arg	Arg	Ala	Ile	Phe	545	550	555	560
Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Val	Pro	Glu	Ser	Ser	Ile	Val	Gln	Asp	565	570	575	
Pro	Ser	Asn	Glu	Val	Val	Ser	Val	Leu	Lys	Ala	Leu	Cys	Glu	Asp	Pro	580	585	590	
Asn	Asn	Thr	Val	Phe	Ile	Val	Ser	Gly	Arg	Gly	Arg	Glu	Ser	Leu	Ser	595	600	605	
Asn	Trp	Leu	Ser	Pro	Cys	Glu	Asn	Leu	Gly	Ile	Ala	Ala	Glu	His	Gly	610	615	620	
Tyr	Phe	Ile	Arg	Trp	Lys	Ser	Lys	Asp	Glu	Trp	Glu	Thr	Cys	Tyr	Ser	625	630	635	640
Pro	Thr	Asp	Thr	Glu	Trp	Arg	Ser	Met	Val	Glu	Pro	Val	Met	Arg	Ser	645	650	655	
Tyr	Met	Glu	Ala	Thr	Asp	Gly	Thr	Ser	Ile	Glu	Phe	Lys	Glu	Ser	Ala	660	665	670	
Leu	Val	Trp	His	His	Gln	Asp	Ala	Asp	Pro	Asp	Phe	Gly	Ser	Cys	Gln	675	680	685	
Ala	Lys	Glu	Met	Leu	Asp	His	Leu	Glu	Ser	Val	Leu	Ala	Asn	Glu	Pro	690	695	700	
Val	Val	Val	Lys	Arg	Gly	Gln	His	Ile	Val	Glu	Val	Lys	Pro	Gln	Gly	705	710	715	720
Val	Ser	Lys	Gly	Leu	Ala	Ala	Glu	Lys	Val	Ile	Arg	Glu	Met	Val	Glu	725	730	735	
Arg	Gly	Glu	Pro	Pro	Glu	Met	Val	Met	Cys	Ile	Gly	Asp	Asp	Arg	Ser	740	745	750	
Asp	Glu	Asp	Met	Phe	Glu	Ser	Ile	Leu	Ser	Thr	Val	Thr	Asn	Pro	Glu	755	760	765	
Leu	Leu	Val	Gln	Pro	Glu	Val	Phe	Ala	Cys	Thr	Val	Gly	Arg	Lys	Pro	770	775	780	
Ser	Lys	Ala	Lys	Tyr	Phe	Leu	Asp	Asp	Glu	Ala	Asp	Val	Leu	Lys	Leu	785	790	795	800

Leu Arg Gly Leu Gly Asp Ser Ser Ser Ser Leu Lys Pro Ser Ser Ser
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His Thr Gln Val Ala Phe Glu Ser Ile Val
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Val Pro Gly Ile Ile Ser Glu Leu Asp Gly Gly Tyr Ser Asp Gly Ser
 35 40 45

Ser Asp Val Asn Ser Ser Asn Ser Ser Arg Glu Arg Lys Ile Ile Val
 50 55 60

Ala Asn Met Leu Pro Leu Gln Ala Lys Arg Asp Thr Glu Thr Gly Gln
 65 70 75 80

Trp Cys Phe Ser Trp Asp Glu Asp Ser Leu Leu Leu Gln Leu Arg Asp
 85 90 95

Gly Phe Ser Ser Asp Thr Glu Phe Val Tyr Ile Gly Ser Leu Asn Ala
 100 105 110

Asp Ile Gly Ile Ser Glu Gln Glu Glu Val Ser His Lys Leu Leu Leu
 115 120 125

Asp Phe Asn Cys Val Pro Thr Phe Leu Pro Lys Glu Met Gln Glu Lys
 130 135 140

Phe Tyr Leu Gly Phe Cys Lys His His Leu Trp Pro Leu Phe His Tyr
 145 150 155 160

Met Leu Pro Met Phe Pro Asp His Gly Asp Arg Phe Asp Arg Arg Leu
 165 170 175

Trp Gln Ala Tyr Val Ser Ala Asn Lys Ile Phe Ser Asp Arg Val Met
 180 185 190

Glu Val Ile Asn Pro Glu Glu Asp Tyr Val Trp Ile His Asp Tyr His
 195 200 205

Leu Met Val Leu Pro Thr Phe Leu Arg Lys Arg Phe Asn Arg Ile Lys
 210 215 220

Leu Gly Phe Phe Leu His Ser Pro Phe Pro Ser Ser Glu Ile Tyr Arg
 225 230 235 240

Thr Leu Pro Val Arg Asp Asp Leu Leu Arg Gly Leu Leu Asn Cys Asp
 245 250 255

Leu Ile Gly Phe His Thr Phe Asp Tyr Ala Arg His Phe Leu Ser Cys
 260 265 270

Cys	Ser	Arg	Met	Leu	Gly	Leu	Asp	Tyr	Glu	Ser	Lys	Arg	Gly	His	Ile	
		275					280					285				
Gly	Leu	Asp	Tyr	Phe	Gly	Arg	Thr	Val	Phe	Ile	Lys	Ile	Leu	Pro	Val	
	290					295					300					
Gly	Ile	His	Met	Gly	Arg	Leu	Glu	Ser	Val	Leu	Asn	Leu	Pro	Ser	Thr	
305					310					315					320	
Ala	Ala	Lys	Met	Lys	Glu	Ile	Gln	Glu	Gln	Phe	Lys	Gly	Lys	Lys	Leu	
				325					330					335		
Ile	Leu	Gly	Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	Gly	Ile	Ser	Leu	Lys	
			340					345					350			
Leu	Ile	Ala	Met	Glu	Arg	Leu	Phe	Glu	Thr	Tyr	Trp	His	Met	Arg	Gly	
		355					360					365				
Lys	Leu	Val	Leu	Ile	Gln	Ile	Val	Asn	Pro	Ala	Arg	Ala	Thr	Gly	Lys	
	370					375					380					
Asp	Val	Glu	Glu	Ala	Lys	Lys	Glu	Thr	Tyr	Ser	Thr	Ala	Lys	Arg	Ile	
385					390					395					400	
Asn	Glu	Arg	Tyr	Gly	Ser	Ala	Gly	Tyr	Gln	Pro	Val	Ile	Leu	Ile	Asp	
				405					410					415		
Arg	Leu	Val	Pro	Arg	Tyr	Glu	Lys	Thr	Ala	Tyr	Tyr	Ala	Met	Ala	Asp	
			420					425					430			
Cys	Cys	Leu	Val	Asn	Ala	Val	Arg	Asp	Gly	Met	Asn	Leu	Val	Pro	Tyr	
		435					440					445				
Lys	Tyr	Ile	Ile	Cys	Arg	Gln	Gly	Thr	Pro	Gly	Met	Asp	Lys	Ala	Met	
	450					455					460					
Gly	Ile	Ser	His	Asp	Ser	Ala	Arg	Thr	Ser	Met	Leu	Val	Val	Ser	Glu	
465					470					475					480	
Phe	Ile	Gly	Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala	Ile	Arg	Val	Asn	Pro	
			485						490					495		
Trp	Asp	Val	Asp	Ala	Val	Ala	Glu	Ala	Val	Asn	Leu	Ala	Leu	Thr	Met	
			500					505					510			
Gly	Glu	Thr	Glu	Lys	Arg	Leu	Arg	His	Glu	Lys	His	Tyr	His	Tyr	Val	
		515					520					525				
Ser	Thr	His	Asp	Val	Gly	Tyr	Trp	Ala	Lys	Ser	Phe	Met	Gln	Asp	Leu	
	530					535					540					
Glu	Arg	Ala	Cys	Arg	Glu	His	Tyr	Asn	Lys	Arg	Cys	Trp	Gly	Ile	Gly	
545					550					555					560	
Phe	Gly	Leu	Ser	Phe	Arg	Val	Leu	Ser	Leu	Ser	Pro	Ser	Phe	Arg	Lys	
				565					570					575		
Leu	Ser	Ile	Asp	His	Ile	Val	Ser	Thr	Tyr	Arg	Asn	Thr	Gln	Arg	Arg	
			580					585					590			
Ala	Ile	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Val	Pro	Glu	Ser	Ser	Ile	
		595					600					605				

Ile Lys Thr Pro Asn Ala Glu Val Leu Ser Val Leu Lys Ser Leu Cys
 610 615 620
 Gly Asp Pro Lys Asn Thr Val Phe Val Val Ser Gly Arg Gly Trp Glu
 625 630 635 640
 Ser Leu Ser Asp Trp Leu Ser Pro Cys Glu Asn Leu Gly Ile Ala Ala
 645 650 655
 Glu His Gly Tyr Phe Ile Arg Trp Ser Ser Lys Lys Glu Trp Glu Thr
 660 665 670
 Cys Tyr Ser Ser Ala Glu Ala Glu Trp Lys Thr Met Val Glu Pro Val
 675 680 685
 Met Arg Ser Tyr Met Asp Ala Thr Asp Gly Ser Thr Ile Glu Tyr Lys
 690 695 700
 Glu Ser Ala Leu Val Trp His His Gln Asp Ala Asp Pro Asp Phe Gly
 705 710 715 720
 Ala Cys Gln Ala Lys Glu Leu Leu Asp His Leu Glu Ser Val Leu Ala
 725 730 735
 Asn Glu Pro Val Val Val Lys Arg Gly Gln His Ile Val Glu Val Lys
 740 745 750
 Pro Gln Gly Val Ser Lys Gly Leu Ala Val Glu Lys Val Ile His Gln
 755 760 765
 Met Val Glu Asp Gly Asn Pro Pro Asp Met Val Met Cys Ile Gly Asp
 770 775 780
 Asp Arg Ser Asp Glu Asp Met Phe Glu Ser Ile Leu Ser Thr Val Thr
 785 790 795 800
 Asn Pro Asp Leu Pro Met Pro Pro Glu Ile Phe Ala Cys Thr Val Gly
 805 810 815
 Arg Lys Pro Ser Lys Ala Lys Tyr Phe Leu Asp Asp Val Ser Asp Val
 820 825 830
 Leu Lys Leu Leu Gly Gly Leu Ala Ala Ala Thr Ser Ser Ser Lys Pro
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 Glu Tyr Gln Gln Gln Ser Ser Ser Leu His Thr Gln Val Ala Phe Glu
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 Ser Ile Ile
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Val	Pro	Gly	Ile	Ile	Ser	Asp	Val	Asp	Gly	Tyr	Gly	Ile	Ser	Asp	Gly	35	40	45	
Asp	Ser	Asp	Val	Ile	Ser	Leu	Pro	Cys	Arg	Glu	Arg	Lys	Ile	Ile	Val	50	55	60	
Ala	Asn	Phe	Leu	Pro	Leu	Asn	Gly	Lys	Lys	Asp	Ser	Glu	Thr	Gly	Lys	65	70	75	80
Trp	Lys	Phe	Ser	Leu	Asp	Asn	Asp	Ser	Pro	Leu	Leu	His	Leu	Lys	Asp	85	90	95	
Gly	Phe	Ser	Pro	Glu	Thr	Glu	Val	Ile	Tyr	Val	Gly	Ser	Leu	Lys	Thr	100	105	110	
His	Val	Asp	Val	Ser	Glu	Gln	Asp	Glu	Val	Ser	His	Asn	Leu	Phe	Glu	115	120	125	
Glu	Phe	Asn	Cys	Val	Ala	Thr	Phe	Leu	Pro	Gln	Asp	Val	His	Lys	Lys	130	135	140	
Phe	Tyr	Leu	Gly	Phe	Cys	Lys	Gln	Gln	Leu	Trp	Pro	Leu	Phe	His	Tyr	145	150	155	160
Met	Leu	Pro	Met	Cys	Pro	Asp	His	Gly	Glu	Arg	Phe	Asp	Arg	Gly	Leu	165	170	175	
Trp	Gln	Ala	Tyr	Val	Ser	Ala	Asn	Lys	Ile	Phe	Ala	Asp	Lys	Val	Met	180	185	190	
Gly	Val	Ile	Asn	Leu	Glu	Glu	Asp	Tyr	Ile	Trp	Ile	His	Asp	Tyr	His	195	200	205	
Leu	Met	Val	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Arg	Phe	His	Arg	Val	Lys	210	215	220	
Leu	Gly	Phe	Phe	Leu	His	Ser	Pro	Phe	Pro	Ser	Ser	Glu	Ile	Tyr	Arg	225	230	235	240
Thr	Leu	Pro	Val	Arg	Glu	Glu	Leu	Leu	Arg	Gly	Leu	Leu	Asn	Cys	Asp	245	250	255	
Leu	Ile	Gly	Phe	His	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	Leu	Ser	Cys	260	265	270	
Cys	Cys	Arg	Met	Leu	Gly	Leu	Glu	Tyr	Glu	Ser	Lys	Arg	Gly	His	Ile	275	280	285	
Ala	Leu	Asp	Tyr	Leu	Gly	Arg	Thr	Val	Phe	Leu	Lys	Ile	Leu	Pro	Ile	290	295	300	
Gly	Ile	His	Met	Gly	Arg	Leu	Glu	Ser	Val	Leu	Asn	Leu	Pro	Ala	Thr	305	310	315	320
Ala	Glu	Lys	Leu	Lys	Glu	Ile	Gln	Glu	Lys	Tyr	Arg	Gly	Lys	Lys	Ile	325	330	335	
Ile	Leu	Gly	Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	Gly	Leu	Ser	Leu	Lys	340	345	350	
Ile	Leu	Ala	Phe	Glu	His	Leu	Leu	Gln	Gln	Tyr	Pro	Ser	Met	Leu	Gly	355	360	365	

Lys Ile Val Leu Ile Gln Ile Val Asn Pro Ala Arg Gly Ser Gly Lys
 370 375 380
 Asp Val Gln Glu Ala Arg Lys Glu Thr Tyr Asp Thr Val Lys Arg Ile
 385 390 395 400
 Asn Glu Arg Tyr Gly Ser His Asp Tyr Glu Pro Val Val Leu Ile Asp
 405 410 415
 Arg Pro Val Pro Arg Phe Glu Lys Ser Ala Tyr Tyr Ala Leu Ala Glu
 420 425 430
 Cys Cys Ile Val Asn Ala Val Arg Asp Gly Met Asn Leu Val Pro Tyr
 435 440 445
 Lys Tyr Thr Val Cys Arg Gln Gly Thr Pro Ser Met Asn Lys Ser Leu
 450 455 460
 Gly Val Ser Asp Asp Leu Pro Arg Thr Ser Thr Leu Val Leu Ser Glu
 465 470 475 480
 Phe Ile Gly Cys Ser Pro Ser Leu Ser Gly Ala Ile Arg Val Asn Pro
 485 490 495
 Trp Asp Val Asp Ala Val Ala Asp Ser Leu Tyr Ser Ala Ile Thr Met
 500 505 510
 Ser Asp Phe Glu Lys Gln Leu Arg His Lys Lys His Phe His Tyr Ile
 515 520 525
 Ser Thr His Asp Val Gly Tyr Trp Ala Arg Ser Phe Ser Gln Asp Leu
 530 535 540
 Glu Arg Ala Ser Arg Asp His Tyr Ser Lys Arg Cys Trp Gly Val Gly
 545 550 555 560
 Trp Gly Leu Gly Phe Arg Leu Val Ala Leu Ser Pro Asn Phe Arg Arg
 565 570 575
 Leu Ser Ile Glu Gln Thr Val Ser Ala Tyr Arg Arg Ser Ser Lys Arg
 580 585 590
 Ala Ile Phe Leu Asp Tyr Asp Gly Thr Leu Val Pro Glu Thr Ser Ile
 595 600 605
 Val Lys Asp Pro Ser Ala Glu Val Ile Ser Ala Leu Lys Ala Leu Cys
 610 615 620
 Ser Asp Pro Asn Asn Thr Ile Phe Ile Val Ser Gly Arg Gly Lys Val
 625 630 635 640
 Ser Leu Ser Glu Trp Leu Ala Pro Cys Glu Asn Leu Gly Ile Ala Ala
 645 650 655
 Glu His Gly Tyr Phe Thr Arg Trp Asn Lys Ser Ser Asp Trp Glu Thr
 660 665 670
 Ser Gly Leu Ser Asp Asp Leu Glu Trp Lys Lys Val Val Glu Pro Ile
 675 680 685
 Met Arg Leu Tyr Thr Glu Thr Thr Asp Gly Ser Asn Ile Glu Ala Lys
 690 695 700

Glu Ser Ala Leu Val Trp His His Gln Asp Ala Asp Pro Asp Phe Gly
 705 710 715 720
 Ser Cys Gln Ala Lys Glu Leu Leu Asp His Leu Glu Thr Val Leu Val
 725 730 735
 Asn Glu Pro Val Ile Val Asn Arg Gly His Gln Ile Val Glu Val Lys
 740 745 750
 Pro Gln Gly Val Ser Lys Gly Leu Val Thr Gly Lys Ile Leu Ser Arg
 755 760 765
 Met Leu Glu Asp Gly Ile Ala Pro Asp Phe Val Val Cys Ile Gly Asp
 770 775 780
 Asp Arg Ser Asp Glu Glu Met Phe Glu Asn Ile Ser Thr Thr Leu Ser
 785 790 795 800
 Ala Gln Ser Ser Ser Met Ser Thr Glu Ile Phe Ala Cys Thr Val Gly
 805 810 815
 Arg Lys Pro Ser Lys Ala Lys Tyr Phe Leu Asp Glu Val Ser Asp Val
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 Leu Ser Gly Leu Glu Thr Asp Asp Pro Asn Gly Gly Ala Trp Val Thr
 35 40 45
 Lys Pro Lys Arg Ile Val Val Ser Asn Gln Leu Pro Leu Arg Ala His
 50 55 60
 Arg Asp Ile Ser Ser Asn Lys Trp Cys Phe Glu Phe Asp Asn Asp Ser
 65 70 75 80
 Leu Tyr Leu Gln Leu Lys Asp Gly Phe Pro Pro Glu Thr Glu Val Val
 85 90 95
 Tyr Val Gly Ser Leu Asn Ala Asp Val Leu Pro Ser Glu Gln Glu Asp
 100 105 110
 Val Ser Gln Phe Leu Leu Glu Lys Phe Gln Cys Val Pro Thr Phe Leu
 115 120 125
 Pro Ser Asp Leu Leu Asn Lys Tyr Tyr His Gly Phe Cys Lys His Tyr
 130 135 140

Leu	Trp	Pro	Ile	Phe	His	Tyr	Leu	Leu	Pro	Met	Thr	Gln	Ala	Gln	Gly
145					150					155					160
Ser	Leu	Phe	Asp	Arg	Ser	Asn	Trp	Arg	Ala	Tyr	Thr	Thr	Val	Asn	Lys
				165					170					175	
Ile	Phe	Ala	Asp	Lys	Ile	Phe	Glu	Val	Leu	Asn	Pro	Asp	Asp	Asp	Tyr
			180					185					190		
Val	Trp	Ile	His	Asp	Tyr	His	Leu	Met	Ile	Leu	Pro	Thr	Phe	Leu	Arg
		195					200					205			
Asn	Arg	Phe	His	Arg	Ile	Lys	Leu	Gly	Ile	Phe	Leu	His	Ser	Pro	Phe
	210					215					220				
Pro	Ser	Ser	Glu	Ile	Tyr	Arg	Thr	Leu	Pro	Val	Arg	Asp	Glu	Ile	Leu
225					230					235					240
Lys	Gly	Phe	Leu	Asn	Cys	Asp	Leu	Val	Gly	Phe	His	Thr	Phe	Asp	Tyr
				245					250					255	
Ala	Arg	His	Phe	Leu	Ser	Cys	Cys	Ser	Arg	Met	Leu	Gly	Leu	Asp	Tyr
			260					265					270		
Glu	Ser	Lys	Arg	Gly	Tyr	Ile	Gly	Leu	Glu	Tyr	Phe	Gly	Arg	Thr	Val
		275					280					285			
Ser	Ile	Lys	Ile	Leu	Pro	Val	Gly	Ile	His	Met	Gly	Gln	Ile	Glu	Ser
	290					295					300				
Ile	Lys	Ala	Ser	Glu	Lys	Thr	Ala	Glu	Lys	Val	Lys	Arg	Leu	Arg	Glu
305					310					315					320
Arg	Phe	Lys	Gly	Asn	Ile	Val	Met	Leu	Gly	Val	Asp	Asp	Leu	Asp	Met
				325					330					335	
Phe	Lys	Gly	Ile	Ser	Leu	Lys	Phe	Trp	Ala	Met	Gly	Gln	Leu	Leu	Glu
			340					345					350		
Gln	Asn	Glu	Glu	Leu	Arg	Gly	Lys	Val	Val	Leu	Val	Gln	Ile	Thr	Asn
		355					360					365			
Pro	Ala	Arg	Ser	Ser	Gly	Lys	Asp	Val	Gln	Asp	Val	Glu	Lys	Gln	Ile
	370					375					380				
Asn	Leu	Ile	Ala	Asp	Glu	Ile	Asn	Ser	Lys	Phe	Gly	Arg	Pro	Gly	Gly
385					390					395					400
Tyr	Lys	Pro	Ile	Val	Phe	Ile	Asn	Gly	Pro	Val	Ser	Thr	Leu	Asp	Lys
				405					410					415	
Val	Ala	Tyr	Tyr	Ala	Ile	Ser	Glu	Cys	Val	Val	Val	Asn	Ala	Val	Arg
			420					425					430		
Asp	Gly	Met	Asn	Leu	Val	Pro	Tyr	Lys	Tyr	Thr	Val	Thr	Arg	Gln	Gly
		435					440					445			
Ser	Pro	Ala	Leu	Asp	Ala	Ala	Leu	Gly	Phe	Gly	Glu	Asp	Asp	Val	Arg
	450					455					460				
Lys	Ser	Val	Ile	Ile	Val	Ser	Glu	Phe	Ile	Gly	Cys	Ser	Pro	Ser	Leu
465					470					475					480

Ser Gly Ala Ile Arg Val Asn Pro Trp Asn Ile Asp Ala Val Thr Asn
 485 490 495
 Ala Met Ser Ser Ala Met Thr Met Ser Asp Lys Glu Lys Asn Leu Arg
 500 505 510
 His Gln Lys His His Lys Tyr Ile Ser Ser His Asn Val Ala Tyr Trp
 515 520 525
 Ala Arg Ser Tyr Asp Gln Asp Leu Gln Arg Ala Cys Lys Asp His Tyr
 530 535 540
 Asn Lys Arg Phe Trp Gly Val Gly Phe Gly Leu Phe Phe Lys Val Val
 545 550 555 560
 Ala Leu Asp Pro Asn Phe Arg Arg Leu Cys Gly Glu Thr Ile Val Pro
 565 570 575
 Ala Tyr Arg Arg Ser Ser Ser Arg Leu Ile Leu Leu Asp Tyr Asp Gly
 580 585 590
 Thr Met Met Asp Gln Asp Thr Leu Asp Lys Arg Pro Ser Asp Asp Leu
 595 600 605
 Ile Ser Leu Leu Asn Arg Leu Cys Asp Asp Pro Ser Asn Leu Val Phe
 610 615 620
 Ile Val Ser Gly Arg Gly Lys Asp Pro Leu Ser Lys Trp Phe Asp Ser
 625 630 635 640
 Cys Pro Asn Leu Gly Ile Ser Ala Glu His Gly Tyr Phe Thr Arg Trp
 645 650 655
 Asn Ser Asn Ser Pro Trp Glu Thr Ser Glu Leu Pro Ala Asp Leu Ser
 660 665 670
 Trp Lys Lys Ile Ala Lys Pro Val Met Asn His Tyr Met Glu Ala Thr
 675 680 685
 Asp Gly Ser Phe Ile Glu Glu Lys Glu Ser Ala Met Val Trp His His
 690 695 700
 Gln Glu Ala Asp His Ser Phe Gly Ser Trp Gln Ala Lys Glu Leu Leu
 705 710 715 720
 Asp His Leu Glu Ser Val Leu Thr Asn Glu Pro Val Val Val Lys Arg
 725 730 735
 Gly Gln His Ile Val Glu Val Lys Pro Gln Gly Val Ser Lys Gly Lys
 740 745 750
 Val Val Glu His Leu Ile Ala Thr Met Arg Asn Thr Lys Gly Lys Arg
 755 760 765
 Pro Asp Phe Leu Leu Cys Ile Gly Asp Asp Arg Ser Asp Glu Asp Met
 770 775 780
 Phe Asp Ser Ile Val Lys His Gln Asp Val Ser Ser Ile Gly Leu Glu
 785 790 795 800
 Glu Val Phe Ala Cys Thr Val Gly Gln Lys Pro Ser Lys Ala Lys Tyr
 805 810 815

Tyr Leu Asp Asp Thr Pro Ser Val Ile Lys Met Leu Glu Trp Leu Ala
 820 825 830
 Ser Ala Ser Asp Gly Ser Lys His Glu Gln Gln Lys Lys Gln Ser Lys
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 Phe Thr Phe Gln Gln Pro Met Gly Gln Cys Arg Lys Lys Ala
 850 855 860

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 Ser Pro Gly Ile Ile Ser Asp Pro Asp Trp Asp Thr Arg Ser Asp Gly
 35 40 45
 Asp Ser Val Gly Ser Ala Ser Ser Val Glu Arg Lys Ile Ile Val Ala
 50 55 60
 Asn Phe Leu Pro Leu Asn Cys Thr Lys Asp Glu Ala Gly Gln Trp Ser
 65 70 75 80
 Phe Ser Arg Asp Asp Asp Ala Leu Leu Met Gln Leu Lys Asp Gly Phe
 85 90 95
 Ser Asn Glu Thr Asp Val Ile Tyr Val Gly Ser Leu Lys Val Gln Val
 100 105 110
 Asp Pro Ser Glu Gln Asp Gln Val Ala Gln Lys Leu Leu Arg Asp Tyr
 115 120 125
 Arg Cys Ile Pro Thr Phe Leu Pro Pro Asp Leu Gln Gln Gln Phe Tyr
 130 135 140
 His Gly Phe Cys Lys Gln Gln Leu Trp Pro Leu Phe His Tyr Met Leu
 145 150 155 160
 Pro Ile Cys Leu Asp Lys Gly Glu Leu Phe Asp Arg Ser Leu Phe Gln
 165 170 175
 Ala Tyr Val Arg Ala Asn Lys Leu Phe Ala Asp Lys Val Met Glu Ala
 180 185 190
 Ile Asn Thr Asp Asp Asp His Val Trp Val His Asp Tyr His Leu Met
 195 200 205
 Leu Leu Pro Thr Phe Leu Arg Lys Arg Leu His Arg Ile Lys Leu Gly
 210 215 220
 Phe Phe Leu His Ser Pro Phe Pro Ser Ser Glu Ile Tyr Arg Ser Leu
 225 230 235 240
 Pro Val Arg Asp Glu Ile Leu Lys Ser Leu Leu Asn Ala Asp Leu Ile
 245 250 255

Gly	Phe	Gln	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	Leu	Ser	Cys	Cys	Ser	260	265	270	
Arg	Leu	Leu	Gly	Leu	His	Tyr	Glu	Ser	Lys	Arg	Gly	Tyr	Ile	Gly	Ile	275	280	285	
Asp	Tyr	Phe	Gly	Arg	Thr	Val	Ser	Leu	Lys	Ile	Leu	Ser	Val	Gly	Val	290	295	300	
His	Val	Gly	Arg	Leu	Glu	Ser	Ile	Leu	Lys	Leu	Pro	Ala	Thr	Val	Lys	305	310	315	320
Lys	Val	Gln	Glu	Ile	Glu	Gln	Arg	Tyr	Lys	Gly	Lys	Met	Leu	Met	Leu	325	330	335	
Gly	Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	Gly	Ile	Ser	Leu	Lys	Leu	Leu	340	345	350	
Gly	Leu	Glu	Leu	Leu	Leu	Asp	Arg	Asn	Pro	Lys	Leu	Arg	Gly	Lys	Val	355	360	365	
Val	Leu	Val	Gln	Ile	Val	Asn	Pro	Ala	Arg	Ser	Thr	Gly	Lys	Asp	Val	370	375	380	
Glu	Glu	Ala	Ile	Thr	Glu	Ser	Val	Ser	Val	Ala	Glu	Arg	Ile	Asn	Leu	385	390	395	400
Lys	Tyr	Gly	Ser	Val	Asp	Tyr	Lys	Pro	Val	Val	Leu	Ile	Asp	His	Arg	405	410	415	
Ile	Pro	Phe	Tyr	Glu	Lys	Ile	Ala	Phe	Tyr	Ala	Ala	Ser	Asp	Cys	Cys	420	425	430	
Ile	Val	Asn	Ala	Leu	Arg	Asp	Gly	Met	Asn	Leu	Val	Pro	Tyr	Glu	Tyr	435	440	445	
Thr	Val	Cys	Arg	Gln	Gly	Asn	Glu	Glu	Ile	Asp	Asn	Ala	Arg	Gly	Ser	450	455	460	
Asp	Thr	Asn	Cys	His	His	Thr	Ser	Thr	Leu	Ile	Val	Ser	Glu	Phe	Val	465	470	475	480
Gly	Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala	Phe	Arg	Val	Asn	Pro	Trp	Ser	485	490	495	
Val	Asp	Asp	Val	Ala	Asp	Ala	Leu	His	His	Ala	Thr	Asp	Leu	Thr	Glu	500	505	510	
Ser	Glu	Lys	Arg	Leu	Arg	His	Glu	Lys	His	Tyr	Arg	Tyr	Val	Arg	Ser	515	520	525	
His	Ser	Val	Ala	Tyr	Trp	Ala	His	Ser	Phe	Ala	Gln	Asp	Leu	Glu	Arg	530	535	540	
Ala	Cys	Lys	Asp	His	Tyr	Ser	Arg	Arg	Cys	Trp	Ala	Ile	Gly	Phe	Gly	545	550	555	560
Leu	Asn	Phe	Arg	Val	Ile	Ala	Leu	Ser	Pro	Gly	Phe	Arg	Lys	Leu	Ser	565	570	575	
Leu	Glu	His	Phe	Ala	Ser	Ser	Tyr	Asn	Lys	Ala	Thr	Arg	Arg	Ala	Ile	580	585	590	

Phe Leu Asp Tyr Asp Gly Thr Leu Val Pro Gln Ser Ser Ile Asn Lys
 595 600 605
 Ala Pro Ser Asp Glu Leu Ile Thr Ile Leu Asn Ser Leu Cys Asp Asp
 610 615 620
 Pro Lys Asn Asp Val Phe Ile Val Ser Gly Arg Ala Arg Ser Leu Leu
 625 630 635 640
 Asp Glu Trp Phe Ala Pro Cys Gln Lys Leu Gly Ile Ala Ala Glu His
 645 650 655
 Gly Tyr Phe Val Arg Trp Asn Lys Ala Ala Glu Trp Glu Ser Ser Tyr
 660 665 670
 Pro Asn His Asp Phe Glu Trp Lys His Ile Ala Glu Pro Val Met Gln
 675 680 685
 Val Tyr Thr Glu Thr Thr Asp Gly Ser Ser Ile Glu Pro Lys Glu Ser
 690 695 700
 Ala Leu Val Trp His Tyr Leu Asp Ala Asp His Asp Phe Gly Ser Cys
 705 710 715 720
 Gln Ala Lys Glu Leu Leu Gly His Leu Glu Arg Val Leu Ser Asn Glu
 725 730 735
 Pro Val Val Val Lys Cys Gly His Tyr Ile Val Glu Val Lys Pro Gln
 740 745 750
 Gly Val Ser Lys Gly Leu Val Val Asp Lys Val Ile His Arg Leu Met
 755 760 765
 Asn Asn Gly Lys Thr Pro Asp Phe Val Val Cys Ile Gly Asn Asp Arg
 770 775 780
 Ser Asp Glu Asp Met Phe Lys Ser Ile Asp Ser Met Thr Ser Ser Ser
 785 790 795 800
 Ala Phe Pro Ala Val Pro Glu Val Phe Ala Cys Ser Val Gly Gln Lys
 805 810 815
 Pro Ser Lys Ala Lys Tyr Tyr Val Asp Asp Ala Gly Glu Val Val Arg
 820 825 830
 Leu Leu Lys Asn Val Ala Gly Ile Ser Ser His Arg Glu Ala Val Ser
 835 840 845
 His Gly Arg Val Thr Phe Arg Asp Val Met Asp Tyr Val Glu
 850 855 860

<210> 9

<211> 862

<212> PRT

<213> *Populus balsamifera* subsp. *trichocarpa*

<400> 9

Met Val Ser Arg Ser Tyr Ser Asn Leu Leu Asp Leu Ala Ser Gly Asp
 1 5 10 15

Ala Pro Ile Pro Ser Phe Gly Arg Glu Arg Lys Arg Phe Pro Arg Val
 20 25 30

Ala	Thr	Val	Ala	Gly	Ile	Leu	Thr	Asp	Leu	Asp	Asp	Glu	Asn	Asn	Val
		35					40					45			
Gly	Ser	Asp	Ser	Pro	Ser	Ser	Val	Ser	Leu	Gly	Arg	Met	Ile	Ile	Val
	50					55					60				
Gly	Asn	Gln	Leu	Pro	Leu	Arg	Ala	His	Arg	Ser	Pro	Asp	Ser	Ser	Gly
65					70					75					80
Gly	Trp	Cys	Phe	Ser	Trp	Asp	Glu	Asp	Ser	Leu	Leu	Leu	Gln	Leu	Lys
				85					90					95	
Asp	Gly	Leu	Gly	Glu	Gly	Val	Glu	Val	Ile	Tyr	Val	Gly	Ser	Leu	Lys
			100					105					110		
Glu	Glu	Ile	Glu	Pro	Ser	Glu	Gln	Asp	Asp	Val	Ala	Gln	Thr	Leu	Leu
		115					120					125			
Glu	Thr	Phe	Lys	Cys	Val	Pro	Ala	Phe	Ile	Pro	Pro	Asp	Leu	Phe	Thr
	130					135					140				
Lys	Phe	Tyr	His	Gly	Phe	Cys	Lys	Gln	His	Leu	Trp	Pro	Leu	Phe	His
145					150					155					160
Tyr	Met	Leu	Pro	Leu	Ser	Pro	Asp	Leu	Gly	Gly	Arg	Phe	Asp	Arg	Ser
				165					170					175	
Leu	Trp	Gln	Ala	Tyr	Val	Ser	Val	Asn	Lys	Ile	Phe	Ala	Asp	Lys	Val
			180					185					190		
Lys	Glu	Val	Ile	Ser	Pro	Glu	Asp	Asp	Tyr	Val	Trp	Val	His	Asp	Tyr
	195						200					205			
His	Leu	Met	Val	Leu	Pro	Thr	Phe	Leu	Arg	Lys	Ile	Phe	Asn	Arg	Val
	210					215					220				
Lys	Leu	Gly	Phe	Phe	Leu	His	Ser	Pro	Phe	Pro	Ser	Ser	Glu	Ile	Tyr
225					230				235						240
Arg	Thr	Leu	Pro	Val	Arg	Asp	Glu	Leu	Leu	Arg	Ala	Leu	Leu	Asn	Ser
				245				250						255	
Asp	Leu	Ile	Gly	Phe	His	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	Leu	Ser
			260					265					270		
Cys	Cys	Ser	Arg	Met	Leu	Gly	Leu	Ser	Tyr	Gln	Ser	Lys	Arg	Gly	Tyr
		275					280					285			
Ile	Gly	Leu	Glu	Tyr	Phe	Gly	Arg	Thr	Val	Ser	Ile	Lys	Ile	Leu	Pro
	290					295					300				
Val	Gly	Ile	His	Ile	Gly	Gln	Leu	Gln	Ser	Val	Leu	Asn	Leu	Pro	Glu
305					310					315					320
Thr	Glu	Ser	Lys	Val	Ala	Glu	Leu	His	Asp	Gln	Phe	Arg	Gly	Gln	Ala
				325					330					335	
Val	Met	Leu	Gly	Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	Gly	Ile	Ser	Leu
			340					345					350		
Lys	Leu	Leu	Ala	Met	Glu	Glu	Leu	Leu	Thr	Gln	His	Pro	Asn	Lys	Arg
			355				360					365			

Gly	Glu	Val	Val	Leu	Val	Gln	Ile	Ala	Asn	Pro	Ala	Arg	Gly	Arg	Gly			
370						375					380							
Arg	Glu	Val	Gln	Glu	Val	Gln	Ser	Glu	Thr	Lys	Ala	Ala	Val	Arg	Arg			
385					390					395					400			
Ile	Asn	Glu	Ala	Phe	Gly	Ser	Pro	Gly	Tyr	Thr	Pro	Val	Val	Leu	Ile			
				405					410					415				
Asp	Arg	Pro	Leu	Gln	Phe	Tyr	Glu	Arg	Ile	Ala	Tyr	Tyr	Ala	Ile	Ala			
			420					425					430					
Glu	Cys	Cys	Leu	Val	Thr	Ala	Val	Arg	Asp	Gly	Met	Asn	Leu	Ile	Pro			
		435					440					445						
Tyr	Glu	Tyr	Ile	Ile	Cys	Arg	Gln	Gly	Asn	Glu	Lys	Leu	Asp	Glu	Thr			
450					455						460							
Leu	Gly	Arg	Asp	Pro	Ser	Ala	Pro	Arg	Lys	Ser	Met	Leu	Val	Leu	Ser			
465					470					475					480			
Glu	Phe	Ile	Gly	Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala	Ile	Arg	Val	Asn			
				485					490					495				
Pro	Trp	Asn	Ile	Asp	Ala	Val	Ala	Glu	Ala	Met	Asn	Ser	Ala	Leu	Val			
			500					505					510					
Val	Pro	Glu	Pro	Glu	Lys	Gln	Met	Arg	His	Glu	Lys	His	His	Arg	Tyr			
		515					520					525						
Val	Ser	Thr	His	Asp	Val	Ala	Tyr	Trp	Ala	Arg	Ser	Phe	Leu	Gln	Asp			
	530					535					540							
Leu	Glu	Arg	Ala	Cys	Arg	Asp	His	Val	Lys	Arg	Arg	Cys	Trp	Gly	Phe			
545					550					555					560			
Gly	Phe	Gly	Leu	Gly	Phe	Arg	Val	Ile	Ala	Leu	Asp	Pro	Asn	Phe	Arg			
				565					570					575				
Lys	Ile	Ser	Val	Glu	His	Ile	Val	Ser	Ala	Tyr	Lys	Arg	Thr	Lys	Asn			
			580					585					590					
Arg	Val	Ile	Leu	Leu	Asp	Tyr	Asp	Gly	Thr	Met	Thr	Leu	Pro	Ser	Ser			
		595					600					605						
Thr	Arg	Thr	Pro	Asn	Met	Glu	Thr	Val	Gly	Val	Leu	Asn	Ser	Leu	Cys			
	610					615					620							
Thr	Asp	Pro	Lys	Asn	Val	Val	Phe	Leu	Val	Ser	Gly	Arg	Asp	Arg	Glu			
625					630					635					640			
Thr	Leu	Thr	Glu	Trp	Phe	Ser	Ser	Cys	Glu	Lys	Leu	Gly	Ile	Ala	Ala			
				645					650					655				
Glu	His	Gly	Tyr	Phe	Val	Arg	Thr	Asn	His	Asp	Ala	Glu	Trp	Glu	Thr			
			660					665					670					
Cys	Val	Ser	Val	Pro	Asp	Phe	Asp	Trp	Lys	Arg	Ile	Ala	Glu	Pro	Val			
		675					680					685						
Met	Lys	Leu	Tyr	Thr	Glu	Thr	Thr	Asp	Gly	Ser	Ala	Ile	Glu	Thr	Lys			
690						695					700							

Glu Ser Ser Leu Ala Trp Asn Tyr Gln Tyr Ala Asp Pro Asp Phe Gly
 705 710 715 720
 Ser Cys Gln Ala Lys Glu Leu Leu Asp His Leu Glu Ser Val Leu Val
 725 730 735
 Asn Glu Pro Val Thr Val Lys Ser Gly Gln His Thr Val Glu Val Lys
 740 745 750
 Pro Gln Gly Val Arg Lys Gly Leu Val Ala Glu Arg Leu Leu Asp Thr
 755 760 765
 Met Lys Leu Lys Gly Lys Leu Pro Asp Phe Val Leu Cys Val Gly Asp
 770 775 780
 Asp Gln Ser Asp Glu Asp Met Phe Glu Val Ile Leu Ser Ala Arg Ser
 785 790 795 800
 Gly Pro Ser Leu Ser Pro Val Ala Glu Val Phe Ala Cys Thr Val Gly
 805 810 815
 Arg Lys Pro Ser Lys Ala Lys Tyr Tyr Leu Glu Asp Thr Ser Glu Ile
 820 825 830
 Leu Arg Met Leu Gln Gly Leu Ala Ser Ala Leu Glu Gln Asp Ala Arg
 835 840 845
 Ser Ala Pro Gln Ser Ser Gln Gln Val Ile Ile Asp Arg Glu
 850 855 860

<210> 10
 <211> 854
 <212> PRT
 <213> *Populus balsamifera* subsp. *trichocarpa*

<400> 10
 Met Val Ser Arg Ser Tyr Ser Asn Leu Leu Glu Leu Ala Ser Gly Glu
 1 5 10 15
 Ser Pro Ser Phe Gly Arg Met Ser Arg Arg Ile Pro Arg Ile Met Thr
 20 25 30
 Val Ala Gly Ile Met Ser Asp Ile Asp Asp Asp Pro Ser Glu Ser Val
 35 40 45
 Cys Ser Asp Pro Ser Ser Ser Ser Thr Pro Lys Asp Arg Ile Ile Ile
 50 55 60
 Val Ala Asn Gln Leu Pro Ile Arg Ala Gln Arg Lys Ser Asp Gly Ser
 65 70 75 80
 Lys Ser Trp Ile Phe Ser Trp Asp Glu Asn Ser Leu Leu Leu Gln Leu
 85 90 95
 Lys Asp Gly Leu Gly Asp Asp Glu Ile Glu Val Ile Tyr Val Gly Cys
 100 105 110
 Leu Lys Glu Glu Val His Pro Asn Glu Gln Asp Glu Val Ser Gln Ile
 115 120 125
 Leu Leu Glu Thr Phe Lys Cys Val Pro Thr Phe Leu Pro Pro Asp Leu
 130 135 140

Phe	Ser	Arg	Tyr	Tyr	His	Gly	Phe	Cys	Lys	Gln	Gln	Leu	Trp	Pro	Leu	145	150	155	160
Phe	His	Tyr	Met	Leu	Pro	Leu	Ser	Pro	Asp	Leu	Gly	Gly	Arg	Phe	Asn	165	170		175
Arg	Ser	Leu	Trp	Gln	Ala	Tyr	Val	Ser	Val	Asn	Lys	Ile	Phe	Ala	Asp	180	185		190
Arg	Ile	Met	Glu	Val	Ile	Asn	Pro	Glu	Asp	Asp	Phe	Val	Trp	Val	His	195	200		205
Asp	Tyr	His	Leu	Met	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Lys	Arg	Phe	Asn	210	215		220
Lys	Val	Lys	Leu	Gly	Phe	Phe	Leu	His	Ser	Pro	Phe	Pro	Ser	Ser	Glu	225	230	235	240
Ile	Tyr	Lys	Thr	Leu	Pro	Ile	Arg	Glu	Glu	Leu	Leu	Arg	Ala	Leu	Leu	245	250		255
Asn	Ser	Asp	Leu	Ile	Gly	Phe	His	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	260	265		270
Leu	Ser	Cys	Cys	Ser	Arg	Met	Leu	Gly	Leu	Ser	Tyr	Glu	Ser	Lys	Arg	275	280		285
Gly	Tyr	Ile	Gly	Ile	Glu	Tyr	Cys	Gly	Arg	Thr	Val	Ser	Ile	Lys	Ile	290	295	300	
Leu	Pro	Val	Gly	Ile	His	Met	Gly	Gln	Leu	Gln	Ser	Val	Leu	Ser	Leu	305	310	315	320
Pro	Glu	Thr	Glu	Ala	Lys	Val	Lys	Glu	Leu	Ile	Lys	Gln	Phe	Ser	Asp	325	330		335
Gln	Asp	Arg	Ile	Met	Leu	Leu	Gly	Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	340	345		350
Gly	Ile	Ser	Leu	Lys	Leu	Leu	Ala	Met	Glu	Gln	Leu	Leu	Met	Gln	His	355	360		365
Pro	Glu	Trp	Gln	Gly	Lys	Ile	Val	Leu	Val	Gln	Ile	Ala	Asn	Pro	Ala	370	375		380
Arg	Gly	Lys	Gly	Lys	Asp	Val	Lys	Glu	Val	Gln	Ala	Glu	Thr	His	Ala	385	390	395	400
Ala	Val	Lys	Arg	Ile	Asn	Glu	Thr	Phe	Gly	Lys	Pro	Gly	Tyr	Asp	Pro	405	410		415
Ile	Val	Leu	Ile	Asp	Ala	Pro	Leu	Lys	Phe	Tyr	Glu	Lys	Val	Ala	Tyr	420	425		430
Tyr	Val	Val	Ala	Glu	Cys	Cys	Leu	Val	Thr	Ala	Val	Arg	Asp	Gly	Met	435	440		445
Asn	Leu	Ile	Pro	Tyr	Glu	Tyr	Ile	Ile	Ser	Arg	Gln	Gly	Asn	Asp	Arg	450	455	460	
Leu	Asn	Lys	Leu	Leu	Gly	Gln	Glu	Pro	Ser	Thr	Pro	Lys	Lys	Ser	Met	465	470	475	480

Leu	Val	Ile	Ser	Glu	Phe	Ile	Gly	Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala		
				485					490					495			
Ile	Arg	Val	Asn	Pro	Trp	Asn	Ile	Asp	Ala	Val	Ala	Asp	Ala	Met	Asp		
			500					505					510				
Phe	Ala	Leu	Glu	Met	Ala	Glu	Pro	Glu	Lys	Gln	Leu	Arg	His	Glu	Lys		
		515					520					525					
His	Tyr	Arg	Tyr	Val	Ser	Thr	His	Asp	Val	Gly	Tyr	Trp	Ala	Arg	Ser		
	530					535					540						
Phe	Leu	Gln	Asp	Leu	Glu	Arg	Thr	Cys	Arg	Asp	His	Ser	Arg	Arg	Arg		
545					550					555					560		
Cys	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ser	Phe	Arg	Val	Val	Ala	Leu	Asp		
				565					570					575			
Pro	Asn	Phe	Lys	Lys	Leu	Ser	Met	Glu	Arg	Ile	Val	Ser	Ala	Tyr	Lys		
			580					585					590				
Arg	Thr	Thr	Thr	Arg	Ala	Ile	Leu	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Met		
		595					600					605					
Pro	Gln	Ala	Ser	Ile	Asp	Lys	Ser	Pro	Ser	Ser	Lys	Ser	Ile	Asp	Ile		
	610					615					620						
Ile	Asn	Asn	Leu	Cys	Arg	Asp	Lys	Asn	Asn	Met	Val	Phe	Leu	Val	Ser		
625					630					635					640		
Ala	Arg	Ser	Arg	Asn	Thr	Val	Ala	Glu	Trp	Phe	Ser	Glu	Cys	Glu	Lys		
				645					650					655			
Leu	Gly	Leu	Ala	Ala	Glu	His	Gly	Tyr	Phe	Leu	Arg	Leu	Lys	Arg	Asp		
			660					665					670				
Ala	Glu	Trp	Glu	Thr	Arg	Val	Pro	Val	Ala	Asp	Thr	Thr	Trp	Lys	Gln		
		675					680					685					
Ile	Ala	Glu	Pro	Val	Met	Gln	Leu	Tyr	Thr	Glu	Thr	Thr	Asp	Gly	Ser		
	690					695						700					
Thr	Ile	Glu	Asp	Lys	Glu	Thr	Ser	Leu	Val	Trp	Cys	Tyr	Glu	Asp	Ala		
705					710					715					720		
Asp	Pro	Asp	Phe	Gly	Ser	Cys	Gln	Ala	Lys	Glu	Leu	Leu	Asp	His	Leu		
				725					730					735			
Glu	Ser	Val	Leu	Ala	Asn	Glu	Pro	Val	Thr	Val	Lys	Ser	Gly	Gln	Asn		
			740					745					750				
Ile	Val	Glu	Val	Lys	Pro	Gln	Gly	Val	Ser	Lys	Gly	Leu	Val	Ala	Lys		
		755					760					765					
Arg	Leu	Leu	Ser	Ile	Met	Gln	Glu	Asn	Glu	Met	Ser	Pro	Asp	Phe	Val		
	770					775					780						
Leu	Cys	Ile	Gly	Asp	Asp	Arg	Ser	Asp	Glu	Asp	Met	Phe	Glu	Val	Ile		
785					790					795					800		
Thr	Thr	Ser	Met	Ala	Gly	Pro	Ser	Ile	Ala	Glu	Asn	Ala	Glu	Val	Phe		
				805					810					815			

Ala Cys Thr Val Gly Arg Lys Pro Ser Lys Ala Lys Tyr Tyr Leu Asp
820 825 830

Asp Thr Ala Glu Ile Val Arg Leu Met Gln Gly Leu Ala Ser Val Ser
835 840 845

Glu Gln Thr Val Thr Val
850

<210> 11
<211> 853
<212> PRT
<213> *Populus balsamifera* subsp. *trichocarpa*

<400> 11
Met Met Ser Arg Ser Tyr Thr Asn Leu Leu Asp Leu Ala Ser Gly Asn
1 5 10 15

Phe Pro Ala Met Gly Gln Pro Arg Glu Arg Lys Arg Leu Pro Arg Val
20 25 30

Met Thr Val Pro Gly Val Ile Ser Glu Leu Asp Asp Asp Val Ala Asn
35 40 45

Ser Val Thr Ser Asp Val Pro Ser Ser Val Val Gln Asp Arg Ile Ile
50 55 60

Ile Val Gly Asn Gln Leu Pro Val Lys Ala Lys Arg Arg Pro Asp Asn
65 70 75 80

Lys Gly Trp Ser Phe Ser Trp Asp Glu Asp Ser Leu Leu Leu Gln Leu
85 90 95

Lys Asp Gly Leu Pro Glu Glu Met Glu Val Leu Tyr Val Gly Ser Leu
100 105 110

Arg Ala Asp Ile Asp Leu Ser Glu Gln Glu Asp Val Ser Gln Ile Leu
115 120 125

Leu Asp Arg Phe Lys Cys Val Pro Ala Phe Leu Pro Pro Asp Ile Leu
130 135 140

Ser Lys Phe Tyr His Gly Phe Cys Lys Gln Tyr Leu Trp Pro Leu Phe
145 150 155 160

His Tyr Met Leu Pro Ile Ser Gly Asn His Gly Gly Arg Phe Asp Arg
165 170 175

Ser Leu Trp Glu Ala Tyr Val Ala Ala Asn Lys Ile Phe Ser Gln Arg
180 185 190

Val Ile Glu Val Ile Asn Pro Glu Asp Asp Tyr Val Trp Ile His Asp
195 200 205

Tyr His Leu Met Val Leu Pro Thr Phe Leu Arg Arg Arg Phe Asn Arg
210 215 220

Leu Arg Met Gly Phe Phe Leu His Ser Pro Phe Pro Ser Ser Glu Ile
225 230 235 240

Tyr Arg Thr Leu Pro Val Arg Glu Glu Ile Leu Lys Ala Leu Leu Asn
245 250 255

Ser Asp Leu Ile Gly Phe His Thr Phe Asp Tyr Ala Arg His Phe Leu
 260 265 270
 Ser Cys Cys Ser Arg Met Leu Gly Leu Glu Tyr Gln Ser Lys Arg Gly
 275 280 285
 Tyr Ile Gly Leu Glu Tyr Tyr Gly Arg Thr Val Gly Ile Lys Ile Met
 290 295 300
 Pro Val Gly Ile His Met Gly Gln Ile Gln Ser Val Leu Lys Leu Ala
 305 310 315 320
 Asp Lys Asp Trp Arg Val Glu Glu Leu Lys Gln Gln Phe Glu Gly Lys
 325 330 335
 Thr Val Leu Leu Gly Val Asp Asp Met Asp Ile Phe Lys Gly Val Asn
 340 345 350
 Leu Lys Leu Leu Ala Met Glu Gln Leu Leu Lys Gln His Pro Lys Trp
 355 360 365
 Gln Arg Arg Ala Val Leu Val Gln Ile Thr Asn Pro Ala Arg Gly Arg
 370 375 380
 Gly Arg Asp Leu Glu Glu Val Gln Ala Glu Ile Gln Glu Ser Cys Arg
 385 390 395 400
 Arg Ile Asn Glu Thr Phe Gly Arg Pro Gly Tyr Glu Pro Val Val Phe
 405 410 415
 Ile Asp Arg Pro Val Ser Leu Ser Glu Arg Ser Ala Tyr Phe Thr Ile
 420 425 430
 Ala Glu Cys Val Val Val Ala Ala Val Arg Asp Gly Met Asn Leu Thr
 435 440 445
 Pro Tyr Glu Tyr Ile Val Cys Arg Gln Gly Val Ser Gly Ser Glu Ser
 450 455 460
 Ser Ser Gly Ser Ser Gly Pro Lys Lys Ser Met Leu Val Val Ser Glu
 465 470 475 480
 Phe Ile Gly Cys Ser Pro Ser Leu Ser Gly Ala Ile Arg Val Asn Pro
 485 490 495
 Trp Asn Ile Glu Ala Thr Ala Glu Ala Met Asn Glu Ala Ile Ser Met
 500 505 510
 Ala Asp Ser Glu Lys Gln Leu Arg His Glu Lys His Tyr Arg Tyr Val
 515 520 525
 Ser Thr His Asp Val Ala Tyr Trp Ser Arg Ser Phe Tyr Gln Asp Met
 530 535 540
 Glu Arg Thr Cys Lys Asp His Phe Arg Arg Arg Cys Trp Gly Ile Gly
 545 550 555 560
 Leu Ser Phe Gly Phe Arg Val Val Ala Leu Asp Pro Asn Phe Lys Lys
 565 570 575
 Leu Asn Ile Asp Gln Ile Glu Ser Ala Tyr Ile Lys Ser Lys Asn Arg
 580 585 590

Ala Ile Leu Leu Asp Tyr Asp Gly Thr Val Met Pro Gln Thr Thr Ile
595 600 605

Asn Lys Thr Pro Asn Gln Glu Val Ile Ser Ile Ile Asn Thr Leu Cys
610 615 620

Ser Asp Val Lys Asn Thr Val Phe Val Val Ser Gly Arg Gly Arg Asp
625 630 635 640

Ser Leu Gly Lys Trp Phe Ala His Cys Lys Lys Leu Gly Ile Ala Ala
645 650 655

Glu His Gly Tyr Phe Met Arg Trp Ser Val Asp Glu Asp Trp Glu Asn
660 665 670

Cys Gly Gln Ser Ser Asp Phe Gly Trp Thr Gln Ile Ala Glu Pro Val
675 680 685

Met Asn Leu Tyr Thr Glu Ala Thr Asp Gly Ser Ser Ile Glu Thr Lys
690 695 700

Glu Ser Ala Leu Val Trp His His Arg Asp Ala Asp Pro Gly Phe Gly
705 710 715 720

Ala Ala Gln Ala Lys Glu Leu Leu Asp His Leu Glu Ser Val Leu Ala
725 730 735

Asn Glu Pro Val Ala Val Lys Ser Gly Gln Cys Ile Val Glu Val Lys
740 745 750

Pro Gln Gly Ile Ser Lys Gly Ser Val Ala Glu Lys Ile Phe Thr Ser
755 760 765

Met Ala Glu Ser Gly Arg Gln Ala Asp Phe Val Leu Cys Ile Gly Asp
770 775 780

Asp Arg Ser Asp Glu Asp Met Phe Glu Ser Ile Asp Asn Ala Ile Ala
785 790 795 800

Asn Gly Ile Leu Thr Ser Ser Lys Ser Val Phe Ala Cys Thr Val Gly
805 810 815

Gln Lys Pro Ser Lys Ala Lys Tyr Tyr Leu Asp Asp Thr Thr Asp Val
820 825 830

Ile Asn Met Leu Glu Ala Leu Ala Glu Ala Ser Asp Pro Ser Pro Ser
835 840 845

Ala Gly Ser Ser Pro
850

<210> 12

<211> 857

<212> PRT

<213> Populus balsamifera subsp. trichocarpa

<400> 12

Met Val Ser Ser Ser Cys Ile Ser Leu Leu Asp Leu Ala Ser Gly Asn
1 5 10 15

Met Met Asn Phe Ser Gln Ala Pro Arg Ala Leu Pro Arg Ile Met Thr
20 25 30

Val	Pro	Gly	Ile	Ile	Ser	Asp	Ile	Asp	Gly	Asp	Gly	Thr	Asn	Asp	Gly	
		35					40					45				
Asn	Ser	Asp	Ala	Pro	Ser	Thr	Val	Lys	Lys	Ile	Ile	Val	Ser	Asn	Phe	
	50					55					60					
Leu	Pro	Leu	Asn	Ala	Gln	Lys	Asp	Leu	Lys	Ser	Gly	Lys	Trp	Ser	Phe	
65					70					75					80	
Ser	Phe	Asp	Glu	Asp	Ser	Leu	Leu	Leu	Gln	Met	Lys	Asp	Gly	Phe	Ser	
				85					90					95		
Glu	Asn	Thr	Glu	Val	Val	Tyr	Val	Gly	Ser	Leu	Arg	Val	Asp	Val	Asp	
			100					105					110			
Thr	Ser	Glu	Gln	Glu	Glu	Val	Ser	Gln	Gln	Leu	Leu	Glu	Glu	Phe	Asn	
		115					120					125				
Cys	Val	Pro	Thr	Phe	Ile	Pro	Ser	Glu	Ile	Tyr	Lys	Asn	Phe	Tyr	His	
	130					135					140					
Gly	Phe	Cys	Lys	His	His	Leu	Trp	Pro	Leu	Phe	His	Tyr	Met	Leu	Pro	
145					150					155					160	
Met	Cys	Pro	Asp	His	Gly	Asn	Arg	Phe	Asp	Arg	Leu	Leu	Trp	Gln	Ser	
				165					170					175		
Tyr	Val	Ser	Thr	Asn	Lys	Ile	Phe	Ala	Asp	Lys	Val	Met	Gly	Val	Ile	
			180					185					190			
Asn	Ser	Glu	Glu	Asp	Tyr	Val	Trp	Val	His	Asp	Tyr	His	Leu	Met	Val	
		195					200					205				
Leu	Pro	Thr	Phe	Leu	Arg	Lys	Arg	Phe	Asn	Arg	Ile	Lys	Leu	Gly	Phe	
	210					215					220					
Phe	Leu	His	Ser	Pro	Phe	Pro	Ser	Ser	Glu	Ile	Tyr	Arg	Thr	Leu	Pro	
225					230					235					240	
Val	Arg	Asp	Glu	Ile	Leu	Lys	Ala	Leu	Leu	Asn	Ala	Asp	Leu	Ile	Gly	
				245					250					255		
Phe	His	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	Leu	Ser	Cys	Cys	Ser	Arg	
			260				265						270			
Met	Leu	Gly	Leu	Tyr	Tyr	Glu	Ser	Lys	Arg	Gly	His	Ile	Gly	Leu	Glu	
		275					280					285				
Tyr	Phe	Gly	Arg	Thr	Val	Tyr	Ile	Lys	Ile	Leu	Pro	Val	Gly	Ile	His	
	290					295					300					
Met	Gly	Arg	Val	Glu	Ser	Ala	Leu	Asn	His	Pro	Ser	Ser	Ser	Ile	Lys	
305					310					315					320	
Val	Lys	Glu	Ile	Gln	Lys	Gln	Phe	Lys	Gly	Lys	Arg	Leu	Val	Val	Gly	
				325					330					335		
Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	Gly	Ile	Ser	Leu	Lys	Leu	Leu	Ala	
			340					345					350			
Met	Glu	His	Leu	Leu	Gln	Gln	Asn	Ser	Gly	Met	Arg	Gly	Lys	Leu	Val	
		355					360					365				

Leu Val Trp His His Gln Asp Ala Asp Pro Asp Phe Gly Ser Cys Gln
 705 710 715 720
 Ala Lys Glu Leu Leu Asp His Leu Glu Asn Val Leu Ala Asn Asp Pro
 725 730 735
 Val Val Val Lys Arg Gly Gln Asn Ile Val Glu Val Lys Pro Gln Gly
 740 745 750
 Val Thr Lys Gly Phe Val Ala Glu Lys Val Leu Ser Ser Met Ile Ala
 755 760 765
 Asn Gly Lys Pro Pro Asp Phe Val Leu Cys Ile Gly Asp Asp Arg Ser
 770 775 780
 Asp Glu Asp Met Phe Glu Ser Met Ser Asn Thr Ala Tyr Gly Ser Ser
 785 790 795 800
 Leu Pro Ser Ala Pro Ala Ile Phe Ala Cys Thr Val Gly Gln Lys Pro
 805 810 815
 Ser Lys Ala Arg Tyr Tyr Leu Asp Asp Thr Val Asp Val Leu Ala Leu
 820 825 830
 Leu Gln Cys Leu Ala Asp Ala Ser Asn Ser Lys Ser Ser Ser Thr Glu
 835 840 845
 Thr Gln Val Ser Phe Asp Asn Val Val
 850 855

 <210> 13
 <211> 865
 <212> PRT
 <213> *Populus balsamifera* subsp. *trichocarpa*

 <400> 13
 Met Val Ser Arg Ser Cys Ile Ser Leu Leu Asp Phe Ala Ser Gly Asn
 1 5 10 15
 Met Met Asn Phe Ser Gln Ser Pro Arg Ser Leu Pro Arg Ile Met Thr
 20 25 30
 Val Pro Gly Ile Ile Ser Asp Val Asp Val Asp Gly Ile Asn Asp Gly
 35 40 45
 Ile Ser Asp Ala Pro Ser Thr Gly Ser Gly Ala Lys Met Ile Ile Val
 50 55 60
 Ser Asn Phe Leu Pro Leu Asn Ala Gln Lys Asp Leu Asn Ser Gly Lys
 65 70 75 80
 Trp Ser Phe Ser Phe Asp Glu Asp Ser Leu Leu Leu Gln Met Lys Asp
 85 90 95
 Gly Phe Ser Ala Ile Pro Glu Val Val Tyr Val Gly Ser Leu Arg Val
 100 105 110
 Asp Val Asp Ser Ser Glu Gln Glu Glu Val Ser Gln Lys Leu Leu Glu
 115 120 125
 Glu Phe Asn Cys Val Pro Thr Phe Ile Pro Pro Asp Ile Tyr Lys Asn
 130 135 140

Phe	Tyr	His	Gly	Phe	Cys	Lys	His	His	Leu	Trp	Pro	Leu	Phe	His	Tyr
145					150					155					160
Met	Leu	Pro	Leu	Cys	Pro	Asp	His	Gly	Asn	Arg	Phe	Asp	Arg	Leu	Leu
				165					170					175	
Trp	Gln	Ala	Tyr	Val	Ser	Ala	Asn	Lys	Ile	Phe	Ala	Asp	Lys	Val	Thr
			180					185					190		
Glu	Val	Ile	Asn	Asn	Thr	Glu	Glu	Asp	Tyr	Val	Trp	Val	His	Asp	Tyr
		195					200					205			
His	Leu	Met	Val	Leu	Pro	Thr	Phe	Leu	Arg	Lys	Arg	Phe	Asn	Arg	Ile
	210					215					220				
Lys	Leu	Gly	Phe	Phe	Leu	His	Ser	Pro	Phe	Pro	Ser	Ser	Glu	Ile	Tyr
225					230					235					240
Arg	Thr	Leu	Leu	Val	Arg	Asp	Glu	Ile	Leu	Lys	Ala	Leu	Leu	Asn	Ala
				245					250					255	
Asp	Leu	Ile	Gly	Phe	His	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	Leu	Ser
			260					265					270		
Cys	Cys	Ser	Arg	Met	Leu	Gly	Leu	Asp	Tyr	Glu	Ser	Lys	Arg	Gly	His
		275					280					285			
Ile	Gly	Leu	Glu	Tyr	Phe	Gly	Arg	Thr	Val	Tyr	Ile	Lys	Ile	Leu	Pro
	290					295					300				
Val	Gly	Ile	His	Met	Gly	Arg	Val	Glu	Ser	Ala	Leu	Asn	His	Pro	Ser
305					310					315					320
Ser	Ser	Ile	Lys	Val	Lys	Glu	Ile	Gln	Glu	Gln	Phe	Lys	Gly	Lys	Arg
				325					330					335	
Leu	Val	Ile	Gly	Val	Asp	Asp	Met	Asp	Ile	Phe	Lys	Gly	Ile	Ser	Leu
			340					345					350		
Lys	Leu	Leu	Ala	Val	Glu	His	Leu	Leu	Leu	Gln	Asn	Ser	Glu	Leu	Arg
		355					360					365			
Gly	Lys	Leu	Val	Leu	Val	Gln	Ile	Val	Asn	Pro	Ala	Arg	Ser	Ser	Gly
	370					375					380				
Lys	Asp	Val	Gln	Glu	Ala	Lys	Met	Glu	Ile	Tyr	Ser	Ile	Thr	Lys	Arg
385					390					395					400
Ile	Asn	Asn	Thr	Phe	Gly	Phe	Pro	Gly	Tyr	Glu	Pro	Val	Val	Leu	Ile
				405					410					415	
Asp	Arg	His	Val	Pro	Phe	Cys	Glu	Lys	Thr	Ala	Tyr	Tyr	Ala	Leu	Ala
			420					425					430		
Glu	Cys	Cys	Ile	Val	Asn	Ala	Val	Arg	Asp	Gly	Met	Asn	Leu	Ile	Pro
		435					440					445			
Tyr	Lys	Tyr	Ile	Val	Cys	Arg	Gln	Gly	Thr	Pro	Lys	Met	Asp	Glu	Ala
	450					455					460				
Leu	Gly	Val	Ala	Ser	Gly	Ser	Arg	His	Thr	Ser	Ser	Leu	Val	Val	Ser
465					470					475					480

Glu	Phe	Thr	Gly	Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala	Ile	Arg	Val	Asn	
				485					490					495		
Pro	Trp	Asp	Ile	Glu	Ala	Val	Ala	Asn	Ala	Val	Asn	Thr	Ala	Ile	Asn	
			500					505					510			
Met	Pro	Asp	Leu	Glu	Lys	Gln	Leu	Arg	His	Gly	Lys	His	Tyr	Cys	Tyr	
		515					520					525				
Val	Ser	Ser	His	Asp	Val	Ala	Tyr	Trp	Ala	Arg	Ser	Phe	Met	Gln	Asp	
	530					535					540					
Leu	Lys	Arg	Ala	Cys	Lys	Asp	His	Tyr	Ser	Lys	Arg	Cys	Trp	Gly	Ile	
545					550					555					560	
Gly	Phe	Gly	Leu	Asn	Phe	Arg	Ile	Leu	Ala	Leu	Ser	Pro	Ser	Phe	Arg	
			565						570					575		
Lys	Leu	Ser	Asn	Asp	Tyr	Ile	Ile	Ser	Ala	Tyr	Lys	Arg	Thr	Ser	Lys	
			580					585					590			
Arg	Ala	Ile	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Met	Val	Pro	His	Thr	Ser	
		595					600					605				
Leu	Ala	Lys	Thr	Pro	Thr	Pro	Glu	Val	Ile	Ser	Val	Leu	Asn	Asn	Leu	
	610					615					620					
Cys	Ala	Asp	Pro	Met	Asn	Ser	Val	Phe	Ile	Val	Ser	Gly	Arg	Gly	Lys	
625					630				635						640	
Lys	Ser	Leu	Ser	Asp	Trp	Phe	Val	Gln	Cys	Glu	Asn	Leu	Gly	Ile	Ala	
			645					650					655			
Ala	Glu	His	Gly	Tyr	Phe	Phe	Arg	Trp	Ser	Gly	Met	Ser	Asp	Trp	Glu	
			660					665					670			
Thr	Ser	Ser	Leu	Ala	Val	Asp	Phe	Asp	Trp	Lys	Asn	Ile	Ala	Glu	Pro	
		675					680					685				
Val	Met	Lys	Leu	Tyr	Thr	Glu	Ala	Thr	Asp	Gly	Ser	Tyr	Ile	Glu	Val	
	690					695					700					
Lys	Glu	Ser	Ala	Leu	Val	Trp	His	His	Gln	Asp	Ala	Asp	Pro	Asp	Phe	
705					710					715					720	
Gly	Ser	Cys	Gln	Ala	Lys	Glu	Leu	Leu	Asp	His	Leu	Glu	Asn	Val	Leu	
			725						730					735		
Ala	Asn	Asp	Pro	Val	Ala	Val	Lys	Arg	Gly	Gln	Asn	Ile	Val	Glu	Val	
			740					745					750			
Lys	Pro	Gln	Gly	Val	Thr	Lys	Gly	Phe	Val	Ala	Glu	Lys	Val	Leu	Ser	
		755					760					765				
Lys	Met	Ile	Ala	Ser	Gly	Lys	Pro	Pro	Gly	Phe	Val	Leu	Cys	Ile	Gly	
	770					775					780					
Asp	Asp	Arg	Ser	Asp	Glu	Asp	Met	Phe	Glu	Ser	Ile	Ser	Lys	Thr	Pro	
785					790					795					800	
Tyr	Ser	Ser	Ser	Leu	Pro	Ser	Ala	Pro	Ala	Ile	Phe	Ala	Cys	Thr	Val	
			805						810					815		

Gly Gln Lys Pro Ser Lys Ala Arg Tyr Tyr Leu Asp Asp Thr Val Asp
 820 825 830
 Val Leu Ala Leu Leu Gln Cys Leu Ala Asp Ala Ser Ser Ser Asn Leu
 835 840 845
 Ser Ser Thr Glu Thr Gln Val Ser Phe Asp Asn Val Val Arg Lys Glu
 850 855 860
 Leu
 865

 <210> 14
 <211> 854
 <212> PRT
 <213> *Populus balsamifera* subsp. *trichocarpa*

 <400> 14
 Met Ile Thr Gln Ser Cys Lys Asp Asn Leu Asp Met Ile Ser Val Asn
 1 5 10 15
 Asp Phe Arg Val Val Asp Arg Ile Pro Arg Ile Met Asn Val Leu Gly
 20 25 30
 Ala Leu Ser Glu Ile Glu Val Gly Glu His Asp Asp Glu Gly Val Thr
 35 40 45
 Ser Pro Val Val Ser Lys Pro Arg Arg Ile Met Val Ala Asn Gln Leu
 50 55 60
 Pro Ile Arg Gly His Arg Asn Glu Glu Thr Lys Gly Trp Ser Phe Glu
 65 70 75 80
 Leu Asp Lys Glu Ser Leu Val Leu Gln Phe Lys Asp Gly Phe Pro Ala
 85 90 95
 Asn Ser Glu Val Trp Tyr Val Gly Leu Leu Lys Val Asp Val Glu Thr
 100 105 110
 Lys Asp Gln Asp Glu Val Ala Arg Leu Leu Phe Ser Met Phe Arg Cys
 115 120 125
 Val Pro Val Phe Leu Thr Asp Asp Gln Lys Asn Lys Tyr Tyr His Gly
 130 135 140
 Phe Cys Lys His Tyr Leu Trp Pro Leu Phe His Tyr Met Leu Pro Leu
 145 150 155 160
 Ser Pro Ser Arg Gly Gly Val Arg Phe Asp Arg Ser Leu Trp Glu Gly
 165 170 175
 Tyr Ile Val Ala Asn Arg Leu Phe Ala Asn Lys Val Thr Glu Ile Leu
 180 185 190
 Arg His His Glu Asp Ser Val Trp Val His Asp Tyr His Leu Met Val
 195 200 205
 Leu Pro Ala Phe Leu Arg Lys Arg Phe Asn Arg Val Lys Leu Gly Phe
 210 215 220
 Phe Leu His Ser Pro Phe Pro Ser Ser Glu Ile Tyr Thr Thr Ile Pro
 225 230 235 240

Val	Arg	Glu	Glu	Ile	Leu	Arg	Ser	Leu	Leu	Asn	Cys	Asp	Leu	Ile	Gly	245	250	255	
Phe	His	Thr	Phe	Asp	Tyr	Ala	Arg	His	Phe	Leu	Ser	Cys	Cys	Ser	Lys	260	265	270	
Met	Leu	Gly	Ile	Asp	Tyr	Gln	Cys	Lys	Arg	Gly	Tyr	Ile	Gly	Leu	Asp	275	280	285	
Tyr	Cys	Gly	Lys	Thr	Ile	Ser	Ile	Lys	Ile	Leu	His	Met	Gly	Ile	His	290	295	300	
Met	Gly	Gln	Leu	Glu	Ser	Val	Leu	Asn	Met	Glu	Gln	Thr	Ala	Thr	Leu	305	310	315	320
Ala	Lys	Gln	Leu	Lys	Glu	Lys	Phe	Glu	Gly	Lys	Ile	Val	Met	Val	Gly	325	330	335	
Val	Asp	Asp	Leu	Asp	Leu	Leu	Lys	Gly	Ile	Ser	Ser	Lys	Phe	Ser	Ala	340	345	350	
Met	Gly	Arg	Leu	Leu	Glu	Met	Arg	Pro	Glu	Leu	Ile	Gly	Lys	Val	Val	355	360	365	
Leu	Val	Gln	Ile	Ala	Asn	Pro	Ala	Arg	Ser	Gln	Gly	Lys	Asp	Val	Gln	370	375	380	
Glu	Val	Gln	Lys	Glu	Thr	Thr	Leu	Ile	Ala	Gln	Gln	Ile	Asn	Gln	Lys	385	390	395	400
Tyr	Gly	Tyr	Glu	Gly	Tyr	Gln	Pro	Ile	Val	Phe	Ile	Asn	Gly	Pro	Val	405	410	415	
Ser	Thr	Leu	Glu	Lys	Ala	Ala	Tyr	Tyr	Ala	Ile	Ser	Glu	Cys	Cys	Val	420	425	430	
Val	Asn	Ala	Leu	Arg	Asp	Gly	Met	Asn	Leu	Val	Ser	Tyr	Lys	Tyr	Thr	435	440	445	
Val	Cys	Arg	Gln	Gly	Ser	Pro	Val	Leu	Asp	Lys	Ala	Leu	Gly	Ile	Asp	450	455	460	
Glu	Ser	Tyr	Pro	Arg	Lys	Ser	Phe	Leu	Ile	Val	Ser	Glu	Phe	Ile	Gly	465	470	475	480
Cys	Ser	Pro	Ser	Leu	Ser	Gly	Ala	Arg	Arg	Val	Asn	Pro	Trp	Asp	Val	485	490	495	
Gly	Ala	Val	Ala	Asp	Ala	Met	Tyr	Ala	Gly	Ile	His	Met	Lys	Asp	Glu	500	505	510	
Glu	Lys	His	Leu	Arg	His	Glu	Lys	His	Tyr	Lys	Tyr	Ile	Ser	Ser	His	515	520	525	
Asp	Val	Ala	Phe	Trp	Ala	Arg	Ser	Phe	Asp	Leu	Asp	Leu	Glu	Arg	Ala	530	535	540	
Cys	Lys	Asp	His	Tyr	Leu	Lys	Arg	Tyr	Tyr	Asn	Val	Gly	Phe	Gly	Leu	545	550	555	560
Asn	Phe	Arg	Val	Ala	Ala	Val	Gly	Thr	Asn	Phe	Arg	Met	Leu	Thr	Thr	565	570	575	

Glu Arg Val Val Ala Ala Tyr Asn Asn Thr Asn Ser Arg Leu Ile Leu
 580 585 590
 Leu Asp Tyr Asp Gly Thr Met Met Pro Gln Cys Ala Val Asp Lys Thr
 595 600 605
 Pro Arg Ser Glu Val Ile Ser Ile Leu Asn Cys Leu Cys Ser Asp Pro
 610 615 620
 Lys Asn Val Val Phe Ile Val Ser Gly Arg Gly Arg Asp Pro Leu Ser
 625 630 635 640
 Lys Trp Phe Ser Pro Cys Glu Thr Leu Gly Ile Ser Ala Glu His Gly
 645 650 655
 Tyr Phe Thr Arg Trp Thr Lys Asn Ser Pro Trp Glu Thr Cys Ser Val
 660 665 670
 Ala Met Asp Cys Asp Trp Lys Lys Ile Val Gln Pro Val Met Glu Arg
 675 680 685
 Tyr Thr Glu Thr Thr Asp Gly Ser Phe Ile Glu Pro Lys Glu Ser Ala
 690 695 700
 Leu Val Trp His His Gln Asp Ala Asp Pro Asp Phe Gly Ser Cys Gln
 705 710 715 720
 Ala Lys Glu Leu Leu Asp His Leu Glu Ser Val Leu Ala Asn Glu Pro
 725 730 735
 Val Val Val Arg Arg Gly Gln Gln Ile Val Glu Val Lys Pro Gln Gly
 740 745 750
 Val Ser Lys Gly Ile Val Val Glu Asn Leu Ile Ser Thr Met Arg Ser
 755 760 765
 Gln Gly Lys Ser Pro Asp Phe Leu Phe Cys Ile Gly Asp Asp Arg Ser
 770 775 780
 Asp Glu Asp Met Phe Glu Ser Ile Ala Arg Leu Val Asp Asn Pro Ser
 785 790 795 800
 Ile Pro Pro Ile Ala Glu Val Phe Ala Cys Thr Val Gly Leu Lys Pro
 805 810 815
 Ser Lys Ala Lys Tyr Tyr Leu Asp Asp Thr Pro Glu Val Ile Lys Leu
 820 825 830
 Leu Gln Gly Leu Ala Thr Ala Ser Val Gly Ser Lys Tyr Ala His Thr
 835 840 845
 Leu Glu Asp Glu Asp Val
 850

<210> 15
 <211> 846
 <212> PRT
 <213> *Populus balsamifera* subsp. *trichocarpa*

<400> 15
 Met Ile Thr Gln Ser Cys Lys Asp Ser Leu Asp Met Ile Ser Val Asn
 1 5 10 15

Asp	Phe	Arg	Gly	Leu	Glu	Arg	Ile	Pro	Ala	Val	Met	Asn	Glu	Leu	Gly	20	25	30
Tyr	Glu	Val	Gly	Asp	Glu	His	Gly	Gln	Gly	Pro	Val	Val	Ser	Lys	Gln	35	40	45
Arg	Arg	Ile	Ile	Val	Ala	Asn	Gln	Leu	Pro	Ile	Arg	Gly	Tyr	Arg	Asn	50	55	60
Glu	Gly	Thr	Lys	Gly	Trp	Phe	Phe	Glu	Phe	Asp	Lys	Asp	Ser	Leu	Val	65	70	75
Leu	Gln	Leu	Lys	Asp	Gly	Phe	Pro	Ala	Asn	Thr	Glu	Val	Trp	Tyr	Val	85	90	95
Gly	Met	Leu	Lys	Val	Asp	Val	Glu	Lys	Glu	Asp	Gln	Glu	Glu	Val	Ala	100	105	110
Gln	Leu	Met	Phe	His	Lys	Phe	Arg	Cys	Val	Pro	Val	Phe	Leu	Thr	Val	115	120	125
Asp	Gln	Lys	Asn	Lys	Phe	Tyr	His	Gly	Phe	Cys	Lys	His	Tyr	Leu	Trp	130	135	140
Pro	Leu	Phe	His	Tyr	Met	Leu	Pro	Leu	Ser	Pro	Ser	His	Gly	Gly	Val	145	150	155
Arg	Phe	Asp	Lys	Ser	Leu	Trp	Glu	Gly	Tyr	Ile	Val	Ala	Asn	Gln	Leu	165	170	175
Phe	Ala	Asn	Lys	Val	Ala	Glu	Ile	Leu	Trp	Pro	Asp	Lys	Asp	Ser	Val	180	185	190
Trp	Val	His	Asp	Tyr	His	Leu	Met	Val	Leu	Pro	Ser	Ile	Leu	Arg	Asn	195	200	205
Arg	Tyr	Thr	Arg	Val	Lys	Leu	Gly	Phe	Phe	Leu	His	Ser	Pro	Phe	Pro	210	215	220
Ser	Ser	Glu	Ile	Tyr	Arg	Thr	Ile	Pro	Val	Arg	Glu	Gln	Ile	Leu	Arg	225	230	235
Ser	Leu	Leu	Asn	Cys	Asp	Leu	Ile	Gly	Phe	His	Thr	Phe	Asp	Tyr	Ala	245	250	255
Arg	His	Phe	Leu	Ser	Cys	Cys	Ser	Arg	Leu	Leu	Gly	Ile	Asp	Tyr	Gln	260	265	270
Cys	Lys	Arg	Gly	Tyr	Ile	Gly	Leu	Asp	Tyr	Cys	Gly	Lys	Thr	Ile	Asn	275	280	285
Ile	Lys	Ile	Leu	Pro	Val	Gly	Ile	His	Met	Gly	Gln	Leu	Glu	Ser	Asp	290	295	300
Leu	Asn	Met	Glu	Gln	Thr	Ala	Thr	Leu	Ala	Lys	Gln	Leu	Lys	Glu	Lys	305	310	315
Phe	Glu	Gly	Lys	Val	Val	Met	Val	Gly	Val	Asp	Asp	Leu	Asp	Met	Phe	325	330	335
Lys	Gly	Ile	Ser	Leu	Lys	Phe	Ser	Ala	Met	Gly	Arg	Leu	Leu	Glu	Met	340	345	350

Ser Phe Ile Glu His Lys Glu Ser Ala Leu Val Trp His Tyr Gln Asp
 690 695 700
 Ala Asp Pro Asp Phe Gly Gly Cys Gln Ala Lys Glu Leu Leu Asp His
 705 710 715 720
 Leu Glu Ser Val Leu Ala Asn Glu Pro Val Val Val Lys Arg Gly Arg
 725 730 735
 Gln Ile Val Glu Val Lys Pro Gln Gly Val Ser Lys Gly Val Val Val
 740 745 750
 Glu Asp Leu Ile Ser Ser Met Arg Ser Lys Gly Lys Ser Pro Asp Phe
 755 760 765
 Leu Phe Cys Ile Gly Asp Asp Arg Ser Asp Glu Asp Met Phe Glu Ser
 770 775 780
 Ile Ala Arg Leu Phe Asp Asn Pro Ser Leu Pro Pro Ile Ala Glu Val
 785 790 795 800
 Phe Ala Cys Thr Val Gly His Lys Pro Ser Lys Ala Lys Tyr Tyr Leu
 805 810 815
 Asp Asp Thr Pro Asp Val Ile Glu Leu Leu Gln Gly Leu Ala Thr Ala
 820 825 830
 Ser Val Gly Pro Lys Val Thr His Thr Leu Glu Glu Asp Ile
 835 840 845

<210> 16
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> Consensus sequence

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Xaa can be G or D

<400> 16
 Leu Asp Tyr Asp Xaa Thr
 1 5

<210> 17
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> Consensus sequence

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa can be R or Q

<400> 17
 Gly Asp Asp Xaa Ser Asp
 1 5

<210> 18
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> Forward primer

<400> 18
 ggggacaagt ttgtacaaaa aagcaggctc cgaagtaact tctacctcc 49

<210> 19
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <223> Reverse primer

<400> 19
 ggggaccact ttgtacaaga aagctgggctc ccatctctaa gttgtaactg 50

<210> 20
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> Forward primer

<400> 20
 cgggatccat ggtgtcaaga tcttgtgcta a 31

<210> 21
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Reverse primer

<400> 21
 aaggcctaac gatgctttca aatgcaactt 30

<210> 22
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Forward primer AtTPS5

<400> 22
 tcctgcttat atcccacctg agc 23

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Reverse primer AtTPS5

<400> 23
 gcgccgctta aagaaggaga a

21

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> left border T-DNA primer

<400> 24
 tggttcacgt agtgggcat cg

22

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Forward primer Genetrap

<400> 25
 ttgggcgcgt agctttatac

20

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Reverse primer Genetrap

<400> 26
 caagaagata tgaaaacagc ctca

24

<210> 27
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20

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CLAIMS:

1. Use of inactivation of the activity of a plant class II trehalose-6-phosphate synthase to increase plant growth.
2. The use according to claim 1, wherein said increase comprises
5 increased root growth, increased stem thickness, increased leave number and/or increased seed size.
3. The use according to claim 1 or 2, whereby said increase is obtained in absence of light.
4. Use of inactivation of the activity of a class II plant trehalose-6-
10 phosphate synthase to increase starch synthesis.
5. The use according to any one of claims 1 to 4, wherein the amino acid sequence of said trehalose-6-phosphate synthase is selected from the group consisting of SEQ ID Nos: 1-15.
6. The use according to any one of claims 1 to 4, wherein the amino acid
15 sequence of said trehalose-6-phosphate synthase is selected from the group consisting of SEQ ID Nos: 1-8.
7. The use according to any one of claims 1 to 4, wherein the amino acid sequence of said trehalose-6-phosphate synthase consists of SEQ ID No: 4.
8. The use according to any one of claims 1 to 4, wherein the amino acid
20 sequence of said trehalose-6-phosphate synthase consists of SEQ ID No: 1.
9. A method for increasing growth of a plant, comprising the step of inactivating class II trehalose-6-phosphate synthase (class II TPS) activity in the plant.

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10. The method according to claim 9, wherein said increase comprises increased root growth, increased stem thickness, increased leave number and/or increased seed size.

11. The method according to claim 9 or 10, wherein said increase is
5 obtained in absence of light.

12. A method for increasing starch synthesis of a plant, comprising the step of inactivating class II trehalose-6-phosphate synthase (class II TPS) activity in the plant.

13. The method according to any one of claims 9 to 12, wherein the step of
10 inactivating class II TPS activity comprises:

(a) knocking out a gene encoding the class II TPS in the plant,

(b) use of RNA interference to inhibit class II TPS expression in the plant,

(c) use of an antisense class II TPS nucleic acid or an inverted repeat of class II TPS nucleic acid to inhibit class II TPS gene expression in the plant, or

15 (d) inactivating the promoter of a gene encoding the class II TPS in the plant.

14. The method according to any one of claims 9 to 13, wherein the amino acid sequence of said class II TPS comprises a sequence selected from the group consisting of SEQ ID Nos: 1 to 15.

15. The method according to any one of claims 9 to 13, wherein the amino
20 acid sequence of said class II TPS comprises a sequence selected from the group consisting of SEQ ID Nos: 1 to 8.

16. The method according to any one of claims 9 to 13, wherein the amino acid sequence of said class II TPS consists of SEQ ID No: 4.

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17. The method according to any one of claims 9 to 13, wherein the amino acid sequence of said class II TPS consists of SEQ ID No: 1.

Application number / numéro de demande: 2636844

Figures: _____

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