PRODUCTION OF LYOSOMAL ENZYMES IN PLANT-BASED EXPRESSION SYSTEMS

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Related U.S. Application Data
Provisional application No. 60/003,737, Sep. 14, 1995.

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ABSTRACT
The invention relates to the production of enzymatically active recombinant human and animal lysosomal enzymes involving construction and expression of recombinant expression constructs comprising coding sequences of human or animal lysosomal enzymes in a plant expression system. The plant expression system provides for post-translational modification and processing to produce a recombinant gene product exhibiting enzymatic activity. The invention is demonstrated by working examples in which transgenic tobacco plants having recombinant expression constructs comprising human hGC and IDUA nucleotide sequences produced enzymatically active modified human glucocerebrosidase and human α-L-iduronidase. The recombinant lysosomal enzymes produced in accordance with the invention may be used for a variety of purposes, including but not limited to enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal storage diseases.
FIG. 6

**Glucosidase Activity (FU/min/ug/ml)**

- **UT Extracts**
- **hGC Extracts**

**Time Post-Induction (hrs)**

0, 8, 12, 24
FIG. 9A

123 ATGGAGTT TTCAAGTCCT TCCAGAGAGG
151 AATGTCCCAA GCCTTTTAGT AGGGTAAGCA TCATGGCTGG CAGCCTCACA
201 GGTTTGCTTC TACTTCAGGC AGTGTCTGTTG GCATCAGGGT CCCGCCCCCTG
251 CATCCCTAAA AGCTTCGCTT ACAGCTCGGT GGTGTGTGTC TGCAATGCCA
301 CATACTGTGA CTTCCTTGAC CCCCCGACCT TTCCTGCCCT TGGTACCTTTC
351 AGCCGCTATG AGAGTACACG CAGTGGGCCA CCGATTGGGGG TGAGTATGGG
401 GCCCATCCAG GCTAATCACA CGGGCACAGG CCTGCTACTG ACCCTGCAGC
451 CAGAACAGAA GTTCCAGAAA GTGAAGGGAT TTGAGGGGCA CATGACAGAT
501 GCTGCTGCTC TCAACATCCT TGCCCTGTCA CCCCCGTCCC AAAATTTGCT
551 ACTTAAATCG TACTTCTCTG AAGAAGGGAAT CCGATATAAC ATCATCCGGG
601 TACCCATGGC CAGCTGTGAC TTCTCCATCC GCACCTACAC ATGAAGGAGCAGAC
651 ACCTCCTGATG ATTTCCAGTT GCACAACTTC AGGCCCTCAG AGGAAGATAC
701 CAAGCTCAAG ATACACCCCTGA TTCACCGAGC CCTGCAGGTT GCCAGCGGTC
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| 1851 | aattcggact |

**FIG. 9C**
1 50
MEFSSPSREE CPKPLSRVS IMAGSLTGGL LLQAVSWASG ARPCIPKSG
51 100
YSSVCVCNA TYCDSFDPP TFPAVTFTSR YESTRSGRRM ELSMGPIQAN
101 150
HTGTGGLLTLE QPEQKFQKV KGFGGAMTDA AALNILALSP PAQNLKSY
151 200
FSEEGIGYNIRVPMASCDFISIETYADTPDDFQHNFSLPEEDTKLK
201 250
IPLIHRLQALQRPSLLASPWTSPWTLKTNAGVNGKGLKQPGDIYH
251 300
QTWARYFVKFLDAYAHEKLFQFWVTAENEPSAGLSSGYPFQCLGFTPHE
301 350
QRDFIARDLGPALTANSTHHNVRLLMLDDQRLLPHWAKVVLTDPEAAKY
351 400
VHGIAVFWYLDFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVR
401 450
LGSWDRGMQYSHSIITNLYHVVGWTWNLALNPEGPWNWRNFVDSPI
451 500
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501 550
PDGSAVVVLNRSKDVPTIKDPAVGFLETISPGYSIHTYLWRRQnsd

FIG. 10
CAATACGATA TTACCGAATA TTATACTAAA TCAAAATTTA ATTTATCATA TCGAATTATT
AAACTGATAT TTCAAATTTT AATATTTAAT ATCTACTTTC AACTATTATT ACCTAATTAT
CAAATGCAAA ATGTATGAGT TATTTCATAA TAGCCCGAGT TCGTATCCAA ATATTTTACA
CTTGACCAGT CAACTTGACT ATATAAAACT TTACTTTCAA AAATAAAAA AAAAAAGAAAG
TATATATTG TAAAAGATAA TACTCCATTC AAAATATAAA ATGAAAAAAG TCCAGGCCGG
CAACCGGGTT CCTCTATAAA TACATTTTCT ACATCTTCTC TTCTCCTCAC ATCCCATCAC
TCTTCTTTTA ACAATTATAC TTGTCAATCA TCAATCCCAAC AAACAACACT TTTTCTCTCC
TCTTTTTTCT CACCGGCAGC AGACTTACCG GTGAATCTA GAGTAAGCAT C

FIG. 11
FIG. 14A

Hours Post-Induction
0  2  4  8  11  27

2.2 kb
IDUA mRNA

FIG. 14B

Hours Post-Induction
0  2  4  8  11  27

92 kDa
IDUA Protein
FIG. 15A

Hours Post-Induction

0  8  24  34

IDUA-9
IDUA-8
IDUA-7

FIG. 15B
FIG. 18

Hours Post-Induction

24  26  36

1  2  3
FIG. 19A

ATCGTCCCTGCCCCTGGGCGGTTGCT

GGCGCTCCTGGCCTCGCTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCCGCACCT

GGTGCAGgTGGACGCGGCCCGCGCGCTGTGGCCCCTGCGGCGCTTCTGGAGGAGCACAGG

CTTCTGCCCCCCGCTGCCACACAGCCAGGCTGACCAGTACGTCCTCAGCTGGGACCAGCA

GCTCAACCTCGCCTATGTGGGCGCCGTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCA

CTGGCTGCTGGAGCTTGTCACCACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAACTT

CACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCCTCCCAGGGTTTGA

CTGGCTGCTGGAGCTTGTCACCACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAACTT

CACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCCTCCCAGGGTTTGA
FIG. 19B
GCTGCTGGCGCTGCTGGATGAGGAGCAGCTCTGGGCCGAAGTGTCGCAGGCCGGGACCGT
CCTGGACAGCAACCACACGGTGGGCGTCCTGGCCAGCGCCCACCGCCCCCAGGGCCCGGC
CGACGCCTGGCGCGCCGCGGTGCTGATCTACGCGAGCGACGACACCCGCGCCCACCCCAA
CGTCACGCGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCGCCTGGG
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CGTCACGCGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCGCCTGGG
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CAATCCATGAGCCTGTGCTGAGCCCCAGTGGGTTGCACCTCCACCGGCAGTCAGCGAGCT

GGGGCTGCACTGTGCCCATGCTGCCCTCCCATCACCCCCTTTGCAATATATTTTT

FIG. 19F
MRPLRRAALLASLALLAAPPVAPAEHPHVDVADRMLWRRWRSTGFZCPRPHLSQ

ADQVLSNDQQLNAVAVPHRSHITRTWTVRTVISLTTGSGLESNTFTLDLDL

LRENQILPGFEMGSASGHTDFDKDQQVFWEKSDLSSARRYYRGLTVYNFVZ

NEPDDHNDVNMQGOMFNYDYACSEGIARASSAPRALRLGGPDHFTPPRLPSGILRHE

CHGNTFFTGAVRYLIDHLHRKGGARSISILEQKVTEQIRQLFPFAPDTPYIE

DPLVWGLPQPRARDTVYAMVGLQHQQVQILLLANTTAFFYALLSSNNAFLSYHEHPF

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1. FIELD OF THE INVENTION

The present invention relates to the production of human and animal lysosomal enzymes in plants comprising expressing the genetic coding sequence of a human or animal lysosomal enzyme in a plant expression system. The plant expression system provides for post-translational modification and processing to produce recombinant protein having enzymatic activity.

The invention is demonstrated herein by working examples in which transgenic tobacco plants produce a modified human glucocerebrosidase (hGC) and a human α-L-iduronidase (IDUA), both of which are enzymatically active.

The recombinant lysosomal enzymes produced in accordance with the invention may be used for a variety of purposes including but not limited to enzyme replacement therapy for the therapeutic treatment of lysosomal storage diseases, research for development of new approaches to medical treatment of lysosomal storage diseases, and industrial processes involving enzymatic substrate hydrolysis.
LYSOSOMAL STORAGE DISEASES

Lysosomes, which are present in all animal cells, are acidic cytoplasmic organelles that contain an assortment of hydrolytic enzymes. These enzymes function in the degradation of internalized and endogenous macromolecular substrates. When there is a lysosomal enzyme deficiency, the deficient enzyme’s undegraded substrates gradually accumulate within the lysosomes causing a progressive increase in the size and number of these organelles within the cell. This accumulation within the cell eventually leads to malfunction of the organ and to the gross pathology of a lysosomal storage disease, with the particular disease depending on the particular enzyme deficiency. More than thirty distinct, inherited lysosomal storage diseases have been characterized in humans.

A few examples of lysosomal storage diseases (and their associated deficient enzymes) include Fabry disease (α-galactosidase), Farber disease (ceramidase), Gaucher disease (glucocerebrosidase), GMS gangliosidoses (β-galactosidase), Tay-Sachs disease (β-hexosaminidase), Niemann-Pick disease (sphingomyelinase), Scheinfeld disease (α-N-acetylgalactosaminidase), Hunter syndrome (iduronate-2-sulfatase), Sly syndrome (β-glucuronidase), Hurler and Hurler/Scheie syndromes (iduronidase), and I-Cell/San Filipo syndrome (mannose 6-phosphate transporter).

One proven treatment for lysosomal storage diseases is enzyme replacement therapy in which an active form of the enzyme is administered directly to the patient. However, abundant, inexpensive and safe supplies of therapeutic lysosomal enzymes are not commercially available for the treatment of any of the lysosomal storage diseases.

2.1.1. GAUCHER DISEASE AND TREATMENT

Gaucher disease is the most common lysosomal storage disease in humans, with the highest frequency encountered in the Ashkenazi Jewish population. About 5,000 to 10,000 people in the United States are afflicted with this disease (Grabowski, 1993, Adv. Hum. Genet. 21:377–441). Gaucher disease results from a deficiency in glucocerebrosidase (hGC; glucosylceramidase; acid β-glucosidase; EC 3.2.1.45). This deficiency leads to an accumulation of the enzyme’s substrate, glucocerebroside, in reticuloendothelial cells of the bone marrow, spleen, and liver, resulting in significant skeletal complications such as bone marrow expansion and bone deterioration, and also hypersplenism, hepatomegaly, thrombocytopenia, anemia and lung complications (Grabowski, 1993, supra; Lee, 1982, Prog. Clin. Biol. Res. 95:177–217; Brady et al., 1965, Biochem. Biophys. Res. Comm. 18:221–225).


Despite the benefits of hGC replacement therapy, the source and high cost of the enzyme seriously restricts its availability. Until recently, the only commercial source of purified hGC has been from pooled human placenta, where ten to twenty kilograms (kg) of placenta yield only 1 milligram (mg) of enzyme. From five hundred to two thousand kilograms of placenta (equivalent to 2,000–8,000 placenta) are required to treat each patient every two weeks. Current costs for HGC replacement therapy range from $55 to $220/kg patient body weight every two weeks, or from $70,000 to $300,000/year for a 50 kg patient. Since the need for therapy essentially lasts for the duration of a patient’s life, costs for the enzyme alone may exceed $15,000,000 during 30 to 70 years of therapy.

A second major problem associated with treating Gaucher patients with glucocerebrosidase isolated from human tissue (and perhaps even from other animal tissues) is the risk of exposing patients to infectious agents which may be present in the pooled placenta, e.g., human immuno-deficiency virus (HIV), hepatitis viruses, and others. Accordingly, a new source of hGC is needed to effectively reduce the cost of treatment and to eliminate the risk of exposing Gaucher patients to infectious agents.

2.1.2. HURLER SYNDROME AND TREATMENT

Hurler syndrome is the most common of the group of human lysosomal storage disorders known as the mucopolysaccharidoses (MPS) involving an inability to degrade dermatan sulfate and heparan sulfate. Hurler patients are deficient in the lysosomal enzyme, α-L-iduronidase (IDUA), and the resulting accumulation of glucosaminoglycans in the lysosomes of affected cells leads to a variety of clinical manifestations (Neufeld & Ashwell, 1980, The Biochemistry of Glycoproteins and Proteoglycans, ed. W. J. Lennarz, Plenum Press, N.Y.; pp. 241–266) including developmental delay, enlargement of the liver and spleen, skeletal abnormalities, mental retardation, coarse facial features, corneal clouding, and respiratory and cardiovascular involvement. Hurler/Scheie syndrome (MPS 1 H/S) and Scheie syndrome (MPS IS) represent less severe forms of the disorder but also involve deficiencies in IDUA. Molecular studies on the genes and cDNAs of MPS I patients has led to an emerging understanding of genotype and clinical phenotype (Scott et al., 1990, Am. J. Hum. Genet. 47:802–807). In addition, both a canine and feline form of MPS I have been characterized (Haskins et al., 1979, Pediat. Res. 13:1294–1297; Haskins and Kakkis, 1995, Am. J. Hum. Genet. 57:A39 Abstr. 194; Shull et al., 1994, Proc. Natl. Acad. Sci. USA, 91:12937–12941) providing an effective in vivo model for testing therapeutic approaches.

The efficacy of enzyme replacement in the canine model of Hurler syndrome using human IDUA generated in CHO cells was recently reported (Kakkis et al., 1995, Am. J. Hum. Genet. 57:A39 (Abstr.); Shull et al., 1994, supra). Weekly doses of approximately 1 mg administered over a period of 3 months resulted in normal levels of the enzyme in liver and spleen, lower but significant levels in kidney and Lungs and very low levels in heart, brain, cartilage and cornea (Shull et al., 1994, supra). Tissue examinations showed normalization of lysosomal storage in the liver, spleen and kidney, but no improvement in heart, brain and corneal tissues. One dog was maintained on treatment for 13 months and was clearly more active with improvement in skeletal deformities, joint stiffness, corneal clouding and weight gain (Kakkis et al., 1995, supra). A single higher-dose experiment was quite promising and showed detectable IDUA activity in the brain and cartilage in addition to tissues which previously showed activity at the lower doses. Additional higher-dose experiments and trials involving longer administration are currently limited by availability of recombinant enzyme. These
experiments underscore the potential of replacement therapy for Hurler patients and the severe constraints on both canine and human trials due to limitations in recombinant enzyme production using current technologies.

2.2. BIOSYNTHESIS OF LYSOSONAL ENZYMES

Soluble lysosomal enzymes share initial steps of biosynthesis with secretory proteins, i.e., synthesis on the ribosome, binding of the N-terminal signal peptide to the surface of the rough endoplasmic reticulum (ER), transport into the lumen of the ER where the signal peptide is cleaved, and addition of oligosaccharides to specific asparagine residues (N-linked), followed by further modifications of the nascent protein in the Golgi apparatus (von Figura and Hasilik, 1986, Annu. Rev. Biochem. 55:167–193). The N-linked oligosaccharides can be complex, diverse and heterogeneous, and may contain high-mannose residues. The proteins undergo further processing in a post-ER, pre-Golgi compartment and in the cis-Golgi to form either an N-linked mannose 6-phosphate (M-6-P) oligosaccharide-dependent or N-linked M-6-P oligosaccharide-independent recognition signal for lysosomal localized enzymes (Kornfeld & Mellman, 1989, Ann. Rev. Cell Biol., 5:483–525; Kaplan et al., 1977, Proc. Natl. Acad. Sci. USA 74:2026). The presence of the M-6-P recognition signal results in the binding of the enzyme to M-6-P receptors (MPR). These bound enzymes remain in the cell, are eventually packaged into lysosomes, and are thus segregated results in the binding of the enzyme to M-6-P receptors (MPR). These bound enzymes remain in the cell, are eventually packaged into lysosomes, and are thus segregated.

Although many lysosomal enzymes are soluble and are transported to lysosomes by MPRs, integral membrane and membrane-associated proteins (notably hGC) are targeted and transported to lysosomes independent of the M-6-P/MPR system (Kornfeld & Mellman, 1989, Erickson et al., 1985). hGC does not become soluble after translation, but instead becomes associated with the lysosomal membrane by means which have not been elucidated (von Figura and Hasilik, 1986, Annu. Rev. Biochem. 55:167–193; Kornfeld and Mellman, 1989, Annu. Rev. Cell Biol. 5:483–525).

hGC is synthesized as a single polypeptide (58 kDa) with a signal sequence (2 kDa) at the amino terminus. The signal sequence is co-translationally cleaved and the enzyme is glycosylated with a heterogeneous group of both complex and high-mannose oligosaccharides to form a precursor. The glycans are predominately involved in protein conformation. The “high mannose” precursor, which has a molecular weight of 63 kDa, is post-translationally processed in the Golgi to a 66 Kda intermediate, which is then further modified in the lysosome to the mature enzyme having a molecular weight of 59 Kda (Jonsson et al., 1987, Eur. J. Biochem. 164:171; Erickson et al., 1985, J. Biol. Chem., 260:14319).

The mature hGC polypeptide is composed of 497 amino acids and contains five N-glycosylation amino acid consensus sequences (Asn-X-Ser/Thr). Four of these sites are normally glycosylated. Glycosylation of the first site is essential for the production of active protein. Both high-mannose and complex oligosaccharide chains have been identified (Berg-Fussman et al., 1993, J. Biol. Chem. 268:14861–14866). hGC from placenta contains 7% carbohydrate, 20% of which is of the high-mannose type (Grace & Grabowski, 1990, Biochem. Biophys. Res. Comm. 168:771–777). Treatment of placental hGC with neuraminidase (yielding an asialo enzyme) results in increased clearance and uptake rates by rat liver cells with a concomitant increase in hepatic enzymatic activity (Furbias et al., 1981, Biochim. Biophys. Acta 673:425–434). This glycan-modified placental hGC is currently used as a therapeutic agent in the treatment of Gaucher’s disease. Biochemical and site-directed mutagenesis studies have provided an initial map of regions and residues important to folding, activator interaction, and active site location (Grace et al., 1994, J. Biol. Chem. 269:2283–2291).

The complete complementary DNA (cDNA) sequence for hGC has been published (Tsuji et al., 1986, J. Biol. Chem. 261:50–53; Sorge et al., 1985, Proc. Natl. Acad. Sci. USA 82:7289–7293), and E. coli containing the hGC cDNA sequence cloned from fibroblasts, as described (Sorge et al., 1985, supra), is available from the American Type Culture Collection (ATCC) (Accession No. 65969).

Recombinant methodologies have the potential to provide a safer and less expensive source of lysosomal enzymes for replacement therapy. However, production of active enzymes, e.g., hGC, in a heterologous system requires correct targeting to the ER, and appropriate N-linked glycosylation at levels or efficiencies that avoid ER-based degradation or aggregation. Since mature lysosomal enzymes must be glycosylated to be active, bacterial systems cannot be used. For example, hGC expressed in E. coli is enzymatically inactive (Grace & Grabowski, 1990, supra).

Active monomers of hGC have been purified from insect cells (SF9 cells) and Chinese hamster ovary (CHO) cells infected or transfected, respectively, with hGC cDNA (Grace & Grabowski, 1990, supra; Grabowski et al., 1989, Enzyme 41:131–142). A method for producing recombinant hGC in CHO cell cultures and in insect cell cultures was recently disclosed in U.S. Pat. No. 5,236,838. Recombinant hGC produced in these heterologous systems had an apparent molecular weight ranging from 64 to 73 kDa and contained from 5 to 15% carbohydrate (Grace & Grabowski, 1990, supra; Grace et al., 1990, J. Biol. Chem. 265:6827–6835). These recombinant hGCs had kinetic properties identical to the natural enzyme isolated from human placenta, as based on analyses using a series of substrate and transition state analogues, negatively-charged lipid activators, protein activators (saposin C), and mechanism-based covalent inhibitors (Grace et al., 1994, supra; Berg-Fussman et al., 1993, supra; Grace et al., 1990, J. Biol. Chem. 265:6827–6835; Grabowski et al., 1989, supra). However, both insect cells and CHO cells retained most of the enzyme rather than secreting it into the medium, significantly increasing the difficulty and cost of harvesting the pure enzyme (Grabowski et al., 1989, supra).

Accordingly, a recombinant system is needed that can produce human or animal lysosomal enzymes in an active form at lower cost, and that will be appropriately targeted for case of recovery.

2.3. MAMMALIAN LYSOSONAL ENZYMES VERSUS PLANT VACUOLES

Because plants are eukaryotes, plant expression systems have advantages over prokaryotic expression systems, particularly with respect to correct processing of eukaryotic gene products. However, unlike animal cells, plant cells do not possess lysosomes. Although the plant vacuole appears functionally analogous to the lysosome, plants do not contain MPRs (Chrispeels, 1991, Ann. Rev. Pl. Phys. Pl. Mol. Biol. 42:21–53; Chrispeels and Tague, 1991, Intl. Rev. Cytol. 125:1–45), and the mechanisms of vacuolar targeting can differ significantly from those of lysosomal targeting. For example, the predominant mechanism of vacuolar targeting in plants does not appear to be glycan-dependent, but appears to be based instead on C- or N-terminal peptide sequences (Gomez & Chrispeels, 1993, Plant Cell 5:1113–1124; Chrispeels & Raikhel, 1992, Cell 68:613–618;
The present invention relates to the production of human or animal lysosomal enzymes in transformed or transfected plants, plant cells or plant tissues, and involves constructing and expressing recombinant expression constructs comprising lysosomal enzyme coding sequences in a plant expression system. The plant expression system provides appropriate co-translational and post-translational modifications of the nascent peptide required for processing, e.g., signal sequence cleavage, glycosylation, and sorting of the expression product so that an enzymatically active protein is produced. Using the methods described herein, recombinant therapeutic enzymes, such as to produce a more effective therapy, and involves constructing pBIB-KAN to form plasmid CTPro1:hGC:FLAG. R and L produce an active product.

The present invention is exemplified by the genetic-engineering of transgenic tobacco plants with three lysosomal enzyme expression constructs. One construct comprises a nucleotide sequence encoding a modified human glucocerebrosidase (hGC), specifically a hGC fused at its C-terminal to the eight amino acid FLAG™ peptide (hGC:FLAG™). Another construct comprises nucleotide sequence encoding a human α-L-iduronidase (IDUA). The third construct comprises a nucleotide sequence encoding a human glucocerebrosidase (hGC). Transgenic tobacco plants having the expression constructs produce lysosomal enzymes that are enzymatically active.

The plant expression systems and the recombinant lysosomal enzymes produced therewith have a variety of uses, including but not limited to: (1) the production of enzymatically active lysosomal enzymes for the treatment of lysosomal storage diseases; (2) the production of altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialized industrial form for research or therapeutic uses, such as to produce a more effective therapeutic enzyme; (3) the production of antibodies against lysosomal enzymes for medical diagnostic use; and (4) use in any commercial process that involves substrate hydrolysis.

3. SUMMARY OF THE INVENTION

The present invention relates to the production of human or animal lysosomal enzymes in transformed or transfected plants, plant cells or plant tissues, and involves constructing and expressing recombinant expression constructs comprising lysosomal enzyme coding sequences in a plant expression system. The plant expression system provides appropriate co-translational and post-translational modifications of the nascent peptide required for processing, e.g., signal sequence cleavage, glycosylation, and sorting of the expression product so that an enzymatically active protein is produced. Using the methods described herein, recombinant therapeutic enzymes, such as to produce a more effective therapy, and involves constructing pBIB-KAN to form plasmid CTPro1:hGC:FLAG. R and L produce an active product.

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4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. hGC:FLAG™ cDNA plant expression construct and transformation vector. The MeGA:hGC:FLAG™ construct in a pBS intermediate vector is excised and inserted into the SstI site of the binary plant transformation vector. The MeGA:hGC:FLAG™ construct comprises nucleotide sequence encoding a human glucocerebrosidase (hGC) derived sequences are in upper case; restriction sites are underlined. Restriction enzymes: E, EcoRI; S, SstI; N, NotI; X, XbaI.

FIGS. 2A–E. Transformation and generation of tobacco plants carrying the MeGA:hGC:FLAG™ construct. FIG. 2A. Agrobacterium-mediated transformation of tobacco leaf discs. Leaf discs were inoculated with a cell suspension of A. tumefaciens strains carrying the plasmid CTPro1:hGC:FLAG. FIG. 2B. Development of shoots on selection media 22 days post-inoculation. FIG. 2C. Development of roots on rooting media 27 days post-inoculation. Use of rooting media containing kanamycin clearly differentiated between transgenic shoots which formed roots and “false positive” shoots which did not form roots on selective media. FIG. 2D. Transformed plants three weeks after transfer to soil. FIG. 2E. Transformed plant 10 weeks after transfer to soil.

FIG. 3. Genomic Southern hybridization analysis of control and transgenic plants. Total genomic DNA was isolated from untransformed control plant (UT) and independent transformants generated from Nicotiana tabacum cv. Xanthi (X-1, X-8, X-9, X-11) and cv. VA116 (V1). Five to 10 μg of total genomic DNA were digested with HindIII and resolved on a TBE agarose gel. The DNA was blotted to nitrocellulose membrane and probed with a 32P-labeled hGC:FLAG™ sequence from a gel-purified 1.7 kb HindIII fragment isolated from the pBS intermediate vector containing the MeGA:hGC:FLAG™ expression construct (see FIG. 1).

FIG. 4. Induction of hGC:FLAG™ mRNA levels in transgenic plants. Total RNA was isolated by standard guanidino-thiocyanate methods from UT and X-11 leaf tissue at 0 and 24 hr post-mechanical gene activation (MGA). Five μg of total RNA was glyoxylated, size-separated on a 1.2% agarose gel, transferred to NitroPure (MSI) filters and probed with a 32P-labeled hGC:FLAG™ gene sequence from a gel-purified 1.7 kb HindIII fragment isolated from the pBS intermediate vector shown in FIG. 1.

FIGS. 5A–B. Induction of hGC:FLAG™ fusion protein in transgenic tobacco plants as detected by Western analysis using anti-FLAG™ antibodies and anti-hGC antibodies. Leaf tissue from X-11 was induced by MGA at time 0 at room temperature, harvested at 2, 4, 8, 16, and 24 hrs, and frozen at −20°C. prior to extraction. hGC:FLAG™ was solubilized by grinding the tissue in a coffee bean grinder with dry ice and homogenized in 1% Triton X-100, 1% taurocholate, 25 mM sodium citrate pH 7.0, 4 mM β-mercaptoethanol, and 5 mM ethylenediaminetetraacetic acid (EDTA), followed by two cycles of freezing and thawing of the homogenate. Both protein concentration and enzyme activity of cell free extracts were determined. FIG. 5A. Ten μg of total soluble protein were analyzed by Western immunoblot using anti-FLAG™ antibodies. Lane 1, 24 ng of FLAG™-tagged control protein; lane 2, X-11 at time 0; lane 3, X-11 at 2 hr; lane 4, X-11 at 4 hrs; lane 5, X-11 at 8 hrs; lane 6, X-11 at 12 hrs; lane 7, X-11 at 24 hrs; lane 8, UT (control plant) at 12 hrs. FIG. 5B. Forty μg of total soluble protein were analyzed by Western immunoblot using anti-hGC antibodies. Lane 1, UT at time 0; lane 2, X-11 at time 0; lane 3, X-11 at 2 hrs; lane 4, X-11 at 4 hrs; lane 5, X-11 at 8 hrs; lane 6, X-11 at 12 hrs; lane 7, X-11 at 24 hrs; lane 8, UT at 8 hrs. The maximum level of hGC:FLAG™ expression was found between 8–12 hrs post-MGA.

FIG. 6. Total β-glucosidase (endogenous plant β-glucosidase and hGC) activity post-MGA of X-11 leaf tissue. One-tenth μg of cell free extract was assayed for...
ability to convert the fluorometric substrate, 4-methylumbelliferyl-D-glucopyranoside (4MuGlc) to 4Mu at 37°C, as measured in a fluorometer (Hoefer DynaQuant-200, Hoefer, Pharmacia, Biotech. Inc.) with excitation at 365 nm and emission at 460 nm. Fluorometer units; Time=hrs post-inducti(on (i.e., wounding of tissue or MGA).

FIGS. 7A–B. Affinity purification of hGCFLAG™ fusion protein. FIG. 7A. Commassie blue stained SDS-PAGE gel and Western analysis of hGCFLAG™ fusion protein. Lane 1, Commassie blue stained SDS-PAGE gel of 0.1 μg FLAG™ affinity-purified hGCFLAG™. Lane 2, Western analysis using anti-hGC antibodies on 0.1 μg FLAG™ affinity-purified hGCFLAG™. FIG. 7B. Commassie blue stained SDS-PAGE gel and Western analysis of ConA-affinity-purified hGCFLAG™. Lane 1, Commassie blue stained SDS-PAGE gel of 10 μg of ConA purified hGCFLAG™. Lane 2, Western analysis of ConA purification of hGCFLAG™ using anti-FLAG™ antibodies. These results indicate that the ConA-purified hGCFLAG™ protein is glycosylated.

FIG. 8. Immuno-slot blot Western analysis using anti-FLAG™ antibodies on fractions from hGCFLAG™ fusion protein purification steps using plant tissue 12 hrs post-MGA. Lane A, hGCFLAG™ fusion protein; lane B, FLAG™-tagged control protein: slot 1, 1 ng; slot 2, 6 ng; slot 3, 8 ng; slot 4, 18 ng; slot 5, 60 ng. Lane B, Fractions 1, 2, and 3, from isolation of hGCFLAG™: slot 1, 0.5 μl/800,000 μl soluble protein from crude cell free extract; slot 2, 0.5 μl/800,000 μl soluble protein from 33% ammonium sulfate (AS) supernatant; slot 3, 2.5 μl/5,000 μl soluble protein from ConA-affinity-purified hGCFLAG™. Lane C: slot 1, 1 μl soluble protein from crude plant tissue extract; slot 2, 1 μl soluble protein from 33% AS supernatant; slot 3, 5 μl soluble protein from ConA-affinity purified hGCFLAG™.

FIG. 9. Nucleotide sequence of hGCFLAG™ construct (SEQ ID NO:3) which was cloned and expressed in tobacco strains X-11 and X-27. The upper case underlined letters represent additions to the hGC amino acid sequence, e.g., the XbaI (ATCC bank cDNA sequence). The lower case letters represent additions to the hGC sequence, e.g., the FLAG™ epitope.

FIG. 10. Deduced amino acid sequence of hGCFLAG™ fusion protein (SEQ ID NO:4). The upper case underlined letters at two positions represent changes to the original hGC amino acid sequence disclosed by E. Neufeld. Lower case letters represent additions to the hGC amino acid sequence. For example, dykdddddh(SEQ ID NO:10)=the FLAG™ epitope.

FIG. 11. Sequence of 456 bases (SEQ ID NO:5) comprising the McGA promoter.

FIG. 12. IDUA expression vector construction strategy. McGA-IDUA and 35SenhIDUA constructs were inserted into the HindIII/SacI site of the binary vector pHBB-KAN. R and I represent T-DNA right and left borders which precisely demarcate the DNA inserted into the plant genome. NPTII is the kanamycin selectable marker, Pnos is the polyadenylation/terminator signal and Pnos a promoter from Agrobacterium tumefaciens nopaline synthetase gene. PCR-products for IDUA were: 1D1, (5'-CTAG tetagaATGGGTCCCTGGGCCCCCGCGC) (SEQ ID NO:6) and 1D2, (5'CGT gattctggagTCATGGAATGGGCCGCCGAGT) (SEQ ID NO:7); IDUA sequences are capitalized, introduced restriction sites are underlined. SP, signal peptide; IDUA, human IDUA coding region; H, HindIII; S, SacI; X, XbaI.

FIGS. 13A–C. Transgenic tobacco expressing the McGA-IDUA construct. FIG. 13A. Germination of first generation seeds on selective medium showing segregation of kanamycin resistant and sensitive sccllings. FIG. 13B. Young plants containing the McGA-IDUA construct (right) and untransformed parent plants grown in parallel. FIG. 13C. Fully mature IDUA-expressing plants in the greenhouse.

FIGS. 14A–B. Induction of IDUA gene in tobacco leaf tissues. Leaf tissue from transgenic plant IDUA-9 was induced by excision into 1.5 mm strips and incubated at room temperature on moist paper towels in sealed plastic bag. Tissue was removed for analysis (stored at —80°C for RNA, —20°C for protein) at 0, 2, 4, 8, 11, and 27 hrs post-induction. FIG. 14A. Northern blot analysis of IDUA mRNA from transgenic tobacco plants. Fifteen μg of total RNA was run on glyoxal agarose gel, blotted onto nitrocellulose membrane, and hybridized with 32P-labeled IDUA cDNA. FIG. 14B. Western blot analysis of total soluble proteins (20 μg) from tobacco leaf extracts using antibodies to denatured IDUA synthesized in CHO cells. Control lane represents IDUA synthesized in CHO cells (98 kDa under our gel conditions). IDUA synthesized from transgenic tobacco has a molecular size of 92 kDa.

FIG. 15. Immunodetection of IDUA secreted by transgenic plants into the incubation buffer. Fifty μl of incubation buffer was boiled and slotted onto OPTITRAN membrane along with control IDUA synthesized in CHO cells. Antibodies to denatured IDUA synthesized in CHO cells were used to detect IDUA.

FIG. 16. IDUA activity in tissue extracts and incubation buffer from transgenic IDUA-9 plant tissue. Panel A: IDUA-9 plant tissue was induced and incubated in buffer, which was collected and replaced at various times after induction as described in the text. Open boxes represent IDUA activity in extracts prepared from induced tissue after incubation in buffer. Shaded boxes represent the IDUA activity in the incubation buffer. Panel B: IDUA-9 plant tissue was induced and incubated without buffer for 34 hours after which an extract was prepared from the induced tissue. The IDUA activity of the extract is shown.

FIG. 17. Comparison of IDUA activity in transgenic tobacco plants IDUA-7, IDUA-8 and IDUA-9: Panel A: Plant tissue was induced and incubated in buffer, which was collected and replaced at various times after induction as described in the text. IDUA activity present in the incubation buffer collected at various times post-induction was plotted. Panel B: Plant tissue was induced and incubated without buffer. Absence of incubation buffer for 34 hours, after which extracts were prepared from the induced tissues. The IDUA activities of the extracts are shown.

FIG. 18. Western slot blot analysis of secreted IDUA from transgenic plant IDUA-9 after three sequential addition and collection of incubation buffer; 24, 26 and 34 hrs post-MGA. The tissue (1.5 gm) was induced and incubated in a moist plastic bag for 24 hrs. Ten ml of incubation buffer was used to wash the tissue; this fraction is denoted as 24 hrs. Fresh buffer (10 ml) was added and incubated at room temperature for 2 hrs; this fraction was denoted as 26 hrs. Fresh buffer (10 ml) was added to the tissue and incubated for 8 hrs and this fraction was denoted as 34 hrs. Fifty μl of incubation buffer from each fraction was boiled and slotted onto OPTITRAN membrane and analyzed with anti-IDUA antibodies.

FIG. 19. The nucleotide sequence of the IDUA coding sequence (SEQ ID NO:8) used in the McGA-IDUA and 35SenhIDUA expression construct.

FIG. 20. The deduced amino acid sequence (SEQ ID NO:9) of the IDUA coding sequence shown in FIG. 19.
FIG. 21. hGC cDNA plant expression construct and transformation vector. The MeGa:hGC expression construct in a PBS intermediate plasmid is excised and inserted into the SstI site of the binary plant transformation vector pBBKAN to form transformation vector pCT50. The PCR-amplification primers for reconstruction of the 3' end of the hGC coding region were: GC23, which has the sequence 5'GCCATGCTGACACAAGTTACAG3' (SEQ ID NO:11); and GC37, whose complementary strand has the sequence 5'TTCTCTGGAGTCACTGGCGACGCCACAGGTA3' (SEQ ID NO:12). The other abbreviations and notations shown are same as those described for FIG. 1.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to the production of recombinant human or animal lysosomal enzymes in plants and in cultured plant cells and plant tissues, involving: (1) construction of recombinant expression constructs comprising lysosomal enzyme coding sequences and transformation vectors containing the expression constructs; (2) transformation or transfecting plant cells, plant tissues or plants with the transformation vectors; (3) expressing the lysosomal enzyme coding sequences in the plant cell, plant tissue or plant; and (4) detecting and purifying expression products having lysosomal enzyme activity.

The plant expression systems and the recombinant lysosomal enzymes produced therewith have a variety of uses, including but not limited to: (1) the production of enzymatically active enzymes for the treatment of lysosomal storage diseases; (2) the production of antibodies against lysosomal enzymes, which antibodies would have medical diagnostic uses; (3) use in any commercial process that involves substrate hydrolysis; and (4) the production of modified enzymes, which antibodies would have medical diagnostic uses.

Once a plant transformant or transfectant is identified that expresses a recombinant lysosomal enzyme, one non-limiting embodiment of the invention involves the cloning and use of that transformant or transfectant in the production and purification of enzymatically active recombinant lysosomal enzyme. In another non-limiting embodiment of the invention, each new generation of progeny plants may be newly screened for the presence of nucleotide sequence coding for a lysosomal enzyme, wherein such screening results in production by subsequent generations of plants of recoverable amounts of active recombinant lysosomal enzyme, and wherefrom the enzyme is then purified.

The invention is divided into the following sections solely for the purpose of description: (a) genes or coding sequences for lysosomal enzymes involved in lysosomal storage diseases; (b) construction of recombinant expression constructs for expressing lysosomal enzyme coding sequences in plant cell; (c) construction of plant transformation vectors comprising the expression constructs; (d) transformation/transfection of plants capable of translating and processing primary translation products in order to express an enzymatically active recombinant lysosomal enzyme; (e) identification and purification of the recombinant lysosomal enzyme so produced; (f) expansion of the number of transformed or transfected plants; and (g) methods of therapeutically using the recombinant lysosomal enzyme.

5.1. GENES OR CODING SEQUENCES FOR ENZYMES INVOLVED IN LYOSOMAL STORAGE DISEASES

The recombinant lysosomal enzymes produced in accordance with this invention will have a variety of uses, probably the most significant being their use in enzyme replacement therapy for lysosomal storage diseases. These lysosomal enzymes include but are not limited to: α-N-acetylgalactosaminidase (Warner et al., Biochem. Biophys. Res. Commun., 1990, 170:13—19; acid lipase; aryl sulfatase A; aspartylglucosaminidase; ceramidase; α-L-fucosidase (de Wet et al., 1984, DNA 3:437—447), α-galactosidase, β-galactosidase, galactosylceramidase, glucocerebrosidase, α-glucosidase, β-glucuronidase, heparin N-sulfatase, β-hexosaminidase, iduronate sulfatase, α-L-iduronidase, α-mannosidase, β-mannosidase, stilidase, and sphingomyelinase. Of these enzymes, cDNAs have been cloned for α-N-acetylgalactosaminidase (Zhu & Goldstein, 1993, Gene 137:309—314); acid lipase (Ames et al., 1994, Eur. J. Biochem. 219:905—914); α-galactosidase (Eng & Desnick, 1994, Hum Mutat. 3:103—111); human glucocerebrosidase
The nucleic acid sequences encoding lysosomal enzymes which can be used in accordance with the invention include but are not limited to any nucleic acid sequence that encodes a lysosomal enzyme, modified lysosomal enzyme, or functional equivalent thereof, including but not limited to: (a) any nucleotide sequence that selects hybridizes to the complement of a human or animal lysosomal enzyme coding sequence under stringent conditions, e.g., washing in 0.1x SSC/0.1% SDS at 68°C (Ausubel et al., 1989, Current Protocols in Molecular Biology, Vol. 1, Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., New York, at page 2.10.3), and encodes a product homologous to the human or animal lysosomal enzyme; and/or (b) any nucleotide sequence that hybridizes to the complement of the human or animal lysosomal enzyme coding sequence under less stringent conditions, such as moderately stringent conditions, e.g., washing in 0.2x SSC/0.1% SDS at 42°C (Ausubel et al., 1989, supra), yet which still encodes a homologous gene product that is enzymatically active; and (c) any nucleotide coding sequence that otherwise encodes) a protein from any organism capable of hydrolyzing a human or animal lysosomal enzyme's native substrate or substrate analogue.

The invention also includes but is not limited to: (a) DNA vectors that contain any of the foregoing nucleotide coding sequences and/or their complements; (b) DNA expression and transformation vectors that contain expression constructs comprising any of the foregoing nucleotide coding sequences operatively associated with a regulatory element that directs expression of the coding sequences in plant cells or plants; and (c) genetically engineered plant cells or plants that contain any of the foregoing coding sequences, operatively associated with a regulatory element that directs the expression of the coding and/or antisense sequences in the plant cell. As used herein, the term "regulatory element" includes but is not limited to inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art to drive and/or regulate gene expression. The invention also includes fragments, derivatives or other modifications of the DNA sequences described herein.

5.2. TRANSFORMATION VECTORS TO DIRECT THE EXPRESSION OF LYOSOMAL ENZYME CODING SEQUENCE

5.2.1. LYOSOMAL ENZYME EXPRESSION CONSTRUCTS

In order to express a lysosomal enzyme in a plant expression system, the lysosomal enzyme coding sequence is inserted into an appropriate expression construct and the expression construct is incorporated into a transformation vector for transfer into cells of the plant. The expression construct is preferably constructed so that the lysosomal enzyme coding sequence is operatively associated with one or more regulatory elements, including, e.g., promoters and/or enhancers, necessary for transcription and translation of the lysosomal enzyme coding sequence. Methods to construct the expression constructs and transformation vectors include standard in vitro genetic recombination and manipulation. See, for example, the techniques described in Weissbach and Weissbach, 1988, Methods For Plant Molecular Biology, Academic Press, Chapters 26–28.

Regulatory elements that may be used in the expression constructs include promoters which may be either heterologous or homologous to the plant cell. The promoter may be a plant promoter or a non-plant promoter which is capable of driving high levels transcription of a linked sequence in plant cells and plants. Non-limiting examples of plant promoters that may be used effectively in practicing the invention include cauliflower mosaic virus (CaMV) 35S, rcbS, the promoter for the chlorophyll a/b binding protein, Adhl, NOS and HMG2, or modifications or derivatives thereof. The promoter may be either constitutive or inducible. For example, and not by way of limitation, an inducible promoter can be a promoter that promotes expression or increased expression of the lysosomal enzyme nucleotide sequence after mechanical gene activation (MGA) of the plant, plant tissue or plant cell. One non-limiting example of such an MGA-inducible plant promoter is MeGA (described infra).

The expression constructs can be additionally modified according to methods known to those skilled in the art to enhance or optimize heterologous gene expression in plants and plant cells. Such modifications include but are not limited to mutating DNA regulatory elements to increase promoter strength or to alter the lysosomal enzyme coding sequence itself. Other modifications include deleting intron sequences or excess non-coding sequences from the 5' and/or 3' ends of the lysosomal enzyme coding sequence in order to minimize sequence- or distance-associated negative effects on expression of hGC, e.g., by minimizing or eliminating message destabilizing sequences.

The expression constructs may be further modified according to methods known to those skilled in the art to add, remove, or otherwise modify peptide signal sequences to alter signal peptide cleavage or to increase or change the targeting of the expressed lysosomal enzyme through the plant endomembrane system. For example, but not by way of limitation, the expression construct can be specifically engineered to target the lysosomal enzyme for secretion, or vacuolar localization, or retention in the endoplasmic reticulum (ER).

In one embodiment, the expression construct can be engineered to incorporate a nucleotide sequence that encodes a signal targeting the lysosomal enzyme to the plant vacuole. For example, and not by way of limitation, the N-terminal 143 amino acid domain derived from the plant vacuolar protein, proaleurain (Holwerda et al., 1992, supra; Holwerda et al., 1990, supra), may be engineered into the expression construct to produce a signal peptide-lysosomal enzyme fusion product upon transcription and translation. The proaleurain signal peptide will direct the lysosomal enzyme to the plant cell vacuole, but is itself cleaved off during transit through the plant endomembrane system to generate the mature protein.

In another non-limiting embodiment, a signal peptide may be engineered into the expression construct to direct the lysosomal enzyme to be secreted from the plant cell. For example, and not by way of limitation, the signal peptide of tobacco PR-1, which is a secreted pathogenesis-related protein (Cornelissen et al., 1986, EMBO J. 5:37–40), can be engineered into the expression construct to direct the secretion of the lysosomal enzyme from the plant cell.

In an additional non-limiting embodiment, the signal peptide or peptide engineered into the expression construct may direct the lysosomal enzyme to be retained within the ER. Such ER-retained lysosomal enzymes may exhibit altered, and perhaps preferable, glycosylation patterns as a result of failure of the peptide to progress through the Golgi
Expression construct may be further modified according to methods known to those skilled in the art to add coding sequences that facilitate purification of the lysosomal enzyme. In one non-limiting embodiment, a nucleotide sequence coding for the target epitope of a monoclonal antibody may be engineered into the expression construct in operative association with the regulatory elements and situated so that the expressed epitope is fused to the lysosomal enzyme. For example, and not by way of limitation, a nucleotide sequence coding for the FLAG™ epitope tag (International Biotechnologies, Inc., [1B]), which is a hydrophilic marker peptide, can be inserted by standard techniques into the expression construct at a point corresponding to the carboxyl-terminus of the lysosomal enzyme. The expressed FLAG™ epitope-lysosomal enzyme fusion product may then be detected and affinity-purified using anti-FLAG™ antibodies.

In another non-limiting embodiment, a nucleotide sequence can be engineered into the expression construct to provide for a cleavable linker sequence between the lysosomal enzyme peptide sequence and any targeting signal, reporter peptide, selectable marker, or detectable marker, as described supra, that has not otherwise been cleaved from the lysosomal enzyme peptide sequence during peptide processing and trafficking through the plant endomembrane system. Such a linker sequence can be selected so that it can be cleaved either chemically or enzymatically during purification of the lysosomal enzyme (Light et al., 1980, Anal. Biochem. 106:199—206).

5.2.2. PLANT TRANSFORMATION VECTORS

The transformation vectors of the invention may be developed from any plant transformation vector known in the art include, but are not limited to, the well-known family of Ti plasmids from Agrobacterium and derivatives thereof, including both integrative and binary vectors, and including but not limited to pBIKAN, pGA471, pEND4K, pGv3850, and pMON505. Also included are DNA and RNA plant viruses, including but not limited to CaMV, geminiviruses, tobacco mosaic virus, and derivatives engineered therefrom, any of which can effectively serve as vectors to transfer a lysosomal enzyme coding sequence, or functional equivalent thereof, with associated regulatory elements, into plant cells and/or autonomously maintain the transferred sequence. In addition, transposable elements may be utilized in conjunction with any vector to transfer the coding sequence and regulatory sequence into a plant cell.

To aid in the selection of transformants and transfectants, the transformation vectors may preferably be modified to comprise a coding sequence for a reporter gene product or selectable marker. Such a coding sequence for a reporter or selectable marker should preferably be in operative association with the regulatory element coding sequence described supra.

Reporter genes which may be useful in the invention include but are not limited to the β-glucuronidase (GUS) gene (Jefferson et al., 1986, Proc. Natl. Acad. Sci. USA, 83:8447), and the luciferase gene (Ow et al., 1986, Science 234:856). Coding sequences that encode selectable markers which may be useful in the invention include but are not limited to those sequences that encode gene products conferring resistance to antibiotics, anti-metabolites or herbicides, including but not limited to kanamycin, hygromycin, streptomycin, phosphinothricin, gentamicin, methotrexate, glyphosate and sulfonylurea herbicides, and include but are not limited to coding sequences that encode enzymes such as neomycin phosphotransferase II (NPTII), chloramphenicol acetyltransferase (CAT), and hygromycin phosphotransferase I (HPT, HYG).

5.3. TRANSFORMATION/TRANSFECTION OF PLANTS

A variety of plant expression systems may be utilized to express the lysosomal enzyme coding sequence or its functional equivalent. Particular plant species may be selected from any dicotyledonous, monocotyledonous species, gymnospermous, lower vascular or non-vascular plant, including any cereal crop or other agriculturally important crop. Such plants include, but are not limited to, alfalfa, Arabidopsis, asparagus, barley, cabbage, carrot, celery, corn, cotton, cucumber, flax, lettuce, oil seed rape, pear, peas, petunia, poplar, potato, rice, soybean, sugar beet, sunflower, tobacco, tomato, wheat and white clover.

Methods by which plants may be transformed or transfected are well-known to those skilled in the art. See, for example, Plant Biotechnology, 1989, Kung & Antzen, eds., Butterworth Publishers, ch. 1, 2. Examples of transformation methods which may be effectively used in the invention include but are not limited to Agrobacterium-mediated transformation of leaf discs or other plant tissues, microinjection of DNA directly into plant cells, electroporation of DNA into plant cell protoplasts, liposome or spheroplast fusion, microprojectile bombardment, and the transfection of plant cells or tissues with appropriately engineered plant viruses.

Plant tissue culture procedures necessary to practice the invention are well-known to those skilled in the art. See, for example, Dixon, 1985, Plant Cell Culture: A Practical Approach, IRL Press. Those tissue culture procedures that may be used effectively to practice the invention include the production and culture of plant protoplasts and cell suspensions, sterile culture propagation of leaf discs or other plant tissues with appropriately engineered strains of transforming agents such as, for example, Agrobacterium or plant virus strains and the regeneration of whole transformed plants from protoplasts, cell suspensions and callus tissues.

The invention may be practiced by transforming or transfecting a plant or plant cell with a transformation vector containing an expression construct comprising a coding sequence for the lysosomal enzyme and selecting for transformants or transfectants that express the lysosomal enzyme. Transformed or transduced plant cells or tissues may be selected by techniques well-known to those of skill in the art, including but not limited to detecting reporter gene products or selecting based on the presence of one of the selectable markers described supra. The transformed or transcribed plant cells or tissues are then grown and whole plants regenerated therefrom. Integration and maintenance of the lysosomal enzyme coding sequence in the plant genome can be confirmed by standard techniques, e.g., by Southern hybridization analysis, PCR analysis, including reverse transcriptase-PCR (RT-PCR), or immunological assays for the expected protein products. Once such a plant transformant or transfectant is identified, a non-limiting embodiment of the invention involves the clonal expansion and use of that transformant or transfectant in the production of lysosomal enzyme.

As one non-limiting example of a transformation procedure, Agrobacterium-mediated transformation of plant
leaf disks can follow procedures that are well known to those skilled in the art. Briefly, leaf disks can be excised from axenically grown plant seedlings, incubated in a bacterial suspension, for example, 10^6 cfu/ml of A. tumefaciens containing an engineered plasmid comprising a selectable marker such as, for example, kanamycin resistance, and transferred to selective “shooting” medium containing, for example, kanamycin, that will block growth of bacteria and untransformed plant cells and induce shoot initiation and leaf formation from transformed cells. Shoots are regenerated and then transferred to selective media to trigger root initiation. Stringent antibiotic selection at the rooting step is useful to permit only stably transformed shoots to generate roots. Small transgenic plantlets may then be transferred to sterile peat, vermiculite, or soil and gradually hardened off for growth in the greenhouse or in the field.

5.4. IDENTIFICATION AND PURIFICATION OF THE LYSOSOMAL ENZYME GENE PRODUCT

Transcription of the lysosomal enzyme coding sequence and production of the lysosomal enzyme in transformed or transplanted plants, plant tissues, or plant cells can be confirmed and characterized by a variety of methods known to those of skill in the art. Transcription of the lysosomal enzyme coding sequence can be analyzed by standard techniques, including but not limited to detecting the presence of lysosomal enzyme messenger ribonucleic acid (mRNA) transcripts in transformed or transplanted plants or plant cells using Northern hybridization analysis or RT-PCR amplification.

Detection of the lysosomal enzyme itself can be carried out using any of a variety of standard techniques, including, but not limited to, detecting lysosomal enzyme activity in plant extracts, e.g., by detecting hydrolysis of either the enzyme’s natural substrate or a substrate analogue. Additionally, the lysosomal enzyme can be detected immunologically using monoclonal or polyclonal antibodies, or immuno-reactive fragments or derivatives thereof, raised against the enzyme, e.g., by Western blot analysis, and limited amino acid sequence determination of the protein.

Indirect identification of enzyme production in a plant can be performed using any detectable marker or reporter linked to the lysosomal enzyme. For example, but not by way of limitation, the FLAG™ epitope, which can be linked to the lysosomal enzyme, as described supra, is detectable in plant tissues and extracts using anti-FLAG M2 monoclonal antibodies (IBI) in conjunction with the Western Exposure™ chemi-luminescent detection system (Clontech).

Lysosomal enzyme production in a transformed or transplanted plant can be confirmed and further characterized by histochemical localization, the methods of which are well known to those skilled in the art. See, for example, Techniques in Immunocytochemistry, Vol I, 1982, Bullock and Petrusz, eds., Academic Press, Inc. For example, but not by way of limitation, either fresh, frozen, or fixed and embedded tissue can be sectioned, and the sections probed with either polyclonal or monoclonal primary antibodies raised against the lysosomal enzyme or, for example, anti-FLAG™ monoclonal antibodies. The primary antibodies can then be detected by standard techniques, e.g., using the biotinylated protein A-alkaline phosphatase-conjugated streptavidin technique, or a secondary antibody bearing a detectable label that binds to the primary antibody.

The expression products can be further purified and characterized as described in the subsections below.

5.4.1. PRODUCTION AND PURIFICATION OF THE LYSOSOMAL ENZYME GENE PRODUCT

One non-limiting method to produce and purify the lysosomal enzyme is described here, wherein the lysosomal enzyme coding sequence is operably associated with an inducible promoter in the expression construct. Leaf or other tissue or cells from a transgenic plant or cell culture transformed or transfected with this expression construct can be processed to induce expression of the lysosomal enzyme coding sequence. This induction process may include inducing the activation of lysosomal genes by one or more methods, applied separately or in combination, including but not limited to physical wounding or other mechanical gene activation (MGA), and application of chemical or pathogenic elicitors or plant hormones. Lysosomal gene activation levels may also be enhanced in plant cells or tissues by factors such as the availability of nutrients, gases such as O_2 and CO_2, and light or heat. After induction of expression, the tissue can be stored, e.g., at -20°C. If the lysosomal protein is targeted for localization within the plant cell, the plant cell wall must be penetrated to extract the protein. Accordingly, the plant tissue can be ground to a fine powder, e.g., by using a tissue grinder and dry ice, or homogenized with a ground glass tissue homogenizer. To resuspend the lysosomal enzyme, plant membranes must be solubilized using an extraction buffer containing a detergent, e.g., a bile detergent such as 1% (w/v) sodium taurocholate, in a buffered solution, e.g., 25 mM sodium citrate, pH 7.0. The homogenate can then be clarified by, for example, centrifugation at 10,000g for 30 min to produce a cell-free homogenate.

The lysosomal enzyme must be further purified if it is to be useful as a therapeutic or research reagent. The lysosomal enzyme can be purified from plant extracts according to methods well known to those of skill in the art (Furbish et al., 1977, Proc. Natl. Acad. Sci. USA 74:3560–3563). Once the presence of the enzyme is confirmed it can be isolated from plant extracts by standard biochemical techniques including, but not limited to, differential ammonium sulfate (AS) precipitation, gel filtration chromatography or affinity chromatography, e.g., utilizing hydrophobic, immunological or lectin binding. At each step of the purification process the yield, purity and activity of the enzyme can be determined by one or more biochemical assays, including but not limited to: (1) detecting hydrolysis of the enzyme’s substrate or a substrate analogue; (2) immunological analysis by use of an enzyme-linked immunosorbent assay (ELISA); (3) sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) analysis; and (4) Western analysis. The enzyme may be alternatively or additionally purified by affinity chromatography wherein the enzyme binds to its inhibitor which is linked, for example, to an inert substrate.

Once solubilized, all enzyme-containing fractions can be maintained, for example, by storage at 4°C, and stabilized if necessary, e.g., with 4 mM β-mercaptoethanol, 5 mM EDTA, and/or possibly with high levels of glycerol or ethylene glycol.

5.4.2. PROTEOLYTIC PROCESSING OF THE SIGNAL PEPTIDE

In order to address whether the plant expression system efficiently recognizes and correctly cleaves the human signal peptide from the lysosomal enzyme, the plant-produced enzyme can be purified and analyzed by N-terminal sequencing. Accordingly, the enzyme can, for example, be treated with Endo-F/N-glucanase (Boehringer Mannheim) to remove N-linked glycans, and the resulting peptide can be repurified by methods described supra. The purity of the enzyme can be determined based, for example, on silver-stained SDS-PAGE. The band containing the enzyme can be excised from the gel, the peptide eluted therefrom, and then analyzed by commercial N-terminal amino acid sequencing to determine whether the correct cleavage of the signal peptide.
peptide has occurred. Incomplete cleavage can be detected, for example, as a double band on SDS-PAGE, or as mixed-N-terminal sequences.

5.4.3. N-LINKED GLYCOSYLATION IN PLANTS VERSUS ANIMALS

The oligosaccharides of native human and animal lysosomal enzymes are typical antennary structures containing N-acetylgalactosamine, mannose, and galactose. The glycoconjugate associated with the lysosomal enzyme of the invention may be determined, for example, by lectin binding studies (Reddy et al., 1985, Biochem. Med. 33:200–210, Cummings, 1994, Meth. Enzymol. 230:66–86).

Plant glycans do not contain sialic acid, which is a prevalent terminal sugar in mammalian glycans. In addition, the complex glycans of plants are generally smaller and contain a β1-2 xylose residue attached to the β-linked mannose residues of the core (Gomez and Chrispeels, 1994, Proc. Natl. Acad. Sci. USA 91:1829–1833).

Determination of the glycan composition and structure of the lysosomal enzyme of the invention is of particular interest because: (a) the glycan composition will indicate the status of the protein’s movement through the Golgi; and (b) the presence of a complex glycan may indicate whether an antigenic response will be triggered in humans.

Several molecular, genetic and chemical approaches can be used to raise the proportion of the high-mannose form of glycans on lysosomal enzymes, making them more similar in structure to the native human protein (Grabowski et al., 1995, Ann. Int. Med. 122:33–39; Berg-Fussman et al., 1993, J. Biol. Chem. 268:14861–14866). For example, but not by way of limitation, the mannose analog, 1-deoxymannojirimycin (dMM), inhibits mannosidase I, the first Golgi-specific enzyme involved in glycan processing. Plant tissues treated with dMM produce glycoproteins which lack fucose and xylose and maintain a glycan profile consistent with inhibition at the mannosidase I step (Vitale et al., 1989, Pl. Physiol. 89:1079–1084). Treatment of lysosomal enzyme-expressing plant tissues with dMM may be useful to produce lysosomal enzymes with a relatively homogeneous high-mannose glycan profile. Such lysosomal enzymes should be highly effective for use in treatment of lysosomal storage diseases in human and animals.

5.5. CLONAL PROPAGATION AND BREEDING OF TRANSGENIC PLANTS

Once a transformed or transfected plant is selected that produces a useful amount of the recombinant lysosomal enzyme of the invention, one embodiment of the invention contemplates the production of clones of this plant either by well-known asexual reproductive methods or by standard plant tissue culture methods. For example, tissues from a plant of interest can be induced to form genetically identical plant regenerants by transferring the lysosomal enzyme coding sequence, as well as all plants in subsequent generations descending from a cross in which at least one of the parents comprised the lysosomal enzyme coding sequence. The invention further encompasses all seeds comprising the lysosomal enzyme coding sequence and from which such plants can be grown, and tissue cultures, including callus tissues, cell suspensions and protoplasts, comprising the lysosomal enzyme coding sequence, whether or not they can be regenerated back to plants.

5.6. METHODS FOR THERAPEUTIC USE OF LYSOSOMAL ENZYMES

The recombinant lysosomal enzymes of the invention are useful for therapeutic treatment of lysosomal storage diseases by providing a therapeutic amount of a particular lysosomal enzyme, or a derivative or modification thereof, to a patient suffering from a lysosomal storage disease or condition resulting from a deficiency of the corresponding human or animal active form of that enzyme.

By “therapeutic amount” is meant an amount of enzymatically active lysosomal enzyme which will cause significant alleviation of clinical symptoms of a particular lysosomal storage disease.

A therapeutic amount causes “significant alleviation of clinical symptoms” of the particular lysosomal storage disease if it serves to reduce one or more of the pathological effects or symptoms of the disease or to reduce the rate of progression of one or more of such pathological effects or symptoms.

An effective dosage and treatment protocol may be determined by conventional means, starting with a low dose in laboratory animals and then increasing the dosage while monitoring the effects, and systematically varying the dosage regimen as well. The amount of recombinant lysosomal enzyme to be administered to a patient suffering from a lysosomal disease or condition will vary. Numerous factors may be taken into consideration by a clinician when determining an optimal dose for a given subject. These factors include the size of the patient, the age of the patient, the general condition of the patient, the particular disease being treated, the severity of the disease, the presence of other drugs in the patient, and the like. Trial dosages would be chosen after consideration of the results of animal studies, and any available clinical literature with respect to past results of replacement therapy for the particular lysosomal storage disease.

For example, therapeutic amounts of recombinant hGC and IDUA and modified hGC and IDUA produced according to the invention may in each instance encompass dosages of between about 10 and about 500 mg per 70 kg patient per month, depending upon the severity of the patient’s symptoms of the Gaucher’s or Hurler’s disease.

The amount of recombinant lysosomal enzyme of the invention administered to the patient may be decreased or increased according to the enzymatic activity of the particular lysosomal enzyme. For example, administration of a recombinant lysosomal enzyme of the invention which has been modified to have increased enzymatic activity relative to the native human or animal enzyme will require administration of a lesser amount to the patient than a native human or animal lysosomal enzyme having lower enzymatic activity.

In addition, the amount of recombinant lysosomal enzyme administered to the patient may be modified over time
depending on a change in the condition of the patient as treatment progresses, the determination of which is within the skill of the attending clinician.

The invention also provides pharmaceutical formulations for use of the recombinant lysosomal enzyme in treating lysosomal storage diseases. The formulations comprise a recombinant lysosomal enzyme of the invention and a pharmaceutically acceptable carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.4% saline, 0.3% glycerine, and the like. The pharmaceutical formulations may also comprise additional components that serve to extend the shelf-life of pharmaceutical formulations, including preservatives, protein stabilizers, and the like. The formulations are preferably sterile and free of particulate matter (for injectable forms). These compositions may be sterilized by conventional, well-known sterilization techniques.

The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, etc.

The formulations may be adapted for various forms of administration, including intramuscularly, subcutaneously, intravenously and the like. The subject formulations may also be formulated so as to provide for the sustained release of a lysosomal enzyme. Actual methods for preparing parenterally administrable compositions and adjustments necessary for administration to subjects will be known or apparent to those skilled in the art and are described in more detail in, for example, Remington's Pharmaceutical Science, 17th Ed., Mack Publishing Company, Easton, Pa. (1985), which is incorporated herein by reference.

The invention is illustrated in the working examples described infra, for the expression of hGC in tobacco.

6. EXAMPLE 1

PRODUCTION AND ISOLATION OF RECOMBINANT MODIFIED hGC FROM TRANSGENIC TOBACCO PLANTS

The subsections below describe the production of an enzymatically active modified human glucocerebrosidase (hGC) in tobacco.

6.1. CONSTRUCTION OF A MODIFIED hGC EXPRESSION CONSTRUCT AND INSERTION INTO A PLANT TRANSFORMATION VECTOR

6.1.1. PROMOTER:hGC EXPRESSION CONSTRUCT

E. coli containing the hGC cDNA sequence cloned from fibroblast cells, as described (Sorge et al., 1985, supra), was obtained from the ATCC (Accession No. 65696). Oligonucleotide primers GC1 (corresponding to the amino terminus of the hGC coding region as shown in FIG. 1), and GC4 (corresponding to the carboxy terminus of the hGC coding region), were used to amplify the hGC cDNA sequence using the polymerase chain reaction (PCR). Primer GC1 was designed to include the hGC ATG initiation codon and to generate a 5' XbaI site. Primer GC4, complementary to hGC mRNA, does not include the stop codon for the gene and was designed to generate an EcoRI restriction site. The design of oligonucleotide GC4 also corrected an altered base in the ATCC sequence (GenBank/EMBL #M11080), thus producing an Arg-Arg-Gln sequence upstream to the site where a FLAG™ epitope will be inserted.

The 1.9 kb fragment generated by PCR was purified by agarose gel elution, digested with XbaI and EcoRI, and ligated into the similarly digested plasmid, Bluescript SK™ (Stratagene). This cloning vector was chosen because of its small size (2.9 kb) and its extensive multiple cloning region.

The MeGA promoter, comprising a 456 bp fragment (FIG. 11) (SEQ ID NO:5) as modified from the tomato HMG2 promoter (Weissenborn et al., 1995, Phys. Plantarum 93:393–400), was used to drive the expression of the hGC gene. The MeGA promoter is inducible and has a low basal expression in unstressed plant tissues, but is highly induced in both immature and mature tissues by the process of mechanical gene activation (MGA), or by a variety of chemicals that induce plant defense responses. MGA includes but is not limited to the mechanical shredding of leaf tissue, for example, into 2 mm strips, followed by storage at room temperature on Whatman 3 MM chromatography paper moistened with sterile water in a sealed plastic bag. The expression of a MeGA:GUS construct has been monitored in transgenic tobacco plants from seedling stage to flowering and it showed no loss of inducible activity as plants reached maturity.

The 456 bp MeGA promoter was PCR-amplified using primers which incorporated a NotI restriction site at the 5' end of the fragment and a XbaI site at the 3' end of the promoter. This fragment also contained the 5'-untranslated leader of its native tomato sequence and thus provided all necessary 5' elements for expression of the fused hGC sequences. Following amplification, the fragment was PAGE-purified, digested with NotI and XbaI, and ligated into the plasmid containing the hGC coding region, which had also been NotI/XbaI digested, to produce a MeGA:hGC fusion.

6.1.2. GENERATION OF A MeGA:hGC:FLAG™ CONSTRUCT

In order to facilitate detection and purification of the hGC gene product, a FLAG™ epitope coding sequence was fused in frame to the C-terminus of the hGC coding sequence. The FLAG™ epitope (IBI) is the octapeptide Asp-Tyr-Lys-Asp-Asp-Asp-Lys (or DYKDDDDK) (SEQ ID NO:10) designed to be a hydrophilic marker peptide situated on a protein surface to facilitate antibody interactions (Shelness, 1992, Epitope: 11:11–17; Hopp et al., 1988, Bio/Tech. 6:1204–1210).

A double-stranded oligonucleotide (FIG. 1) was synthesized which incorporated: (a) a 5' EcoRI restriction site which creates an in-frame fusion with the engineered hGC C-terminus EcoRI site; (b) the FLAG™ octapeptide coding region; (c) a stop codon following the epitope; and (d) a 3' SmaI/EcoRI site. The DNA encoding FLAG™ was PAGE-purified, digested with EcoRI, and the fragment encoding FLAG™ inserted into the EcoRI site of the MeGA:hGC plasmid, and tested for insert orientation.

The translational fusion was tested by in vitro transcription using T3 RNA polymerase driven by the T3 promoter in the pBluescript SK- vector following excision of the MeGA promoter, and in vitro translation in the presence of 35S-methionine using rabbit reticulocyte lysates (BRL). The major translation product was about 56–59 kDa, consistent with the expected size of the hGC:FLAG™ fusion protein (59 kDa). In addition, the hGC:FLAG™ fusion construct was completely sequenced using the dideoxy-sequenase system (USB). The nucleotide sequence of the hGC:FLAG™ fusion (SEQ ID NO:3) is shown in FIG. 9; the deduced amino acid sequence (SEQ ID NO:4) is shown in FIG. 10. The construction altered amino acid residue 545 to an arginine (R) and added ten amino acid residues, including the FLAG™ octapeptide, to the carboxyterminal of hGC. See FIG. 10.
6.1.3. INSERTION OF THE MeGA:hGC:FLAG™ CONSTRUCT INTO A PLANT TRANSFORMATION VECTOR

The MeGA:hGC:FLAG™ expression construct was excised from the pBluescript vector by digestion with SstI and ligated into the corresponding restriction site in the multiple cloning region of the plant binary vector pBIN-KAN (Becker, 1990, Nucl. Acids Res. 18:203) to form plasmid CTProl:hGC:FLAG™. As shown in Fig. 1, insertion of the MeGA:hGC:FLAG™ expression construct correctly positioned a plant transcriptional terminator for the construct. In addition, the binary vector carries an NPTII gene within the transfer DNA (T-DNA) which allows for selection of transformed plant cells based on kanamycin resistance. The engineered plasmid was transformed into E. coli strain DH5α and tested for correct insertion prior to mobilization into Agrobacterium tumefaciens strain LBA4404 (Hoeckma et al., 1983, Nature 303:179—180).

6.2. INTRODUCTION OF THE MeGA:hGC:FLAG™ EXPRESSION CONSTRUCT INTO TOBACCO AND ASSESSMENT OF hGC:FLAG™ EXPRESSION

6.2.1. GENERATION OF TRANSGENIC TOBACCO PLANTS CONTAINING THE MeGA:hGC:FLAG™ CONSTRUCT

Agrobacterium-mediated transformation (Horsch et al., 1984, Science 223:98—98) was used to stably integrate the modified T-DNA sequence containing the MeGA:hGC:FLAG™ construct into the genome of tobacco. Leaf discs excised from aseptically grown seedlings of tobacco (Nicotiana tabacum) cv. Xanthi (a non-commercial variety) and VA116 (a commercial, flue-cured variety) were briefly incubated in a bacterial suspension (10⁸ cfu/ml) of A. tumefaciens containing the engineered plasmid (Fig. 2A), and co-cultivated on plates containing a nurse-culture of Agrobacterium tumefaciens strain LBA4404 (Hoeckma et al., 1983, Nature 303:179—180).

Shoots were observed three weeks post-inoculation (Fig. 2B) and were excised and placed on selective rooting media (100 mg/L kanamycin, 10 μM indole-3-acetic acid in MS medium). After 1 week, the rooted plantlets (Fig. 2C) were transferred to sterile potting soil and placed in the greenhouse (Fig. 2D). Additional shoots were excised and rooted over the next 4 weeks with a total of 45 individual transgenic plant tissue was isolated by standard guanidino-thiocyanate methods from 35 plants of the 45 transformants described above were harvested (and thereby wounded) to induce transgene expression.

6.2.2. SOUTHERN ANALYSIS OF MeGA:hGC:FLAG™ INSERTIONS IN TRANSGENIC PLANTS

The stable insertion of the MeGA:hGC:FLAG™ construct was confirmed by genomic Southern hybridization analysis. Total DNA was isolated from leaf tissue of eight young regenerants and digested with HindIII, which cuts only once within the introduced DNA (see Fig. 1). The second HindIII site flanks the introduced DNA and is located within the plant’s genomic DNA. Thus, when probed with hGC cDNA sequences (1.7 kb HindIII fragment from pBluescript intermediate vector) 3' of the HindIII site, each fragment should be a distinctive size and represent an independent insertion event within the plant genome.

Five of the eight putative transformants tested showed multiple hGC inserts (Fig. 3). Four of these plants (X-1, X-8, X-9 and X-11) were derived from the Xanthi cultivar. One plant (V-1) was derived from cultivar VA116. Transformed X-8 had less DNA loaded and showed two bands upon longer autoradiographic exposure. In addition, high levels of hGC were detected in other transformants for which Southern hybridizations were not carried out, including a plant designated X-27.

6.2.3. NORTHERN ANALYSIS OF TRANSCRIPTIONAL ACTIVATION OF THE MeGA:hGC:FLAG™ TRANSGENE

As described supra, the MeGA promoter is essentially inactive in unstressed leaves, but is activated by MGA (see Fig. 4) or by treatment with chemicals that induce plant defense responses. In order to demonstrate that transgenic plants express hGC:FLAG™ mRNA in the expected inducible expression pattern, transformed plant tissue was induced by MGA, i.e., by shredding the leaf tissue into 2 mm strips, followed by incubation of Whatman #1 paper moistened with sterile water within a Ziploc™ plastic bag and incubated at room temperature for 24 hrs. Total RNA was isolated using standard guanidino-thiocyanate methods from leaf tissue of untransformed and transformed plants immediately upon excision (time 0), or at 24 hr after MGA.

As shown in Fig. 4, hGC:FLAG™ mRNA levels were undetectable in leaves of X-11 at the time 0, but showed a marked increase in hGC transcript levels 24 hr after MGA. A more detailed time course of a second plant, V-1, showed detectable mRNA by 4 hr, maximal RNA levels at 24 hr, and mRNA levels declining at 48 hr. In addition, transcript levels increased in response to chemical defense elicitors compared to MGA. This pattern of expression is exactly what is expected of a transgene construct linked to the MeGA promoter (Park et al., 1992, Pl. Mol. Biol. 20:327—331; Yang et al., 1991, Pl. Cell 3:397—405).

6.2.4. IMMUNODETECTION OF THE hGC:FLAG™ PROTEIN IN TRANSGENIC PLANT EXTRACTS

As described supra, the hGC:FLAG™ fusion construct was designed to utilize the FLAG™ epitope to facilitate detection and purification of the hGC:FLAG™ fusion protein. Seven weeks after plants were potted in soil, leaf discs from 35 plants of the 45 transformants described above were harvested (and thereby wounded) to induce transgene expression.

Extracts from the leaf discs of control plants and transgenic plants were spotted on nitrocellulose membranes for immunoblot blot analysis. Monoclonal antibodies (anti-FLAG M2, IBI) against the FLAG™ epitope, in conjunction with the Western Exposure™ chemiluminescent detection system (Clontech, Inc.), were used to test for immune-reactive material. Of the 35 plants tested, 25 showed significant transgene expression.

Western analysis of extracts from wounded leaves of untransformed plants and transformed plants were tested for immuno-reactivity to polyclonal antibodies raised against hGC (Fig. 5B). These antibodies have not shown binding to any mammalian proteins other than the acid β-glucosidase, i.e., glucocerebrosidase of chimpanzees. Extracts from transgenic plants showed strong immuno-reactivity by a single protein band with an apparent molecular weight of about 66—69 kDa (Fig. 5B). The size of the immuno-reactive protein was reduced to about 58 kDa after N-acetylation treatment, indicating that the enzyme was glycosylated. Analogous Western immunoblots probed with anti-FLAG™ antibodies showed additional similar molecular weight bands (Fig. 5A), suggesting that both the polyclonal antibody to hGC and the anti-FLAG™ antibody recognize the same fusion protein product.
6.2.5. ENZYMATIC ACTIVITY IN TOBACCO EXTRACTS

Plant tissues were tested for hGC activity using a sensitive and convenient assay that is widely utilized in Gaucher disease research (Grabowski et al., 1990, in: Critical Reviews in Biochemistry and Molecular Biology, 25:385–414, CRC Press, Inc.). This assay uses the fluorometric substrate, 4-methylumbelliferyl-β-D-glucopyranoside (4MuGlc) (the “4MuGlc assay”). An increase in absorbance at 460 nm results from cleavage of 4MuGlc, and indicates the presence of enzymatic activity. 4MuGlc also serves as a substrate for endogenous plant β-glucosidases which have been detected in leaves of both control and transgenic plants. However, several distinctive properties of hGC were used to distinguish between endogenous glucosidase activity and hGC activity (TABLE 1). The differences in solubility together with the use of anti-FLAG™ affinity system for purification of the hGC-FLAG™ were employed to solve the problem of separating hGC:FLAG™ from the endogenous plant β-glucosidases (Table 2, FIG. 8).

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<th>TABLE 1</th>
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<td><strong>CHARACTERISTICS</strong></td>
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6.2.6. ACCUMULATION OF hGC:FLAG™ PROTEIN IN TOBACCO TISSUES

In order to determine the best length of incubation time post-MGA for optimum yield of hGC:FLAG™ protein and hGC enzyme activity, extracts were analyzed from transgenic leaves at 0, 2, 4, 8, 16, and 24 hrs post-MGA. Plant tissue (0.5 gm) was ground using dry ice and a coffee bean grinder. To solubilize hGC:FLAG™, the ground tissue was resuspended in 1 ml of extraction buffer containing 25 mM sodium citrate pH 7.0, 1% (v/v) sodium taurocholate, 4 mM β-mercaptoethanol, and 5 mM EDTA. The homogenate was frozen in a dry ice/ethanol bath for 30 min and thawed at 4°C. Cell debris was pelleted at 14,000 x g for 30 min. The supernatant was filtered through a layer of cheese cloth and the filtrate was saved. An 1 ml aliquot was stored at 500 μg/ml, followed by 2 x 1 ml at 250 μg/ml. Eluted material was subjected to SDS-PAGE, and stained with Commassie blue to determine relative purity (FIG. 7A). No immuno-reactive material was eluted in the first fraction since release of the bound hGC:FLAG™ protein requires equilibration with the peptide. As a consequence, the second and third eluted fractions contained the majority of immuno-reactive material. SDS-PAGE analysis of anti-FLAG™-purified hGC:FLAG™ protein showed a single band co-migrating with the anti-FLAG™ immuno-reactive band (FIG. 7A).

In order to utilize the properties of the glycans present on the hGC:FLAG™ protein for purification purposes, hGC:FLAG™ protein was also isolated using a concanavalin-A (ConA) affinity column (Sigma). Concentrated tissue extract (1.5 ml) was loaded onto a 1.5 ml bed volume of ConA in column buffer (0.1M sodium citrate pH 6.5, 0.15M sodium chloride). An equal volume of column buffer was added to the concentrated extract and passed through the column twice at 4°C. The ConA column was washed three times with column buffer using three times the bed volume of buffer. The bound hGC:FLAG™ was eluted with 5 mls of 0.1M methyl α-D-mannopyranoside (Sigma) followed by 5 mls of 1M methyl α-D-mannopyranoside. Fractions were

The differences in solubility together with the use of anti-FLAG™ affinity system for purification of the hGC-FLAG™ were employed to solve the problem of separating hGC:FLAG™ from the endogenous plant β-glucosidases (Table 2, FIG. 8).

6.3. PURIFICATION OF hGC:FLAG™ FROM TOBACCO EXTRACTS

Forty gms of post-wounded (12 hrs) tissue was ground to a fine powder using dry ice and a coffee bean grinder. One hundred mls of extract buffer were added and the sample was made into a slurry using a polytron (Brinkman Scientific). The extract was frozen in a dry ice/ethanol bath for 1 hr and thawed for 16 hrs at 4°C. Cell debris was pelleted at 14,000 x g for 30 min. The supernatant was filtered through a layer of cheese cloth and the filtrate was saved. An 1 ml aliquot was stored at 500 μg/ml, followed by 2 x 1 ml at 250 μg/ml. Eluted material was subjected to SDS-PAGE, and stained with Commassie blue to determine relative purity (FIG. 7A). No immuno-reactive material was eluted in the first fraction since release of the bound hGC:FLAG™ protein requires equilibration with the peptide. As a consequence, the second and third eluted fractions contained the majority of immuno-reactive material. SDS-PAGE analysis of anti-FLAG™-purified hGC:FLAG™ protein showed a single band co-migrating with the anti-FLAG™ immuno-reactive band (FIG. 7A).

In order to utilize the properties of the glycans present on the hGC:FLAG™ protein for purification purposes, hGC:FLAG™ protein was also isolated using a concanavalin-A (ConA) affinity column (Sigma). Concentrated tissue extract (1.5 ml) was loaded onto a 1.5 ml bed volume of ConA in column buffer (0.1M sodium citrate pH 6.5, 0.15M sodium chloride). An equal volume of column buffer was added to the concentrated extract and passed through the column twice at 4°C. The ConA column was washed three times with column buffer using three times the bed volume of buffer. The bound hGC:FLAG™ was eluted with 5 mls of 0.1M methyl α-D-mannopyranoside (Sigma) followed by 5 mls of 1M methyl α-D-mannopyranoside. Fractions were
collected and assayed for protein content and hGC enzymatic activity. All fractions containing hGC enzyme activity were concentrated (Amicon, YM30 filters) to a final volume of 0.5 ml. To stabilize the hGC enzymatic activity of the hGC:FLAG™ protein, the concentrated extract was made 40% (v/v) in glycerol and stored at 4°C. SDS-PAGE analysis of the ConA purified hGC:FLAG™ protein (FIG. 7B) showed a band migrating at 66—69 kd and three lower molecular weight bands that stained equally with Comassie blue.

Enzyme activity and protein determination of fractions from each step in the purification indicate that the most effective method to purify hGC:FLAGm was to employ anti-FLAG™ affinity chromatography followed by the ConA affinity chromatography (see Table 2 and FIGS. 7A—B).

### TABLE 2

**PURIFICATION OF hGC:FLAG™ FROM TOBACCO EXTRACTS**

<table>
<thead>
<tr>
<th>Fraction</th>
<th>Protein Conc. (mg/ml)</th>
<th>Specific activity (4 MU/min/mg protein)</th>
<th>% Activity Recovered</th>
<th>Fold Purification</th>
</tr>
</thead>
<tbody>
<tr>
<td>40 gms FW</td>
<td>2 mg/ml</td>
<td>+0.027</td>
<td>100</td>
<td>1</td>
</tr>
<tr>
<td>35% A8-sup</td>
<td>2.5 mg/ml</td>
<td>+0.625</td>
<td>100</td>
<td>12</td>
</tr>
<tr>
<td>ConA</td>
<td>0.1 mg/ml</td>
<td>+0.81</td>
<td>12.5</td>
<td>240</td>
</tr>
<tr>
<td>FLAG</td>
<td>7.2 µg/ml</td>
<td>+0.84</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
</tbody>
</table>

*Since 4 MU Glc is not a specific substrate, this specific activity represents both plant glucosidase and hGC activity.

### 6.4. PRODUCTION OF hGC:FLAG™ PROTEIN FROM TOBACCO PLANTS

An estimation can be made on the amount of hGC:FLAG™ extracted per g of fresh weight of tobacco plant tissue or per mg soluble protein from slot blot western analysis of initial crude extracts using anti-FLAG™. Approximately 2 mg/ml of soluble protein were extracted per 0.5 g of fresh weight plant tissue. Western blot slot analysis of 1 µl of crude extract indicates the presence of approximately 0.5 to 0.6 µg of hGC:FLAG™ (FIG. 8).

Based on these results, a single mature tobacco plant comprising about 1.6 kg of fresh weight of tissue will contain about 2.5 g of hGC:FLAG™ per plant. Accordingly, a standard acre of tobacco planted to 6,000 plants could potentially produce 15 kg of hGC:FLAG™ (Table 3).

### TABLE 3

**EXTRACTABLE hGC:FLAG™ PER ACRE OF TOBACCO**

<table>
<thead>
<tr>
<th>Tissue</th>
<th>Soluble Protein</th>
<th>hGC:FLAG™</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 gm</td>
<td>4.5 mg</td>
<td>1.5 mg</td>
</tr>
<tr>
<td>1.6 kg/plant</td>
<td>6-8 gm</td>
<td>2.4 gm</td>
</tr>
<tr>
<td>6,000 PLANTS/ACRE (Stunted field)</td>
<td>38-48 kg</td>
<td>14.4 kg</td>
</tr>
<tr>
<td>9,600 kg</td>
<td>40-50 kg</td>
<td></td>
</tr>
</tbody>
</table>

*These estimations are based on slot blot westerns using anti-FLAG and crude extracts from 0.5 g to 50 g of post-wounded tissue.

### 7. EXAMPLE 2

**PRODUCTION AND PURIFICATION OF IDUA IN TRANSGENIC TOBACCO PLANTS**

The subsections below describe the production of enzymatically active recombinant human α-L-iduronidase (IDUA) in transgenic tobacco plants.

#### 7.1. CONSTRUCTION OF A PLANT TRANSFORMATION VECTOR CONTAINING AN IDUA EXPRESSION CONSTRUCT

The first step in the construction of the desired plant transformation vector was to generate the human IDUA coding region with appropriate flanking restriction site to facilitate fusion to specific plant promoters and insertion into plant transformation vectors. A full-length human IDUA cDNA clone was provided by E. Neufeld (University of California, Los Angeles). In this clones, the IDUA cDNA sequence was inserted into the EcoRI site of pB9 plasmid (Moskowitz et al., 1992, FASEB J. 6: A77; Murray, 1987, Methods in Enzymol. 149: 25—42). This IDUA cDNA sequence has been expressed in animal cell lines (Moskowitz et al., 1992, supra, 1987, supra) and shown to contain all the information necessary to produce enzymatically active IDUA (Murray, 1987, supra). The IDUA cDNA encodes a 653 amino acid protein (66 kDa) including the 26 amino-terminal signal peptide which is cleaved as it passes through the ER membrane. To aid in the insertion of the IDUA cDNA into the plant vector, unique flanking XbaI and SacI sites were introduced by PCR using 5'-primer ID1 and 3'-primer ID2, Pfu polymerase (Stratagene, La Jolla, Calif.); as shown in FIG. 12. The 1.9 kb fragment generated by PCR was purified by agarose gel electrophoresis, digested with XbaI and SacI, and ligated into pBS and pSp64polys (Gibco, a vector for in vitro transcription/translation). The PCR-amplified IDUA coding sequence was sequenced prior to insertion into the expression constructs.

The nucleotide and deduced amino acid sequences of the amplified IDUA coding sequence are shown in FIGS. 19 (SEQ ID NO: 8) and 20 (SEQ ID NO: 9), respectively. The PCR-amplified IDUA coding sequence differs from that originally published by E. Neufeld at positions 931 and 932. The PCR-amplified IDUA sequence has the dinucleotide CG instead of the original GC at those positions. Accordingly, the deduced amino acid sequence of the PCR-amplified IDUA has a glutamate, instead of a glutamine, residue at position 282. In vitro transcription of the PCR-amplified IDUA sequence in a pSp64polys:IDUA vector and rabbit reticulocyte lysate- mediated in vitro translation of the resultant transcript produced protein having a molecular size expected for IDUA.

The PCR-amplified IDUA coding region was inserted downstream of two distinct regulated plant promoters: 1) the MeGA promoter and 2) the 35SPconf promoter. As discussed above, the MeGA promoter shows little or no expression in most plant tissues but is strongly inducible resulting in significant transgene product accumulation 12 to 48 hours after induction of the MeGA promoter. The 35SPconf promoter is a widely used high-level constitutive promoter consisting of a modified CaMV 3SS promoter containing double enhancer which is fused to a translational enhancer from the tobacco etch virus. See Cramer et al., 1996, “High-Level of Enzymatically Active Human Lysosomal Proteins in Transgenic Tobacco”, Transgenic Plants: A Production System for Industrial and Pharmaceutical Proteins, eds., Owens & Pen, John Wiley & Sons; Chriseps, 1991, Annu. Rev. Plant Physiol. Plan. Biol. 42: 21—53; and Haskins et al., 1979, Pediat. Res. 13:128—1297. Each promoter was ligated as a HindIII-XbaI fragment upstream of the IDUA cDNA (see FIG. 12).

#### 7.1.2. IDUA EXPRESSION/TRANSFORMATION VECTORS

During the subcloning and vector analysis steps, bacterial transformants having any vector containing the 5'-end of the
IDUA cDNA were recovered at lower than expected frequencies. For example, multiple ligation and transformations of competent E. coli cells DH5α with pBS containing the 1.9 kb PCR amplified IDUA cDNA were required to generate fewer than 100 transformants. Among the 70 transformants analyzed by restriction analysis of the plasmid DNA, only 2 clones contained the proper sized 1.9 kb fragment. One of the two clones was sequenced and found to contain the complete IDUA coding sequence. Colony size of IDUA containing transformant was reduced. These reduced efficiencies were independent of plasmid vector, presence or absence of plant promoter, IDUA expression (not fused to a bacterially active promoter) or bacterial host. Independent subcloning of the 3'-versus 5'-end of the IDUA cDNA localized an "obnoxious" region to the 5'-end of the IDUA sequence. DNA secondary structure or the high GC content of this region may cause intolerance in heterologous organisms. This effect by the 5'-end of the IDUA cDNA has also been noticed in yeast and animal cell expression systems. These limitations in transformation of the IDUA sequence, however, did not preclude successful isolation and characterization of the desired IDUA expression and transformation constructs.

For both promoter constructs, the promoter:IDUA cDNA fusions were excised as HindIII/SacI fragments and ligated into HindIII and SacI-digested pBB-B-KAN (FIG. 12). pBB-B-Kan is a large (>13 kb) plant transformation vector that provides a terminator/poladenylation signal (pAnos) for kzinamycin resistance) for transformed plant cells, and blly integratethe 35SENH:IDUA and MeGA:IDUA constructs into the genome of tobacco. Approximately 80 leaf discs were harvested, induced by mechanical wounding and incubated at room temperature under high humidity (i.e., the wounded leaves are wrapped in moist filter paper in sealed bags or layered in a container with buffer gently swirled over the tissue) to allow de novo synthesis of the transgene product. In an initial screen of ten MeGA:IDUA-containing plants, tissue extracts were used for immunodot-blot analyses (see above). The extracts showed little or no IDUA content for all plants. Later analyses revealed that IDUA was secreted from the leaves and leached out onto the filter paper during the incubation step. This was somewhat surprising because recovery of extracellular proteins from intact leaf generally requires vacuum-induced buffer infiltration of the leaf (see Parent & Asselin, 1987, Can. J. Bot. 62:2564—569; Regalado & Ricardo, 1996, Plant Physiol. 110:227—232). As described below, the expression procedure was subsequently modified to include a post-induction incubation step that involved gentle rotation of buffer over the wounded tissue, which permitted recovery of IDUA protein and activity in the incubation buffer. Subsequent analyses were focused primarily on one plant, IDUA-9 also known as CT40-9, since preliminary tests show detectable levels of IDUA activity and anti-IDUA immuno-reactive material. IDUA-9 contains 3 copies of the MeGA:IDUA construct.
7.4.2. NORTHERN ANALYSIS SHOWS ACTIVATION OF THE MEGA:IDUA TRANSGENE

In order to demonstrate induction of the MEGA promoter and accumulation of IDUA mRNA, total RNA was isolated (Rutter, 1981, J. Biol. Chem. 91:468–478) from IDUA-9 leaves before and after induction. As shown in FIG. 14A, IDUA mRNA of the expected size (approximately 2.2 kb) was detected at low basal levels in uninduced tissue and showed a marked increase at 8 hrs post-induction and reached a maximum level at 27 hrs post-induction. This pattern is similar to transgene induction kinetics seen with other MEGA-driven constructs (e.g., hGC:FLAG™). The smaller hybridizing RNA species also accumulated after induction. Analogous lower molecular weight RNAs have not been detected in hGC:FLAG™ expressing plants and may be unique to the IDUA-9 plant or a consequence of the IDUA sequence.

7.4.3. WESTERN ANALYSIS OF HUMAN IDUA LOCALIZED TO TOBACCO

The induced IDUA-9 tissues were also used for protein extracts. Western blot analysis showed CHO-derived IDUA and IDUA from tobacco tissue migrated very similarly in SDS-PAGE (FIG. 14B). The IDUA (92 kD) from IDUA-9 tobacco extract migrated slightly faster than secreted IDUA from CHO cells. This presumably is due to differences in glycan composition. However, the similarity in size suggests that the tobacco produced recombinant IDUA was also glycosylated.

7.4.4. IDUA SYNTHESIZED IN TRANSGENIC TOBACCO IS SECRETED

As discussed above, CHO cells secrete recombinant IDUA into the media. To determine if tobacco also secretes recombinant IDUA into the media, leaf tissue from transgenic IDUA-7, -8 and -9 plants were indferred for 0 to 34 hrs and placed in a plastic petri dish with incubation buffer (PBS). At 0 hr, incubation buffer was used to wash the induced tissue and the wash stored frozen. Fresh buffer was added to the induced tissue and incubated at room temperature. At 8 hrs, the buffer was removed and frozen. Fresh buffer was added to the induced tissue and incubated further. The buffer was removed at 24 hrs post-induction. Fresh buffer was added to the induced tissue and further incubated. The final incubation buffer was removed 34 hrs post-induction and a tissue extract was prepared from the incubated leaf tissue. Fifty µl of each incubation buffer and tissue extract was boiled and slotted onto OPITRTAN membrane. A range of control IDUA protein from 0 to 40 µg was also blotted and IDUA was detected using anti-IDUA antibodies. As shown in FIG. 15, IDUA protein was present in the incubation buffer following induction in all of the transgenic tissue analyzed. This indicates that transgenic tobacco secretes IDUA after induction.

7.4.5. THE TOBACCO-SYNTHESIZED IDUA IS ENZYMATICALLY ACTIVE

One of the most critical factors in assessing the utility of plant-synthesized recombinant IDUA is whether the IDUA is enzymatically active. Enzyme activity of human lysosomal hydrolases requires appropriate glycosylation and folding and heterologous expression systems often result in endoplasmic reticulum-localized degradation or accumulation of insoluble and inactive aggregates. To determine whether the recombinant IDUA synthesized in transgenic leaves has enzymatic activity, a sensitive fluorometric assay using the substrate, 4-Methylumbelliferyl-α-L-iduronide (4-MUI) (Calbiochem, LaJolla, Calif.) was used (see Neufeld, E. F., 1991, Ann. Rev. Biochem. 60:257–280). Untransformed tobacco extracts were shown to contain no endogenous IDUA activity. When CHO-derived recombinant IDUA was seeded into crude extracts of untransformed tobacco leaves, no detectable inhibition of activity was found. When the tissue extracts from IDUA-9 transgenic plant were assayed, the extracts showed IDUA activity at reproducible but at relatively low levels (0.2 to 0.4 m mole 4-MU/hr/gm tissue). This confirms that tobacco has all the necessary machinery to synthesize and process IDUA into an active form. Consistent with IDUA distribution shown by immuno-detection, significantly higher IDUA activities were detected in the secreted fraction as described below.

7.4.6. SECRETION AND RECOVERY OF TOBACCO-SYNTHESIZED RECOMBINANT IDUA

Significant portion of the recombinant IDUA produced in transgenic tobacco was recovered in the incubation buffer following induction of the MEGA:IDUA gene construct (FIG. 15). Localization of the majority of active IDUA after induction and incubation was determined. This was done by comparing the IDUA activity and anti-IDUA immuno-reactivity of tissue extract with those of the incubation buffer. As shown in FIG. 16, there was much higher levels of IDUA activity in the incubation buffer than in the tissue extract after induction and incubation. Moreover, the IDUA activity in the incubation buffer showed strong correlation with the the amount of anti-IDUA immuno-reactive material found in the incubation buffer, as reveal by the data presented in FIG. 15. Thus, IDUA-expressing transgenic tobacco secrete most of its active IDUA (about 67%) into the incubation buffer after induction and incubation.

Based on activity assays and Western analysis, the specific activity of secreted IDUA was estimated to be about 64 U/µg protein. In comparison, purified IDUA enzyme from engineered CHO cells has a specific activity of about 242 U/µg protein.

Variation in transgene expression levels is very common in transgenic plants due to “positional” effects caused by the site of transgene insertion within the host genome. The IDUA activity levels in three independent IDUA-expressing transgenic plants (i.e., IDUA-7, IDUA-8 and IDUA-9) were examined. Among these transgenic plants, IDUA-9 has the highest IDUA activity (FIG. 17). The relative amount of active IDUA remaining in the cell, as reflected by the activity present in tissue extract, after 34 hrs of incubation ranged from 14% to 35% of the total activity (FIG. 17).

The above-identified three transgenic plants were identified in a screen of about fifty independently transformed plants. This is a relatively small scale screen. It is reasonable to expect that larger scale screenings of IDUA-engineered plants will yield plants that produce active IDUA at levels higher than those of the plants disclosed herein.

7.4.7. PURIFICATION AND YIELD OF IDUA FROM TRANSGENIC TOBACCO

The yield of recombinant IDUA from IDUA-9 was estimated to be about 6 µg/gm fresh tissue. This estimate was based on the material present in the incubation buffer after 34 hrs of incubation (see FIG. 18). However, neither the induction nor the IDUA recovery procedure used was optimized. Thus, it is likely that higher IDUA yields may be achieved through optimization of induction and recovery procedures. It should be noted that the transgenic tobacco plants yielded an average of greater than 1 kg fresh weight of leaf at maturity, and that leaves can be periodically harvested from greenhouse-grown plants for over an year. Accordingly, cultivation of transgenic tobacco plants either in the field of the greenhouse offers a convenient and effective means for producing large amounts of IDUA.

8. EXAMPLE 3

PRODUCTION OF TRANSGENIC TOBACCO PLANTS CONTAINING AN UNMODIFIED hGC EXPRESSION CONSTRUCT

A 3' end segment of the hGC coding sequence was PCR-amplified from the cDNA clone in E. coli ATCC65696
using as the 5' primer GC23 oligo, 5'GCCTATGCTGAGCACAAGTTACAG3' (SEQ ID NO:11), whose 5' end corresponds to nucleotide 894 of the hGC:FLAG sequence shown in FIG. 9, and as the 3' primer GC37 oligo, whose complementary strand has the sequence 5' TTCCTTGAGCTCGtcaCTGGCGACGCCACAGGTA3' (SEQ ID NO:12), a SalI restriction site is shown with an underline and a stop codon that is in-frame to the amplified hGC coding sequence is shown in lower case. The site of the 5' primer in the hGC coding sequence is 5' upstream of a SalI restriction site. Accordingly, the amplified DNA was cut with SalI and SacI, and the SalI/SacI fragment containing the 3' end of hGC coding sequence was inserted into the pBS intermediate vector containing the MeGa:hGC:FLAG™ expression construct (see FIG. 1 and Section 6.1.2., supra) which had been cut with SalI and SacI. Clones were identified that had replaced the 3' end of the MeGa:hGC:FLAG™ construct with the 3' end of hGC coding sequence yielding a MeGa:hGC expression construct. This construction eliminated the ten amino acid addition at the carboxyl terminal and corrected the amino acid substitution at residue 545 in the hGC:FLAG™ fusion, and thereby reconstructing an unmodified hGC coding sequence. The MeGa:hGC expression construct was excised from the pBS intermediate vector by SacI digestion and inserted into pBIB-KAN to form the transformation vector pCT54. A schematic of the construction of the pCT54 vector is shown in FIG. 21.

Agrobacterium containing pCT54 was used to transformed plants and transgenic tobacco plants containing the MeGa:hGC expression construct were produced according to procedures described above. Transgenic tobacco plants containing the MeGa:hGC expression construct were identified and assigned the designations CT54-1 to -40. Analyses of hGC enzymatic activity and presence of hGC in the induced tissues of transgenic plants are carried out using the enzymatic assay described in Section 6.2.5. and the Western blot analysis using anti-hGC antibodies described in Section 6.2.6. Purification of the hGC produced in transgenic tobacco tissue is carried out using the procedure described in Section 6.3., except the anti-FLAG™ affinity chromatography step was omitted, which procedure is further modified accordingly to strategies and methods known in the art for purifying the hGC enzyme.

9. DEPOSIT OF BIOLOGICAL MATERIALS

The following biological materials have been deposited with the American Type Culture Collection (ATCC) at 12301 Parklawn Drive, Rockville, Md. 20852, in compliance with the requirements of the Budapest Treaty On The International Recognition Of The Deposit Of Microorganisms For The Purpose Of Patent Procedure, on the dates and were assigned the ATCC accession numbers indicated below.

<table>
<thead>
<tr>
<th>Deposited Material</th>
<th>Deposit Date</th>
<th>Accession No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA of pCTPr01:hGC:FLAG</td>
<td>Sept. 14, 1995</td>
<td>97277</td>
</tr>
<tr>
<td>seeds of tobacco plant</td>
<td>Sept. 14, 1995</td>
<td>97275</td>
</tr>
<tr>
<td>hGC X-11</td>
<td></td>
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<td>seeds of tobacco plant</td>
<td>Sept. 14, 1995</td>
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<tr>
<td>hGC X-27</td>
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<td>DNA of pCT22</td>
<td>Aug. 30, 1996</td>
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<td>DNA of pCT22</td>
<td>Aug. 30, 1996</td>
<td>97700</td>
</tr>
<tr>
<td>DNA of pCT54</td>
<td>Oct. 17, 1996</td>
<td>97770</td>
</tr>
</tbody>
</table>

The present invention is not to be limited in scope by the biological material deposited since the deposited embodiments are intended as illustrations of the individual aspects of the invention, and any biological material, or constructs which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various references are cited herein; these are incorporated by reference in their entirety.
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"
(x) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: CDNA
(x) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGTTTT CAAGTCCTTC CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC 60
ATGGCTGGCA GCCTCACAGG TTTGCTTCTA CTTCAGGCAG TGTCGTGGGC ATCAGGTGCC 120
CGCCCCTGCA TCCCTTAAAG CTCGGCCCTC ACCTGGCGTG TGCTGGCTAG CAATGCGACA 180
TACTGTGACT CTTTGAACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG 240
AGTACAGCCA GTGGCAGCGC GATGGGGGCT AGTATGGGGC CATCCAGCGC CTACCGACAC 300
GGCACAGCCA GCACACCTGC TCTGCCAAGC GAAGAAATGG TCTCTCTTCC GAGGGGTGTA 360
GGACGGCCCA TGACGAGATG TGGTGTCTCT ACAATCTCTTG CCCTGACCAC CCTGCCGCAA 420
AATTTCTTCT TTAATGCTGA CTCTCTCTGA GAAAGAAGTG GATATAAGCT AATCTGCAGT 480
CCCATGGCACA GCTGGGCTCT GGTCCCCGCA ACCTCCACGC ATCACACGCA CCGGATGTCC 540
TTCCGATTGC AACAACCGGC CCTCCCCAGG CTTACGGCGT AACTCTTCTC CGGGGGGGGA 600
CAGGGGGGCA CGAGGCTGGT CAGGCGCGGC CACAAGGAGG TGGGTTTCTG TGCCAGATGC 660
GGAGGGCCCA TGAGGCAAGG CAGACATGGT AGGAGCACTG GAGAGGAGAG TCTGTATGCC 720
GAGACACACC TCTCCTGTCA ACCCAAGAGG ATTTTCGAGC GTTGTCTGCT AGAGAGAGAG 780
GACACAGGCA CGCTGGCAGG CCCTGCAAGC CAACACACAC AGGAGGAGAG CTTTCATGCC 840
AATTAAGGCA CTGGGAGAGG TGGGAGAGAG TGGGAGAGAG TGGGAGAGAG TGGGAGAGAG 900
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GCTAAATGCT TTCTGCGCTG TTGTAGATGC TGGGCTTGCT GGGGGCTGGA TGCTGCGCTG 1080
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(A) LENGTH: 546 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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35     40     45
Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser  
50     55     60
Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu  
65     70     75     80
Ser Thr Arg Ser Gly Arg Met Glu Leu Ser Met Gly Pro Ile Gln  
85    90     95
Ala Asn His Thr Gly Thr Gly Leu Leu Thr Leu Gln Pro Glu Gln  
100   105    110
Lys Phe Glu Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala  
115    120    125
Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gin Asn Leu Leu Leu  
130    135    140
Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val  
148    150    155    160
Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp  
165    170    175
Thr Pro Asp Asp Phe Glu Leu His Asn Phe Ser Leu Pro Glu Gln Asp  
180    185    190
Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gin Leu Leu Ala Gln  
195    200    205
Arg Pro Val Ser Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu  
210    215    220
Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gin Pro  
225    230    235    240
Gly Asp Ile Tyr His Gin Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu  
245    250    255
Asp Ala Tyr Ala Glu His Lys Leu Gin Phe Trp Ala Val Thr Ala Gln  
260    265    270
Asn Glu Pro Ser Ala Gly Leu Ser Gly Tyr Pro Phe Gin Cys Leu  
275    280    285
Gly Phe Thr Pro Glu His Gin Arg Asp Phe Ile Ala Arg Asp Leu Gly  
290    295    300
Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu  
305    310    315    320
Asp Asp Gin Arg Leu Leu Leu Pro His Trp Ala Lys Val Leu Thr  
325    330    335
Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr  
340    345    350
Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg  
355    360    365
Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
370 375 380
Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
385 390 395 400
Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
405 410 415
Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
420 425 430
Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp
435 440 445
Thr Phe Tyr Lys Glu Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
450 455 460
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
465 470 475 480
Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
485 490 495
Val Val Val Leu Asn Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
500 505 510
Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
515 520 525
His Thr Tyr Leu Trp Arg Gln Asn Ser Asp Tyr Lys Asp Asp Asp
530 535 540
Asp Lys
545

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = \"MeGA Promoter\"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAATACGATA AAACTGATAT CAAATGCAAA CTCTGACCAGT
60
TATATTATTG CAACCGGGTT TCTTCTTTTA TCTTTTTCCT
120
TCTTGACC GTCAACTTGACT TAAAAGATAA CCTCTATAAA
180
ACAATTATAC CACCGGCGGC TTATACTAAA AATATTTAAT
240
TATTTCATAA ATATAAAACT TACTCCATTC TACATTTCCT
300
TTGTCAATCA AGACTTACCG TCAAAATTTA ATCTACTTTC
360
TTACTTCAAA AAAATATAAA TAGCCCGAGT ACATCTTCTC
420
GTGAAATCTA CCAACGCGTT CCTCATATAA TACATTTCCT ACATCTTCTC ATCCCATCAC
480
TCTCTTTTAA ACAATGTCAT TGGPTCAATCA TCAATCCAC AAAACAACACT TTTTCTCTCC
540
TCTTTTCTC CACCOCGCGC AGACTTACCG GTGARAAATCTA GAGTAGAGCAT C
600

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = \"PCR primer\"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDINESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCGAG CTCTCATGGA TTGCCCGGGG ATG

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2067 base pairs
(B) TYPE: nucleic acid
(C) STRANDINESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGCGTCCCC TGCGCCCCCG CGCCGCGCTG CTGGCGCTCC TGGCCTCGCT CCTGGCCGCG 60
CCCCCGCGAC GCCGGGCAGG CGCCGGGCCG GCCGGGGAGG GCCGGGCCC GGGGGGAGG 120
TGCCCCCGGC GCCGGCAGAG GCCGGGAGG GCCGGGGAGG GCCGGGCCC GGGGGGAGG 180
GCTGAAGACT CAGTGCCAG CGCCGGGAGG CGCCGGGCCG GCCGGGGAGG GCCGGGCCC GGGGGGAGG 240
CTGCCGCCAG GCCGCCAGAG GCCGGGAGG GCCGGGGAGG GCCGGGCCC GGGGGGAGG 300
GGCGCTTCAC GCCGGGAGG CGCCGGGCCG GCCGGGGAGG GCCGGGCCC GGGGGGAGG 360
CTGCCGCCAG GCCGCCAGAG GCCGGGAGG GCCGGGGAGG GCCGGGCCC GGGGGGAGG 420
AGGAGAATA CTGGGCACC GCGAGCTTGA CTGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG 480
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AATGGGCAGC ACCACAGCA TCCTTCAAAC GCTGGCTGCTG GACAGCTTGA CTGGCTGGCTG 600
TACTGACATG CTGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 660
CCGGGGAGG CTCGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 720
TGCGGAGT GATTCAGCTG CTTGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 780
CTGCCTTCA CAGGGGAGG CTCGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 840
CACGAGCTTCA CAGGGGAGG CTCGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 900
GACGAGCTTCA CAGGGGAGG CTCGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 960
ATGGTGCTGA GACAGCTTCA CAGGGGAGG CTCGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 1020
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CTTTGGCGCG ATGGTGCTGA GACAGCTTGA CTGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 1320
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CTGGCGGGTC ATGGTGCTGA GACAGCTTGA CTGGCTGGCTG GCGAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG GACAGCTTGA CTGGCTGGCTG 1500
(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Leu Ala Ser 1 5 10 15
Leu Leu Ala Ala Pro Val Ala Pro Ala Glu Ala Pro His Leu Val 20 25 30
His Val Asp Ala Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg 35 40 45
Ser Thr Gly Phe Cys Pro Leu Pro Pro Ser Gin Ala Asp Gin Tyr 50 55 60
Val Leu Ser Trp Asp Gin Gin Leu Asn Leu Ala Tyr Val Gly Ala Val 65 70 75 90
Pro His Arg Gly Ile Lys Gin Val Arg Thr His Trp Leu Leu Gly Leu 85 90 95
Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr 100 105 110
His Leu Asp Gly Thr Leu Asp Leu Arg Glu Asn Gin Leu Leu Pro 115 120 125
Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu 130 135 140
Asp Gin Gin Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala 145 150 155 160
Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn 165 170 175
Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser 180 185 190
Met Thr Met Glu Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly 195 200 205
Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser 210 215 220
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His 225 230 235 240
Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu 245 250 255 260
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(2) INFORMATION FOR SEQ ID NO:10:
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLGY: unknown

(ii) MOLECULE TYPE: peptide

(x) SEQUENCE DESCRIPTION: SEQ ID NO:10:
Asp Tyr Lys Asp Asp Asp Asp Lys

1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
GCCTATGCTG AGCACAAGTT ACAG

3

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Complementary sequence of a PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
TCCCTTGAGC TCGTCACTGG CGACGCCACA GGTA

3

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
CAGAATTCGG ACTACAAGGA CGACGATGAC AAGTAGGAGC TCGAATTC

48

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
Asn Ser Asp Tyr Lys Asp Asp Asp Asp Lys

1 5 10

(2) INFORMATION FOR SEQ ID NO:15:
What is claimed is:
1. A method for producing a lysosomal enzyme which is enzymatically active, comprising:
   recovering the lysosomal enzyme from (i) a transgenic plant cell or (ii) a cell, tissue or organ of a transgenic plant, which transgenic plant cell or plant is transformed or transfected with a recombinant expression construct comprising a nucleotide sequence encoding the lysosomal enzyme and a promoter that regulates expression of the nucleotide sequence so that the lysosomal enzyme is expressed by the transgenic plant cell or plant.
2. The method according to claim 1, in which the promoter is an inducible promoter.
3. The method according to claim 2, in which the inducible promoter is induced by mechanical gene activation.
4. The method according to claim 3, in which the inducible promoter comprises SEQ ID NO:5.
5. The method according to claim 2, which is carried out with the transgenic plant and additionally comprises a step of inducing the inducible promoter before or after the transgenic plant is harvested, which inducing step is carried out before recovering the lysosomal enzyme from the cell, tissue or organ of the transgenic plant.
6. The method according to claim 1, in which the lysosomal enzyme is a modified lysosomal enzyme which is enzymatically active and comprises:
   (a) an enzymatically-active fragment of a human or animal lysosomal enzyme;
   (b) the human or animal lysosomal enzyme or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human or animal lysosomal enzyme or (a); or
   (c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.
7. The method according to claim 6, in which the modified lysosomal enzyme comprises a signal peptide or detectable marker peptide at the amino or carboxyl terminal of the modified lysosomal enzyme.
8. The method according to claim 7, in which the modified lysosomal enzyme is recovered from (i) the transgenic plant cell or (ii) the cell, tissue or organ of the transgenic plant by reacting with an antibody that binds the detectable marker peptide.
9. The method according to claim 7, in which the antibody is a monoclonal antibody.
10. The method according to claim 7, in which the detectable marker peptide comprises SEQ ID NO:10.
11. The method according to claim 6, in which the modified lysosomal enzyme comprises:
   (a) an enzymatically-active fragment of an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase; and
   (b) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a); or
   (c) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.
12. The method according to claim 11, in which the modified lysosomal enzyme comprises:
   (a) an enzymatically-active fragment of a human glucocerebrosidase or human α-L-iduronidase enzyme;
   (b) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human glucocerebrosidase, human α-L-iduronidase or (a); or
   (c) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.
13. The method according to claim 6, in which the modified lysosomal enzyme is a fusion protein comprising:
   (l) the enzymatically-active fragment of the human or animal lysosomal enzyme,
   (b) the human or animal lysosomal enzyme, or
   (c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions,
   and
   (II) a cleavable linker fused to the amino or carboxyl terminus of (I); and the method comprises:
   (i) recovering the fusion protein from the transgenic plant cell, or the cell, tissue or organ of the transgenic plant;
   (ii) treating the fusion protein with a substance that cleaves the cleavable linker so that (I) is separated from the cleavable linker and any sequence attached thereto; and
   (iii) recovering the separated (I).
14. The method according to claim 1, in which the transgenic plant is a transgenic tobacco plant.
15. The method according to claim 1, in which the lysosomal enzyme is a human or animal lysosomal enzyme.
16. The method according to claim 15, in which the lysosomal enzyme is an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase.

Lys Asp Glu Leu
17. The method according to claim 16, in which the lysosomal enzyme is a human glucocerebrosidase or human α-L-iduronidase.

18. The method according to claim 1, in which the organ is leaf, stem, root, flower, fruit or seed.

19. A recombinant expression construct comprising a nucleotide sequence encoding a lysosomal enzyme and a promoter that regulates the expression of the nucleotide sequence in a plant cell.

20. The recombinant expression construct of claim 19, in which the promoter is an inducible promoter.

21. The recombinant expression construct of claim 20, in which the inducible promoter is induced by mechanical gene activation.

22. The recombinant expression construct of claim 20, in which the inducible promoter comprises SEQ ID NO:5.

23. The recombinant expression construct of claim 19, in which the lysosomal enzyme is a modified lysosomal enzyme which is enzymatically active and comprises:

- (a) an enzymatically-active fragment of a human or animal lysosomal enzyme;
- (b) the human or animal lysosomal enzyme or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human or animal lysosomal enzyme or (a); or
- (c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

24. The recombinant expression construct of claim 23, in which the modified lysosomal enzyme comprises a signal peptide or detectable marker peptide at the amino or carboxyl terminus of the lysosomal enzyme.

25. The recombinant expression construct of claim 24, in which the detectable marker peptide comprises SEQ ID NO:10.

26. The recombinant expression construct of claim 23, in which the modified lysosomal enzyme comprises:

- (a) an enzymatically-active fragment of an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase;
- (b) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase; or
- (c) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a); or
- (d) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase or (c) having one or more naturally-occurring amino acid additions, deletions or substitutions.

27. The recombinant expression construct of claim 26, in which the modified lysosomal enzyme comprises:

- (a) an enzymatically-active fragment of a human glucocerebrosidase or human α-L-iduronidase enzyme;
- (b) the human glucocerebrosidase or human α-L-iduronidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human glucocerebrosidase, human α-L-iduronidase or (a); or
- (c) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

28. The expression construct of claim 23, in which the modified lysosomal enzyme is a fusion protein comprising:

- (I) (a) the enzymatically-active fragment of the human or animal lysosomal enzyme,
- (b) the human or animal lysosomal enzyme, or
- (c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions, and

- (II) a cleavable linker fused to the amino or carboxyl terminus of (I).

29. The recombinant expression construct of claim 19, in which the lysosomal enzyme is a human or animal lysosomal enzyme.

30. The recombinant expression construct of claim 29, in which the lysosomal enzyme is an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase.

31. The recombinant expression construct of claim 30, in which the lysosomal enzyme is a human glucocerebrosidase or human α-L-iduronidase.

32. A plant transformation vector comprising the recombinant expression construct of claim 19, 20, 24, 29, 31, 23, 27 or 28.

33. A plant which is transformed or transfected with the recombinant expression construct of claim 19, 20, 24, 29, 31, 23, 27 or 28.

34. A plant cell, tissue or organ which is transformed or transfected with the recombinant expression construct of claim 19, 20, 24, 29, 31, 23, 27 or 28.

35. A plant transformation vector comprising the recombinant expression construct of claim 19, 20, 24, 29, 31, 23, 27 or 28.

36. A plasmid comprising the recombinant expression construct of claim 19, 20, 24, 29, 31, 23, 27 or 28.

37. A plasmid CTProI:GCFLAG:FLAG having the ATCC accession number 97277.

38. A plasmid pCT22 having the ATCC accession number 97701.

39. A plasmid pCTS4 having the ATCC accession number 97770.

40. A transgenic plant or plant cell capable of producing a lysosomal enzyme which is enzymatically active, which transgenic plant or plant cell is transformed or transfected with a recombinant expression construct comprising a nucleotide sequence encoding a lysosomal enzyme and a promoter that regulates the expression of the nucleotide sequence in the transgenic plant or plant cell.

41. The transgenic plant or plant cell of claim 40, in which the promoter is an inducible promoter.

42. The transgenic plant or plant cell of claim 41, in which the inducible promoter is induced by mechanical gene activation.

43. The transgenic plant or plant cell of claim 42, in which the inducible promoter comprises SEQ ID NO:5.

44. The transgenic plant or plant cell of claim 40, in which the lysosomal enzyme which is a modified lysosomal enzyme which is enzymatically active and which comprises:

- (a) an enzymatically-active fragment of a human or animal lysosomal enzyme;
- (b) the human or animal lysosomal enzyme or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human or animal lysosomal enzyme or (a); or
- (c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.
45. The transgenic plant or plant cell of claim 44, in which the modified lysosomal enzyme comprises a signal peptide or detectable marker peptide at the amino or carboxyl terminal of the modified lysosomal enzyme.

46. The transgenic plant or plant cell of claim 45, in which the detectable marker peptide comprises SEQ ID NO:10.

47. The transgenic plant or plant cell of claim 44, in which the modified lysosomal enzyme comprises:

(a) an enzymatically-active fragment of an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase;

(b) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a); or

(c) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

48. The transgenic plant or plant cell of claim 47, in which the modified lysosomal enzyme comprises:

(a) an enzymatically-active fragment of a human glucocerebrosidase or human α-L-iduronidase enzyme;

(b) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human glucocerebrosidase, human α-L-iduronidase or (a); or

(c) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

49. The transgenic plant or plant cell of claim 44, in which the modified lysosomal enzyme is a fusion protein comprising:

(I) (a) the enzymatically-active fragment of the human or animal lysosomal enzyme,

(b) the human or animal lysosomal enzyme, or

(c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions, and

(II) a cleavable linker fused to the amino or carboxyl terminus of (I).

50. The transgenic plant or plant cell of claim 40, in which the transgenic plant or plant cell is a transgenic tobacco plant or tobacco cell.

51. The transgenic plant or plant cell of claim 40, in which the lysosomal enzyme is a human or animal lysosomal enzyme.

52. The transgenic plant or plant cell of claim 51, in which the lysosomal enzyme is an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase.

53. The transgenic plant or plant cell of claim 52, in which the lysosomal enzyme is a human glucocerebrosidase or human α-L-iduronidase.

54. A leaf, stem, root, flower or seed of the transgenic plant of claim 40, 41, 45, 50, 51, 53, 44, 48 or 49.

55. A seed of plant line hGC X-11, which seed has the ATCC Accession No. 97275.

56. A seed of plant line hGC X-27, which seed has the ATCC Accession No. 97276.

57. A seed of plant line CT-40-9, which seed has the ATCC Accession No. 97700.

58. A plant grown from the seed of claim 55, 56 or 57.

59. A lysosomal enzyme which is enzymatically active and is produced according to a process comprising:

recovering the lysosomal enzyme from (i) a transgenic plant cell or (ii) a cell, tissue or organ of a transgenic plant which transgenic plant cell or plant is transformed or transfected with a recombinant expression construct comprising a nucleotide sequence encoding the lysosomal enzyme and a promoter that regulates expression of the nucleotide sequence so that the lysosomal enzyme is expressed by the transgenic plant cell or plant.

60. The lysosomal enzyme of claim 59, in which the promoter is an inducible promoter.

61. The lysosomal enzyme of claim 60, in which the inducible promoter comprises SEQ ID NO:5.

62. The lysosomal enzyme of claim 60, which process is carried out with the transgenic plant and additionally comprises a step of inducing the inducible promoter before or after the transgenic plant is harvested, which inducing step is carried out before recovering the lysosomal enzyme from the cell, tissue or organ of the transgenic plant.

63. The lysosomal enzyme of claim 59, in which a modified lysosomal enzyme which is enzymatically active and comprises:

(a) an enzymatically-active fragment of a human or animal lysosomal enzyme;

(b) the human or animal lysosomal enzyme or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human or animal lysosomal enzyme or (a); or

(c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

64. The lysosomal enzyme of claim 63, in which the modified lysosomal enzyme comprises a signal peptide or detectable marker peptide at the amino or carboxyl terminal of the modified lysosomal enzyme.

65. The modified lysosomal enzyme of claim 64, in which the detectable marker peptide comprises SEQ ID NO:10.

66. The lysosomal enzyme of claim 63, in which the modified lysosomal enzyme comprises:

(a) an enzymatically-active fragment of an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase;

(b) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions, and

(c) the α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase, sialidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

67. The lysosomal enzyme of claim 66, in which the modified lysosomal enzyme comprises:

(a) an enzymatically-active fragment of a human glucocerebrosidase or human α-L-iduronidase enzyme;
(b) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more amino acid residues added to the amino or carboxyl terminus of the human glucocerebrosidase, human α-L-iduronidase or (a); or
(c) the human glucocerebrosidase, human α-L-iduronidase or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions.

68. The lysosomal enzyme of claim 63, in which the modified lysosomal enzyme is a fusion protein comprising:
(I) (a) the enzymatically-active fragment of the human or animal lysosomal enzyme,
(b) the human or animal lysosomal enzyme, or
(c) the human or animal lysosomal enzyme or (a) having one or more naturally-occurring amino acid additions, deletions or substitutions, and
(II) a cleavable linker fused to the amino or carboxyl terminus of (I).

69. The lysosomal enzyme of claim 59, in which the transgenic plant is a transgenic tobacco plant.
70. The lysosomal enzyme of claim 39, in which the lysosomal enzyme is a human or animal lysosomal enzyme.
71. The lysosomal enzyme of claim 70, in which the lysosomal enzyme is an α-N-acetylgalactosaminidase, acid lipase, α-galactosidase, glucocerebrosidase, α-L-iduronidase, iduronate sulfatase, α-mannosidase or sialidase.
72. The lysosomal enzyme of claim 71, in which the lysosomal enzyme is a human glucocerebrosidase or human α-L-iduronidase.
73. The lysosomal enzyme of claim 59, in which the organ is leaf, stem, root, flower, fruit or seed.