Identification and Expression of Acid β-Glucosidase Mutations Causing Severe Type 1 and Neurologic Type 2 Gaucher Disease in Non-Jewish Patients

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Abstract

Gaucher disease, the most prevalent lysosomal storage disease, occurs in three subtypes, all resulting from mutations in the acid β-glucosidase gene. Molecular studies in five severely affected type 1 and two type 2 Gaucher disease patients of non-Jewish descent identified six new mutations: K74X, W179X, G195E, S271N, V352L, and a two-base deletion in exon 10 (1450del2). Two additional mutations identified in these patients (R48W and G202R) have been reported previously, but were not expressed or characterized. Heterologous expression in SF9 cells using the baculovirus system revealed that the missense mutations, R48W and V352L, had 14 and 7%, respectively, of the specific activity based on cross-reacting immunologic material expressed by the normal allele. In contrast, the G195E, G202R, and S271N mutant alleles were more severely compromised with only 1–2% of the normal expressed specific activity based on cross-reacting immunologic material. Structural distortion at the active site was probed by comparing the interaction of the mutant enzymes with active site–directed inhibitors (castanospermine, conduritol B epoxide and deoxynojirimycin). R48W, G202R, and S271N were normally inhibited, whereas V352L and G195E mutant enzymes had significantly decreased binding affinity. These mutations further expand the genetic heterogeneity in the lesions causing Gaucher disease types 1 and 2, and further delineate genotype/phenotype correlations and functional domains within the acid β-glucosidase gene. (J. Clin. Invest. 1997. 99:2530–2537.) Key words: Baculoviridae • mutagenesis, site-directed • recombinant • enzymology • genotype

Introduction

Gaucher disease (GD),¹ the most prevalent lysosomal storage disorder, results from the deficient activity of acid β-glucosidase, and the accumulation of glucosylceramide in monocytes/macrophages (1, 2). The disease is an autosomal recessive disorder (1, 2) resulting from mutations in the acid β-glucosidase (EC.3.2.1.45) gene, which has been localized to the chromosomal region 1q21–q31 (3–5). Three clinical subtypes have been delineated based on the absence (type 1) or presence and severity (acute type 2 and subacute type 3) of neurological involvement. Although prevalent among individuals of Ashkenazi Jewish descent, the disease is panethnic. Almost 80 gene alterations leading to the defective activity of this lysosomal hydrolase have been identified (for review see Beutler and Gelbart, reference 6). Four defects (N370S, 84insG, L444P, and IVS2-1G), account for 90–96% of the disease-causing changes among patients of Ashkenazi descent (7, 8). In non-Jewish patients, the N370S and L444P mutations account for 38 and 33% of disease alleles, respectively (9). Of the remaining mutations reported, most are unique or “private,” having been detected in only one or a few GD families.

The full length cDNA and genomic sequences for acid β-glucosidase have been isolated and characterized (10–12). Of note, a pseudogene transcribable into mRNA, but unable to produce a functional gene product (13), is located 16 kb downstream from the structural gene (12), and several mutations causing GD derived from homologous recombination and/or gene conversion have been reported. The structural gene codes for a 497 amino acid mature protein of 59–67 kD, depending on the state of glycosidic processing. Acid β-glucosidase is active as a monomer and requires saposin C, a small glycoprotein activator, for physiological activity (14). Detailed characterization studies of heterologously expressed normal and mutagenized acid β-glucosidases have localized residues important for substrate and activator binding to the last third of the protein (15–17) and identified Glu486 as the catalytic nucleophile (18).

The identification and expression of mutations in the acid β-glucosidase gene is useful for structure/function studies and for genotype/phenotype correlations. In this communication, the identification and characterization of six new and two previously uncharacterized mutations in five moderately to severely affected type 1 patients and two severely affected type 2 patients, all of non-Jewish ancestry, are described. Heterologous expression of the missense mutations was undertaken to characterize the mutant enzymes’ stability and catalytic function, confirming causality for GD. An additional mutation, the substitution of the glutamate at position 235 by glycine (E235G), was engineered to probe this residue’s putative mechanistic role as the acid catalyst (19). These studies led to further delineation of functional regions and identification of individual residues important for maintaining normal acid β-glucosidase function.

Methods

Patient descriptions. Patient 1 is a 20-yr-old female of Indian descent with severe type 1 GD who presented with cachexia and massive

1. Abbreviations used in this paper: 4MU-Glc, 4-methylumbelliferyl-β-D-glucopyranoside; CBE, conduritol B epoxide; CRIM, cross-reacting immunologic material; CRIM SA, CRIM specific activity; CS, castanospermine; DNM, deoxynojirimycin; GD, Gaucher disease; Hgb, hemoglobin; NBD-GC, NBD-glucosylceramide.
hepatosplenomegaly (liver and spleen volumes of 3,095 and 6,545 ml, respectively), ascites, and portal hypertension. She had marked anemia (hemoglobin [Hgb], 9.7 g%) and hepatosplenomegaly (liver and spleen volumes of 3,095 and 6,545 ml, respectively), ascites, and portal hypertension. She had marked anemia (hemoglobin [Hgb], 9.7 g%), hepatosplenomegaly (three times normal liver volume), and diminished leukocyte acid β-glucosidase activity (0.7 nmol/h per mg). She experienced extreme fatigue before enzyme therapy that has resolved together with significant improvement in her hemoglobin and normalization of her spleen volume.

Patient 5 is an 18-yr-old female of Hispanic (Peruvian) descent with moderate type 1 GD. She presented with easy bruising and bone disease characterized by lytic femoral head deformities and pathological pelvic fracture during a pregnancy at age 26. She had anemia (Hgb, 10.3 g%), hepatomegaly (three times normal liver volume), and diminished leukocyte acid β-glucosidase activity (0.7 nmol/h per mg). She experienced extreme fatigue before enzyme therapy that has resolved together with significant improvement in her hemoglobin and normalization of her spleen volume.

Table I. Oligonucleotide Primers Used to Amplify Exons 3, 4, 6, 7, 8, and 10 of the Acid β-Glucosidase Structural Gene

<table>
<thead>
<tr>
<th>Exon</th>
<th>Sense primers</th>
<th>Antisense primers</th>
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<tr>
<td>3</td>
<td>5'-CATGTCCTTATCATGACGTCCTCAC-3'</td>
<td>5'-CACAGGGATAAAGGGATCAG-3'</td>
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<tr>
<td>4</td>
<td>5'-GCTGGTTACTGAATCCTATG-3'</td>
<td>5'-TGCCGAGATGATCAGTCTG-3'</td>
</tr>
<tr>
<td>6</td>
<td>5'-GCTTCTCTCTCTCTCCTTT-3'</td>
<td>5'-GCTGACAGAGAGAGAGACTCC-3'</td>
</tr>
<tr>
<td>7</td>
<td>5'-GCTTCTCTCTCTCTCTCTTGG-3'</td>
<td>5'-GTTGGAAGGCGCACAAGTGGT-3'</td>
</tr>
<tr>
<td>8</td>
<td>5'-AGCTCATGCTGAGGAGGATC-3'</td>
<td>5'-GTAAGGAGATGAGGCTCTGTA-3'</td>
</tr>
<tr>
<td>10</td>
<td>5'-CTAACTTGTGTCGACATCAG-3'</td>
<td>5'-ATAAGGCACTCAGACTGTA-3'</td>
</tr>
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produced in cloned S. frugiperda (S9) cells by calcium phosphate–mediated transfection and homologous recombination between the expression plasmid and baculovirus genomic DNA (Baculogold®) as described (31). Pure recombinant baculovirus clones containing the normal or mutant cDNA for acid β-glucosidase were isolated by plaque hybridization, amplified, titrated, and used at a multiplicity of infection >10 to infect S9 cells (31).

**Immunoblotting.** Immunoelectroblotting using a polyclonal antihuman acid β-glucosidase antibody was conducted as described (15–17). In brief, S9 cells infected with pure recombinant virus were harvested 3 d after infection. The pellets were sonicated in 0.04 M citrate/phosphate buffer, pH 5.5, containing 1 mM EDTA, 4 mM β-mercaptoethanol, 0.1% Triton X-100, and 0.1% sodium taurocholate, using a cup sonicator (Cell Disruptor 200; 80 watts, pulse times of 30, 20, and 20 s). Aliquots of the clarified (875 g; 20 min) crude sonicates containing determined amounts of protein and enzymatic activity were run on tricine-SDS-polyacrylamide gels (32) and immunoblotted. Specific activities based on the amount of cross-reacting immunological material (CRIM) specific activity (CRIM SA) were determined as described (15, 16). The relative amounts of CRIM per unit of glucosylceramide-cleaving activity for each mutant was determined by visual inspection of immunoblotting membranes and referenced to that of the normal enzyme.

**Enzyme assays.** Aliquots of the crude sonicates, prepared as described above, were assayed for acid β-glucosidase activity using the fluorescently labeled natural substrate (NBD-glucopyranosylceramide or 12-[N-methyl-N-(7-nitrobenz-2-oxa-1,3-diazol-4-yl)]dodecylglycosylphosphatidyl-1-O-β-D-glucopyranoside; NBD-GC) or the synthetic substrate (4-methylumbelliferyl-β-D-glucopyranoside; 4MU-Glc). The final reaction mixtures contained either 0.3 mM NBD-GC (100 μl final reaction vol) or 4 mM 4MU-Glc (200 μl final reaction vol) in 0.04 M citrate/phosphate buffer, pH 5.5, 1 mM EDTA, 4 mM β-mercaptoethanol, 0.25% Triton X-100, and 0.25% sodium taurocholate. The 4MU-Glc reaction was terminated by raising the pH with the addition of 2.3 ml of a 0.1 M aqueous solution of ethylenediamine. The fluorescence of the samples was then read with the fluorometer. The NBD-GC assays were terminated and processed as described (33). The fluorescence of the extracted reaction products were read using an Optical System 3 spectrofluorometer. Background levels were determined by comparison with results obtained from S9 cells infected with recombinant baculovirus containing the cDNA for acid β-glucosidase in the antisense direction. 1 U acid β-glucosidase activity is the amount of enzyme that hydrolyzed 1 μM substrate/min at 37°C.

The effect of the addition of sodium azide on the activity of the E235G mutant was measured using the stopped assays outlined above with the natural (NBD-GC) and synthetic (4MU-Glc) substrates and a continuous assay with 2,4-dinitrophenol-phosphate as the substrate. Initial rates of hydrolysis towards both NBD-GC and 4MU-Glc (100 and 200 μl final reaction vol, respectively) were determined in the presence of 0, 10, 250, and 500 mM sodium azide by the addition of aliquots from a concentrated (4.8 M) aqueous sodium azide solution just before addition of crude E235G lysate. For the continuous assay, the reaction mixture containing 0.39 mM DNP-Glu in 0.04 M citrate/phosphate buffer, pH 5.5, 0.25% Triton X-100, and 0.25% sodium taurocholate with or without 200 mM sodium azide was preincubated at 37°C in a thermostatted cell holder. An aliquot of E235G lysate was added and the release of dinitrophenolate was followed continuously by measuring the increase in absorbance at 400 nm at 10-s intervals.

**Inhibition of expressed normal and mutant acid β-glucosidases.** Aliquots of crude lysates were assayed in the absence or presence of each of the following active site-directed inhibitors: conduritol B epoxide (CBE; 0–600 μM), deoxynojirimycin (DNM; 0–600 μM), and castanospermine (CS; 0–80 μM). Concentrated aqueous stock solutions of the inhibitors were made such that aliquots between 0 and 50 μl gave the desired final concentrations in the reaction assay. The synthetic substrate (4MU-Glc) was used. The final reaction mixture contained 4 mM 4MU-Glc (200 μl final reaction vol) and the appropriate amount of inhibitor in 0.04 M citrate/phosphate buffer, pH 5.5, containing 0.25% Triton X-100 and 0.25% sodium taurocholate. The IC₅₀ for each inhibitor for the normal and mutant (R48W, G195E, G202R, S271N, and V352L) acid β-glucosidases was determined from a plot of activity remaining versus inhibitor concentration. The previously characterized (15–17) common mutations, N370S and L444P, were reexpressed for comparative purposes.

**N-Glycanase treatment of expressed normal and mutant acid β-glucosidases.** S9 cells expressing normal acid β-glucosidase and two of the mutants, R48W and V352L, were harvested and sonicated in 0.2 M phosphate buffer, pH 7.5, (200 μl) as described above. Aliquots of the crude lysates (100 μl) were adjusted to 0.5% SDS and 0.1 M β-mercaptoethanol and boiled for 5 min. Octyl-β-glucopyranoside (10% stock solution) was added to a final concentration of 2.6% (i.e., a sevenfold excess over the final SDS concentration of 0.37%). Each sample was divided in half. Recombinant N-Glycanase® (0.3 U) was added to one aliquot of each sample, while the other served as the untreated control. After 8 h, the deglycosylation reaction was terminated by addition of the protein gel loading dye. The samples were analyzed by tricine-SDS-PAGE (10% acrylamide gel) and Western blotting, as previously described (16, 17).

**Results**

Identification of novel point mutations. Complete sequencing of the acid β-glucosidase coding region and intron/exon boundaries from seven non-Jewish patients with GD (Table II) resulted in the identification of five new point mutations (K74X, W179X, G195E, S271N, and V352L), and a novel 2-bp deletion in exon 10 (1450del2), as well as two known but uncharacterized mutations (R48W and G202R) (34, 35). Other alleles found included the common N370S, the complex RecNcil, and the rare but previously expressed F213I (22, 36) lesions. Table III summarizes the identified nucleotide substitutions and the resulting changes at the protein level.

Six of the novel mutations were found in five patients with nonneurologic disease. Patient 1, with severe GD type 1, was heteroallelic for R48W and W179X. Although the nucleotide substitution at position 259 in the cDNA causing the R48W mutation corresponds to the pseudogene sequence at the analogous site, it did not derive from a crossover event between the structural gene and the pseudogene since other pseudogene-like substitutions at contiguous sites were not present (nucleotides 257–261 for the normal allele, GAC→GG). Moreover, it occurred at a CpG dinucleotide, a known mutational hotspot (37, 38). Patient 2, with severe type 1 disease, did not carry a normal V352 codon and appeared homoallelic for V352L (Fig. 1A). The genomic DNAs

<table>
<thead>
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<th>Patient</th>
<th>Phenotype</th>
<th>Ancestry</th>
<th>Genotype</th>
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<tbody>
<tr>
<td>1</td>
<td>Type 1, severe</td>
<td>Indian</td>
<td>R48W/W179X</td>
</tr>
<tr>
<td>2</td>
<td>Type 1, severe</td>
<td>African-American</td>
<td>V352Ldel</td>
</tr>
<tr>
<td>3</td>
<td>Type 1, severe</td>
<td>English</td>
<td>S271N/RecNcil</td>
</tr>
<tr>
<td>4</td>
<td>Type 1, moderate</td>
<td>Hispanic (Peruvian)</td>
<td>G195E/N370S</td>
</tr>
<tr>
<td>5</td>
<td>Type 1, moderate</td>
<td>Hispanic (Spanish)</td>
<td>1450del2/N370S</td>
</tr>
<tr>
<td>6</td>
<td>Type 2</td>
<td>Hispanic (Puerto Rican)</td>
<td>K74X/F213I</td>
</tr>
<tr>
<td>7</td>
<td>Type 2</td>
<td>Italian</td>
<td>G202R/G202R</td>
</tr>
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</table>
from both parents were amplified across exon 8 and sequenced. The mother was heteroallelic for the V352L mutation, while codon 352 in the father was normal, suggesting that both the father and the son had an unamplifiable allele (i.e., deletion). Efforts to define the limits of the deletion are underway. Patient 3, with moderate to severe type 1 disease, was heteroallelic for the S271N mutation and the common complex allele, RecNcil (L444P+A456P+V460V). Patient 4, with moderate type 1 disease, was heteroallelic for G195E and N370S, the common exon 9 defect. Patient 5, with moderate to severe type 1 disease, was heteroallelic for a two-base deletion after nucleotide 1450 in exon 10 (1450del2) (Fig. 1) and the common N370S allele. The deletion of the two bases at nucleotide positions 1451 and 1452 in codon 445 causes a shift in reading frame and the translation of eight altered bases after position 452. The deleted area includes residues required for substrate and activator binding (17).

The remaining two mutations were identified in two patients with the most severe neurologic form of the disease, type 2. Patient 6 was heteroallelic for K74X and F213I. The F213I substitution mimics the base substitution in the pseudogene at the analogous site.

The K74X and W179X alleles are predicted to produce unstable protein products that terminate before all the active site residues identified to date (17). The 452 amino acid truncated protein expressed from the 1450del2 allele would be missing residues important for completing the active site. These three severely compromised alleles were not characterized further.

Expression and characterization of missense mutations. The R48W, G195E, G202R, S271N, and V352L, missense alleles, as well as the sense and antisense acid β-glucosidase alleles, were expressed in the baculovirus system and characterized (Table IV). The previously studied N370S and L444P alleles (15, 17) were reexpressed for comparative purposes. In addition, the mutation, E235G, which was created by the substitution of an adenine at position 821 in the cDNA (genomic position 4178) by guanine (GAG→GGG), leading to the replacement of the glutamate at residue 235 by glycine, was also included in these studies to probe the putative role of Glu235 as the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19). Using the fluorescently labeled natural substrate, NBD-GC, the normal sense construct expressed the acid catalyst (19).
human acid β-glucosidase antibody. The smallest band ($M_r \sim 56,000$) can be clearly seen on the immunoblot from the more heavily loaded gel (Fig. 2, lane 9). Similar patterns were obtained for all of the expressed mutant cDNAs. No CRIM was detected in the cells expressing the antisense construct. The origin of the multiband pattern was explored using the expressed normal enzyme and the two mutants, R48W and V352L. The bands ($M_r$, ranging from 63,000 to $\sim 56,000$) represented differentially glycosylated forms of acid β-glucosidase, since after treatment with N-Glycanase (Fig. 3), a single species of $\sim 55,600$ D was observed, consistent with that of the deglycosylated mature acid β-glucosidase protein (1). Interestingly, the migration pattern of the lowest band in the untreated normal and mutant samples remained unchanged after N-Glycanase treatment. The molecular weight of this lower band is identical to that of the mature deglycosylated protein, indicating that it has undergone appropriate signal peptide cleavage in the endoplasmic reticulum, but no cotranslational glycosidic processing. Presumably, the high levels of protein synthesis achieved in Sf9 cells with the baculovirus expression vectors overwhelmed the glycosylation machinery in the ER, resulting in unglycosylated and underglycosylated species.

All sense cDNAs gave strong CRIM signals (Fig. 2), indicating similar stabilities for the normal and mutant enzyme species. To assess the level of catalytic efficiency ($k_{cat}$) for each mutant allele, the amount of CRIM SA was calculated for each relative to the expressed normal acid β-glucosidase (Table IV). In comparison with the signal from the expressed normal enzyme in the immunoblot in Fig. 2, the lane containing R48W had approximately three times the CRIM (i.e., three times the amount of acid β-glucosidase protein). Since only 41% of the normal activity was loaded, the R48W enzyme had a 7.3-fold reduction in catalytic efficiency compared with the expressed normal enzyme. Similarly, comparison of the CRIM signals and activities for the normal and V352L proteins indicated a 15-fold reduction in catalytic efficiency for the V352L-expressed enzyme. The effects of the remaining mutations were much more deleterious, all causing an $\sim 100$-fold (G195E, G202R, and S271N) or greater (E235G) reduction in turnover rate or $k_{cat}$.

To probe the effect of the various amino acid substitutions on the structural integrity of the active site of each mutant protein species, the affinity of various active site-directed inhibitors (DNM, CBE, and CS) was determined by determination of the concentration of each inhibitor required for inhibition of 50% of the initial activity ($IC_{50}$). Three of the mutants, R48W, G202R, and S271N, interacted normally with the series of inhibitors tested (as did L444P) and had $IC_{50}$ values that overlapped with those for the expressed normal enzyme. As was the case with N370S, the mutants, G195E and V352L, demonstrated significantly reduced affinity for DNM and CBE. Interestingly, the range for the $IC_{50}$ values for CS towards the G195E mutant enzyme was considerably higher than any mutant characterized to date (15–17). The extremely low residual activity of the E235G mutant precluded its inclusion in the inhibition studies. This mutant was, however, tested for a gain of activity in the presence of a strong competitive nucleophile, sodium azide. This criterion has been used to identify the acid catalyst.
in *Agrobacterium faecalis* β-glucosidase (39). There was no change in activity of E235G towards glucosylceramide or 4MU-Glc in the presence of up to 250 mM sodium azide or towards 2,4-dinitrophenol-β-glucopyranoside in the presence of 200 mM sodium azide.

**Discussion**

The identification of these mutations and their individual expression in the baculovirus system provided insight into the molecular basis of the GD subtypes and structure/function relationships in normal acid β-glucosidase. The deleterious effects of introducing these substitutions into the cDNA for acid β-glucosidase on the catalytic turnover rate of the expressed proteins demonstrate causality of these mutations for GD. As these and earlier (15–17) studies demonstrate, there is, in general, good correlation between the properties of the mutant proteins overexpressed in Sf9 cells and the severity of the disease manifestations in Gaucher patients. This Sf9 expression system permits the overexpression of sufficient protein for further assessment of defective enzyme function, such as binding affinities, thermal stability, pH sensitivity, and activation by phosphatidylserine or saposin C (17). Our findings extend the earlier assignments of functional domains of acid β-glucosidase (17), although more definite identification of residues comprising the active site, as well as activator binding sites, awaits a crystal structure.

For the R48W mutant, the nonconservative substitution of tryptophan for arginine at residue 48 involves the loss of a positive charge and the introduction of a more sterically bulky, side chain, and thus could be expected to be a very deleterious defect. However, the normal stability and interaction of the R48W mutant enzyme with active site-directed inhibitors argued against a gross structural distortion of the expressed protein, in particular at the catalytic site, and suggested that residue 48 may lie near the surface of the protein or in a location where such a substitution could be better accommodated. To date, characterization of the NH-terminus of human acid β-glucosidase has been limited. Only three other patient-derived single missense mutations (T43I, reference 34, and V15L and G46E, reference 40) have been reported in the first 100 amino acids of the human enzyme, but only the very conservative V15L mutant has been expressed (40) and shown to retain significant residual activity (~14% of the normal). Earlier mutagenesis studies in this laboratory (15) involving the engineered (i.e., not patient-derived) mutation T43K strongly supported the hypothesis that the region encompassing this amino acid is not buried within the protein core, since introduction of this highly unfavorable substitution (polar, uncharged threonine for the large positively charged lysine) had no effect on activity. Additionally, the presence of oligosaccharide chains attached at Asn19 and Asn49 (proven sites of N-glycosylation; reference 41) would be expected to bring these residues and the surrounding regions to the surface.

In the S271N allele, serine is replaced by the bulkier asparagine, which also has an uncharged polar R group. Studies have shown that this substitution is generally nondisruptive (42), unless buried inside the protein in a region of very tight packing. Since Asn70 has been shown to be one of four sites of N-glycosylation in acid β-glucosidase (41), the S271N lesion should be near the surface. Although only the presence of a proline in the second position of the consensus sequence for N-glycosylation (Asn-Xaa-Ser/Thr, where Xaa ≠ Pro) prevents attachment of oligosaccharide chains (43), the severe reduction in activity in the S271N mutant (normal sequence, Asn-Ser171-Thr-His; and mutant sequence, Asn-Asn171-Thr-His) may be due to interference with the frequency of site occupancy of Asn171.

The reduced activity and altered affinity towards active site-directed inhibitors by the V352L, G202R, and G195E mutant polypeptides localize residues 352, 202, and 195 to the active site of acid β-glucosidase. Substitution of leucine for valine is generally considered a conservative (44, 45) or favorable (42) substitution since both have nonpolar R groups varying only by one methylene group. However, residue 352 lies within the region of acid β-glucosidase containing the substrate and activator binding domains (residues 323–463) (17) and the catalytic nucleophile (Glu340) (18). Compared with that of the normally expressed enzyme, the reduced CRIM SA of the V352L enzyme and its lower affinity for the active site-directed inhibitors (especially DNM and CBE) suggest an altered substrate binding region, presumably accounting for its 15-fold reduction in catalytic efficiency. With respect to the G202R allele, the substitution of the bulky, polar arginine for the small, nonpolar glycine is considered unfavorable, especially if amino acid position 202 is in a tightly packed region of the folded protein (42). That Gly202 contributes to active site structure, either directly by proximity or indirectly via folding, is supported by the decreased affinity of the mutant enzyme for CS, DNM, and CBE, indicating a distorted catalytic site. With the unfavorable substitution of the small, neutral side chain of glycine by the bulky, negatively charged chain of glutamate, the G195E allele had a predictably greatly reduced catalytic efficiency and an altered active site (indicated by the higher IC50 values). G195E is the first mutation demonstrated to significantly interfere with the binding of CS at the active site. Since mutations at other positions in the active site (e.g., N370S and V394L) selectively interfered with the binding of DNM and CBE, but not significantly with CS (15–17), the side chain of Glu95 in the G195E mutant must have a specific unfavorable interaction with the rigid bicyclic CS in the aberrant glycopeptide.

Of the numerous residues that have been localized to the active site region of acid β-glucosidase, only E340 has been assigned a direct mechanistic role (i.e., the catalytic nucleophile) (18). The acid catalyst has yet to be identified. Using hydrophobic cluster analysis to theoretically predict catalytic residues in several lysosomal glycosidases, Henrissat et al. (19) proposed that Glu235 is the acid catalyst in acid β-glucosidase. The mutagenesis results presented here confirm that Glu235 is required to maintain enzymatic activity, since its substitution by glycine (E235G) resulted in a stable protein with a >1000-fold reduction in rate constant. However, a mechanistic role of Glu235 as the acid catalyst could not be confirmed, since no effect on the initial rates of hydrolysis of a panel of substrates with varying leaving group abilities was observed in the presence of a competitive nucleophile (sodium azide). This criterion has been used to assign mechanistic roles to putative acid/base catalysts in fungal glycosidases (39).

The characteristics of these newly identified mutations in acid β-glucosidase were generally consistent with the observed phenotypes of the respective types 1 and 2 patients. As expected from the results of large population screening studies (23, 46, 47) and earlier structure/function studies (15–17), the
presence of one N370S allele protected against the development of neurological manifestations, even if the heteroallelic mutation was severely compromised, as in patients 4 (N370S/G195E) and 5 (N370S/1450del12). With a CRIM SA value similar to that of N370S, the R48W mutant also had sufficient residual activity to protect against the neurogenicform of GD, as indicated by the type 1 phenotype of Patient 1 (R48W/W179X), where the truncated W179X does not produce any active acid β-glucosidase protein. While these studies were in progress, the R48W mutation was identified (but not expressed or characterized) in two GD patients with mild (R48W/1450del12; African-American) and moderate to severe (R48W/L444P; Bedouin descent) type 1 disease (34).

The type 1 phenotypes of patients 2 and 3 suggest that the V352L and S271N alleles each have sufficient residual activity to prevent neurologic disease, since the heteroalleles in these patients (i.e., a “deletion” and RecNcl, respectively) most likely contribute little, if any, residual activity. The protective effect of S271N would not be predicted from its low CRIM SA (~0.02, average of four experiments), illustrating the limits of an in vitro detergent-based assay (which may not always reflect a mutant’s intracellular activity at the lysosomal level) or that other factors (such as a modifier gene) in addition to acid β-glucosidase deficiency may influence the phenotypic expression of GD. The role of a modifier gene is clearly indicated by the range of phenotypes (asymptomatic to mild to severe disease) observed in Gaucher type 1 patients who are homoallelic for N370S.

The homoygous presence of the severely compromised G202R mutant allele, with its 100-fold reduction in turnover rate, is in agreement with the type 2 phenotype of Patient 7 and with the findings of Beutler et al. (35), who identified the G202R mutation in two GD patients with the least severe type 1 phenotype (G202R/N370S) and in one type 2 patient (G202R/L444P). The combination of the inactive truncation allele, K74X, and the severely compromised F213I allele (36) also is consistent with the observed type 2 phenotype of patient 6. Interestingly, the F213I allele has been identified in all three types of GD (22, 36), including an English type 1 patient whose heteroallele was the severely deficient P289L allele (22), which again suggests a role for a modifier gene in the phenotypic expression of this disease.

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