

Reciprocal and Nonreciprocal Recombination at the Glucocerebrosidase Gene Region: Implications for Complexity in Gaucher Disease

Nahid Tayebi, Barbara K. Stubblefield, Joseph K. Park, Eduard Orvisky, Jamie M. Walker, Mary E. LaMarca, and Ellen Sidransky

Clinical Neuroscience Branch, National Institute of Mental Health, and Medical Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda

Gaucher disease results from an autosomal recessive deficiency of the lysosomal enzyme glucocerebrosidase. The glucocerebrosidase gene is located in a gene-rich region of 1q21 that contains six genes and two pseudogenes within 75 kb. The presence of contiguous, highly homologous pseudogenes for both glucocerebrosidase and metaxin at the locus increases the likelihood of DNA rearrangements in this region. These recombinations can complicate genotyping in patients with Gaucher disease and contribute to the difficulty in interpreting genotype-phenotype correlations in this disorder. In the present study, DNA samples from 240 patients with Gaucher disease were examined using several complementary approaches to identify and characterize recombinant alleles, including direct sequencing, long-template polymerase chain reaction, polymorphic microsatellite repeats, and Southern blots. Among the 480 alleles studied, 59 recombinant alleles were identified, including 34 gene conversions, 18 fusions, and 7 downstream duplications. Twenty-two percent of the patients evaluated had at least one recombinant allele. Twenty-six recombinant alleles were found among 310 alleles from patients with type 1 disease, 18 among 74 alleles from patients with type 2 disease, and 15 among 96 alleles from patients with type 3 disease. Several patients carried two recombinations or mutations on the same allele. Generally, alleles resulting from nonreciprocal recombination (gene conversion) could be distinguished from those arising by reciprocal recombination (crossover and exchange), and the length of the converted sequence was determined. Homozygosity for a recombinant allele was associated with early lethality. Ten different sites of crossover and a shared pentamer motif sequence (CACCA) that could be a hotspot for recombination were identified. These findings contribute to a better understanding of genotype-phenotype relationships in Gaucher disease and may provide insights into the mechanisms of DNA rearrangement in other disorders.

Introduction

In mammalian cells, DNA rearrangement occurs by chromosomal pairing, breakage, and crossover between two nonsister chromatids during meiosis and is an essential cellular process. However, recombination between homologous sequences of DNA may also introduce harmful mutations resulting from the unequal pairing of chromosomes. The frequency of nonequal chromosomal pairing and DNA rearrangement is influenced by the degree of DNA sequence homology that exists between corresponding segments on the two chromosomes. The occurrence of homologous recombination can be enhanced by the presence of highly repetitive DNA sequence families, low-copy repeats, a processed or nonprocessed pseu-

dogene sequence, or the duplication of a region within the locus (Chen et al. 1997; Purandare and Patel 1997; Strachan and Read 1999; Stankiewicz and Lupski 2002a). Misalignment and recombination of homologous sequences cause DNA rearrangements that lead to genetic disorders and include deletions, duplications, inversions, fusions, and gene conversions (Mazzarella and Schlessinger 1998; Emanuel and Shaikh 2001; Hurler 2001; Inoue et al. 2001; Stankiewicz and Lupski 2002b). Human disorders resulting from DNA rearrangements due to structural features of the genome have been referred to as “genomic disorders” (Lupski 1998). Analyzing the results of homologous recombination in human genes can provide insights into the mechanisms of DNA rearrangement and may also enhance our understanding of factors contributing to the complexity seen in specific disorders. In the present study, we have evaluated the frequency and possible phenotypic consequences of crossover events and gene conversion occurring between the glucocerebrosidase (GBA) gene and its nonprocessed pseudogene located on the same chromosome.

The human GBA gene (GenBank accession number

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Address for correspondence and reprints: Dr. Ellen Sidransky, Section on Molecular Neurogenetics, 49 Convent Drive MSC4405, 49/B1EE16, Bethesda, MD 20892-4405. E-mail: sidrans@irp.nih.gov

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J03059), located on chromosome 1q21, has a pseudogene (GenBank accession number J03060) that shares 96% exonic sequence homology, located 16 kb downstream of the functional gene (Horowitz et al. 1989; Winfield et al. 1997). The 1q21 region is gene rich, with seven genes and two pseudogenes located in close proximity (GenBank accession number AF023263) (Winfield et al. 1997). The gene for metaxin (MTX) is located immediately downstream of the GBA pseudogene and is convergently transcribed, encoding a protein of 317 amino acids that appears to be part of a preprotein import complex in the outer membrane of mitochondria (Armstrong et al. 1997). MTX also has a pseudogene located between the GBA gene and pseudogene, immediately adjacent to the 3' end of the functional GBA gene (Long et al. 1996). These genes can serve as a model to demonstrate the effects of unequal pairing and recombination on gene function.

Gaucher disease (MIM 230800), the autosomal recessive inherited deficiency of lysosomal glucocerebrosidase (EC 3.2.1.45), presents with many diverse clinical phenotypes (Stone et al. 2000; Beutler and Grabowski 2001). On the basis of the presence and rate of progression of neurological symptoms, Gaucher disease has been divided into type 1 (nonneuronopathic), type 2 (acute neuronopathic), and type 3 (subacute neuronopathic) forms. The gene for glucocerebrosidase is organized into 11 exons coding for 498 amino acids, and, to date, >200 different mutations have been identified (Beutler and Gelbart 1998; Hodanova et al. 1999; Koprivica et al. 2000; Orvisky et al. 2002; GeneDis Databank). Studies of genotype-phenotype correlation indicate that clinically similar patients have many different genotypes and that patients sharing the same PCR-defined point mutations can have a spectrum of clinical manifestations (Koprivica et al. 2000; Zhao and Grabowski 2002). Most mutations resulting in Gaucher disease are point mutations that are distributed throughout the gene, with a majority clustered between exons 8 and 11. Several missense mutations, particularly N370S and L444P, are encountered with an increased frequency. Other mutations include frameshifts, deletions (with or without insertions), and splice-site mutations.

Another important group of mutations result from homologous recombination between the GBA gene and pseudogene. Patients with a recombinant allele containing three single point mutations—two that introduce the amino acid substitutions L444P and A456P, and a silent mutation, V460V, in exon 10 (Rec *NciI*)—were first reported in 1990 (Eyal et al. 1990; Latham et al. 1990). This allele is referred to as “recombinant 1” (Rec 1) in the present study. Subsequently, another recombinant allele was described, encompassing the same three changes with an additional amino acid substitution, D409H, in exon 9 (Rec TL or Rec 2) (Eyal et

al. 1990; Zimran and Horowitz 1994). Homologous recombination resulting in a fusion that includes the 5' segment of the GBA functional gene extending from exon 1 to intron 9, with the remainder of the sequence corresponding to the pseudogene, was shown by Zimran et al. (1990). Strasberg et al. (1994) first reported homozygosity for a recombinant allele in a patient with lethal type 2 Gaucher disease. Another type of mutant allele, a 55-bp deletion in exon 9 resulting from gene conversion from the pseudogene sequence, has also been reported (Walley and Harris 1993; Beutler et al. 1995; Tayebi et al. 1996b). Furthermore, recombinant alleles that include the 55-bp deletion, D409H, L444P, A456P, and V460V (Rec 3) have been identified, in which the site of crossover is located within the region extending from the end of intron 8 to the beginning of exon 9 (Hatton et al. 1997; Tayebi et al. 1998). Several reports have described fusion alleles in which the recombination occurred in the upstream portion of the gene, including introns 2, 3, and 6, introducing a larger segment of pseudogene into the recombinant allele (Reissner et al. 1998; Cormand et al. 2000; Filocamo et al. 2000). Patients with a crossover site in the 3' UTR of the GBA gene or the adjacent MTX pseudogene have also been identified (Stone et al. 2000; Tayebi et al. 2000, 2001).

To improve upon previous genotype-phenotype studies, we performed detailed molecular analyses of the GBA gene mutations in 480 alleles from clinically diverse patients with Gaucher disease. Because the high sequence homology between genes and pseudogenes at this locus increases the likelihood of recombination, we set out to determine the frequency, type, location, and mechanisms of recombination and whether different recombinant alleles had different phenotypic consequences.

Subjects and Methods

Patients

DNA samples from 240 patients with Gaucher disease were analyzed, including 155 patients with type 1, 37 patients with type 2, and 48 patients with type 3 Gaucher disease. Medical records were reviewed. DNA was also collected from selected family members. The patients and relatives provided informed consent through a protocol approved by the National Institute of Mental Health institutional review board. The series also included several cell lines purchased from the National Institute of General Medical Sciences Human Genetic Mutant Cell Repository.

DNA Preparation

High-molecular-weight DNA was isolated from lymphocytes, cultured fibroblasts, and/or EBV transformed lymphoblast cell lines from normal, affected, and carrier individuals, by standard protocols (Sambrook et al. 1989).

Mutation Analysis

Genomic DNA samples were screened for five common point mutations—N370S, L444P, R463C, c.84-85insG, and IVS2+1G→A—and the 55-bp deletion, through use of PCR, the amplification refraction mutation system (ARMS), restriction-enzyme digestion, and direct sequencing methods, as described by Mistry et al. (1992) and Tayebi et al. (1996a, 1997). After this screening, DNA from any patient with an unidentified mutation, a homozygous genotype, or a mutant allele that derived from pseudogene sequence was subjected to further analysis.

To confirm the presence of the mutations identified by screening and to search for unknown mutations, each of the 11 exonic regions of the GBA gene, including flanking intronic sequences and a 1-kb fragment of the 5' UTR, were selectively amplified using PCR primers that were designed to amplify the functional GBA gene but not the pseudogene (Reissner et al. 1998; Stone et al. 2000). Direct sequencing of the PCR products in both directions was performed by cycle sequencing using the fluorescent dideoxy termination method according to standard protocols. Fluorometric sequences were analyzed using the 373A DNA Sequencer (Applied Biosystems).

Long-template PCR was performed in selected cases, as described by Tayebi et al. (1996a, 1998). The bands corresponding to the recombinant alleles were isolated and sequenced to confirm the recombination and the site of crossover.

Southern Blot Analyses

Genomic DNA (10–15 µg) was isolated from patients and normal control individuals and was digested overnight at 37°C with the restriction enzymes *SstII*, *SspI*, *EcoRI*, or *HincII*. The digested DNAs were electrophoresed on a 0.6% I.D.NA (FMC Bioproducts) agarose gel for 16–18 h (for *SspI* and *HincII*) or for 40–48 h (for the restriction enzymes *SstII* and *EcoRI*). The gels were transferred to a supported nitrocellulose filter (Schleicher and Schuell) and were hybridized with ³²P-labeled GBA cDNA or MTX cDNA probes.

In addition, Southern blots prepared with *HincII*-digested DNA were hybridized to three shorter GBA cDNA probes. The first probe was a 250-bp fragment encompassing exons 2–4, which was amplified using the

forward primer 5'-CAGGCAGTGTCTGGGCATC-3' and the reverse primer 5'-CAGAACAGAAGTTCCAGAAA-3' (annealing temperature 60°C). A second probe, a 476-bp fragment covering exons 4–7, was amplified with the forward primer 5'-CTGCTGCTCTCAACATCCTT-3' and the reverse primer 5'-TGTTGAGTGGATACCCCTTC-3' (annealing temperature 60°C), and a third 762-bp fragment, containing exons 7–11, was amplified using the forward primer 5'-TTCCTGGATGCCTATGCTGA-3' and the reverse primer 5'-GCTCCTCTAAGGATGTCCC-3' (annealing temperature 60°C). Southern blots of *HincII*-digested DNA were also hybridized to an MTX cDNA probe.

Analysis of Polymorphic Sites

Genotypes at two polymorphic microsatellite sites, a dinucleotide (CT) repeat located upstream of the GBA gene and a tetranucleotide (AAAT) repeat located downstream of the GBA gene, were determined as described by Lau et al. (1999).

Analysis of Motif Sequences

To identify DNA regions representing shared motif sequences at specific crossover sites in the GBA gene, all sequences surrounding the approximate sites of recombination were aligned using the GCG and Sequencher software programs (Gene Codes).

Nomenclature for Recombinant Alleles

The approximate initiation point for a gene conversion or reciprocal recombination event was determined by examination of known mismatches between the functional gene and pseudogene sequences. The crossover region was defined as the sequence between the last mismatch corresponding to the functional GBA gene and the first mismatch corresponding to pseudogene. In the case of gene conversions, the length of converted sequence was determined by identifying where the functional gene sequence resumed.

The different recombinant alleles are referred to as Rec 1–7, depending upon the exonic site at which pseudogene sequence was first detected (table 1). Recombinant alleles resulting from a nonreciprocal event such as gene conversion are further defined with an “a.” These alleles carried only a small converted segment originating from the pseudogene (table 2). Recombinant alleles resulting from reciprocal recombination are designated with a “b” (table 3). These alleles may carry either a fusion between the gene and pseudogene or a duplicated allele.

The site at which conversion begins in the “a” group can be similar to the site of crossover observed in the “b” group (tables 1, 2, and 3). For example, although Rec 1a and Rec 1b both have sequence in exon 10 de-

Table 1**Recombinant Alleles Resulting from Crossover or Gene Conversion between the GBA Gene and Pseudogene**

Recombination	Description
Rec 1a or b	The allele carries mutations L444P, A456P, and V460V. Crossover sites include Ex9-Int-9, Int-9 or Int9-Ex10. (See fig. 1e, 1f, and 1g).
Rec 2a or b	The allele carries mutations D409H, L444P, A456P, and V460V. Crossover site is in Ex9. (See fig. 1d).
Rec 3a or b	The allele carries the 55-bp deletion in exon 9, as well as point mutations D409H, L444P, A456P, and V460V. Crossover site is in the Int8-Ex9 region (see fig. 1c).
Rec 4a or b	The allele carries pseudogene sequence beginning from intron 3. Crossover site is in Int3 (see fig. 1a).
Rec 5a or b	The allele carries the pseudogene sequence beginning from intron 4. Crossover site is in Int4 (see fig. 1b).
Rec 6a or b	The allele carries the pseudogene sequence beginning from intron 10 or has a duplicated pseudogene with a fusion between metaxin and pseudometaxin. Crossover site is in the Int10-Ex11 region (see fig. 1b).
Rec 7a or b	The allele carries the pseudogene sequence beginning from the 3' UTR or has a duplicated pseudogene with a fusion between MTX and pseudometaxin. Crossover site is in the 3' UTR (see fig. 1i) or in MTX.

rived from the pseudogene, Rec 1a results from a gene conversion and Rec 1b is a fusion allele. Because the beginning and extent of a crossover or gene conversion can be detected only by the identification of pseudogene sequence that is not homologous to that of the functional gene, the location of the initiation of the recombination is not exact. Although seven different groups of recombinations are defined, 10 different sites of recombination are described, as shown in figure 1.

Results

We analyzed 480 alleles from 240 patients with Gaucher disease. This analysis included mutation detection and total and/or partial sequencing of the 11 exons and flanking intronic regions in 422 alleles. In ~20% of these alleles, the sequencing focused on the region from exon 8 to exon 11, whereas, for the rest, the entire gene was sequenced. All patients with mutation L444P or any other pseudogene-derived mutation were analyzed by Southern blots. Moreover, patients with a homozygous genotype were examined by long PCR template and/or Southern blots, and, when possible, parental DNA was studied to exclude the possibility of a deletion on one allele. The final result was the identification of 59 recombinant alleles, representing 12% of the alleles studied, and the type, frequency, and distribution of recombinant alleles among patients with different types of Gaucher disease are summarized in table 4. Twenty-two percent of the patients evaluated had at least one recombinant allele present. However, since Southern blots and full sequencing were not performed on every proband, this may be an underrepresentation of the total number.

Sequencing data showed that a significant number of the patients with point mutations previously identified by PCR screening for individual mutations actually carried recombinant alleles with more than one point mutation derived from the pseudogene sequence. The se-

quence was examined carefully, focusing on every site at which the sequence for the gene and pseudogene were known to differ, and the length of the pseudogene/functional gene substitutions and the site of crossover or gene conversion were estimated (tables 1, 2, and 3).

To pinpoint the crossover site and the type of recombination for the remaining recombinant alleles, long PCR results and Southern blot analyses were examined. Long PCR indicated that several patients had smaller fusion alleles. The fusion alleles detected by this method resulted from recombination between the GBA gene and its pseudogene, with crossover sites located in the 5' regions of the gene. Since the GBA pseudogene has large deletions in introns 2, 4, 6, and 7 (Horowitz et al. 1989), long PCR demonstrates two separate bands, which represent the normal allele (6.6 kb) and a shorter recombinant allele (~5 kb). By examining the long PCR results, two fusion alleles, designated as "Rec 4b" and "Rec 5b" (table 3; patients 13 and 17), were identified with a crossover in the 5' region of the gene. Sequencing of the mutant band demonstrated the specific crossover sites.

In general, alleles with reciprocal recombinations including fusions and duplications could be detected by Southern blots using the restriction enzymes *Sst*II, *Ssp*I, and *Eco*RI (fig. 2A, 2B, and 2C). On the other hand, recombinations resulting from gene conversion had a normal pattern on Southern blots. The restriction enzyme *Hinc*II, which cleaves at several sites within the GBA gene but not the pseudogene (fig. 2D), was used to localize the crossover region. Three short probes (from exons 2–4, 4–7, and 7–11) were hybridized to Southern blots of *Hinc*II-digested DNA, which enabled the identification of the site of crossover in better detail in some cases.

Alleles Resulting from Gene Conversion Events

Table 2 summarizes the molecular and clinical data in patients with type 1, 2, and 3 Gaucher disease who had gene conversion events or nonreciprocal recombi-

Table 2

Genotype/Phenotype Data on Patients with an Allele Resulting from Nonreciprocal Recombination

Disease Type and Patient Number	Ethnic Background	Age at Diagnosis/ Evaluation (years)	Genotype ^a	Site Where Gene Conversion Starts ^b	Maximum Possible Size of Converted Sequence (bp)	Southern Blot Results	Clinical Features
Type 1:							
1	European American	2/3	<u>N370S/Rec 1a</u>	Ex9-Int9	824	Normal	Hepatosplenomegaly, anemia, thrombocytopenia
2	Ashkenazi	NA	<u>N370S/c.1263-1317del-a</u>	Int8-Ex9	288	Missing exon 9 site on <i>HincII</i>	Hepatosplenomegaly, anemia, thrombocytopenia
3	Hispanic	13/48	<u>N370S/Rec 1a</u>	Ex9-Int9	824	Normal	Splenectomy, hepatomegaly, bone disease
4	African American	14/15	<u>c.222-224delTAC/Rec 1a+Rec 6b</u>	Ex9-Int9	824	Pseudogene duplication	Hepatosplenomegaly, anemia, thrombocytopenia
5	Hispanic	10/34	<u>N370S/Rec 1a</u>	Ex9-Int9	824	Normal	Splenectomy, hepatomegaly, bone disease
6	European American	4/8	<u>N370S/c.1263-1317del-a</u>	Int8-Ex9	288	Missing exon 9 site on <i>HincII</i>	Hepatosplenomegaly
7	African American	2/5	<u>V352L/Rec 1a+Rec7b</u>	Ex9-Int9	824	Pseudogene duplication	Splenectomy, hepatomegaly
8	European American	6/21	<u>N370S/Rec 1a</u>	Int9-Ex10	475	Normal	Hepatosplenomegaly, thrombocytopenia, bone disease
9	European American	8/28	<u>N370S/L444Pa</u>	Int9	194	Normal	Splenectomy, hepatomegaly, bone disease
10	French	NA	<u>N370S/Rec 1a</u>	Int9	824	Normal	Parkinsonism
11	African American	1/1	<u>N117D/Rec 1a</u>	Int9-Ex10	424	Normal	Splenectomy, bone disease, hepatomegaly, anemia, thrombocytopenia
12	European American	13/16	<u>N370S/Rec 1a</u>	Ex9-Int9	824	Normal	Hepatosplenomegaly, thrombocytopenia
13	NA	NA	<u>N370S/c.1263-1317del-a</u>	Int8-Ex9	288	NA	NA
14	French	24	<u>N370S/c.1263-1317del-a</u>	Int8-Ex9	288	Missing exon 9 site on <i>HincII</i>	Thrombocytopenia, splenectomy, parkinsonism
15	NA	NA	<u>N370S/Rec 1a</u>	Ex9-Int9	824	Normal	NA
Type 2:							
16	European American	5 mo	<u>L444P/Rec 1a</u>	Int9-Ex10	424	Normal	Hepatosplenomegaly, seizures
17	Greek	Birth	<u>H225Q/Rec 3a</u>	Int8-Ex9	849	Normal	Hepatosplenomegaly, seizures, opisthotonus
18	NA	Birth	<u>Rec 1a/Rec 1a</u>	Ex9-Int9	824	Normal	Hydrops
19	Lebanese	Birth	<u>Rec 1a/Rec 1a</u>	Ex9-Int9	824	Normal	Hydrops
20	Australian	Birth	<u>R257Q/c.1263-1317del-a</u>	Int8-Ex9	288	Normal	Ichthyosis, hepatosplenomegaly
21	European American	Birth	<u>Rec 2a/Rec 2a</u>	Ex9	1193	Missing exon 9 site on <i>HincII</i>	Hydrops
22	European American	NA	<u>L444P/Rec 1a</u>	Int9-Ex10	424	Normal	NA
23	European American	NA	<u>R285H/c.1263-1317del-a</u>	Int8-Ex9	288	Missing exon 9 site on <i>HincII</i>	NA
24	European American	11 mo	<u>L444P/Rec 1a</u>	Ex9-Int9	824	Normal	Hepatosplenomegaly, seizures, opisthotonus
Type 3:							
25	European American	1/6	<u>D409H/Rec 1a</u>	Ex9-Int9	824	Normal	Hepatosplenomegaly, cardiac fibrosis, abnormal horizontal saccades
26	European American	4/28	<u>F216Y/c.1263-1317del-a</u>	Int8-Ex9	288	Missing exon 9 site on <i>HincII</i>	Renal disease, bone disease, myoclonic epilepsy
27	European American	4/13	<u>R463C/Rec 1a+Rec7b</u>	Ex9-Int9	824	Pseudogene duplication	Abnormal horizontal saccades, splenectomy, hepatomegaly, bone disease
28	Ashkenazi/Sephardic	5/9	<u>V394L/Rec 1a</u>	Int9-Ex 10	824	Normal	Abnormal horizontal saccades, hepatosplenomegaly, myoclonic epilepsy, developmental delay, lung disease
29	African American	38/40	<u>N188S/Rec 1a</u>	Int9-Ex10	824	Normal	Hepatosplenomegaly, abnormal horizontal saccades, myoclonic epilepsy
30	French	1/4	<u>V394L/Rec 1a</u>	Int9-Ex10	824	Normal	Hepatosplenomegaly, abnormal horizontal saccades, myoclonic epilepsy, developmental delay
31	Mexican	4/6	<u>F213I/L444Pa</u>	Ex9-Int9	510	Normal	Hepatosplenomegaly, abnormal horizontal saccades, myoclonic epilepsy, developmental delay

NOTE.—NA = not available.

^a Alleles discussed in this table are underlined.

^b Refer to figure 1 for precise description of sites.

Table 3

Genotype/Phenotype Data on Patients with an Allele Resulting from Reciprocal Recombination

Disease Type and Patient Number	Ethnic Background	Age at Diagnosis/Evaluation (years)	Genotype ^a	Site of Crossover ^b	Southern Blot Results	Clinical Features
Type 1:						
1	European American	1/12	N370S/ <u>Rec 2b</u>	Ex9	Fusion	Hepatosplenomegaly, anemia, thrombocytopenia
2	African American	2/5	R170C/L444P+ <u>Rec 7b</u>	3' UTR or MTX	Pseudogene duplication	Hepatosplenomegaly, anemia, thrombocytopenia, bone disease
3	European American	3/18	R463C/ <u>Rec 1b</u>	Ex9-Int9	Fusion	Splenectomy, hepatomegaly, thrombocytopenia, renal disease
4	European American	1/7	N370S/ <u>Rec 1b</u>	Int9-Ex10	Fusion	Hepatosplenomegaly
5	African American	14/15	c.222-224delTAC/ <u>Rec 1a+Rec 6b</u>	Int10-Ex11	Pseudogene duplication	Hepatosplenomegaly, anemia, thrombocytopenia
6	African American	2/5	V352L/ <u>Rec 1a+Rec 7b</u>	3' UTR or MTX	Pseudogene duplication	Splenectomy, hepatomegaly, bone disease
7	African American	13/22	c.153-154insTACAGC/ <u>Rec 1b</u>	Ex9-Int9	Fusion	Hepatosplenomegaly, anemia, thrombocytopenia, bone disease
8	NA	NA	N370S/ <u>Rec 1b</u>	Ex9-Int9	Fusion	NA
9	European American	30/30	N370S/ <u>Rec 3b</u>	Int8-Ex9	Fusion	Hepatosplenomegaly, bone disease, thrombocytopenia
10	European American	5/28	N370S/ <u>Rec 1b</u>	Int9-Ex10	Fusion	Hepatosplenomegaly, thrombocytopenia
11	European American	10/21	R463C/ <u>Rec 1b</u>	Ex9-Int9	Fusion	Splenectomy, anemia, thrombocytopenia, liver disease
Type 2:						
12	European American	6 mo	R257Q/L444P+ <u>Rec 6b</u>	Int10-Ex11	Fusion	Hepatosplenomegaly, seizures
13	Ashkenazi	Fetus	IVS10+2T→G/ <u>Rec 4b</u>	Int3	Fusion	Hydrops
14	African American	8 mo	E41K/ <u>Rec 1b</u>	Int9	Fusion	Hepatosplenomegaly, seizures, developmental delay
15	European American	NA	<u>Rec 1b/Rec 1b</u>	Ex9-Int9	Fusion	NA
16	Mexican	NA	L444P+E326K/L444P+ <u>Rec 7b</u>	MTX	Fusion in MTX	Hepatosplenomegaly, opisthotonus
Type 3:						
17	Korean	22/22	N188S/ <u>Rec 5b</u>	Int4	Fusion	Myoclonic epilepsy
18	European American	3/13	R463C/ <u>Rec 1b</u>	Ex9-Int9	Fusion	Hepatosplenomegaly, abnormal horizontal saccades
19	European American	4/13	R463C/ <u>Rec 1a+Rec 7b</u>	3' UTR or MTX	Pseudogene duplication	Hepatomegaly, abnormal horizontal saccades, splenectomy, bone disease
20	European American	18/45	L444P/D409H+ <u>Rec 7b</u>	MTX	Pseudogene duplication	Parkinsonism, splenectomy
21	European American	7/28	N188S/ <u>Rec 1b</u>	Int9-Ex10	Fusion	Abnormal horizontal saccades, myoclonic epilepsy, dementia
22	European American	5/9	R463C/ <u>Rec 1b</u>	Ex9-Int9	Fusion	Hepatomegaly, splenectomy, lung disease, bone disease, abnormal horizontal saccades
23	European American	1/1	L444P/L444P+ <u>Rec 7b</u>	3' UTR or MTX	Pseudogene duplication	Hepatosplenomegaly, abnormal horizontal saccades, developmental delay
24	European American	1/4	G202R/L444P+ <u>Rec 7b</u>	3' UTR or MTX	Pseudogene duplication	Abnormal horizontal saccades, developmental delay, myoclonic epilepsy

NOTE.—NA = not available.

^a Alleles discussed in this table are underlined.

^b Refer to figure 1 for precise description of sites.

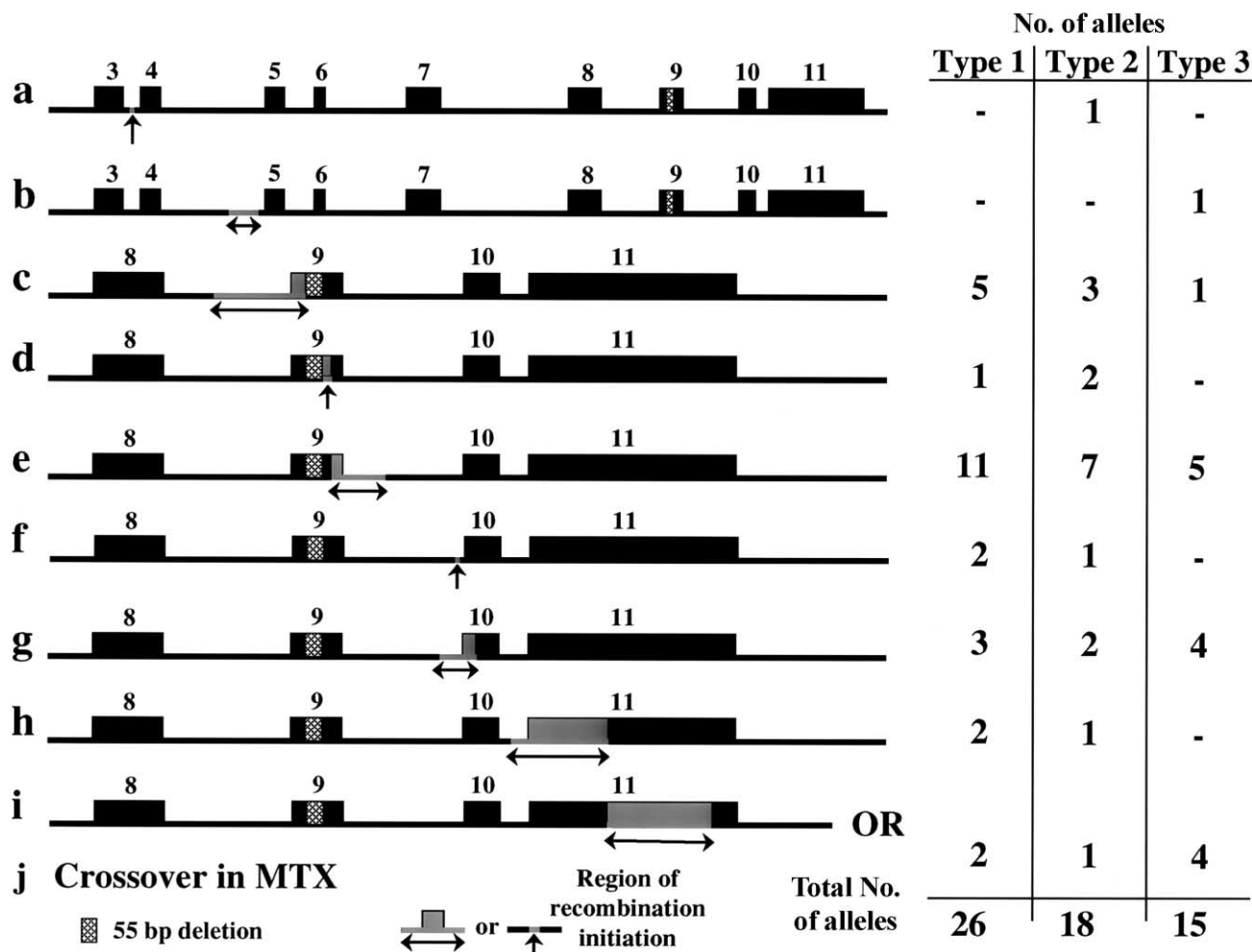


Figure 1 Recombination initiation sites and allele frequencies. The initiation regions for recombination events were determined by comparing mismatches between the GBA functional gene and pseudogene sequences. The region where a recombination starts is defined as the sequence between the last mismatch containing functional gene sequence and the first mismatch carrying pseudogene sequence. The schematics show the exonic structure of GBA, with the different initiation regions indicated in gray, with arrows below. The number of alleles found in patients with type 1, 2, or 3 Gaucher disease with either reciprocal or nonreciprocal recombinations starting within the given region are shown next to each schematic map. The abbreviations for each initiation region are used in tables 1, 2, and 3. *a*, Int3; the recombination starts within 26 bp in intron 3. *b*, Int4; the recombination starts within 98 bp in intron 4. *c*, Int8-Ex9; the recombination starts within 288 bp encompassing the intron 8/exon 9 junction. *d*, Ex9; the recombination starts within 23 bp of exon 9 following the 55 bp that are deleted in pseudogene. *e*, Ex9-Int9; the recombination starts within 186 bp encompassing the exon 9/intron 9 junction. *f*, Int9; the recombination starts within 30 bp at the end of intron 9. *g*, Int9-Ex10; the recombination starts within 126 bp encompassing the intron 9/exon 10 junction. *h*, Int10-Ex11; the recombination starts within 300 bp encompassing the intron 10/exon 11 junction. *i*, 3' UTR; the recombination starts within 304 bp in the 3' UTR. *j*, MTX (not shown); the recombination starts within the MTX pseudogene.

nations. Thirty-four (58%) of the 59 recombinant alleles fell in this category, including 58% of all recombinant alleles in patients with type 1, 67% in patients with type 2, and 47% in patients with type 3 (table 4). A wide range of mutations was encountered on the second allele, as shown in table 2. In all 31 patients with these alleles, the site of gene conversion appeared to begin between exon 8 and intron 9 (fig. 1). It is possible that the gene conversion data is an underestimate, since not all intronic regions and, in some cases, not all of the 5' exonic

regions were sequenced. For the recombinant alleles in table 2, the maximum possible length of the converted sequence ranged between 194 bp and 1,193 bp. The Southern blot results for this group were normal except for the six patients who carried the 55-bp deletion in exon 9, where a *HincII* site is lost (see representative example, fig. 2D). There were two alleles carrying L444P (table 2; patients 9 and 31), in which the mutation appears to have resulted from a gene conversion event and not as an individual point mutation, since pseudogene

Table 4
Summary of Recombinant Allele Frequencies

GAUCHER DISEASE TYPE	NO. OF PATIENTS/ NO. OF ALLELES EXAMINED	NO. (%) OF PATIENTS WITH RECOMBINANT ALLELES	NO. (%) OF RECOMBINANT ALLELES ^a	NO. OF ALLELES FOR EACH TYPE OF RECOMBINATION		
				Gene Conversion	Fusion	Duplication
1	155/310	24 (16)	26 (8)	15	8	3
2	37/74	14 (38)	18 (24)	12	6	0
3	<u>48/96</u>	<u>14</u> (29)	<u>15</u> (16)	<u>7</u>	<u>4</u>	<u>4</u>
Total	240/480	52 (22)	59 (12)	34	18	7

^a Several patients had more than one recombination on the same allele.

sequence was also present in intron 9. Patient 9, with type 1 disease, carried only one pseudogene mismatch, whereas patient 31, with type 3 disease, had two sites corresponding to pseudogene sequence in intron 9.

Alleles Resulting from Reciprocal Recombination

Table 3 describes the alleles resulting from reciprocal recombination that carried either a fusion between the GBA gene and pseudogene or a duplication. For each of the 25 alleles identified (42% of all recombinants), Southern blots using the four restriction enzymes confirmed the reciprocal recombination (see fig. 2 for representative examples). Reciprocal recombinations were found in 42% of recombinant alleles from patients with type 1, 33% from patients with type 2, and 53% from patients with type 3 disease (table 4).

Seven alleles carried a duplication of the GBA pseudogene and a fusion between the MTX gene and pseudometaxin, resulting from a crossover at the 3' region of the gene (Tayebi et al. 2000). The site of crossover was identified by sequencing and by Southern blots using the restriction enzymes *HincII* and *EcoRI* (fig. 2C and 2D). In three of these patients, the presence of a duplication was confirmed through studies of the tetranucleotide repeat polymorphism ITG6.2, located in the region between the GBA gene and pseudogene. In these individuals, three allelic forms (318 bp, 322 bp, and 326 bp) were found. The site of crossover for these recombinant alleles was pinpointed by sequencing and is referred to as "Rec 6b" (crossover initiates between Int10 and Ex11) or "Rec 7b" (crossover within a 304-bp sequence at the 3' UTR or between MTX and pseudometaxin). Southern blots prepared using *HincII*-digested DNA were also hybridized to an MTX cDNA probe (data not shown). The results confirmed the duplication and fusion alleles found in the 3' region.

Although 18 fusion alleles were identified, the size of the fusion product seen on the Southern blots varied because of different sites of crossover (fig. 2). The sites were mostly clustered between intron 8 and exon 11 of the GBA gene, with the exception of two alleles in which the site of crossover was in intron 3 (table 3, patient 13)

or intron 4 (table 3, patient 17) and two unique fusion alleles resulting from crossovers within intron 10 to exon 11 or within pseudometaxin (table 3, patients 12 and 16). The latter two alleles both had fusions between the MTX gene and pseudogene. One patient (table 3, patient 15) was homozygous for a fusion allele in which the site of crossover occurred within the last 186 bp of exon 9 or in the beginning of intron 9. Homozygosity for a fusion allele has not previously been reported. Among the patients with reciprocal crossover, there was also a wide range of mutations present on the second allele.

Nine alleles with a reciprocal recombination in the 3' region of the GBA gene, two with fusions and seven with duplications, also carried a point mutation or another recombinant allele. An analysis of parental DNA showed that the 3' region recombinations (Rec 6b and Rec 7b) were located on the allele with L444P or Rec 1a, except for one case (table 3; patient 20) in which Rec 7b and D409H were on the same allele. To determine which was the original mutation on these alleles and whether the first mutation increases the likelihood of a second mutation, studies of several successive generations will be needed.

Sites of Recombination and Motif Sequences

The examination of the 59 recombinant alleles by Southern blots and detailed sequencing led to the identification of 10 different sites of crossover or gene conversion. An accurate identification of the site where the crossover event occurred was dependent upon the degree of gene/pseudogene homology in a specific region. Seven of the 10 sites were located between intron 8 and the 3' UTR (fig. 1).

The sequences within the regions surrounding the 10 sites were compared to identify one or more possible motif sequences that might predispose to crossover. A pentamer sequence (CACCA) was found in five of the crossover regions and was identified in 35 of 59 recombinant alleles. A similar tetramer sequence (CACC) was found at two additional sites in 11 patient alleles. The remaining two sites without this sequence shared a dif-

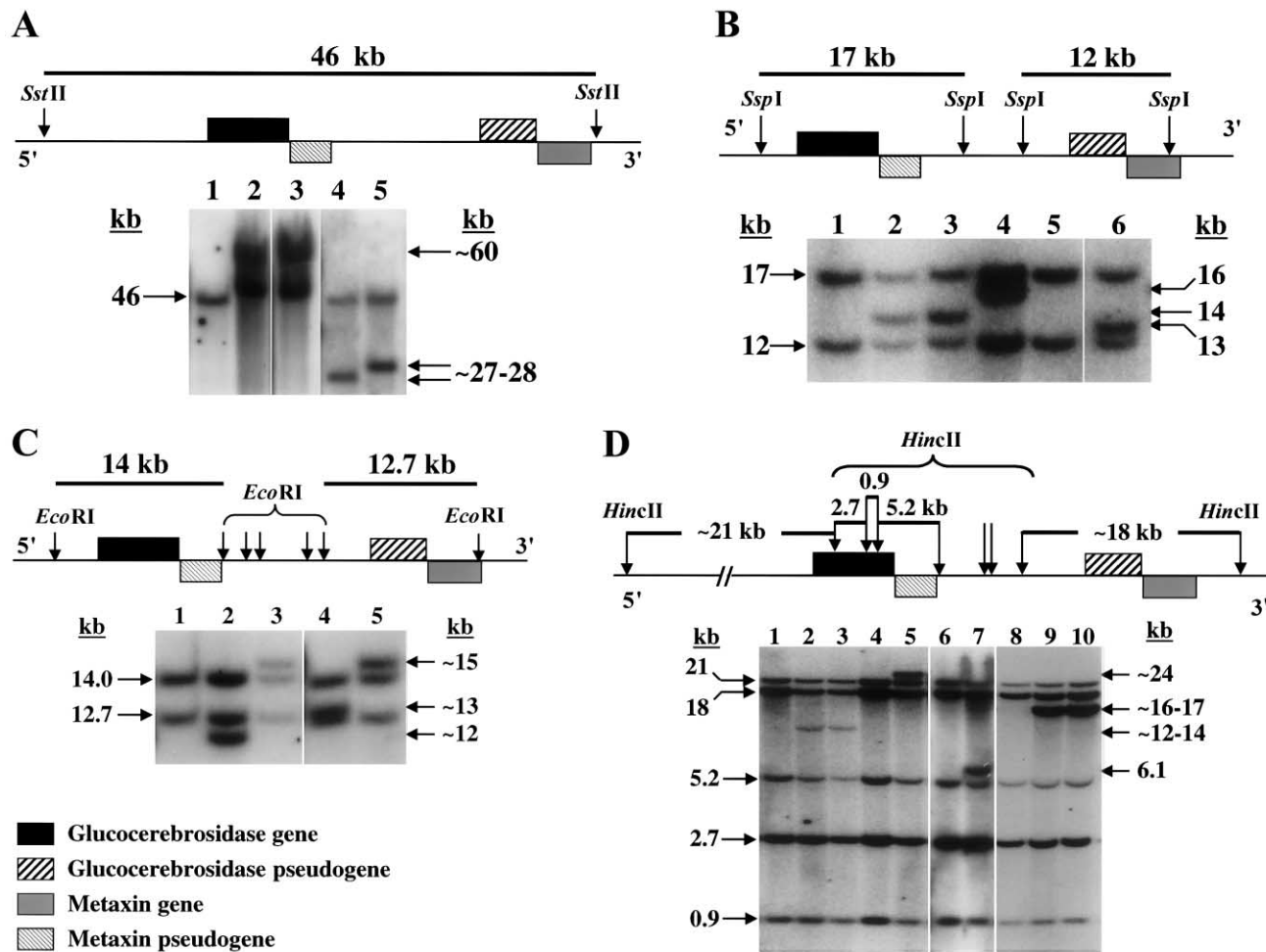


Figure 2 Southern blots of the GBA gene and pseudogene. Genomic DNAs were digested using four different restriction enzymes and were hybridized to a human GBA cDNA probe. A representative selection of patients with different recombinant alleles is shown in each panel. Included are schematic maps showing the normal restriction sites. Samples in each lane are identified by the table, patient number, and the recombinant allele they demonstrate (i.e., T2-2, Rec 7b is table 2, patient 2 with Rec 7b). The approximate sizes of the abnormal bands are shown to the right of each blot. **A**, *SstII*-digested DNA samples: lane 1, normal control demonstrating a single 46-kb band; lane 2, T3-2, Rec 7b; lane 3, T3-20, Rec 7b; lane 4, T3-13, Rec 4b; and lane 5, T3-14, Rec 1b. **B**, *SspI*-digested DNA samples: lane 1, normal control with 17- and 12-kb bands; lane 2, T3-11, Rec 1b; lane 3, T3-1, Rec 2b; lane 4, T3-20, Rec 7b; lane 5, T2-20, c.1263-1317del-a; and lane 6, T3-17, Rec 5b. **C**, *EcoRI*-digested DNA samples: lane 1, normal control with 14- and 12.7-kb bands; lane 2, T3-24, Rec 7b; lane 3, T3-12, Rec 6b; lane 4, T3-13, Rec 4b; and lane 5, T3-14, Rec 1b. **D**, *HincII*-digested DNA samples: lanes 1, 6, and 8, normal controls showing 21-, 18-, 5.2-, 2.7-, and 0.9-kb bands; lane 2, T3-16, Rec 7b; lane 3, T3-11, Rec 1b; lane 4, T2-5, Rec 1a; lane 5, T3-13, Rec 4a; lane 7, T2-20, c.1263-1317del-a; lane 9, T3-2, Rec 7b; and lane 10, T3-5, Rec 6b.

ferent tetramer sequence (TGGG), which was found in 13 recombinant alleles.

Correlation with Clinical Data

The ethnic or racial backgrounds of patients carrying recombinant alleles were quite varied. Of note, although nine recombinant alleles were identified in 10 African American patients with Gaucher disease, the recombinations included both fusions and gene conversions, suggesting that this was not due to a founder effect.

The majority of the 24 patients with type 1 Gaucher disease carrying recombinant alleles had significant dis-

ease manifestations. Twenty-one of the subjects whose clinical data were available were diagnosed by adolescence, and a majority had hepatosplenomegaly and cytopenia. Eight had undergone splenectomy and seven were described as having bone disease. Seventeen of these patients had mutation N370S on their second allele. Although the patients with genotype N370S/Rec had a wide range of disease severity, the severity in those with recombinant alleles resulting from reciprocal recombination did not differ significantly from those with gene conversions.

Among the 14 patients with type 2 Gaucher disease,

nine had recombinant alleles resulting from gene conversion. In the three cases in which there was homozygosity for a gene conversion allele (table 2, patients 18, 19, and 21), death resulted from hydrops fetalis, although the three patients did not all share the same site of recombination. Three other patients with L444P/Rec1a (table 2, patients 16, 22, and 24) lived for approximately one year. Of the five patients with fusion alleles, one had a hydrops fetalis phenotype. This fetus (table 3, patient 13) carried a fusion allele that resulted from a crossover in intron 3, along with a splice site mutation in exon 10 on the second allele. Another patient was found to be homozygous for a fusion allele (table 3, patient 15). One infant with a classic type 2 phenotype had genotype L444P/L444P (table 3, patient 16), a genotype not normally associated with type 2 Gaucher disease. However, each L444P allele also had a second alteration that might have a modifying effect on the phenotype. One carried the presumed polymorphism E326K (Park et al. 2002a) and the other a 3'-region duplication within the sequence for pseudome-taxin (Rec 7b) (Tayebi et al. 2000).

Among the 14 patients with type 3 Gaucher disease carrying recombinant alleles, six had a recombination resulting from gene conversion, seven as a result of reciprocal recombination, and one patient had both types of recombinant alleles. Clinically, patients with alleles resulting from both reciprocal and nonreciprocal recombinations were similar, with a diagnosis in early childhood in all but three patients. Of note, half of the subjects with either type of recombinant allele had myoclonic epilepsy associated with their other disease manifestations. Mutation N188S was found together with recombinant alleles in three patients with type 3 Gaucher disease (table 2, patient 29; and table 3, patients 17 and 21). While each of the three had a different recombinant allele, all three patients were adults with uncontrolled myoclonic epilepsy. The two patients with genotype V394L/Rec 1a (table 2, patients 28 and 30) shared a similar phenotype, with progressive myoclonic epilepsy in childhood. Three patients with type 3 disease, one with R463C/Rec 1a (table 2, patient 27) and two with R463C/Rec 1b (table 3, patients 18 and 22), had aggressive visceral and skeletal disease and slowing of the horizontal saccades as their principal neurologic manifestation. However, two other patients with R463C/Rec 1b (table 3, patients 3 and 11) had a type 1 phenotype with no neurologic symptoms.

Discussion

Homologous recombination, both reciprocal and nonreciprocal, has been implicated as the cause of mutations in many human disorders. Repeated DNA sequences can be one of the forces driving recombination and have been

classified on the basis of the location, distribution and length of the repeat sequence, and the number of repeats (Purandare and Patel 1997). *Alu* sequences, a specific class of repeat sequences, are one of the major sources of DNA rearrangement and are implicated in several genetic disorders (Brooks et al. 2001; Martinez et al. 2001; Batzer and Deininger 2002; Lutskiy et al. 2002). Another cause of recombination is the presence of duplicated gene sequences or "duplicons," which can mediate local deletions, duplications, fusions, inversions, and gene conversion (Ji et al. 2000; Eichler 2001). Duplicons can consist of tandemly repeated sequences or low-copy repeat sequences (LCRs), including gene clusters, gene fragments, pseudogenes, or repeat elements flanking unique sequence. LCRs are usually 10–400 kb in size and exhibit 95%–98% homology (Stankiewicz and Lupski 2002a). The likelihood of DNA rearrangement is increased when repeated fragments are located near one another on the same chromosome but are not directly adjacent. Recombinant alleles resulting in human disease can be categorized by the type of recombination, either nonreciprocal or reciprocal. This distinction proved very useful in our characterization of recombinations at the GBA gene locus.

The nonreciprocal exchange of homologous sequence, also known as gene conversion, has been extensively examined in lower eukaryotes, in which, unlike mammalian systems, the results of meiosis can be easily recovered and studied. In nonreciprocal genetic exchange, the transient pairing of two similar, although not identical, genes or alleles is followed by conversion of one sequence to that of the other. The donor sequence is not changed, but the acceptor sequence is altered by the incorporation of sequence copied from the donor sequence (fig. 3A) (Strachan and Read 1999).

In general, gene conversion results from nonreciprocal sequence exchange between either nonallelic or allelic DNA sequences. Gene conversion facilitated by nonallelic tandem repeat sequences has been implicated in some clustered human gene families, including the globins (Papadakis and Patrinos 1999) and immunoglobulins (Sitnikova and Su 1998). Gene conversion involving allelic exchanges is more likely to occur when the gene in question has a nearby pseudogene or is part of a gene cluster located on the same chromosome, as in the HLA genes (Blanco-Gelaz et al. 2001), 21- β hydroxylase deficiency (Tusie-Luna and White 1995), and polycystic kidney disease (Watnick et al. 1998; Bogdanova et al. 2001). Allelic exchanges are a likely mechanism for the DNA rearrangements observed in the GBA locus.

Although gene conversion cannot easily be distinguished from double crossover events, double crossovers occurring in very close proximity would not normally be expected. The sizes of the converted sequences

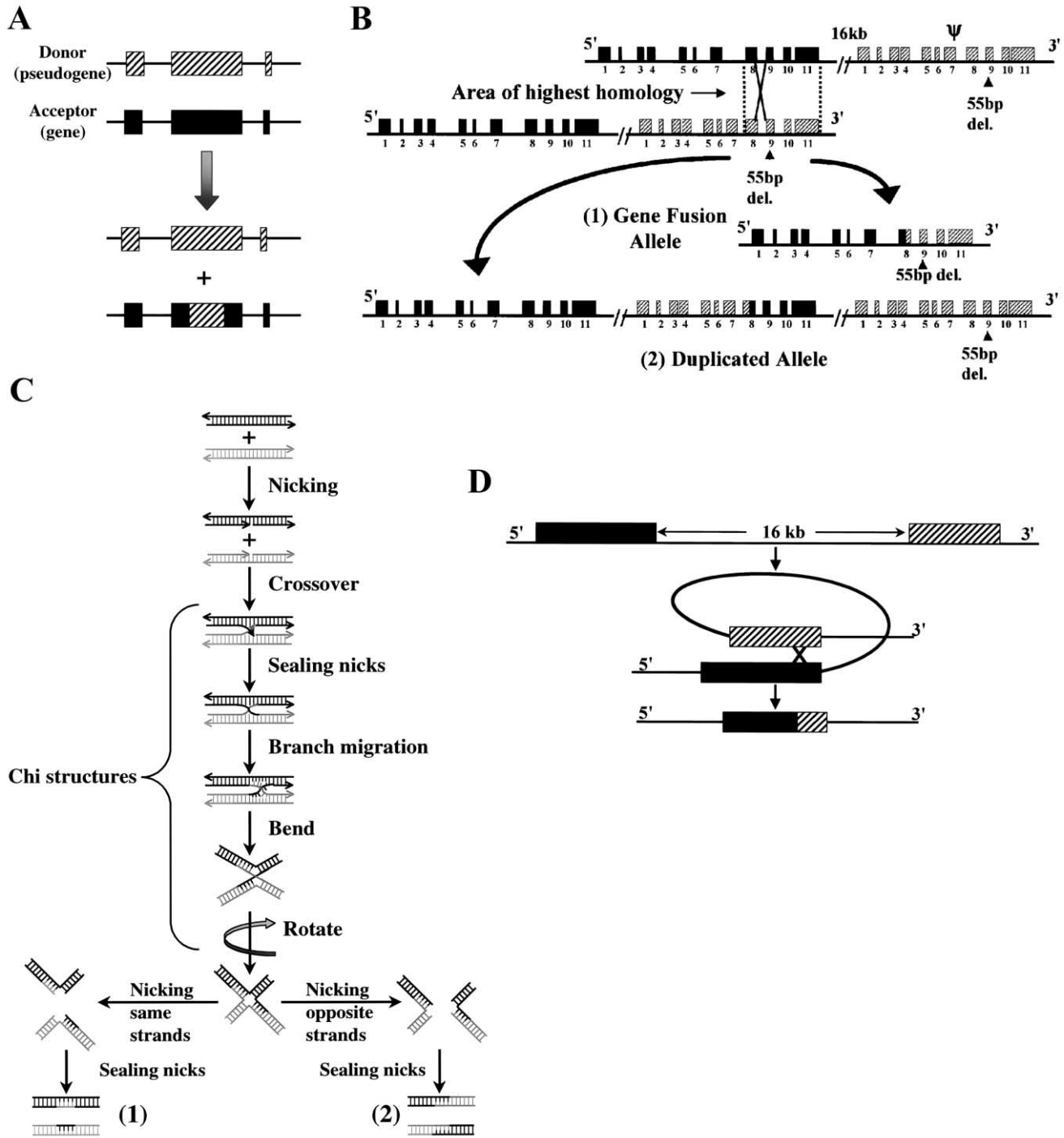


Figure 3 Illustrations of proposed mechanisms for recombination events occurring between the GBA gene and its pseudogene. *A*, Allelic gene conversion. This is a nonreciprocal sequence exchange, facilitated by sequence homology between allelic genes. The donor sequence is unaltered, but the acceptor sequence is changed by the incorporation of regions copied from the donor sequence. *B*, Reciprocal crossover between homologous regions. This event results in two possible gene rearrangements. One is a fusion between the gene and its pseudogene and a deletion of the intergenic region shown in (1). The second is a partial duplication of the pseudogene and gene sequences, which are fused together (2). *C*, Holliday model. This is a mechanism of recombination that includes nicking and reunion between two homologous sequences. Nicking occurs in the same location in both homologous sequences (i.e., in the GBA gene and pseudogene). Crossover, exchanges, and sealing nicks create chi structures. Branch migration and breaking in some base pairs in the four strands increase the chance of bending, rotation, and exchange between strands, resulting in two possible gene conversion-like alleles (1) and two possible fusion-like alleles (2). Figure adapted from Weaver and Hedrick (1989). *D*, Intramolecular crossover. This is another proposed model for recombination between the GBA gene and pseudogene on the same chromosome, resulting in a fusion allele. In this case, the intergenic region and portions of the gene and pseudogene are removed as an extrachromosomal fragment and are lost.

identified in this series, ranging from 190 bp to 1,193 bp, are presumably far too short to be the result of a double crossover. Liskay et al. (1987) demonstrated, in cultured mammalian cells, that when duplicated chromosomal sequences had regions of shared homology ranging between 295 bp and 1.8 kb in length, gene conversion events were efficient, with the rate being directly proportional to the extent of homology.

Our results demonstrate that the regions where the GBA gene and pseudogene share the greatest sequence homology are those with the highest rate of gene conversion (table 2). The sequence homology shared between the GBA gene and its pseudogene in the region between intron 8 and the 3' UTR is ~98% and includes five segments of exact identity, each >200 bp in length.

The second major type of homologous exchange, reciprocal recombination, can arise by several possible mechanisms. Gene rearrangement during meiosis or, rarely, mitosis, can occur by direct crossover between identical or very similar DNA sequences. This usually involves the breakage of a pair of homologous chromosomes and a rejoining of the fragments to generate new recombinant strands.

Tandemly repeated genes or gene clusters are subject to reciprocal rearrangements leading to disease. For example, reciprocal recombination events between the clustered, highly homologous red and green visual pigment genes at the color vision locus at Xq28 introduce deletions or fusions, resulting in red/green color blindness (Vollrath et al. 1988; Jagla et al. 2002). In the thalassemias, crossover between duplicated sequences at the β -globin gene cluster on 11p15.5 cause the deletion of the β gene, resulting in β -thalassemia, while the same type of crossover in the α -globin gene cluster on 16p13.3 can cause α -thalassemia (Hattori 1999; Papadakis and Patrinos 1999; Wayne et al. 2001). Fusion genes resulting from unequal crossing over are also seen in the β -globin gene cluster (Metzenberg et al. 1991).

Reciprocal DNA rearrangements involving LCRs can cause duplications and deletions associated with diseases. Nonallelic homologous recombination between two LCRs on 17p12 sharing 98.7% sequence homology can result in a 1.4-Mb duplication found in Charcot Marie Tooth disease type IA, and a deletion of the region causes hereditary neuropathy with liability to pressure palsies (Lopes et al. 1999; Ji et al. 2000; Hurles 2001; Stankiewicz and Lupski 2002b). Likewise, recombination between complex LCRs at the proximal and distal regions of 17p11.2 can result in the deletion of a 4-Mb genomic segment in patients with Smith-Magenis syndrome or a duplication of the region in patients with dup(17)(p11.2 p11.2) syndrome (Lucas et al. 2001; Park et al. 2002b; Shaw et al. 2002).

In a similar fashion, the presence of a pseudogene can increase the likelihood of reciprocal recombination and,

hence, disease. Unequal crossover or unequal sister chromatid exchange between a functional gene and a related pseudogene can result in deletion of the functional gene or the formation of fusion genes carrying a segment derived from the pseudogene (Purandare and Patel 1997; Timms et al. 1997; Lobato et al. 1998; Stone et al. 2000). In steroid 21-hydroxylase deficiency and Hunter syndrome, most of the mutations arise as a result of such sequence exchanges between the functional gene and a very closely related pseudogene (Biro et al. 1996; Karsten et al. 1997; Bunge et al. 1998; Wedell 1998; Dracopoulou-Vabouli et al. 2001).

As demonstrated in the present study, recombinations between the GBA gene and its pseudogene, resulting in gene fusions or duplications, provide a prime example of the consequences of reciprocal crossover (fig. 3B). Fusion alleles with the 5' sequence deriving from the gene and 3' sequence from the pseudogene were the most prevalent. Moreover, in several instances, recombination occurred as a result of crossover between the nearby gene and pseudogene for MTX.

Another mechanism of recombination demonstrated in simple organisms that may be relevant to Gaucher disease is the Holliday junction model, which occurs during meiosis. In figure 3C, the different steps of the Holliday model observed in plasmid DNA are shown (Weaver and Hedrick 1989; Fu et al. 1994). An essential step in this model occurs when the two homologous strands cross over and the new branches are sealed by DNA ligase in a form called the "chi structure" or "half chiasma." The branch in the half chiasma can migrate in either direction simply by breaking old base pairs and forming new ones. The chi structure is first shown with two of its strands crossed, but a 180° rotation of either the upper or the lower uncrossed strands can give rise to different alleles, such as fusion alleles and gene conversion-like alleles (a short sequence of the donor strand can be inserted into an acceptor sequence). The Holliday junction mechanism has also been used to explain recombinant alleles in yeast (Petes 2001).

A third possible mechanism to explain reciprocal fusions within the GBA locus is intramolecular crossover (fig. 3D) (Weaver and Hedrick 1989). When two regions sharing similar sequence are located nearby on one chromosome but are separated by ≥ 10 kb, the chance of an intramolecular crossover with a loop formation occurring during the cell cycle is increased. As a result, one daughter cell carries an allele with a fusion between the gene and pseudogene, and the other daughter cell carries a small extrachromosomal loop consisting of a short fragment of gene and pseudogene and the intergenic region (fig. 3D).

In higher organisms, clearly one cannot demonstrate directly which mechanism occurred during the cell cycle. However, extrapolating from prokaryotes and yeast,

several possible mechanisms can be considered. The gene conversion alleles identified in this study could be explained either by the classic gene conversion model or the Holliday junction model. Likewise, the fusion alleles encountered could arise either by direct crossover, intramolecular recombination or by the Holliday junction model.

Crossover hotspot regions in prokaryotes and eukaryotes have been analyzed, and some of the factors that regulate or initiate recombination have been identified (Bell et al. 1998; Wahls 1998; Petes 2001). In a number of different human disorders caused by DNA rearrangements, several short DNA sequences or repeat sequences have been identified at the crossover break points. It is hypothesized that these sequences might represent a motif that leads to a recombination hotspot (Karsten et al. 1997; Bunge et al. 1998; Aarskog and Vedeler 2001; Kutsche et al. 2002). The motif sequence (CACCA) identified in the present study may be helpful in demonstrating other recombination sites in the GBA gene.

Earlier genotype/phenotype studies in Gaucher disease led to an appreciation that while there are certain generalizations regarding the ability to predict phenotype from genotype, many exceptions remain. On the basis of the present study, PCR-based genotyping is clearly not adequate to accurately describe the mutant alleles in at least 22% of the patients with Gaucher disease analyzed. This observation is of utmost importance to laboratories engaged in molecular diagnostics for Gaucher disease.

Based upon the current genotype/phenotype analyses, it appears that recombinant alleles are essentially null alleles. Homozygosity for a recombinant allele results in very early lethality, usually in utero or in the first days of life. Genotype L444P/recombinant allele is associated with classic type 2 Gaucher disease, although homozygosity for L444P results in a milder phenotype. Likewise, genotypes V394L/Rec 1a, N188S/Rec 5b, and N188S/Rec1a were encountered in patients with type 3 Gaucher disease and myoclonic epilepsy, although homozygosity for V394L and N188S have been seen in patients with type 1 disease. These examples suggest a dose response, in which one copy of a point mutation together with a null allele is more detrimental than two copies of the missense allele.

The current study demonstrates the frequency and the type of recombinations in a broad population of patients with Gaucher disease. Both gene conversion and reciprocal recombination occur at this locus far more frequently than previously appreciated. Although it could not be established whether different mechanisms or sites of recombination made specific contributions to phenotype, it can be concluded that a recombinant allele has a deleterious effect, regardless of how it arose. The one exception were patients who carried the 3' dupli-

cation or Rec 7b. While this recombination alone did not appear to result in Gaucher disease, it still could potentially have a modifying effect on phenotype.

The region surrounding the human GBA gene on chromosome 1 is particularly gene rich, with seven genes and two pseudogenes located within ~85 kb of sequence (Winfield et al. 1997). It is particularly interesting to speculate that some of the recombinations occurring within this locus could potentially disrupt other nearby genes with phenotypic consequences. Certainly, this gene-rich region provides fertile ground for a deeper study of the mechanisms of recombination in the human genome.

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Electronic-Database Information

Accession numbers and URLs for data presented herein are as follows:

GenBank, <http://www.ncbi.nlm.nih.gov/Genbank/> (for human GBA [accession number J03059], the human GBA pseudogene [accession number J03060], and the sequences of genes surrounding human GBA [accession number AF023263])

Human Genetic Disease Databank (GeneDis), <http://life2.tau.ac.il/GeneDis/> (for compilation of mutations in human glucocerebrosidase)

Online Mendelian Inheritance in Man (OMIM), <http://www.ncbi.nlm.nih.gov/Omim/> (for Gaucher disease [MIM 230800], Gaucher disease type 2 [MIM 230900], and Gaucher disease type 3 [MIM 231000])

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