Identification of 12 novel mutations in the α -N-acetylglucosaminidase gene in 14 patients with Sanfilippo syndrome type B (mucopolysaccharidosis type IIIB)

Clare E Beesley, Elisabeth P Young, Ashok Vellodi, Bryan G Winchester

Abstract

Sanfilippo syndrome type B or mucopolysaccharidosis type IIIB (MPS IIIB) is one of a group of lysosomal storage disorders that are characterised by the inability to breakdown heparan sulphate. In MPS IIIB, there is a deficiency in the enzyme α -N-acetylglucosaminidase (NAGLU) and early clinical symptoms include aggressive behaviour and hyperactivity followed by progressive mental retardation. The disease is autosomal recessive and the gene for NAGLU, which is situated on chromosome 17q21, is approximately 8.5 kb in length and contains six exons. Primers were designed to amplify the entire coding region and intron/exon boundaries of the NAGLU gene in 10 fragments. The PCR products were analysed for sequence changes using SSCP analysis and fluorescent DNA sequencing technology. Sixteen different putative mutations were detected in DNA from 14 MPS IIIB patients, 12 of which have not been found previously. The mutations include four deletions (219-237del19, 334-358del25, 1335delC, 2099delA), two insertions (1447-1448insT, 1932-1933insGCTAC), two nonsense mutations (R297X, R626X), and eight missense mutations (F48C, Y140C, R234C, W268R, P521L, R565W, L591P, E705K). In this study, the Y140C, R297X, and R626X mutations were all found in more than one patient and together accounted for 25% of mutant alleles.

(*J Med Genet* 1998;35:910-914)

Keywords: Sanfilippo syndrome type B; mucopolysaccharidosis IIIB; α -N-acetylglucosaminidase; mutations

Sanfilippo syndrome type B or mucopolysaccharidosis type IIIB (MPS IIIB) is a lysosomal storage disorder that is caused by the deficiency of the enzyme α -N-acetylglucosaminidase (NAGLU). NAGLU catalyses the removal of the N-acetylglucosamine residues from the non-reducing terminal of heparan sulphate during lysosomal degradation. The deficiency results in the accumulation inside lysosomes and excretion in the urine of heparan sulphate. Diagnosis is based on detection of excessive urinary heparan sulphate and by demonstration of a deficiency of NAGLU in white blood cells, plasma, or fibroblasts.¹ Clinical symptoms are initially characterised by

intractable hyperactivity and aggressive behaviour, followed by progressive mental retardation with death usually in the late teens. A more slowly progressive form of the disease with later onset, known as the attenuated phenotype, has been described in a small number of MPS IIIB patients.²⁻⁴

MPS IIIB is autosomal recessive and the gene encoding the α -N-acetylglucosaminidase enzyme (NAGLU) has been characterised recently.⁵⁻⁶ The gene which is situated on chromosome 17q21, is approximately 8.5 kb in length and contains six exons. The cDNA is 8.2 kb long and encodes a protein of 743 amino acids. Characterisation of the genomic structure of the NAGLU gene (Genbank accession number U43572) has made it possible to start mutational analysis. There is evidence of clinical variability among MPS IIIB patients and this variation may be the result, in part, of the involvement of different allelic mutations.³ At present, 23 different mutations have been identified in the NAGLU gene from MPS IIIB patients including two deletions, two insertions, five nonsense mutations, and 14 missense mutations.⁶⁻⁹ There appears to be extensive heterogeneity in MPS IIIB. In this study, the NAGLU gene from 14 patients has been analysed by PCR, SSCP analysis, and automated DNA sequencing. Sixteen different mutations have been found, 12 of which were previously unknown. The novel mutations include four deletions (219-237del19, 334-358del25, 1335delC, 2099delA), two insertions (1447-1448insT, 1932-1933insGCTAC), and six missense mutations (F48C, R234C, W268R, R565W, L591P, E705K).

Materials and methods

GENOMIC DNA EXTRACTION AND PCR

The group of 14 MPS IIIB patients were all diagnosed with the severe form of the disease with a NAGLU enzyme activity in white blood cells of <0.1 nmol/h/mg protein (ref range 1.2-4.6). Age of onset was during early childhood. Genomic DNA was extracted from either venous blood or fibroblast cell lines of the patients using a modified version of the ammonium acetate salting out method.^{10,11}

Intronic primers were designed to amplify the coding region and intron/exon boundaries of the NAGLU gene. Exon 1 (715 bp) was amplified as two PCR products and exon 6 (1422 bp) as four products (table 1). The sense and antisense primers were tagged at their 5' ends with the M13 (-21) forward primer

Biochemistry, Endocrinology, and Metabolism Unit, Institute of Child Health, 30 Guilford Street, London WC1N 1EH, UK
C E Beesley
E P Young
A Vellodi
B G Winchester

Correspondence to:
Dr Beesley.

Received 23 February 1998
Revised version accepted for publication 3 April 1998

Table 1 Primers and PCR conditions required for amplification of NAGLU gene

Fragment	Primer	Nucleotide position*	Sequence	Product size (bp)	MgCl ₂ conc (mmol/l)	Annealing temp (°C)	Restriction enzyme before SSCP (fragment sizes (bp))
1a	SFB1a(+)	1292–1307	M13 (-21)- GGAAGCCGCGACTCCT	338	1.0	62	BsaI (132+206)
	SFB1a(-)	1593–1578	M13 rev- CTTGGCAGCCAGAGCG				
1b	SFB1b(+)	1451–1466	M13 (-21)- TCCTTCTCCTGGCCGG	535	1.0	62	AvaII (292+243)
	SFB1b(-)	1949–1933	M13 rev-AGTGGCTGGCTCAAGGC				
2	SFB2(+)	2436–2450	M13 (-21)- AGTTTGGAGCCCTCCC	410	1.5	60	KpnI (128+282)
	SFB2(-)	2809–2790	M13 rev-ACTGTGCACGTTGAAAGCAC				
3	SFB3(+)	3388–3407	M13 (-21)- CCAGCACAAAGAAGCAATGA	401	1.5	62	PstI (258+143)
	SFB3(-)	3752–3733	M13 rev- ATCTCCAGGATACACGCAG				
4	SFB4(+)	3740–3758	M13 (-21)- TATCCTGGGAGATGAGGGC	344	1.0	62	AvaI (161+183)
	SFB4(-)	4047–4031	M13 rev- GGTGATCCGCCCACTC				
5	SFB5(+)	6002–6023	M13 (-21)- AGCTGTAGAGAAGTTGGCAAGG	430	1.0	62	MspI (190+240)
	SFB5(-)	6395–6377	M13 rev- TCTTTTGGAGGCTCTGGGG				
6a	SFB6a(+)	8058–8074	M13 (-21)- GGGGAAGCCATGACCTGG	474	1.0	64	AvaII (249+225)
	SFB6a(-)	8495–8480	M13 rev- CTGGCTGATGCCCTCG				
6b	SFB6b(+)	8402–8421	M13 (-21)- CCTAGAGGCTGTGAACGGAG	435	1.0	64	PstI (291+144)
	SFB6b(-)	8800–8785	M13 rev- GTGGCCAGGGAGGGAG				
6c	SFB6c(+)	8740–8760	M13 (-21)- ACCGATCTGATGTGTTTGAGG	478	1.0	64	HhaI (169+309)
	SFB6c(-)	9181–9166	M13 rev- AGGAAAAGCCGCCAGC				
6d	SFB6d(+)	9092–9107	M13 (-21)- GGGGCCAGAAGGCAAC	489	1.5	64	RsaI (216+273)
	SFB6d(-)	9544–9528	M13 rev- GTGGTGGAGGGCAGGTC				

*Positions of primers are numbered according to Genbank database entry U43572.⁶

sequence (5'-TGTAACACGACGGCCAGT-3') and the M13 reverse primer sequence (5'-CAGGAAACAGCTATGACC-3'), respectively. These universal primer binding sites at the 5' and 3' termini of the PCR products were used for DNA sequencing.

A typical PCR reaction using 100 ng of genomic DNA contained 25 pmol of each primer, 1 × NH₄ reaction buffer (Bioline), 4% (v/v) DMSO (dimethylsulphoxide), 0.2 mmol/l dNTPs, 0.5 µl (2.5 units) BioPro^{TM} DNA polymerase (Bioline) (added after “hot start”). Details of annealing temperatures and MgCl₂ concentrations for each particular amplification reaction are provided in table 1. Cycling conditions were typically 96°C for 10 minutes, followed by 35 cycles of one minute at 96°C, one minute at 60–64°C, one minute at 72°C, and a final extension at 72°C for 10 minutes.

SSCP ANALYSIS AND DNA SEQUENCING

Following amplification, the PCR products were subjected to SSCP (single strand conformation polymorphism) analysis using MDE^{TM} gel (Mutation Detection Enhancement, FMC Bio-products). The 10 PCR products were digested with a restriction enzyme before SSCP analysis

(table 1). Two µl of a loading dye mixture (95% (v/v) formamide, 10 mmol/l NaOH, 0.25% (w/v) bromophenol blue, 0.25% (w/v) xylene cyanol) were added to 5 µl of digestion mix. The samples were denatured at 94°C for four minutes before loading onto a 0.5 × MDE^{TM} gel. Electrophoresis was carried out in 0.5 × TBE at 15 W overnight at 4°C. Bands were detected using a silver staining procedure.¹²

Fragments of interest were concentrated and purified from excess primers and dNTPs by ultrafiltration through Microcon^{TM}-100 columns (Millipore) before sequencing. Products were sequenced in both the forward and reverse direction using the appropriate M13 dye labelled primer kits (Perkin Elmer Applied Biosystems). Reactions were performed as instructed and samples were analysed on an ABI Prism^{TM} 377 DNA Sequencer (Perkin Elmer Applied Biosystems); 25% (v/v) DMSO was included in the sequencing reaction mixes for exons 1a, 1b, and 2 because of their high GC content.

Sequence changes were confirmed by either digestion with a restriction enzyme or by ACRS (amplification created restriction site) PCR.¹³ Primer sequences, annealing

Table 2 Primers and PCR conditions for ACRS reactions

Mutation	Sense primer (nucleotide position)*	Antisense primer (table 1)	Product size (bp)	Annealing temp (°C)	MgCl ₂ conc (mmol/l)	Restriction enzyme (fragment sizes (bp))
F48C	GGCTGCTGGGGCCAGGCCCGCGGCCGACA (1529–1558)	SFB1b(-)	439	64	1.5	+AluI (31+178+39+37+94+18+42)
219-237del19	CTGGGCGGGCGGCGGCGGCTCCACGGGCA (1615–1663)	SFB1b(-)	334	68	1.5	+NlaIII (32+302)
W268R	CCTCAGGTCAATGTCACGAAGATGGGCAGC (6098–6127)	SFB5(-)	316	64	1.5	+NaeI (31+285)
R297X	ATATTCGCCATCATCGGGAGCCTCTTCCAG (6185–6214)	SFB5(-)	229	62	2.0	+BsrI (25+204)
1447-1448insT	CCTGGGTGACCAGCTTTGCCGCCCGGCGGC (8563–8592)	SFB6b(-)	257	64	1.5	-NlaIII (257)
R565W	GCCTTCCGCTACGACCTGCTGGACCTCACA (8808–8837)	SFB6c(-)	392	64	2.0	+NlaIII (28+364)
L591P	GCGCCTACCTGAGCAAGGAGCTGGCCTCCG (8887–8916)	SFB6c(-)	313	66	1.5	+BstUI (30+283)
1932-1933insGCTAC	AGGCCGATTTCTACGAGCAGAACAGCCGCG (9046–9075)	SFB6c(-)	159	64	1.0	+HgaI (39+120)
E705K	CACCAAGTTTGACAAAAATGTCTTCCAACCTT (9228–9257)	SFB6d(-)	335	62	1.5	+AflII (28+307)

*Positions of primers are numbered according to Genbank database entry U43572.⁶

Table 3 Mutations found in the NAGLU gene from patients with MPS IIIB in this study

Exon (fragment)	Mutation*	Nucleotide alteration*	Protein alteration	SSCP shift	RE test	ACRS test (table 2)
1 (1a)	F48C	TTC→TGC 143T>G	Phe→Cys	+		+A _{lu} I
1 (1b)	219-237del19	19 bp del	41 altered aa, term	+		+N _{la} III
1 (1b)	334-358del25	25 bp del	1 altered aa, term	+	-N _{ci} I +F _{nu} 4HI	
2 (2)	Y140C†§	TAC→TGC 419A>G	Tyr→Cys	+		
4 (4)	R234C	CGC→TGC 700C>T	Arg→Cys	+	-H _{ha} I	
5 (5)	W268R	TGG→CGG 802T>C	Trp→Arg	+		+N _{ci} I
5 (5)	R297X†	CGA→TGA 889C>T	Arg→Stop	-		+B _{sr} I
6 (6b)	1335delC	1 bp del	29 altered aa, term	+	+B _{gl} I	
6 (6b)	1447-1448insT	1 bp ins	32 altered aa, term	+		-N _{la} III
6 (6b)	P521L§	CCG→CTG 1562C>T	Pro→Leu	+	-E _{ag} I	
6 (6c)	R565W	CGG→TGG 1693C>T	Arg→Trp	+		+N _{la} III
6 (6c)	L591P	CTG→CCG 1772T>C	Leu→Pro	-		+B _{st} UI
6 (6c)	R626X†	CGA→TGA 1876C>T	Arg→Stop	+	+S _{tu} I	
6 (6c)	1932-1933insGCTAC	5 bp ins	3 altered aa, term	+		+H _{ga} I
6 (6d)	2099delA	1 bp del	106 altered aa, term	+	+A _{hd} I	
6 (6d)	E705K	GAG→AAG 2113G>A	Glu→Lys	+		+A _{fl} III

*Number of codons and nucleotides according to ref 6.
†‡§Found previously by refs 6, 8, 9, respectively.

temperatures, and MgCl₂ concentrations for the ACRS PCR reactions are provided in table 2. All other parameters were as described for the typical PCR reaction.

Results

The six exons and the intron/exon boundaries of the NAGLU gene from 14 patients with the severe form of MPS IIIB were amplified by PCR. All of the 10 fragments were digested

with a restriction enzyme before SSCP analysis. Fragments showing a shift were purified and sequenced directly using fluorescent DNA sequencing technology (Perkin Elmer Applied Biosystems). In patient samples where no or only one heterozygous shift was observed (21.4%), all of the amplified PCR products were directly sequenced. Using these techniques, 16 different mutations were found, 12 of which have not been previously reported

Figure 1 Six novel mutations in the genomic sequences of the NAGLU gene from patients with MPS IIIB. Sequence analysis was performed directly on PCR amplified genomic DNA using an ABI Prism™ M13 (-21) Dye Primer FS Cycle Sequencing Ready Reaction Kit, and products were run on an ABI Prism™ 377 DNA Sequencer (Perkin Elmer Applied Biosystems). (A) L591P, (B) W268R, (C) 2099delA, (D) 1447-1448insT, (E) 1335delC, (F) 334-358del25. Mutations A, C, and D are heterozygous, B, E, and F are homozygous. Base changes, insertions, and deletions are underlined. M=mutant sequence, N=normal sequence.

Table 4 Genotype and national origin of MPS IIIB patients in this study

Patient	Allele 1	Allele 2	National origin
1	219-237del19	Y140C	UK
2	1335delC	1335delC	Pakistan
3	1932-1933insGCTAC	R297X	Eastern Europe
4	R234C	R234C	Spain
5	334-358del25	334-358del25	Greece
6	P521L	P521L	UK
7	L591P	R297X	UK
8	R565W	1447-1448insT	UK
9	E705K	R297X	UK
10	R626X	R626X	UK
11	F48C	F48C	Pakistan
12	2099delA	2099delA	UK
13	W268R	W268R	Pakistan
14	Y140C	R626X	Greece

Table 3 lists these mutations and fig 1 shows the sequence data obtained for six of the mutations. R297X, R626X, Y140C, and P521L are mutations which have been reported previously.^{6,8,9} Of the 12 novel mutations, four are deletions (219-237del19, 334-358del25, 1335delC, 2099delA), two are insertions (1447-1448insT, 1932-1933insGCTAC), and six are missense mutations (F48C, R234C, W268R, R565W, L591P, E705K). Seven of the 16 sequence changes were confirmed by restriction enzyme digestion (table 3). For the remaining nine sequence changes, region specific primers were designed that would lead to the creation or loss of restriction sites at those known mutation sites, a technique known as ACRS PCR.¹³ Table 2 details the necessary amplification conditions for the ACRS reactions and the resulting restriction enzyme analysis.

Two putative mutations were identified in all 14 MPS IIIB patients. Table 4 details the genotype of the patients including their national origin. Eight of the patients were homozygous for their mutations and the remaining six were compound heterozygotes. Three of the mutations, Y140C, R297X, and R626X, were found in more than one patient.

The pathogenic nature of the six novel missense mutations on enzyme function has yet to be ascertained, but 94 control chromosomes were screened to determine if the changes were present in the general population. SSCP analysis was used to screen for four of the changes (F48C, W268R, R565W, E705K). Digestion with the restriction enzyme *HhaI* was used to detect R234C. ACRS PCR and *BstUI* digestion was used to screen for L591P. None of the changes was found in any of the 94 control chromosomes. Two polymorphisms in which the amino acid sequence was not altered were found in the control chromosomes. They were R519R (AGG→AGA: 1557G>A) and P719P (CCG→CCA: 2157G>A). Each occurred in heterozygous form in a single control and both appear to be very rare (1.1%).

Discussion

Mutational analysis on 14 patients with the severe classical form of MPS IIIB has resulted in the identification of 16 putative mutations, 12 of which have not been previously described. Two putative mutations have been found in all 14 patients. Eight patients were homozygous for the sequence changes and the remaining six were compound heterozygotes.

Among the 12 novel sequence changes there were four deletions and two insertions. In the larger insertions and deletions, analysis of the sequence adjacent to or within the affected region shows the presence of direct repeat elements which have probably played a role in the mutation event.^{14,15} In the 219-237del19 mutation, where there has been a deletion of 19 bp, there is a 7 bp direct repeat element (GCGCGGC) just before the deletion site and at the 3' end of the deleted fragment. The 334-358del25 mutation, a deletion of 25 bp, shows a similar pattern with a 5 bp direct repeat element TGCCG; however, there has been a deletion of an additional four G residues from the sequence just after the second direct repeat. There is a 3 bp direct repeat element GCT present in the vicinity of the 1932-1933insGCTAC mutation where five bases have been inserted between nucleotides 1932 and 1933. Two of the single base pair deletions, 2099delA and 1335delC, have occurred after a sequence of four A residues or four C residues, respectively. The 1447-1448insT mutation has occurred after a single T residue. All three have clearly arisen as a result of slipped mispairing during DNA replication.^{14,15} These insertions and deletions will be pathogenic since all of them cause a shift in the reading frame and five of the six will result in premature termination. The exception is 2099delA which occurs close to the C-terminus of the protein. The last 44 amino acids of the normal protein will be altered and an additional 22 amino acids added to the C-terminus (the new stop codon will be situated in the polyadenylation signal AT-TAAA). Since the C-terminus is a critical part of the protein, any alteration will affect its secondary structure and ultimately its function.

Two nonsense mutations were found in the group of patients studied, R297X and R626X, both of which have been previously reported.^{6,9} Only these two mutations and the pathogenic Y140C mutation⁸ were found in more than one MPS IIIB patient. Together they account for 25% of mutant alleles and are therefore relatively common. They occur in several different populations (table 4) and since the two premature stop mutations occur at CpG dinucleotides they have probably occurred independently in different parts of the world. In contrast, the Y140C mutation, which does not occur at a CpG dinucleotide, may be an ancient mutation. In the seven UK patients, the three "common" mutations account for 36% of mutant alleles and such information will be important for future screening of newly diagnosed MPS IIIB patients in the UK.

CpG dinucleotides in a gene sequence are known to be "mutational hotspots".¹⁶ Of the 10 point mutations, five occur at a CpG dinucleotide. Eight of the point mutations were missense and none of the six novel missense mutations was found in 94 control chromosomes. In the patients who were homozygous for a particular missense mutation, no other sequence changes were found. This provides preliminary evidence for the pathogenic nature of these changes. Three of the mutations (W268R, R565W, E705K) alter the charge of

the amino acid side chain, which is likely to affect the conformation, stability, or catalytic function of the NAGLU enzyme. Two of the mutations (F48C, R234C) result in the introduction of an extra cysteine residue into the protein chain and this may alter disulphide bridge formation. There is no alteration in the charge of the side chain in the L591P mutation, but the acquisition of a proline residue is likely to affect secondary structure formation.

A previous study found that nine out of 10 missense mutations were clustered in one of two regions of the protein, between codons 92 and 153, and codons 612 and 682.⁸ It was suggested that these regions may be important in the transport or function of the enzyme.⁸ However, none of the six novel missense mutations found in this study lie in either of these two regions. Since very little is known about the catalytic site of the enzyme, it is very difficult to draw any conclusions as to the effect of the missense mutations on enzyme function. Six potential N-glycosylation sites with the NXS/T motif have been proposed.⁶ None of the mutations presented in this report disrupt any of these potential N-glycosylation sites. The mouse NAGLU enzyme has been characterised recently (Genbank accession number MMU85247)⁸ and shows 84% homology at the amino acid level to the human form. The six novel missense mutations in this report result in the substitution of residues that are conserved in the mouse and human NAGLU enzymes. Future analysis of the precise effect of these missense mutations on enzyme transport and function will lead to a greater understanding of the structural and functional characteristics of the enzyme.

Including the results from this study, the total number of mutations identified so far in the NAGLU gene of MPS IIIB patients is now 35. Only seven of these mutations (P115S, Y140C, R297X, Y455C, R626X, R674C, R674H)^{6,8,9} have been found in more than one family, the remaining 28 are, so far, confined to individual pedigrees. These results further highlight the heterogeneity of MPS IIIB at the molecular level.

The authors would like to thank the Enzyme Laboratory of the Chemical Pathology Services at GOSH NHS Trust for carrying out the enzyme diagnosis of the MPS IIIB patients. We thank Mr Alan Cooper and colleagues at the Willink Biochemical Genetics Centre in Manchester for supplying two of the patient samples. We are grateful for the help and support of the parents from The Society for Mucopolysaccharide Diseases in the UK. Financial support was provided by The Society for Mucopolysaccharide Diseases with funds raised by the charity Jeans For Genes. Funding for the ABI Prism™ 377 DNA sequencer was provided by The Wellcome Trust.

- Whiteman P, Young E. The laboratory diagnosis of Sanfilippo disease. *Clin Chim Acta* 1977;76:139-47.
- Andria G, Di Natale P, Del Giudice E, Strisciunglio P, Murino P. Sanfilippo B syndrome (MPS III B): mild and severe forms within the same sibship. *Clin Genet* 1979;15:500-4.
- van de Kamp JJ, Niermeijer MF, von Figura K, Giesberts MA. Genetic heterogeneity and clinical variability in the Sanfilippo syndrome (types A, B, and C). *Clin Genet* 1981;20:152-60.
- Ballabio A, Pallini R, Di NP. Mucopolysaccharidosis III B: hybridization studies on fibroblasts from a mild case and fibroblasts from severe patients. *Clin Genet* 1984;25:191-5.
- Weber B, Blanch L, Clements PR, Scott HS, Hopwood JJ. Cloning and expression of the gene involved in Sanfilippo B syndrome (mucopolysaccharidosis IIIB). *Hum Mol Genet* 1996;5:771-7.
- Zhao HG, Li HH, Bach G, Schmidtchen A, Neufeld EF. The molecular basis of Sanfilippo syndrome type B. *Proc Natl Acad Sci USA* 1996;93:6101-5.
- Aronovich EL, Zhao HG, Neufeld EF, Whitley CB. Mutation analysis in Sanfilippo syndrome type B by automated sequencing of the NAGLU coding region. *Am J Hum Genet Suppl* 1996;59:A246.
- Schmidtchen A, Greenberg D, Zhao HG, et al. NAGLU mutations underlying Sanfilippo syndrome type B. *Am J Hum Genet* 1998;62:64-9.
- Zhao HG, Aronovich EL, Whitley CB. Genotype-phenotype correspondence in Sanfilippo syndrome type B. *Am J Hum Genet* 1998;62:53-63.
- Miller MA. A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Res* 1988;16:1215.
- Davies JP, Winchester BG, Malcolm S. Sequence variations in the first exon of α -galactosidase. *Am J Med Genet* 1993;30:658-63.
- Tyson J, Ellis D, Fairbrother U, et al. Hereditary demyelinating neuropathy of infancy. A genetically complex syndrome. *Brain* 1997;120:47-63.
- Haliassos A, Chomel JC, Tesson L, et al. Modification of enzymatically amplified DNA for the detection of point mutations. *Nucleic Acids Res* 1989;17:3606.
- Cooper DN, Krawczak M. Mechanisms of insertional mutagenesis in human genes causing genetic disease. *Hum Genet* 1991;87:409-15.
- Krawczak M, Cooper DN. Gene deletions causing human genetic disease: mechanisms of mutagenesis and the role of the local DNA sequence environment. *Hum Genet* 1991;86:425-41.
- Cooper DN, Krawczak M, Antonarakis SEM. The nature and mechanisms of human gene mutation. In: Scriver CR, Beaudet AL, Sly WS, Valle D, eds. *The metabolic and molecular bases of inherited disease*. New York: McGraw-Hill, 1995:259-92.