Am. J. Hum. Genet. 66:790–818, 2000

Minor Lesion Mutational Spectrum of the Entire *NF1* Gene Does Not Explain Its High Mutability but Points to a Functional Domain Upstream of the GAP-Related Domain

Raimund Fahsold,[1,*] Sven Hoffmeyer,[2,*] Claudia Mischung,[3] Christoph Gille,[3,4] Christian Ehlers,[1] Nazan Kücükceylan,[5] Maher Abdel-Nour,[3] Andreas Gewies,[3] Hartmut Peters,[3] Dieter Kaufmann,[5] Annegret Buske,[3] Sigrid Tinschert,[3] and Peter Nürnberg[3]

[1]Gemeinschaftspraxis B. Prager & A. Junge, Dresden; [2]Epidauros AG, Bernried; [3]Institut für Medizinische Genetik, Universitätsklinikum Charité, Berlin; [4] Institut für Biochemie, Universitätsklinikum Charité, Berlin; [5]Abteilung Humangenetik, Universität Ulm, Ulm

More than 500 unrelated patients with neurofibromatosis type 1 (NF1) were screened for mutations in the *NF1* gene. For each patient, the whole coding sequence and all splice sites were studied for aberrations, either by the protein truncation test (PTT), temperature-gradient gel electrophoresis (TGGE) of genomic PCR products, or, most often, by direct genomic sequencing (DGS) of all individual exons. A total of 301 sequence variants, including 278 bona fide pathogenic mutations, were identified. As many as 216 or 183 of the genuine mutations, comprising 179 or 161 different ones, can be considered novel when compared to the recent findings of Upadhyaya and Cooper, or to the NNFF mutation database. Mutation-detection efficiencies of the various screening methods were similar: 47.1% for PTT, 53.7% for TGGE, and 54.9% for DGS. Some 224 mutations (80.2%) yielded directly or indirectly premature termination codons. These mutations showed even distribution over the whole gene from exon 1 to exon 47. Of all sequence variants determined in our study, <20% represent C→T or G→A transitions within a CpG dinucleotide, and only six different mutations also occur in *NF1* pseudogenes, with five being typical C→T transitions in a CpG. Thus, neither frequent deamination of 5-methylcytosines nor interchromosomal gene conversion may account for the high mutation rate of the *NF1* gene. As opposed to the truncating mutations, the 28 (10.1%) missense or single-amino-acid-deletion mutations identified clustered in two distinct regions, the GAP-related domain (GRD) and an upstream gene segment comprising exons 11–17. The latter forms a so-called cysteine/serine-rich domain with three cysteine pairs suggestive of ATP binding, as well as three potential cAMP-dependent protein kinase (PKA) recognition sites obviously phosphorylated by PKA. Coincidence of mutated amino acids and those conserved between human and *Drosophila* strongly suggest significant functional relevance of this region, with major roles played by exons 12a and 15 and part of exon 16.

Introduction

Neurofibromatosis type 1 (NF1; also known as "von Recklinghausen neurofibromatosis" [MIM 162200]) is a common autosomal dominant disorder affecting ~1 per 3,000–5,000 people. It is fully penetrant and exhibits a mutation rate some 10-fold higher than that reported for most other disease genes. As a consequence, a high number of sporadic cases (up to 50%) is observed (Upadhyaya and Cooper 1998). NF1 is clinically characterized by cutaneous neurofibromas, café-au-lait spots, iris hamartomas (Lisch nodules), and freckling of axillary and inguinal regions. These features are present in >90% of patients at puberty. Further manifestations, such as deeply situated and arbitrarily located neurofibromas, plexiform neurofibromas, optic glioma, macrocephaly, short stature, learning difficulties, scoliosis, and pseudarthrosis, as well as certain malignancies, occur less frequently among patients with NF1 (Riccardi 1992; Huson and Hughes 1994; Friedman and Birch 1997). NF1 is notable for its extreme phenotypic variability, both within and between families (Riccardi 1992). In addition to multiple allelism of the *NF1* locus, the influence of modifying genes (Easton et al. 1993) and the impact of stochastic events (Riccardi et al. 1993) have been suggested as causes of this variability. So far, none of these hypotheses has been tested satisfactorily. A comprehensive analysis of the mutational spectrum might help to elucidate the role of different *NF1* mutations.

The *NF1* gene maps to chromosome 17q11.2 and is considered to be a tumor-suppressor gene, because loss-of-function mutations have been associated with the oc-

Received August 19,1999; accepted for publication October 14,1999; electronically published March 10, 2000.

Address for correspondence and reprints: Dr. Peter Nürnberg, Institut für Medizinische Genetik, Universitätsklinikum Charité, D-10098 Berlin, GERMANY. E-mail: peter.nuernberg@charite.de

* These authors contributed equally to this work.

0002-9297/2000/6603-0006$02.00

Table1

Pre-Amplification PCR Primers and Conditions for Nested PCRs in the TGGE Approach

Exon	Primer Sequences[a] (5′→3′)	Fragment Size (bp)	T_a (°C)[b]
1	CAGACCCTCTCCTTGCCTCTT GGATGGAGGGTCGGAGGCTG	433	66
7	TAATTTGCTATAATATTAGCTAC ATAATACTTATGCTAGAAAATTC	323	54
9	AGAAATAATCTGCTTTTTTTTTTC TACAATTTAACTCAGTGATACTC	1,341	59
14 - 18	CTCTGCCTAAGTTGTAGATAGTGAAG TTAGGGAAATTTGAGAAGAGATGT	3,595	53→51
23–1	TTTGTATCATTCATTTTGTGTGTA AAAAACAGCGGTTCTATGTGAAAAG	282	56
23–2	CTTAATGTCTGTATAAGAGTCTC ACTTTAGATTAATAATGGTAATCTC	268	56
23a	AGCCAGAAATAGTAGACATGATTGGGT CTATTTTGTGCCAGAATTAGTAGA	446	56
24	TTGAACTCTTTGTTTTCATGTCTT GGAATTTAAGATAGCTAGATTATC	266	58
32–36	TTGATTAGGCTGTTCCAATGAATA TCATAAATATTTGGGAGAAGTGAGG	1,936	53→50

[a] Primers for the amplification of exons 1, 23-1, 23-2, 23a, and 24 are from Purandare et al. (1995).

[b] Two different annealing temperatures (T_a) connected with an arrow indicate a touch-down PCR protocol with the first 8 cycles being performed at the higher temperature.

currence of benign and malignant tumors in neural-crest–derived tissues (Legius et al. 1993; Colman et al. 1995; Serra et al. 1997) as well as myeloid malignancies (Shannon et al. 1994). The *NF1* gene was cloned in 1990 (White and O'Connell 1991). It spans over 350 kb of genomic DNA comprising ⩾60 exons. The open-reading frame codes for 2,867 amino acids, including three alternatively spliced exons. The most common transcript codes for a polypeptide of 2,818 amino acids called neurofibromin (Marchuk et al. 1991; Danglot et al. 1995; Li et al. 1995). A central region of about 360 amino acids shows significant homology to the mammalian GTPase-activating protein (GAP) (Xu et al. 1990). This region, the NF1 GAP-related domain (GRD), is encoded by the exons 20–27a and has been found to interact with $p21^{ras}$ (Martin et al. 1990). As a result of this interaction, GTP•Ras levels may be elevated in human NF1 peripheral nerve tumors, in which neurofibromin is usually found to be totally absent or, at least, dramatically reduced (Guha et al. 1996). Commensurate with its pivotal functional significance, several missense mutations were identified in the GRD (Li et al. 1992; Upadhyaya et al. 1997; Kim and Tamanoi 1998; Klose et al. 1998*a*).

In general, mutation analysis of the *NF1* gene has turned out to be a major challenge, for several reasons. The large size of the gene under investigation and the diversity of the underlying pathological lesions (Korf 1998; Upadhyaya and Cooper 1998) make analysis problematic. In addition, the presence in the genome of several unprocessed *NF1* pseudogenes severely hampers PCR approaches to the analysis of genomic DNA samples, because of coamplification of homologous sequences of the *NF1*-like loci at other chromosomes (Purandare et al. 1995; Régnier et al. 1997). Most of the *NF1* mutations are point mutations or other small lesions leading to premature termination codons (PTCs) (Upadhyaya and Cooper 1998). Hence, the application of the protein truncation test (PTT) was thought to substantially accelerate the rate of identification of *NF1* mutations. In an initial study, mutations were identified in 14 (67%) of 21 individuals (Heim et al. 1995). Before PTT was introduced, the best results had been obtained by using chemical mismatch cleavage analysis. In a study covering 70% of the coding sequence, seven mutations were found in 25 patients (28%) (Purandare et al. 1994). In a more recent study, by using a combined heteroduplex/SSCP approach, researchers identified only 13 disease-causing mutations in 67 unrelated NF1 patients (a 19% detection rate), even though as many as 45 exons were tested (Abernathy et al. 1997). Most other analyses focused on one or a few arbitrarily selected exons but sometimes were performed in very large cohorts of NF1 patients (e.g., Maynard et al. 1997).

Together with multiple reports of isolated mutations,

Table 2

TGGE-PCR Primers and Conditions

Exon[a]	Primer Sequences (5′→3′)[b]	Fragment Size (bp)	T_a (°C)[c]	TGGE Conditions[d] (gradient, running time × voltage)
1 (nested)	TATTCTCTCCGTCGCCCCCC	137	59	30–60°C, 2 h × 300 V
	p-AACCCCCACTCCGCTCCC			
2	TAAGGATAAGCTGTTAACGTG	221	55	25–55°C, 3 h × 300 V
	p-AATTCCCCAAAACACAGTA			
3	*p*-AATGGTAGCAGAAAGTGAAAC	175	58	35–60°C, 1 h 30 min × 300 V
	AATTCACAAAGCCTGCCTAC			
4a	TTGTTCTGTGTGTGTGTTTG	316	56	32–53°C, 2 h 30 min × 300 V
	p-A-ACTTCAGTAGTCCCATGTGG			(35–70°C, 5 h × 300 V)[e]
4b	CTGTCCCCTAATACTTAATT	209	52	29–52°C, 3 h 15 min × 300 V
	p-A-ATACTAGTTTTTGACCCAGT			
4c	*p*-AA-GCTCTGAGTTGTATTTGTGT	190	51	27–53°C, 3 h 15 min × 300 V
	ACAACAGCAAATTTTACATC			
5	GAAGGAAGTTAGAAGTTTGTG	213	54	30–60°C, 1 h 30 min × 300 V
	p-AA-CACAAGTAGGCATTTAAAAGA			
6	*p*-A-AATGCCAGGGATTTTGT	247	47	35–60°C, 1 h 30 min × 300 V
	p-AA-TAGATATAATGGAAATAATTTTG			
7 (nested)	GAAACTTCATATATTATCTTA	254	52	30–60°C, 2 h 30 min × 300 V
	p-AA-CTTAAAGTTTGTAGTAGA			
8	*p*-AA-TTGTGTGGGTAATGTGTTGA	248	52	30–60°C, 2 h 15 min × 300 V
	AAATATAGTTAGATAAAAACCAATG			
9 (nested)	*p*-AATCTGCTTTTTTTTTTCTTT	136	51	30–60°C, 1 h 30 min × 300 V
	p-AA-TTTAGTAATTTAGCAATAC			
	AATCTGCTTTTTTTTTTCTTT	136	51	30–60°C, 2 h × 300 V
	p-AA-TTTAGTAATTTAGCAATAC			
9br	*p*-AATTGTGAAATATTTTTGTCTAC	102	52	32–62°C, 55 min × 300 V
	CTTGGAACCCAGAAAGGAA			
10a	*p*-AATTTTGTACTTTTTCTTCC	217	53	30–60°C, 2 h 10 min × 300 V
	AATAGAAAGGAGGTGAGA			
10b	*p*-A-ATTATCCTGAGTCTTACGTC	229	51	30–70°C, 50 min × 300 V
	p-AA-TAACTTAGTGTGATAATTT			
10c	ATTTTTTTTAATTGAAGTTTC	186	50	30–60°C, 2 h 30 min × 300 V
	p-AA-TTCCTTCAAGAACATGGAA			
11	AAGTACTCCAGTGTTATGTTTAC	205	52	20–45°C, 3 h × 300 V
	p-A-ACAAAATAAAATTTAAAAGTTGAA			
12a	CTAAGCTTCTCTAAACTTGTATTCA	297	62	25–55°C, 3 h × 300 V
	p-AATCTCTCACCATTACCATTCC			
12b	GTGTTTATTCCTCTTGGTTGTC	274	59	25–55°C, 3 h 30 min × 300 V
	p-AA-ATTCAGAAAACAAACAGAGCAC			
13	CCCAAGTTGCAAATATATGTC	277	60	35–65°C, 4 h 30 min × 300 V
	p-A-ATTGCTGACAGAGGCAAACTC			
	CTCTTGCCCAACTATAACAC	89	58	35–65°C, 2 h 30 min × 300 V
	p-A-AGTAAAAAAAACCACTATTCAC			
14 (nested)	*p*-AA-CCTACTCCTTTTGGGTGGAGCTTA	191	55	31–61°C, 2 h 40 min × 400 V
	GGGGTGTTTCTGTTGCTA			
15 (nested)	*p*-AATATACATCAAGTTTGAAACTT	208	55	28–60°C, 2 h 10 min × 400 V
	AGTTAACAGACAAAAGTCAACTT			
16 (nested)	*p*-AATGTTGGATAAAGCATAATTT	330	55	31–61°C, 2 h 40 min × 400 V
	p-AA-CGTTTCCCTCTGAAGACA			
	p-AAGGGTTCTATGATTTCATGAT	275	55	31–61°C, 2 h 40 min × 400 V
	p-AA-CACTCTATTCATAGAGAAAGGTG			
17 (nested)	*p*-AA-TCATCTCTCTAGGGGGTCT	240	55	31–61°C, 2 h 40 min × 400 V
	ATGTTTCTGCTACATTTCAGTA			
	GATGGCAAATCATTAATGTAT	204	55	28–60°C, 2 h 10 min × 400 V
	p-AATGTTTCTGCTACATTTCAG			
18 (nested)	*p*-AA-TGATAATTTTTTTATTGTTTCTATG	230	55	31–61°C, 2 h 40 min × 400 V
	TGTACTTCATTGGACATATTAAGATTTACA			
	p-AA-TATTTAGAATGCCTTCTCTTTTG	222	55	28–60°C, 2 h 10 min × 400 V
	TACAAGACCCTACATTGCTC			

(*continued*)

Table 2 Continued

Exon[a]	Primer Sequences (5′→3′)[b]	Fragment Size (bp)	T_a (°C)[c]	TGGE Conditions[d] (gradient, running time × voltage)
19a	GTGTGTGTGTGGCTTCAAAA	192	60	30–55°C, 3 h 30 min × 300 V
	p-AACTCTCACAGTAAAACCCACTAA			
19b	TTTTTTTTCAGAGATTTGGACCA	174	58	30–55°C, 3 h 3 min × 300 V
	p-AA-GCTTTATTTGCTTTTTGCTTTA			
20	*p*-A-ATACGGCCTTCACTATGTAAAGGT	276	58	30–60°C, 3 h × 300 V
	GCCAGTTCTCTAGGTTTTGT			
21	*p*-AA-GCATGTAAGAGAAGCAAAAATTA	328	55	35–60°C, 3 h × 300 V
	CTATGTGCCAGGCACTTTTC			
22	TCTTTAGCTTCCTACCTAAGAA	262	59	30–55°C, 4 h × 300 V
	p-A-ACACACATACACACAAAATGAA			
23-1 (nested)	*p*-AAGGTAAAATATATGGAGCAG	191	63	25–55°C, 3 h × 300 V
	AAAACAGCGGTTCTATGTG			
23-2 (nested)	*p*-AAGTGTTAGGATTTTATTTTTATTTTTT	93	59	35–65°C, 1 h 30 min × 300 V
	TTTTCAGTCATCTGAAGGAGG			
	GTTAGAACCATCAGAGAGC	159	59	33–63°C, 3 h 30 min × 300 V
	p-AA-GTAATCTCTAACTGTAAGCAT			
23a (nested)	GCTGTATGTAGTCGGTGCT	78	58	33–63°C, 1 h 30 min × 300 V
	p-AA-TTTATTCAGTAGGGAGTGGCA			
	TGCTCATCTCTGTTCTGTA	113	55→53	33–63°C, 1 h 15 min × 300 V
	p-AACAGCTAATAAAAAGTTCTCC			
24 (nested)	AACTCCTTGTTTTTAGGTGG	171	56	37–67°C, 2 h 30 min × 400 V
	p-AA-GACATTAACTTCAAGCCC			
	ACCTTTGAACTCTTTGTTTTCAT	230	52	37–67°C, 2 h 30 min × 400 V
	p-AA-GACATTAACTTCAAGCCC			
	p-AA-TTCAAACCTTATACTCAATTC	238	48	30–60°C, 2 h 10 min × 400 V
	AAGGGGAATTTAAGATAGCTAG			
25	*p*-AACCCTGTTTTATTGTGTAG	138	62	30–60°C, 5 h 20 min × 300 V
	GTAAGTGGCAAGAAAATTAC			
26	TGAAAATTCTAATGACTTTGC	212	64	30–60°C, 2 h 40 min × 300 V
	p-A-AGTGTTCACTATCCCCATGAC			
27a	TGTGTAGTGCTAAATGTG	263	54	30–60°C, 2 h 30 min × 300 V
	p-AA-GCAAACTCTCCTTCTCAAC			
27b	*p*-AA-CTACTCAGTAGACAACAT	195	55	25–55°C, 3 h × 300 V
	GTTAAGAGACCCAAAACATAG			
28	TCTTTGTCTTTTTTGTCATTTTCC	509	60	SSCP[d]
	AGTCAAGAAAAGCAATGAATCGT			
29	TCACCCCGTCACCACCACTTT	411	60	SSCP[d]
	GCAACAACCCCCAAATCAAACTGA			
30	*p*-AA-GGAACTATAAGGAAAAATACG	181	57	25–55°C, 3 h 30 min × 300 V
	ACTAATAGAGACAATAAAGAGGG			
	GCCAGTTACTAGAGACAT	182	50	25–55°C, 3 h 30 min × 300 V
	p-AATAATTGTTAGTATTAAAGAAAA			
31	*p*-A-ATTGACCATCACATGCTAATAG	260	62	30–55°C, 2 h 30 min × 300 V
	CTAGATAAATATTTGAGCAAACTC			
32 (nested)	*p*-AA-TGATTAGGCTGTTCCAATGAATA	156	48	30–64°C, 2 h 30 min × 400 V
	p-AA-TGATCCCAAGCCACCTGTT			
	p-AA-CTTGATGTTGTACTAGACAGTT	156	48	30–64°C, 2 h 30 min × 400 V
	p-AA-TACAGAAGGCAAAAGAAAAGTGAT			
33 (nested)	*p*-AATTAAACTGAACTTTTTTGTGCTA	204	48	30–64°C, 2 h 30 min × 400 V
	p-AA-GAAGGACAGCATCAGCATGTA			
	p-A-ATGTGGGATGATATTGCTATTTTA	202	48	30–64°C, 2 h 30 min × 400 V
	p-AATGAAGCTGTGAACAAGTACA			
	p-A-ATGGACTGGTCATTAATATCATT	114	48	30–64°C, 2 h 30 min × 400 V
	p-AA-GAAGTAAAATGGAGAAAGGAACT			
34 (nested)	*p*-A-ATGGAACTTTAGAAATTAAAAAGTA	187	48	30–64°C, 2 h 30 min × 400 V
	p-AA-CCCGGTAACTGGAACGGAA			
	p-AA-CAAAGTCAAGTCAGCTGCTGT	179	48	30–64°C, 2 h 30 min × 400 V
	p-AAGATTTTAACTTAGTTTCTTATCA			

(*continued*)

Table 2 Continued

Exon[a]	Primer Sequences (5′→3′)[b]	Fragment Size (bp)	T_a (°C)[c]	TGGE Conditions[d] (gradient, running time × voltage)
35 (nested)	*p*-A-ATCATAATAAACATTATTTAAACAGTT *p*-AA-TTTACAACTTATATTTAATTTAGGA	168	48	30–60°C, 2 h 30 min × 400 V
36 (nested)	*p*-AAGGTTTTTATAAGTTCTGTGGAT *p*-AA-CATAAATATTTGGGAGAAGTGAGG	189	48	30–60°C, 2 h 30 min × 400 V
37	TCCGAGATTCAGTTTAGGAGT *p*-AATGCACTCATTTTCTATACAGTA	203	51	25–55°C, 3 h × 300 V
38	*p*-AA-TTGAAAGAGACTATGTCATGAT *p*-AA-GAGTAATCTAGGAACCTCAAG	235	62	30–60°C, 2 h × 300 V
39	CCTTTAAAGAAAGCTACTG *p*-A-ATAAAAATATTCTAAATAAGGC	215	48	30–60°C, 2 h × 300 V
40	*p*-A-AGATGCTTGTTCAAAAAATTA TATATATAGATGTAGCAAGAT	241	52	30–60°C, 4 h × 300 V
	AAGATGCTTGTTCAAAAAATTA *p*-AA-TATATATAGATGTAGCAAGAT	241	52	30–60°C, 4 h × 300 V
41	GAGACTGTAAGAAGTTCATC *p*-AATTGAAACTTGATTATGATTA	268	50	25–49°C, 2 h 30 min × 300 V
42	*p*-AA-TAATTGATTTTTCTCTATTG AATAATAAAAAAAATCTACATAAT	230	52	30–60°C, 4 h 30 min × 300 V
43	*p*-A-ATGTCCAAACATTTTCTTTTT CCACCTTATTTTCAATGATC	251	53	30–60°C, 3 h 30 min × 300 V
44	*p*-AACATTGAAATAGTTAGGTGAA TAGACTGGAATAAAAATTTG	253	52	35–65°C, 2 h 45 min × 300 V
45	*p*-AA-CCACAAAGTAAAAATGTTGT AAGGTGAATTAAAATCAAAA	179	49	30–58°C, 2 h 15 min × 300 V
46	*p*-A-ATTTTCATTTAATTTTCCTCT ATGTTAGCAAGTTCATCAAC	246	48	30–55°C, 1 h 50 min × 300 V
47	*p*-A-ATTTAATTTCTGTTACAATT CAAAAGTTAGAGAAAAATAT	143	44	26–52°C, 3 h × 300 V
48	*p*-AACTAAAATAATTTCCTATTTTCC *p*-AA-GTCTTATATTGTTGCTCAAAGT	294	58	35–55°C, 3 h 45 min × 300 V
48a	*p*-AATCTTATGAACATCACTTACTT CGTGCAAAGATGATGAAAA	134	54	35–55°C, 2 h × 300 V
49	CCTGGAAGGAAAAGAAGA *p*-AA-GATTTTAAAAAAGAAAGCAA	216	56	35–60°C, 4 h × 300 V

[a] For TGGE, exons were amplified directly from genomic DNA or, as indicated, from a preamplified PCR product (see table 1) using nested TGGE-PCR primers.

[b] Psoralen modification is indicated by "*p*-"; note that psoralen is followed by two adenosine residues irrespective of the target sequence.

[c] T_a is the annealing temperature for the primers during PCR.

[d] The exons 28 and 29 were investigated by single-strand conformation polymorphism (SSCP) analysis in lieu of TGGE (see Peters et al. [1999*b*]).

[e] A second TGGE analysis of exon 4a was performed after digesting the PCR product with *Tru 9* I.

most of these data have been submitted to the NF1 Genetic Analysis Consortium. The consortium was organized in the autumn of 1992 to facilitate mutation detection in the *NF1* gene and to pool mutation data into a common database for better interpretation of the growing body of information. By November 1997 a total of 240 mutations, including 173 minor lesions (72%) had been reported to the consortium (Korf 1998). The mutational spectrum obtained from these data, however, suffers from a strong bias towards more thoroughly investigated regions of the *NF1* gene. To overcome this drawback, we launched a mutation-screening project in Germany aimed at the complete analysis of the entire *NF1* gene in a large cohort of unrelated NF1 patients. According to the preferences of the participating centers, PTT, temperature-gradient gel electrophoresis (TGGE) analysis (Riesner et al. 1989; Wartell et al. 1990), and direct genomic sequencing (DGS) of all individual exons were used for our analysis.

Materials and Methods

Patient Samples

The study was approved by the ethics committee of the Charité University Hospital. NF1 diagnostic criteria

Table 3

DGS-PCR Primers and Conditions

Exon	Primer Sequences[a] (5′→3′)	Fragment Size (bp)	T_a(°C)[b]
1	CACAGACCCTCTCCTTGCCTCTTC TACCTCCCCTCACCTACTCTGTCC	233	66
2	TCTGTGGTTGATGCAGTTTTCC TATATCCAAAGTCCACAGAAAATC	371	62
3	TGGTAGCAGAAAGTGAAACTA ATAGGACTGTCTCTGGTCCATC	224	56
4a	GTTTGAAAATTTTCATAATAGAAAATG GGAGGTCAAAGCTGCTGTGAG	419	60
4b	GAACTCCTGGCCTCAAGTGGTC ATGTCATTATAAAATCCAGTTTGGTG	349	62
4c	GCAAAAGTAATACGTAAATGGAAAG TGATGTACCCAAGCAACAAAGAC	904	62
5	(amplification as for 4c) [TGACTTGAGTGATAGTTTCACAT]	904	62
6	CATGTTTATCTTTTAAAAATGTTGCC TTGAGTAAAATAAACTGCTTCACAT	C333	62
7	ATTTGCTATAATATTAGCTACATCTGG AAAGCAAGTCCTATGAACTTATCAAC	387	62
8	GGATTTTACTGCCATTTGTGTG TAACAGCATCAGTAAATATAGTTAGATA	237	60
9	CTTAGTGTTTTTTTTTTAQAACTTTCTA ATTTTTTTAGTAATTTAGCAATACC	224	54
9br	GCTTAAAATTTGTATACAATAAAC ATGCATGAAGCACCACTCCAGG	193	62
10a	GATAAAACTTAAAAQCTACAGTGATAAACAG GCAATAGAAAGGAGGTGAGATTC	270	62
10b	CTTTAAAGTGATAGCTATTACCTGAGTC CTAAAAAGTATCCTCCAGGTCTTG	288	60
10c	AAACTTGGTACCCTTTAGCAGTC GTATAGACATAAACATACCATTTC	348	60
11	GTACTCCAGTGTTATGTTTACC AAAACCTTTGGAAGTGTAAGTTTTAC	268	64
12a	TGTATTCATTATGGGAGAATGCC ATTACCATTCCAAATATTCTTCCA	267	64
12b	AAGTTGGGGCATAGAGATTGAGAG GATGAAATTTACCAAATTTCATTCAG	363	66
13	CACAGTTTATTGCATTGTTAG GCCATGTGCTTTGAGGCAG	376	60
14	TCCTACTCCTTTTGGGTGGAG TTAACAGATAAAAGTCAACTTTACAG	511	54
15	(amplification as for 14) [TGTGATCAGGAATAGCTTTTG]	511	54
16	TGGATAAAGCATAATTTGTCAAGT GGAAATTTTTAAAAACTGTGAGTACC TCAGTGAACGTAAGGGTTCTATG	628	60
17	GGTGCACTTACTCTGTGTGTTTAG GGGAAATTTGAGAAGAGATGTAGAG	808	64
18	(amplification as for 17) [GCCATTCTTTACTGCACACAAAC]	808	64
19a	GCCATTCTTTACTGCACACAAAC AAACAAAAGTTTGACATCTCAAAAG [TCATGTCACTTAGGTTATCTGG]	985	60
19b	ATTTAAGGGGAAGTGAAAGAAC TGGTGGGGGGCTTTATTTGC	242	56
20	CTATATCAGGTAAAATCATGTCCAAC GATTTGCTATGTGCCAGGGAC	758	62
21	(amplification as for 20) [GGTCTCATGCACTCCATAGGTG]	758	62

(*continued*)

Table 3 Continued

Exon	Primer Sequences[a] (5′→3′)	Fragment Size (bp)	T_a(°C)[b]
22	GCTACTCTTTAGCTTCCTACCTAAG AAAAACAGCGGTTCTATGTGAAAAG [CCTTAAAAGAAGACAATCAGCC]	518	60
23-1	(amplification as for 22) [TTTGTATCATTCATTTTGTGTGTA]	518	60
23-2	GGCTTAATGTCTGTATAAGAGTCTC ACTTTAGATTAATAATGGTAATCTC	270	60
23a	AGCCAGAAATAGTATACATGATTGGGT CTATTTTCTGCCAGAATTAGTAGA	448	60
24	AATAAGACAAGCTATGTCTTGACCTAG GAGTTTTTATGCAAAGTTTGACC	1023	60
25	(amplification as for 24) [TTAAGTACTAGCAGAAATTATATCAATGAG]	1023	60
26	GCTTTGTCTAATGTCAAGTCAC TTAAACGGAGAGTGTTCACTATC	339	62
27a	ATGGTCCTGAGGTCTTTTTG CTAACAAGTGGCCTGGTGGC	360	66
27b	TTGCTTTTAAAATATTTTTTCATTTTAG ACCTCCTGTTAAGTCAACTGGG	329	56
28	TTTAAAAAATGAATCCAGACTTTGAAG GCCTTACGTGACATTTTATACACCAC [TGCAAAGCCATATGAAATTGTAGTG]	696	62
29	GTTGGTTTCTGGAGCCTTTTAG AAATGGTCTCATTTTAAAAGCAAC	489	60
30	TTAAGGGGTATTTTGGTTTTACTG AGGATACCACAGATATAAAATCAGAAG	530	62
31	TTTTTTCCCCGAATTCTTTATG GTGAGTGTCTACATGCTTTCTGAAG	429	56
32	TGACAGGCCTGTAAATAAAATCTAG TTTTGGTAATATTTCATGTCATTACTG	885	58
33	(amplification as for 32) [TTTTGGTAATATTTCATGTCATTACTG]	885	58
34	GTTTGATTTAGGGAACATGAT CTGCAATTAAAAGATCCACAGAAC	794	62
35	(amplification as for 34) [CTGTGTTATTGGTAACAGGTCAC]	794	62
36	GCTGGACCAGTGGACAGAAC TCATTGACCTCAAATTTAAACGTC	392	62
37	ATAGCATGAGAAATCATTCTAG CAAGCGCTTGAGAACATACTATC	439	62
38	GTTCTCAGTCCAGCTAACAGTGTC ATGTAAAAAATATGCATTCAAGTTTAC	530	60
39	TGCTTGACTGTCTTGCACCAG CAAGTGATCCTCCTGCCTCAG	511	66
40	ATTCACATATGCATGTTTTACCTTC GATAACAGAGAGCCACTGTAGTGTC	556	64
41	TGCTTATTAAATCTCTCTGTATATTTC TTTCACTTACTCTTCCTAGGCCATC	436	64
42	CCTAGGGATACACCAAGAGTTTG ACATGGAAAATTTTGATAATCCTG	428	62
43	CTCAGTGAAAGCTTAAACACTTTATG AAAGCTAAAATCACTATCACAATATCTC	1144	60
44	(amplification as for 43) [CGAATAGTAATTCTCTATGATGTTTATG]	1144	60
45	(amplification as for 43) [CCCTCAAATTTTTATTCCAGTC]	1144	60
46	ATTGTAGAAAATTTGGAAAATGAAG ATGAGAAACTTTTTATAAAAGTAACATATG	856	58

(*continued*)

Table 3 Continued

Exon	Primer Sequences[a] (5′→3′)	Fragment Size (bp)	T_a(°C)[b]
47	(amplification as for 46) [TTTAGTTGCTTTGACACTCATTC]	856	58
48	AAGGAAGAAAAATAGTAAATTAAGTCC AAGGAGCAAAATTTGCTATAAAC	421	60
48a	ATTCAATAATTAAAACCAGATTCC GGTGGCTTTACAAGTTCCTAAAG	327	64
49	TTCCTAGAATGTGTCCCCGTTG ATATATGTGGTCGCACTTATTTTCCTG [CCATGTTGTAATGCTGCACTTC]	931	62

[a] Primers used for sequencing but not for amplification are shown in square brackets.

[b] T_a is the annealing temperature for the primers during PCR.

(Gutmann et al. 1997) were used to identify 521 unrelated patients with NF1, all of whom were of German or Turkish descent. Once informed consent was obtained, DNA from peripheral blood was obtained from each patient, applying one of several standard procedures. RNA was also obtained from some patients, either from fresh blood or from cell cultures (i.e., fibroblast-like cells or Epstein-Barr virus–transformed lymphocytes) by using the RNeasy total RNA purification kit (Qiagen). The SuperScript preamplification system (BRL Gibco) was used to prepare cDNA from the RNA samples. The cDNA reaction was performed in a 20-μl reaction volume containing 2–3 μg total RNA, 1.5 μg random hexamers (BRL Gibco), 0.5 μg single-stranded binding protein (Promega), 20 units RNAsin (Promega), 4 mM each dNTP, and 300 U Superscript II reverse transcriptase (RT) (BRL Gibco). cDNA was stored at -20°C.

Analysis of NF1 *Gene Expression*

Allele-specific expression level studies were performed by RT-PCR reactions by using the following primer pair to amplify the polymorphic exon 5 (Hoffmeyer and Assum 1994) from cDNA: 5′-TAGTCGCATTTCTACCAGGTTA-3′ (sense primer) and 5′-GAGAATGGCTTACTTGGATTAAA-3′ (antisense primer). Thirty PCR cycles of 1 min at 92°C, 1 min at 54°C, and 1 min at 72°C were used. After *Rsa*I restriction, the fragments were analyzed by agarose gel electrophoresis and ethidium bromide staining. Subsequently, the band intensities were measured densitometrically by using a charge-coupled-device camera and the ImageQuant software package distributed with the Phosphoimager from Molecular Dynamics.

PTT

RT-PCR.—Hot-start PCR reactions to amplify each of the five overlapping segments required that 2.5–3 μl cDNA be added to a lower-phase PCR mixture containing 1 × PCR buffer (50 mM KCl, 10 mM Tris, pH 8.3, and 2 mM $MgCl_2$), 0.8 mM each dNTP, and 10 pmol each primer (primer sequences were as described elsewhere (Heim et al. 1995) in a total volume of 40 μl. A wax gem (Perkin Elmer) was added to each tube. Reaction mixtures were heated to 80°C for 5 min, followed by cooling to room temperature. A 10-μl upper-phase mixture containing 1 × PCR buffer, 0.25 μg single-stranded binding protein, and 2.5 units *Taq* polymerase (Pharmacia) was layered onto the solidified wax. Reactions were performed in a Cetus model 9600 thermal cycler (PE Biosystems), under the following conditions: 95°C for 1 min; 40 cycles of 95°C for 30 s, 61.5°C for 30 s, and 72°C for 90 s; and 72°C for 10 min. The PCR products were analyzed by agarose gel electrophoresis. Apparent splice defects, for example, exon skipping events, were verified by cDNA sequencing by using radioactive labeling and the Thermo Sequenase kit (Amersham Life Science). Subsequently, the presumably mutated exons or exon/intron boundaries were sequenced from the patients' genomic DNA samples.

In vitro transcription/translation and analysis of the peptides.—For each in vitro transcription/translation reaction, 4–9.5 μl PCR product (volume depends on the quality of the PCR product) and 0.5 μl ^{35}S-methionine (specific activity: >1000 Ci/mmol; Amersham) were added to the commercially available TNT™ Coupled Reticulocyte Lysate System (Promega). Reactions were performed under conditions recommended by the manufacturer, with 1 exception: for all components, only a one-half volume was added to the PTT reaction (e.g., 12.5 μl TNT Rabbit Reticulocyte Lysate). After incubation of the complete reaction for 1.5 h at 30°C, 5 μl

of the reaction was added to 5 μl loading buffer (10% glycerol, 5% 2-mercaptoethanol, 2% SDS, and 0.1% bromphenol blue), and was heated for 5 min, then placed on ice. Samples were subjected to electrophoresis in a 14% SDS-polyacrylamide gel for 1.5–2 h at 40 mA (Rainbow ^{14}C methylated protein (Amersham) was used as a protein-weight marker). The gel was fixed in a solution of 40% methanol and 10% acetic acid and dried for 1.5 h at 80°C in a gel dryer. The synthesized polypeptides were visualized by means of a Phosphoimager (Molecular Dynamics) after the gel had been exposed overnight to a special film slide (Molecular Dynamics). On the basis of the determined fragment size, the positions of the mutations causing shortened polypeptides in the PTT were predicted and the presumably affected exons were sequenced from the patient DNA samples. Either the Thermo Sequenase kit (Amersham Life Science) and radioactive labeling were used for DNA sequencing or samples were analyzed on an ABI 377 PRISM DNA Sequencer by using the Big Dye terminator chemistry (see below).

TGGE

For TGGE analysis, the individual *NF1* exons were usually amplified directly from genomic DNA. For several exons, however, preamplification of a larger genomic fragment was necessary (see table 1) to improve specificity—that is, either to avoid coamplification of *NF1* pseudogenes or simply to relieve constraints of TGGE primer design. Final TGGE primers were chosen by using the programs MELT87 and SQHTX (Lerman and Silverstein 1987), which allow prediction of the impact of mutations on the melting behavior of the PCR products. Sequences containing two or more melting domains were split into several overlapping fragments. One or both oligonucleotides of each primer pair were 5′-modified with psoralen (table 2). Using two psoralen-modified primers in one reaction results in bipolar clamping of the fragments that may improve the sensitivity of mutation detection (Gille et al. 1998). For PCR, some 100 ng of genomic DNA (for the nested PCRs, 50 ng PCR product is required) were added to 25 μl standard Perkin Elmer PCR buffer containing 1.5 mM $MgCl_2$, 200 μM each dNTP, 0.2 μM each primer, and 0.5 U *Taq* polymerase. All reactions were performed on a Perkin Elmer thermocycler (model T1), under the following conditions: 95°C for 3 min; 35 amplification cycles of 95°C for 30 s, specific annealing temperature T_a (seetable 2) for 30 s, and 72°C for 50 s (final extension for 10 min). A commercially available apparatus was used for TGGE (Diagen GmbH, Germany). Prior to electrophoresis, the PCR products were placed directly under a portable UV light source (365 nm) for 15 min to permit cross-linking of the psoralen moiety to the thymine residues of the opposite DNA strand. For exons 2–49, TGGE was done on an 8% polyacrylamide gel with 8 M urea in 3–*N*-morpholino–propanesulfonic acid (MOPS) buffer. For exon 1, an 8% polyacrylamide gel with 7 M urea and 35% formamide in MOPS buffer was used. The individual running conditions for each exon are given intable 2. Silver staining was used for visualization of bands. Samples that showed altered mobility patterns were subjected to DNA sequencing, as described below. Alternatively, radioactive labeling and the Thermo Sequenase kit (Amersham Life Science) were used for sequencing.

DGS

For DGS-PCR, samples were cycled with a first activating step for HotStar*Taq* (Qiagen) at 95°C for 3 min. Primer sequences, fragment sizes, and annealing temperatures are given in table 3. Each cycle consisted of a denaturation step at 95°C for 90 s, annealing for 40 s (48°C to 65°C, see table 3) and an extension step for 1 min at 72°C. 35 cycles were performed in a 20-μl reaction volume on a 9700 thermal cycler (PE Applied Biosystems). PCR products were purified by using the PCR Product Purification Kit (Qiagen) according to the manufacturer's protocol. Cycle sequencing was performed in a 5-μl volume at 60°C with 25 cycles. Sequencing products were purified on Sephadex G-50-80 columns (Sigma) and analyzed on an ABI 377 automated DNA sequencer (PE Applied Biosystems).

Results

Synopsis of Mutation Screening

We analyzed 521 unrelated patients with NF1 by means of PTT, TGGE, or DGS for mutations in the whole coding sequence and the splice sites of the *NF1* gene. Twenty patients were included in both the PTT and the TGGE screening program. In total, we identified 301 sequence changes (table 4), 278 of which were considered pathogenic. The detection rates for the different methods were 40/85 (47.1%) for PTT, 65/121 (53.7%) for TGGE, and 184/335 (54.9%) for DGS. The mutations of 11 patients were identified independently by PTT as well as by TGGE. Among the 278 mutations identified, we observed 84 (30.2%) nonsense mutations and 140 (50.4%) frameshift mutations, comprising 78 deletions and 32 insertions of one or a few base pairs, as well as 30 out-of-frame exon skipping events. Thus, as many as 224 (80.6%) mutations caused, directly or indirectly, a premature termination codon (PTC). Another 25 (9.0%) of the mutations caused in-frame exon skipping. Furthermore, 28 (10.1%) missense mutations and one initiation codon mutation were also observed. Most mutations were found only once in any one pa-

Table 4

Summary of *NF1* Mutations and Sequence Variants Detected with PTT, TGGE, and DGS

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,e]	Mutation Type	Reference; NF1 Mutation Database No.
2318	Exon 1	T2C			M1T; initiation at M68, M102 or M108 (?)	(Missense); faulty initiation	This report
34	Exon 1	G26A	No		W9X	Nonsense	This report
650	Exon 1	G55T			E19X	Nonsense	This report
1852	Exon 2	C147G			Y49X	Nonsense	This report
348	Exon 2	C168T	Yes		S56S	Silent	This report
2732	Exon 2	C168T	Yes		S56S	Silent	This report
2938	Intron 2	204+1G→T		Skip of exon 2 (?)	In frame; −48 aa	Splice site	This report
710	Intron 2	204+2T→G		Skip of exon 2 (?)	In frame; −48 aa	Splice site	This report
1972	Intron 2	205−1G→A	No	Skip of exon 3 (?)	In frame; −28 aa	Splice site	This report
119	Exon 3	220delG			aa 74; PTC 84	1-bp deletion	This report
214	Exon 3	227insA			aa 76; PTC 106	1-bp insertion	This report
2170	Exon 4a	426delATTTT			aa 142−144; PTC 153	5-bp deletion	This report
2253	Exon 4b	T482A			L161X	Nonsense	This report
420	Exon 4b	496delGT			aa 166; PTC 172	2-bp deletion	Toliat et al. (1999); 844
461	Exon 4b	499delTGTT			aa 167-168; PTC 176	4-bp deletion	This report
1062	Exon 4b	499delTGTT			aa 167-168; PTC 176	4-bp deletion	This report
110	Exon 4b	499delTGTT			aa 167-168; PTC 176	4-bp deletion	Toliat et al. (1999); 843
U-36/375	Exon 4b	499delTGTT			aa 167-168; PTC 176	4-bp deletion	Toliat et al. (1999); 848
E13795	Exon 4b	499delTGTT			aa 167-168; PTC 176	4-bp deletion	Toliat et al. (1999)
E13332	Exon 4b	499delTGTT			aa 167-168; PTC 176	4-bp deletion	Toliat et al. (1999)
696	Exon 4b	527delA			aa 176; PTC 177	1-bp deletion	This report
1899	Exon 4b	T528A			D176E	(Missense); polymorphism	This report
2406	Exon 4b	T528A			D176E	(Missense); polymorphism	This report
190	Exon 4b	T528A			D176E	(Missense); polymorphism	Toliat et al. (1999); 545
702	Exon 4b	T528A			D176E	(Missense); polymorphism	Toliat et al. (1999); 849
422	Exon 4b	T539A			L180X	Nonsense	Toliat et al. (1999); 845
NF58a/124	Exon 4b	540insA		Unequal expression	aa 180; PTC 200	1-bp insertion	Däschner et al. (1997); 97-003
1559	Exon 4b	C574T	Yes		R192X	Nonsense	This report
380	Exon 4b	C574T	Yes	Unequal expression	R192X	Nonsense	Toliat et al. (1999); 847
1511	Intron 4b	586+1delG		Skip of exon 4b (?)	Out of frame; PTC 164	1-bp deletion; splice site	This report
3399	Intron 4b	586+1G→A	No	Skip of exon 4b (?)	Out of frame; PTC 164	Splice site	This report
U-76	Intron 4b	586+1G→A	No	Skip of exon 4b; unequal expression	Out of frame; PTC 164	Splice site	This report
2395	Exon 4c	T647C			L216P	Missense	This report
U-61	Intron 4c	655−2A→T		Skip of exon 5	Out of frame; PTC 255	Splice site	This report
314	Intron 4c	655−1G→A	No	Skip of exon 5	Out of frame; PTC 255	Splice site	Horn et al. (1996); 550
2048	Exon 5	703delTA			aa 235; PTC 240	2-bp deletion	This report
434	Exon 5	C715T	(Yes)		Q239X	Nonsense	Horn et al. (1996); 549
3358	Exon 6	754delT			aa 252; PTC 280	1-bp deletion	This report
2880	Exon 6	G801A	No		W267X	Nonsense	This report
1862	Exon 6	838delATAA			aa 280-281; PTC 293	4-bp deletion	This report
NF84a	Exon 6	887delA		Unequal expression	aa 296; PTC 316	1-bp deletion	This report
1008	Intron 6	888+1G→A	No	Skip of exon 6 (?)	Out of frame; PTC 261	Splice site	This report
3080	Intron 6	888+1G→A	No	Skip of exon 6 (?)	Out of frame; PTC 261	Splice site	This report
620	Intron 6	889−2A→G		Skip of exon 7	In frame; −58 aa	Splice site	Klose et al. (1999)
U-15	Exon 7	C910T*	Yes	Skip of exon 7; unequal expression	R304X; in frame; −58 aa	(Nonsense); splice error	Hoffmeyer et al. (1998), 0156

(*continued*)

Table 4 Continued

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,e]	Mutation Type	Reference; NF1 Mutation Database No.
2180	Exon 7	C910T*	Yes	Skip of exon 7 (?)	R304X; in frame; −58 aa	(Nonsense); splice error	This report
U-5	Exon 7	918delT		No exon skipping	aa 306; PTC 316	1-bp deletion	Hoffmeyer et al. (1998), 97-012
1815	Exon 7	918delT			aa 306; PTC 316	1-bp deletion	This report
1163	Exon 7	955delAG			aa 319; PTC 328	2-bp deletion	This report
3109	Exon 7	1019delCT			aa 340; PTC 351	2-bp deletion	This report
3293	Exon 7	1019delCT			aa 340; PTC 351	2-bp deletion	This report
737	Exon 7	1019delCT			aa 340; PTC 351	2-bp deletion	This report
750	Exon 7	A1060T			K354X	Nonsense	This report
448	Exon 7	G1062A	No	Skip of exon 7; unequal expression	K354K; inframe; −58 aa	(Silent); splice site	This report
2719	Intron 7	1062+67T→C		?	?	Splice error ?	This report
2239	Intron 7	1063−13G→A	No	?	?	Splice error ?	This report
2837	Exon 8	T1070C			L357P	Missense	This report
256	Exon 8	1111insT			aa 371; PTC 378	1-bp insertion	This report
NF172	Intron 8	1185+1G→A	No	Skip of exon 8; unequal expression	In frame;−41 aa	Splice site	Hoffmeyer et al. (1995); report w/o no.
59	Intron 8	1185+1G→T		Skip of exon 8	In frame;−41 aa	Splice site	Horn et al. (1996); 551
889	Intron 8	1185+3insTAAA		Skip of exon 8 (?)	In frame;−41 aa	4-bp insertion; splice site	This report
763	Exon 9	T1224G			Y408X	Nonsense	This report
U-51	Exon 9	C1246T	Yes		R416X	Nonsense	This report
NF56	Exon 9	C1246T	Yes	Unequal expression	R416X	Nonsense	This report
1994	Exon 9	C1246T	Yes		R416X	Nonsense	This report
2413	Exon 9	C1246T	Yes		R416X	Nonsense	This report
1023	Exon 9	1255delA			aa 419; PTC 472	1-bp deletion	This report
248	Exon 10a	G1275A	No		W425X	Nonsense	This report
U-65	Exon 10a	C1318T	Yes		R440X	Nonsense	This report
1138	Exon 10a	C1318T	Yes		R440X	Nonsense	This report
2349	Exon 10a	C1318T	Yes		R440X	Nonsense	This report
1571	Exon 10a	1338delA			aa 446; PTC 472	1-bp deletion	This report
E11034	Exon 10a	C1381T	Yes		R461X	Nonsense	This report
U-57	Exon 10b	1398insT			aa 466; PTC 469	1-bp insertion	This report
33	Exon 10b	1436insA			aa 479; PTC 490	1-bp insertion	This report
2788	Exon 10b	A1466G		Skip of the 3′ end of Exon 10b (?)	Y489C; out of frame; PTC 489	(Missense); splice error	This report
250	Exon 10b	A1472G			Y491C	Missense	This report
936	Exon 10b	A1472G			Y491C	Missense	This report
1917	Exon 10b	1484delCC			aa 495; PTC 509	2-bp deletion	This report
2859	Exon 10b	1519insT			aa 507; PTC 509	1-bp insertion	This report
1288	Intron 10b	1527+1delG		Skip of exon 10b (?)	In frame; −45 aa	1-bp deletion; splice site	This report
22	Exon 10c	1541delAG			aa 514; PTC 556	2-bp deletion	Robinson et al. (1996); 544
190	Exon 10c	1541delAG		No exon skipping	aa 514; PTC 556	2-bp deletion	Robinson et al. (1996); 545
535	Exon 10c	1541delAG			aa 514; PTC 556	2-bp deletion	This report
1169	Exon 10c	1546delC			aa 516; PTC 525	1-bp deletion	This report
2243	Intron 10c	1641+1G→T		Skip of exon 10c (?)	In frame; −38 aa	Splice site	This report
3918	Intron 10c	1642−8A→G		Exon 11 enlarged by 7 bp (?)	Out of frame; PTC 559 (?)	Splice error	This report
1003	Exon 11	T1646C			L549P	Missense	This report
279	Exon 11	G1721C		Skip of exon 11 (?)	S574T; out of frame; PTC 560	(Missense); splice site	This report
945	Exon 11	G1721A	No	Skip of exon 11 (?)	S574N; out of frame; PTC 560	(Missense); splice site	This report
1070	Intron 11	1721+3A→G		Skip of exon 11 (?)	Out of frame; PTC 560	Splice site	This report
1377	Intron 11	1721+3A→G		Skip of exon 11 (?)	Out of frame; PTC 560	Splice site	This report
3855	Exon 12a	T1742C			1581T	Missense	This report

(*continued*)

Table 4 Continued

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,c]	Mutation Type	Reference; NF1 Mutation Database No.
1584	Exon 12a	A1748G			K583R	Missense	This report
1700	Exon 12a	A1748G			K583R	Missense	This report
3853	Exon 12a	1756delACTA			aa 586-587; PTC 603	4-bp deletion	This report
2869	Exon 12a	1817insT			aa 606; PTC 609	1-bp insertion	This report
753	Intron 12a	1845+1delGTAAG		Skip of exon 12a (?)	Out of frame; PTC 589	5-bp insertion; splice site	This report
2273	Exon 12b	1935delG			aa 645; PTC 687	1-bp deletion	This report
2760	Exon 12b	C1994T	No		S665F	Missense	This report
NF92	Exon 12b	1998insCCTCT			aa 666; PTC 689	5-bp insertion	Böddrich et al. (1995); 546
2889	Exon 13	2027delC			aa 676; PTC 687	1-bp deletion	This report
3259	Exon 13	2027insC			aa 676; PTC 699	1-bp insertion	This report
NF176	Exon 13	2033insC		Unequal expression	aa 678; PTC 699	1-bp insertion	97-014
212	Exon 13	C2041T*	Yes		R681X	Nonsense	This report
666	Exon 13	C2041T*	Yes		R681X	Nonsense	This report
2052	Exon 13	C2041T*	Yes		R681X	Nonsense	This report
3806	Exon 13	C2041T*	Yes		R681X	Nonsense	This report
2296	Exon 13	C2076G			Y692X	Nonsense	This report
1982	Exon 13	T2084C			L695P	Missense	This report
4132	Exon 13	2190delCCTCT			aa 730-732; PTC 734	5-bp deletion	This report
520	Intron 13	2252−31A→T				Polymorphism	This report
E11225	Intron 13	2252−31A→T		No exon skipping		Polymorphism	This report
E13339	Intron 13	2252−31A→T				Polymorphism	This report
168	Exon 14	2272delAG			aa 758; PTC 766	2-bp deletion	552
173	Exon 14	T2288C			L763P	Missense	553
66	Exon 15	G2330C			W777S	Missense	This report
640	Exon 15	C2339A			T780K	Missense	554
1137	Exon 15	A2342C			H781P	Missense	This report
U-55	Exon 15	C2356T	No		Q786X	Nonsense	This report
1624	Exon 16	2427insGTCTT/2430delG			aa 810; PTC 815	Insertion/deletion	This report
U-62	Exon 16	C2446T	Yes	No exon skipping; equal expression	R816X	Nonsense	This report
1551	Exon 16	C2446T	Yes		R816X	Nonsense	This report
2746	Exon 16	C2446T	Yes		R816X	Nonsense	This report
942	Exon 16	T2540C			L847P	Missense	This report
NF213	Exon 16	2590insTATA		Unequal expression	aa 864; PTC 865	4-bp insertion	Report w/o no.
2332	Exon 16	2666delC			aa 889; PTC 901	1-bp deletion	This report
633	Exon 16	2674delA			aa 892; PTC 901	1-bp deletion	This report
626	Exon 16	C2842T	No		Q948X	Nonsense	This report
1031	Exon 16	2844delA			aa 948; PTC 953	1-bp deletion	This report
3212	Exon 16	2845insT			aa 949; PTC 955	1-bp insertion	This report
2803	Exon 16	2850insTT			aa 950; PTC 954	2-bp insertion	This report
1742	Exon 17	2970delAAT			aa 990-991; 991delM	3-bp deletion	This report
E13563	Exon 17	2970delAAT			aa 990-991; 991delM	3-bp deletion	This report
NF183	Exon 17	2972insT		Unequal expression	aa 991; PTC 1020	1-bp insertion	97-013
U-88	Intron 17	2991−2A→G		Skip of exon 18; equal expression	In frame; −41 aa	Splice site	This report
646	Intron 17	2991−1G→A	No	Skip of exon 18; equal expression	In frame; −41 aa	Splice error	This report
U-27/507	Intron 17	2991−1G→C		Skip of exon 18; equal expression	In frame; −41 aa	Splice site	This report
3365	Exon 18	T2994A			Y998X	Nonsense	This report
858	Exon 18	3060delA			aa 1020; PTC 1021	1-bp deletion	This report
223	Exon 19a	3178delG			aa 1060; PTC 1061	1-bp deletion	This report
NF23	Exon 19a	3193insA			aa 1065; PTC 1087	1-bp insertion	Klose et al. (1998*c*); 440
1572	Exon 20	3394insAG			aa 1132; PTC 1142	2-bp insertion	This report
3400	Exon 20	3456delACTC			aa 1152-1153; PTC 1156	4-bp deletion	This report

(*continued*)

Table 4 Continued

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,e]	Mutation Type	Reference; NF1 Mutation Database No.
255	Exon 20	3456delACTC			aa 1152-1153; PTC 1156	4-bp deletion	This report
460	Exon 20	3456delACTC			aa 1152-1153; PTC 1156	4-bp deletion	This report
3809	Exon 20	A3467G*			N1156S	Missense	This report
520	Intron 20	3496+2T→C		Skip of exon 20	Out of frame; PTC 1133	Splice site	Klose et al. (1998*c*); 444
1747	Exon 21	3525delAA			aa 1175-1176; PTC 1193	2-bp deletion	This report
2861	Exon 21	3525delAA			aa 1175-1176; PTC 1193	2-bp deletion	This report
3340	Exon 21	G3628T			E1210X	Nonsense	This report
878	Exon 21	3643delATG			1215delM	3-bp deletion	This report
2340	Exon 21	G3707A	No		W1236X	Nonsense	This report
742	Exon 22	C3721T*	Yes	No exon skipping	R1241X	Nonsense	This report
2266	Exon 22	3737delTGTT			aa 1246-1247; PTC 1264	4-bp deletion	This report
1528	Exon 22	G3749C			R1250P	Missense	This report
76	Exon 22	G3773A	(Yes)		W1258X	Nonsense	This report
51	Exon 22	3822delCT			aa 1274-1275; PTC 1282	2-bp deletion	This report
1186	Exon 22	C3826T*	Yes		R1276X	Nonsense	This report
157	Exon 22	C3826T*	Yes		R1276X	Nonsense	Klose et al. (1998*b*); 441
U-63	Exon 22	C3826T*	Yes		R1276X	Nonsense	This report
1899	Exon 22	G3827A	Yes		R1276Q	Missense	This report
1939	Exon 22	G3827A	Yes		R1276Q	Missense	This report
364	Exon 22	G3827C		No exon skipping	R1276P	Missense	Klose et al. (1998*a*); 442
288	Exon 22	C3831T	No		G1277G	Silent	This report
2235	Exon 23-1	3909dclT			aa 1303; PTC 1308	1-bp deletion	This report
578	Exon 23-1	3911dclT			aa 1304; PTC 1308	1-bp deletion	This report
258	Exon 23-1	C3916T	Yes	"CpG, RNA editing site"	R1306X	Nonsense	This report
2601	Exon 23-1	C3916T	Yes	"CpG, RNA editing site"	R1306X	Nonsense	This report
71	Exon 23-1	C3916T	Yes	"CpG, RNA editing site"	R1306X	Nonsense	This report
3979	Exon 23-1	C3916T	Yes	"CpG, RNA editing site"	R1306X	Nonsense	This report
82	Intron 23-1	3975−2A→G		Skip of exon 23-2; equal expression	Out of frame; PTC 1339	Splice site	This report
796	Exon 23-2	C4006T	(Yes)		Q1336X	Nonsense	This report
471	Exon 23-2	4016delT			aa 1339; PTC 1342	1-bp deletion	This report
206	Exon 23-2	C4084T	Yes	No exon skipping	R1362X	Nonsense	This report
415	Exon 23-2	C4084T	Yes		R1362X	Nonsense	This report
E13562	Intron 23-2	4110+1G→C		Skip of exon 23-2; unequal expression	Out of frame; PTC 1339	Splice site	This report
U-19	Exon 24	G4243T			E1415X	Nonsense	This report
1765	Exon 24	4247ins74-bp from intron 25			aa 1416; PTC 1422	74-bp insertion	This report
895	Exon 25	T4274C			L1425P	Missense	This report
219	Exon 25	T4274C			L1425P	Missense	Peters et al. (1999*a*)
278	Exon 25	4311delAGAA			aa 1437-1438; PTC 1446	4-bp deletion	This report
238	Intron 25	4368−46G→C				rare variant	This report
333	Intron 25	4368−1G→T		Skip of exon 26	In frame; −49 aa	Splice site	This report
3745	Exon 26	4374insT			aa 1459; PTC 1460	1-bp insertion	This report
1517	Exon 26	4431delC			aa 1477; PTC 1478	1-bp deletion	This report
U-77	Exon 26	G4473A	No		W1491X	Nonsense	This report
31	Exon 26	4486delA			aa 1496; PTC 1552	1-bp deletion	This report
U-66	Exon 26	4497insG			aa 1499; PTC 1508	1-bp insertion	This report
831	Intron 26	4514+1G→A	No	Skip of exon 26 (?)	In frame; −49 aa	Splice site	This report
2928	Intron 26	4515−2A→G		Skip of exon 27a (?)	In frame; −49 aa	Splice site	This report
U-39	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report
U-40	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report
401	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report

(*continued*)

Table 4 Continued

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,c]	Mutation Type	Reference; NF1 Mutation Database No.
740	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report
2488	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report
2713	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report
2789	Exon 27a	C4537T*	Yes		R1513X	Nonsense	This report
U-87a	Exon 27a	G4614A	No		W1538X	Nonsense	This report
966	Exon 27a	4649insG			aa 1550; PTC 1554	1-bp insertion	This report
U-29	Exon 27b	4703delC			aa 1558; PTC 1569	1-bp deletion	This report
1784	Exon 27b	C4719G			Y1573X	Nonsense	This report
2646	Exon 27b	A4750G			11584V	Missense	This report
486	Exon 28	T4839G		No exon skipping; unequal expression	Y1613X	Nonsense	Peters et al. (1999*b*); 97-001
3696	Exon 28	4936insT			aa 1646; PTC 1660	1-bp insertion	This report
56	Exon 28	5050delAGGCTTG			aa 1684-1686; PTC 1686	7-bp deletion	This report
102	Exon 28	5055insT			aa 1686; PTC 1696	1-bp insertion	Peters et al. (1999*b*); 450
345	Exon 28	A5106G			Q1702Q	Silent	Peters et al. (1999*b*)
734	Exon 28	5152delG			aa 1718; PTC 1725	1-bp deletion	This report
B-212	Exon 28	5168delTC			aa 1723; PTC 1734	2-bp deletion	Peters et al. (1999*b*); 842
342	Exon 28	G5172A	No		K1724K	Silent	Peters et al. (1999*b*)
186	Exon 28	G5172A	No		K1724K	Silent	Peters et al. (1999*b*)
B-250	Exon 28	5205delAGTAA		Skip of exon 28 (?)	Out of frame; PTC 1599	5-bp deletion; splice site	Peters et al. (1999*b*); 97-002
1218	Exon 29	C5242T	Yes		R1748X	Nonsense	This report
2886	Exon 29	C5242T	Yes		R1748X	Nonsense	This report
U-34/40	Exon 29	C5242T	Yes	No exon skipping	R1748X	Nonsense	Peters et al. (1999*b*); 97-011
68	Exon 29	5248delAAA			1750delK	3-bp deletion	This report
1079	Exon 29	T5286G			Y1762X	Nonsense	This report
388	Exon 29	C5329T	(Yes)		Q1777X	Nonsense	This report
528	Exon 29	T5339A			L1780X	Nonsense	This report
1698	Exon 29	T5339A			L1780X	Nonsense	This report
3443	Exon 29	C5353T	(Yes)		Q1785X	Nonsense	This report
1038	Exon 29	5399delT			aa 1800; PTC 1841	1-bp deletion	This report
63	Exon 29	C5458T	No		Q1820X	Nonsense	Peters et al. (1999*b*); 97-010
3344	Exon 29	5484delT			aa 1828; PTC 1841	1-bp deletion	This report
U-25/702	Exon 29	G5546A	Yes	Skip of exon 29	R1849Q; Out of frame; PTC 1740	(Missense); splice site	This report
1990	Exon 29	G5546A	Yes	Skip of exon 29 (?)	R1849Q; Out of frame; PTC 1740	(Missense); splice site	This report
2191	Intron 29	5546+1G→A	(Yes)	Skip of exon 29 (?)	Out of frame; 1740	Splice site	This report
NF113	Intron 29	5546+2T→G		Skip of exon 29; unequal expression	Out of frame; PTC 1740	Splice site	report w/o no.
1164	Exon 30	5584delAC			aa 1862; PTC 1863	2-bp deletion	This report
527	Exon 30	5592delTTTAA			aa 1864-1866; PTC 1889	5-bp deletion	Harder et al. ((1999)); 439
224	Exon 31	C5839T	Yes		R1947X	Nonsense	Klose et al. (1999); 437
1197	Exon 31	C5839T	Yes		R1947X	Nonsense	This report
2672	Exon 31	C5839T	Yes		R1947X	Nonsense	This report
394	Exon 31	5847delAG			aa 1949-1950; PTC 1954	2-bp deletion	This report
2097	Intron 31	5943+1G→A	No	Skip of exon 31 (?)	Out of frame; PTC 1922	Splice site	This report

(*continued*)

Table 4 Continued

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,c]	Mutation Type	Reference; NF1 Mutation Database No.
472	Intron 31	5944−5A→G		Skip of exon 32 (?)	In frame; −47 aa	Splice site	This report
1215	Intron 31	5944−2A→G		Skip of exon 32 (?)	In frame; −47 aa	Splice site	This report
2369	Exon 33	6220delG			aa 2074; PTC 2089	1-bp deletion	This report
2774	Exon 34	6468delC			aa 2156; PTC 2178	1-bp deletion	This report
608	Exon 34	6470delT			aa 2157; PTC 2178	1-bp deletion	This report
2912	Exon 34	6471delC			aa 2157; PTC 2178	1-bp deletion	This report
16	Exon 34	T6566A			L2189X	Nonsense	This report
U-64	Intron 34	6579+2T→G		Skip of exon 34; unequal expression	Out of frame; PTC 2148	Splice site	This report
1126	Intron 34	6579+45T→A		?	?	Splice error ?	This report
514	Intron 34	6579+87G→A	No	?	?	Splice error ?	This report
2086	Exon 35	6604delT			aa 2202; PTC 2211	1-bp deletion	This report
234	Exon 35	G6628T			E2210X	Nonsense	This report
3568	Intron 35	6641+2delT		Skip of exon 35 (?)	Out of frame; PTC 2199	1-bp deletion; splice site	This report
2406	Intron 35	6642-1G→T		Skip of exon 36 (?)	Out of frame; PTC 2220	Splice site	This report
1832	Exon 36	C6709T	Yes		R2237X	Nonsense	This report
U-67/572	Exon 36	C6709T	Yes		R2237X	Nonsense	This report
3634	Exon 36	C6709T	Yes		R2237X	Nonsense	This report
952	Intron 36	6756+1G→A	No	Skip of exon 36 (?)	Out of frame; PTC 2220	Splice site	This report
NF33	Exon 37	6789delTTAC			aa 2263-2264; PTC 2268	4-bp deletion	Hoffmeyer et al. (1998)
U116	Exon 37	6789delTTAC		No exon skipping	aa 2263-2264; PTC 2268	4-bp deletion	Robinson et al (1995); 543
342	Exon 37	6789delTTAC		No exon skipping; equal expression	aa 2263-2264; PTC 2268	4-bp deletion	Böddrich et al. (1997); 547
1706	Exon 37	6789delTTAC			aa 2263-2264; PTC 2268	4-bp deletion	This report
3467	Exon 37	6789delTTAC			aa 2263-2264; PTC 2268	4-bp deletion	This report
407	Exon 37	6790insTT		No exon skipping; equal expression	aa 2264; PTC 2270	2-bp insertion	Böddrich et al. (1997); 548
1354	Exon 37	6791insA			aa 2264; PTC 2285	1-bp insertion	This report
25	Exon 37	C6792A		Skip of exon 37; equal expression	Y2264X; in frame; −34 aa	(Nonsense); splice error	Robinson et al. (1995); 541
1	Exon 37	C6792A		Skip of exon 37; equal expression	Y2264X; in frame; −34 aa	(Nonsense); splice error	Robinson et al. (1995); 542
E11225	Exon 37	C6792A		Skip of exon 37; equal expression	Y2264X; in frame; −34 aa	(Nonsense); splice error	This report
1828	Exon 37	C6792G		Skip of exon 37 (?)	Y2264X; in frame; −34 aa	(Nonsense); splice error	This report
2472	Exon 37	6792insA			aa 2265; PTC 2285	1-bp insertion	This report
U-43/547	Exon 37	6797delGT		No exon skipping	aa 2266; PTC 2284	2-bp deletion	This report
1920	Exon 37	T6839G			L2280X	Nonsense	This report
3110	Exon 39	7080insA			aa 2361; PTC 2364	1-bp insertion	This report
3578	Exon 39	7095delT			aa 2365; PTC 2374	1-bp deletion	This report
E15470	Exon 40	7208delGA			aa 2403; PTC 2405	2-bp deletion	This report
260	Exon 40	C7237T	(Yes)		Q2413X	Nonsense	This report
61	Exon 40	G7258C		Skip of exon 40 (?)	A2420P; in frame; −44 aa	(Missense); splice site	This report
B-214	Intron 40	7259−17C→T	No	?	?	Splice error?	841
B-212	Intron 40	7259−14C→T	Yes			rare variant	842
400	Exon 41	7268delCA			aa 2423; PTC 2425	2-bp deletion	This report
3541	Exon 41	7285delC			aa 2429; PTC 2434	1-bp deletion	This report
1777	Exon 41	C7285T	Yes		R2429X	Nonsense	This report
E14377	Exon 41	C7285T	Yes		R2429X	Nonsense	This report
E14071	Exon 41	7367delCC			aa 2456; PTC 2460	2-bp deletion	This report
395	Intron 41	7395−1G→A	(Yes)	Skip of exon 42 (?)	Out of frame; PTC 2471	Splice site	850
U-20/9723	Exon 42	CT7424AG			S2475X	Nonsense	This report
1000	Exon 42	C7457T	No		T24861	Missense	This report
934	Exon 42	C7486T	Yes		R2496X	Nonsense	This report
2717	Exon 42	C7486T	Yes		R2496X	Nonsense	This report

(*continued*)

Table 4 Continued

Patient[a]	Location	Sequence Change[b]	CpG[c] (CpNpG)	RNA Level[d]	Protein Level[d,e]	Mutation Type	Reference; NF1 Mutation Database No.
U-46	Exon 42	7528ins1 bp		Duplication of bases 7515-7528	aa 2510; PTC 2531	14-bp insertion	This report
698	Exon 42	7544insGA			aa 2515; PTC 2527	2-bp insertion	This report
2714	Exon 43	7569delT			aa 2523; PTC 2526	1-bp deletion	This report
1675	Exon 43	7633insC			aa 2545; PTC 2555	1-bp insertion	This report
U-87b	Exon 44	C7699T	No		Q2567X	Nonsense	This report
2253	Exon 44	A7701G			Q2567Q	Silent	This report
90	Exon 44	C7702T	(Yes)		Q2568X	Nonsense	This report
2973	Exon 44	C7702T	(Yes)		Q2568X	Nonsense	This report
2569	Exon 45	C7846T	Yes		R2616X	Nonsense	This report
383	Intron 45	7907+1G→A	No	Skip of exon 45	Out of frame; PTC 2604	Splice site	*555*
735	Intron 45	7908-2A→G		Skip of exon 46 (?)	Out of frame; PTC 2640	Splice site	This report
1480	Exon 46	7926insT			aa 2643; PTC 2643	1-bp insertion	This report
2499	Exon 46	8024delC			aa 2675; PTC 2717	1-bp deletion	This report
578	Intron 46	8050+20A→G		No exon skipping		Polymorphism	This report
586	Intron 46	5080+20A→G				Polymorphism	This report
U-82/310	Exon 47	8092insTT			aa 2698; PTC 2718	2-bp insertion	This report

[a] The same patient may have different ID numbers because some patients were included in both the PTT and the TGGE screening panels. Some patients appear twice in the list because two separate sequence changes were identified (see table 5).

[b] Numbering system based on *NF1* cDNA (Genbank M82814), 1 = first base of methionine (ATG) at start of cDNA. The asterisk indicates congruence to *NF1* pseudogene sequences: C910T to D26141/AC004527 (#21); C2041T to U35696 (#14); A3467G, C3721T, C3826T, and C4537T to M84131 (#15).

[c] All G→A and C→T transitions were checked to see whether they occurred in a CpG or a CpNpG motif. In the latter case, "yes" was put in parentheses.

[d] A question mark in parentheses means "predicted but not tested." A question mark without parentheses means "highly speculative" and that the underlying mutations were not considered pathogenic.

[e] In the case of frameshift mutations, the affected amino acid (aa) positions are given, as well as the position of the premature termination codon (PTC) in the predicted aberrant polypeptide. In the case of in-frame deletions caused by exon skipping, the number of amino acids (aa) expected to be lost in the predicted aberrant polypeptide is given.

tient. The total number of different mutations identified was 216. Among the recurrent mutations, the three most common were R1513X in exon 27a (7 patients), 499delTGTT in exon 4b (6 patients), and 6789delTTAC in exon 37 (five patients). Furthermore, we found that 216 of our mutations, of which 179 were different, were not listed in the most recent review in the field (Upadhyaya and Cooper 1998). Overall, the total number of different minor lesion mutations of the *NF1* gene described to date well exceeds 276, because 97 other mutations of this type have been published before (Upadhyaya and Cooper 1998) and some more unpublished mutations have been reported to the International NF1 Genetic Analysis Consortium.

Distribution of NF1 Mutations

To get an idea of their distribution over the *NF1* gene, we plotted the 278 pathogenic mutations exon by exon into a diagram (fig. 1). Intronic mutations were allocated to the nearest exon. Direct comparison with the 173 minor lesions that had been reported to the International NF1 Genetic Analysis Consortium by November 1997 (Korf 1998) (white columns in fig. 1) underscores the strong bias towards central parts of the *NF1* gene inherent in these data. In particular, exons 28–36—the 9 exons that were described first (Cawthon et al. 1990)—and the GRD region were analyzed in hundreds of NF1 patients by the consortium members, whereas exons of other regions, mainly at the 5′ end of the gene, were not investigated at all. In our study, all parts of the gene were analyzed with equal intensity. Thus, we suppose our data to be an approximate representation of the actual distribution of mutations over the *NF1* gene, at least in our study population, which is mainly of German origin, but includes also some patients of Turkish extraction. As indicated by figure 1, it appears likely that all regions of the *NF1* gene are subject to mutation to a similar extent. However, if data are weighed for exon size (fig. 2*a*), exons 4b and 37 stand out as sites of a remarkably high mutation density. The reason for this may be found in some structural elements prone to mutation, a short tandem repeat structure in exon 4b (Toliat et al. 1999) and a quasisymmetric element in exon 37 (Robinson et al. 1995; Böddrich et al. 1997).

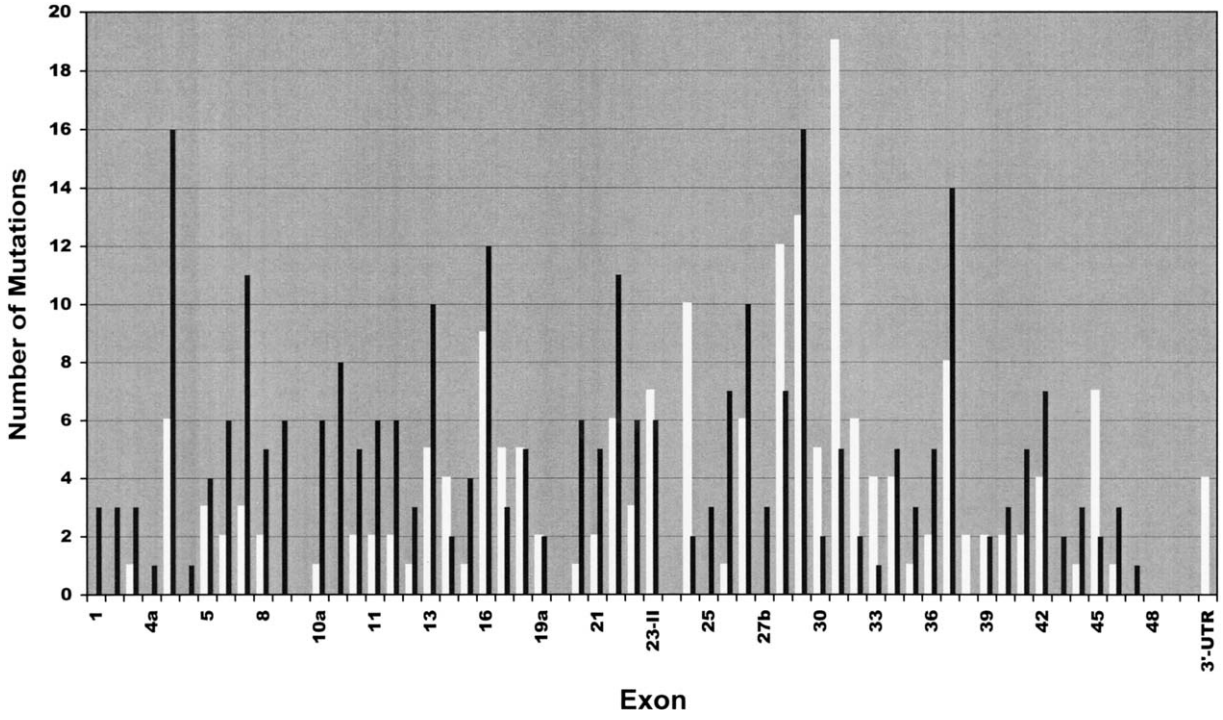

Figure 1 Histogram of number of mutations, exon by exon. Black columns represent the 278 pathogenic mutations of table 4. White columns represent the mutations reported to the NF1 Genetic Analysis Consortium as of November 1997 (Korf 1998).

If presented in a logarithmic mode (fig. 2*b*), the data reveal a slight tendency to fewer mutations towards the 3′ end of the gene that may be caused by the distribution of the missense mutations, as discussed later. Furthermore, several exons are easily recognized in which no mutation was found (exons 9br, 19b, 23a, 38, and 48–49) or that are extremely underrepresented (exons 4a and 33).

Cryptic Splice Mutations

We identified a total of 55 splicing-error mutations (19.8% of all the mutations we found). In 22 cases, an exon skip was revealed in the patients' mRNA. Several mutations were found to affect the splicing process, although they do not pertain to the group of typical splice-site mutations. At first glance, many of these were interpreted as faults, but analysis of mRNA as part of the PTT made us aware of the problem, and we initiated a routine checking of mRNA in all ambiguous cases (if mRNA was available). As reported elsewhere (Hoffmeyer et al. 1998), the two nonsense mutations (R304X and Y2264X) result in a skipping of exons 7 and 37, respectively. The mutation Y2264X may be caused by either of two transversions, C6792A or C6792G, both of which result in skipping of exon 37 (Messiaen et al. 1997). Five other nonsense mutations, as well as six small deletions or insertions, were also tested thoroughly, but did not show any influence on the splicing process (see table 4). However, in addition to the nonsense mutations, we identified a silent mutation (K354K) and several missense mutations (Y489C, S574T, S574N, R1849Q, and A2420P) that also cause exon skipping, presumably or definitely (see table 4). Most of these mutations affect the last base of the exon that is part of the splice donor and is usually a guanine (Krawczak et al. 1992). Messiaen et al. (1998) reported that mutation Y489C generates a new splice donor converting the 3′ end of exon 10b into an intronic sequence that is subsequently removed during splicing as part of intron 10b. The mutation Y491C might act in the same manner; however, no mRNA was available to test this possibility.

Two Sequence Changes

All 60 exons were analyzed in all patients; therefore, multiple sequence changes should have been identified if present. In addition to the known biallelic polymorphisms in exons 5 (702A/G) and 13 (2034G/A) and those in introns 28 (5205+23C/T) and 41 (7395-29A/G), we identified three novel biallelic polymorphisms: 1528-29delT, 1641+39C/T, and 3315-130G/C (located in introns 10b, 10c, and 19b, respectively) with allele frequencies higher than 30% for both alleles. The frequent

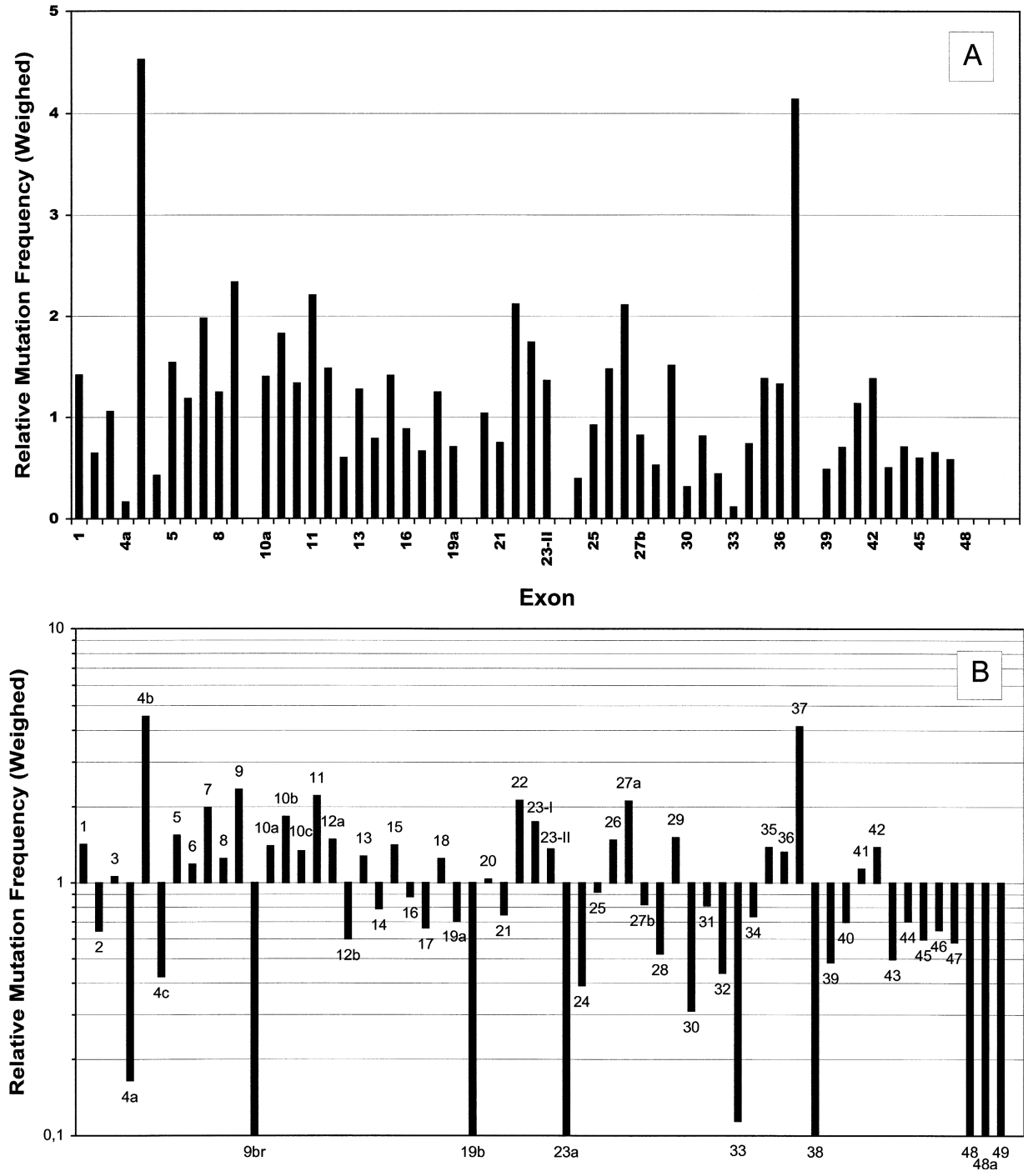

Figure 2 Weighed distribution of mutations over the *NF1* gene. For each exon, the number of pathogenic mutations was divided by the number of base pairs (bp). Ten bp were added to each exon, to allow for splice-site mutations. Values shown are ratios between the exon-specific mutation densities and the average mutation density for the whole gene (278/9,204 bp). *A*, linear presentation. *B*, logarithmic presentation.

polymorphisms were not taken into account when looking for additional sequence changes in the *NF1* gene, yet two rare sequence changes were found in 10 of the patients (table 5). Determining which change is pathogenic is straightforward if a truncating mutation is observed among them; however, the occurrence of two pathogenic mutations is possible. We tested the mutations 2252-31A→T and 8050+20A→G for their influence on the

Table 5

Patients with Two Sequence Changes in the *NF1* Gene

Patient	First Sequence Change, Nonpathogenic	Second Sequence Change, Pathogenic
1899	T528A = D176E (exon 4b)	G3827A = R1276Q (exon 22)
2406	T528A = D176E (exon 4b)	6642-1G→T (intron 35)
190	T528A = D176E (exon 4b)	1541delAG (exon 10c)
702 = U-25	T528A = D176E (exon 4b)	G5546A = R1849Q (skip of exon 29)
520	2252-31A→T (intron 13)	3496+2T→C (intron 20)
E11225	2252-31A→T (intron 13)	C6792A = Y2264X (skip of exon 37)
342	G5172A = K1724K (exon 28)	6789del4bp (exon 37)
B-212	7259-14C→T (intron 40)	5168delTC (exon 28)
2253	A7701G = Q2567Q (exon 44)	T482A = L161X (exon 4b)
578	8050+20A→G (intron 46)	3911delT (exon 23-1)

splicing process, but no exon skipping was observed. In the case of patient 1899, a choice between two missense mutations, D176E and R1276Q, was necessary; the position of the latter gives a helpful hint. Arg1276 is the arginine finger of the GRD—the most essential catalytic element for RasGAP activity. Its mutation into proline was shown to completely disable GAP activity without impairing the secondary and tertiary protein structure (Klose et al. 1998*a*). Mutation R1276Q compromises GAP-stimulated GTP hydrolysis some 500-fold (Ahmadian et al. 1997). Compared with the 8,000-fold reduction by mutation R1276P (Klose et al. 1998*a*), this is still a remarkable residual activity. However, it may be sufficient to cause NF1, because other missense mutations of the GRD with moderate reduction of GAP activity have already been reported (Kim and Tamanoi 1998). It is tempting to speculate about a modifying effect of D176E on the NF1 phenotype. This might occur in *cis* as well as *trans* to another missense mutation or in *trans* to any other pathogenic mutation. In the instance of patient 1899, it is not known whether D176E and R1276Q are situated on the same allele or on different alleles. In the other three cases, both sequence changes cosegregate; that is, D176E is in *cis* to a truncating mutation, with little or no chance of exerting an effect on the phenotype because of the absence of the mutant gene product normally observed with this type of mutation (Hoffmeyer et al. 1995). Recently, we analyzed the unaffected father of patient 702, who is a sporadic case himself. Because the father is also a carrier of D176E, we were able to determine that this amino acid exchange alone is not sufficient to cause NF1.

CpG Mutations

CpG dinucleotides show a high mutation rate in the human genome caused by spontaneous deamination of 5-methylcytosine; ~25% of all single base-pair substitutions involve this dinucleotide (Cooper and Krawczak 1993). In the coding region of the *NF1* gene, there are 118 CpGs, and a C→T transition on either the coding or noncoding strand of 91 of these would result in a disease-related mutation (Krkljus et al. 1997). Methylation of CpGs is a prerequisite for this type of mutation. Interestingly, methylated CpGs have been reported to occur within and around the *NF1* gene; for example, 92% of CpGs in exons 28, 29, and 31 were found to be methylated in sperm DNA (Rodenhiser et al. 1993; Andrews et al. 1996). This prompted us to check our data for typical CpG mutations. Among the 301 sequence changes, we identified 57 (18.9%) C→T or G→A transitions within a CpG dinucleotide (table 4). The 301 sequence changes include 181 single base-pair substitutions, and only 31.5% of these represent a typical CpG mutation. Twenty-one different CpGs from the coding region are involved; that is, 17.8% of the 118 CpGs present in the coding region. They include 1 silent, 2 missense, and 18 nonsense mutations. One of these CpG mutations, R1513X, is the most frequently observed recurrent mutation among all 278 mutations. In addition to CpGs, we identified 9 CpNpG motifs that were subject to a C→T or G→A transition in 10 patients. Although DNA methylation at these sites has also been reported (Clark et al. 1995), it is evident from our data that they do not play a significant role in *NF1* mutagenesis.

Relations to Pseudogene Variants

Genetic variation within pseudogenes may serve as a template for pathological lesions in the original gene by means of gene conversion even if located on different chromosomes (Eikenboom et al. 1994). In view of the large number of *NF1* pseudogenes, it has been hypothesized that they are reservoirs of preformed mutations and may account for the high mutation rate of the *NF1* gene (Cummings et al. 1993). Therefore, we analyzed all *NF1*-like sequences available from the public databases for any sequence deviation from the authentic *NF1* gene. We located 31 entries (table 6) and identified 235 discrepancies (of which 196 were different) between the

Table 6

***NF1* Pseudogene Sequences in the Public Databases**

Accession Number	Exons	Chromosome	Reference
AC004527	7–9	21	R. B. Weiss et al.,[a] unpublished data
D26141	7–11	21	H. Suzuki, unpublished data
U35688	8	18	Purandare et al. (1995)
U35689	9	18	Purandare et al. (1995)
U35696	13	18	Purandare et al. (1995)
YO7853	13–15	17	Régnier et al. (1997)
YO7854	13–15	14	Régnier et al. (1997)
YO7855	13–15	14	Régnier et al. (1997)
YO7856	13–15	15	Régnier et al. (1997)
YO7857	13–15	15	Régnier et al. (1997)
YO7858	13–15	2	Régnier et al. (1997)
YO7859	13–15	22	Régnier et al. (1997)
AF011743	14	15q11.2	Kehrer-Sawatzki et al. (1997)
AF011744	15	15q11.2	Kehrer-Sawatzki et al. (1997)
AF011746	15	15q11.2	Kehrer-Sawatzki et al. (1997)
U35684	15	14	Purandare et al. (1995)
U35685	15	15	Purandare et al. (1995)
U35686	16	12	Purandare et al. (1995)
U35687	16	14	Purandare et al. (1995)
U35690	18	14	Purandare et al. (1995)
U35691	18	15	Purandare et al. (1995)
U35692	18	22	Purandare et al. (1995)
U35693	19b	15	Purandare et al. (1995)
M84131	20–22	15	Legius et al. (1992)
AF011748	21	15q11.2	Kehrer-Sawatzki et al. (1997)
U35694	23-1	15	Purandare et al. (1995)
U35695	24	15	Purandare et al. (1995)
AF011745	24	15q11.2	Kehrer-Sawatzki et al. (1997)
AF011747	24	15q11.2	Kehrer-Sawatzki et al. (1997)
AF011749	24	15q11.2	Kehrer-Sawatzki et al. (1997)
X72619	24	15q24-qter	Gasparini et al. (1993)
M84131	25–27b	15	Legius et al. (1992)

[a] Unpublished data from R. B. Weiss, D. M. Dunn, A. Aoyagi, L. Banks, B. Duval, C. Hamil, C. Holmes, M. Mahmoud, R. Rose, R. Stokes, M. D. Stump, P. Yu, L. Zhou, Y. Gitin, J. Nelson, and A. von Niederhausen.

sequences of the pseudogenes and the *NF1* gene (not shown). Only 6 (3.1%) of the 196 pseudogene variations were also found among the *NF1* mutations in table 4 (indicated by an asterisk); however, 4 of the 6 were recurrent mutations (including R1513X, which was found in seven patients). Unfortunately, all but 1 of the 18 mutations with a pseudogene equivalent happened to occur at highly mutable CpG sites (see above). This definitely weakens further the evidence of *NF1* gene conversion. Moreover, for gene conversion to explain the high mutation rate, mutations should predominantly affect the central part of the gene, which is not the case.

Missense Mutations

Formally, we identified a total of 39 missense mutations or deletions of single amino acids. However, as discussed earlier, D176E has to be considered a polymorphism, and others were shown to be splice mutations. Furthermore, substitution of threonine for the first methionine will cause a false start in translation, with one of the following methionines acting as the initiation codon (Neote et al. 1990; Patten et al. 1990). Hence, strictly speaking, only 28 are genuine missense mutations causing changes or losses of a particular amino acid in the polypeptide chain. The distribution of these mutations is shown in figure 3. It is evident that the mutations cluster in two regions: the GRD, and upstream between exons 10b and 17. If we assume the mutation Y491C to be a splice mutation like Y489C (see above), this region would shrink even further, to an interval from exon 11 to exon 17. Interestingly, a total of 11 substitutions into proline (39%) were found among the 28 missense mutations. Proline is known to destabilize helices and beta sheets.

Except for patient 1899, who carries two missense mutations, R1276Q and D176E, all of the other 28 genuine missense mutations turned out to be the only sequence change present in the entire *NF1* gene. This sug-

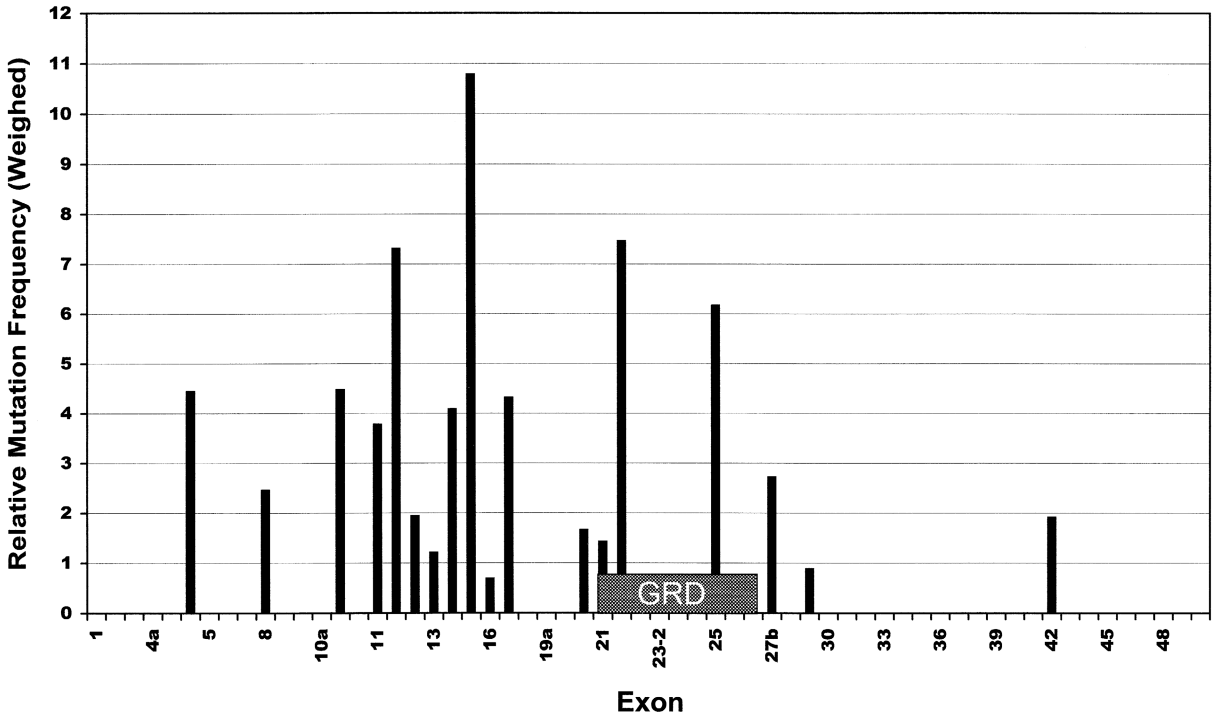

Figure 3 Weighed distribution of missense mutations over the *NF1* gene. For each exon, the number of genuine missense or single-amino-acid-deletion mutations was divided by the number of base pairs (bp). Values shown are ratios between the exon-specific mutation densities and the average mutation density for the whole gene (28/8457 bp). Location of the GRD is indicated by the box.

gests that these mutations cause the disease, yet further evidence is needed to verify this hypothesis. To date, functional and structural assessment of particular amino acids has been obtained only for the GRD. For other regions, information about evolutionary conservation may help to evaluate the significance of an amino acid exchange. Therefore, we generated an amino acid sequence alignment (program PILEUP of the GCG-Wisconsin package, version 9; gap weight 12 and gap length weight 4) between the sequences of the human and the *Drosophila NF1* proteins that are 60% identical over their entire length (The et al. 1997). As many as 15 of the 23 amino acid positions affected by missense mutation in our patients with NF1 turned out to be invariant, whereas, at two further positions, the amino acids were replaced by similar ones in the *Drosophila* protein (Ile1584 by Val and Arg1250 by Lys). At the other six positions nonconservative substitutions were found or the alignment generated a gap in the *Drosophila* protein (Y491: M; K583: Q; S665:−; H781: F; M1215: I; T2486:−). Moreover, we performed a similarity plot between the human and *Drosophila* sequences. Most of the mutations are situated on top of the similarity peaks or, at least, in regions of higher similarity, which may represent helices or beta sheets (fig. 4). Exceptions are Y491C—which might, in fact, be a splice mutation—S665F, and T2486I. These findings raise the possibility that the latter two mutations may actually be nonpathogenic.

Discussion

The systematic analysis of germline mutations in NF1 patients has been a major challenge for many laboratories during the last couple of years. Here, we present for the first time a comprehensive screen of minor lesions of the *NF1* gene in a large cohort of >500 unrelated patients that is free of any assessment bias for special exons or regions. We launched this project hoping that the data would allow us to answer some long-standing questions about the *NF1* gene and its proneness to mutate. Some of the questions were answered, but new questions were raised as well.

The Mutational Spectrum

A preponderance of truncating mutations is one of the most prominent features of *NF1* mutations. Some 80% of all small lesions result in a PTC; that is, about one half of all *NF1* mutations may be direct- or indirect-

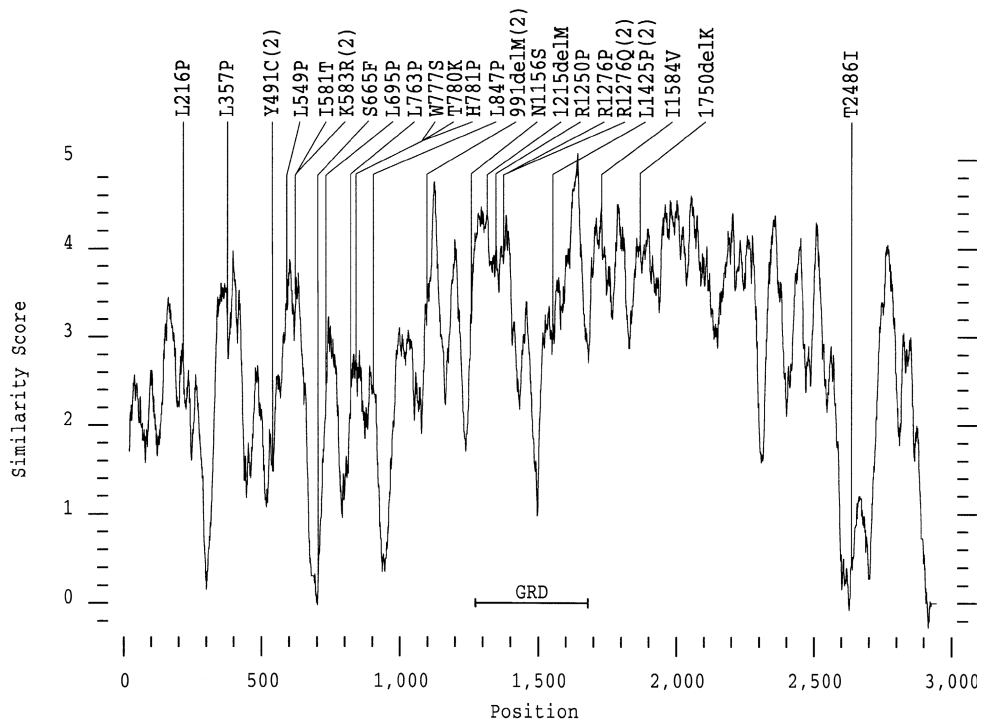

Figure 4 Missense mutations in the similarity plot of human versus *Drosophila* NF1 protein. The program PLOTSIMILARITY of the GCG-Wisconsin package, version 9 was used to calculate the amino-acid-sequence similarity profile of the human and *Drosophila* neurofibromins (accession numbers AAA59925 and AAB58976, respectively). A sliding window of 40 amino acids was chosen. Note that there are 2,963 instead of 2,839 amino acid positions in the alignment (program PILEUP; gap weight = 12 and gap-length weight = 4). For the first 20 and the last 20 positions, a value could not be calculated, because of the chosen window size. Mutations are located primarily in regions of higher similarity. Usually, helices and beta sheets have a higher local sequence similarity than coils.

stop mutations. Distribution of this type of mutation is very even over the coding sequence. We identified the first one in exon 1 and the last in exon 47. At first glance, no difference in phenotype was observed; however, a detailed analysis of a possible relation between clinical features and position of the PTC is in progress and will be presented elsewhere (S. Tinschert, A. Buske, B. Müller-Myhsok, I. Naumann, C. Mischung, R. Fahsold, S. Hoffmeyer, D. Kaufmann, H. Peters, P. Nürnberg, unpublished data). Unequal expression of both *NF1* alleles is a common observation in NF1 and has been related to the high number of truncating mutations (Hoffmeyer et al. 1995). This might explain the absence of a position effect of PTCs; however, we also observed equal expression in some cases, including patients U-62, 82, 342, and 407 (table 4). Of all mutations identified in this study, ~20% were splice defects, with nearly one-half of the latter causing in-frame exon skipping. Hence, analysis of mRNA, in combination with a PTC screening as performed in the PTT, is a good choice for mutation detection in NF1. In our hands, the detection rate was 47.1%, which is lower than the 67% detection rate originally reported (Heim et al. 1995) but in line with the genomic-screening methods applied in this study, taking into account the fact that missense mutations cannot be detected by this approach. According to our data, missense mutations represent ~10% of all small *NF1* lesions.

The identification of a recurrent *NF1* mutation has often been heralded as the discovery of a mutation hotspot. The most widely known example is the mutation R1947X in exon 31 (Valero et al. 1994; Lázaro et al. 1995). At least 10 unrelated patients with NF1, among 563 tested, were reported to carry this mutation (recurrence rate ~2%) (Upadhyaya and Cooper 1998). In our screening of 521 unrelated patients with NF1, however, only 3 presented with this mutation. The most frequent mutation in our study was R1513X in exon 27a found in seven patients. However, when looking for the highest density of mutations, exons 4b and 37 outnumbered all other exons with a value 4- to 5-fold higher than average. This suggests these exons include some minor hotspots. Nevertheless, with the large number of novel mutations presented in this paper, it becomes obvious that

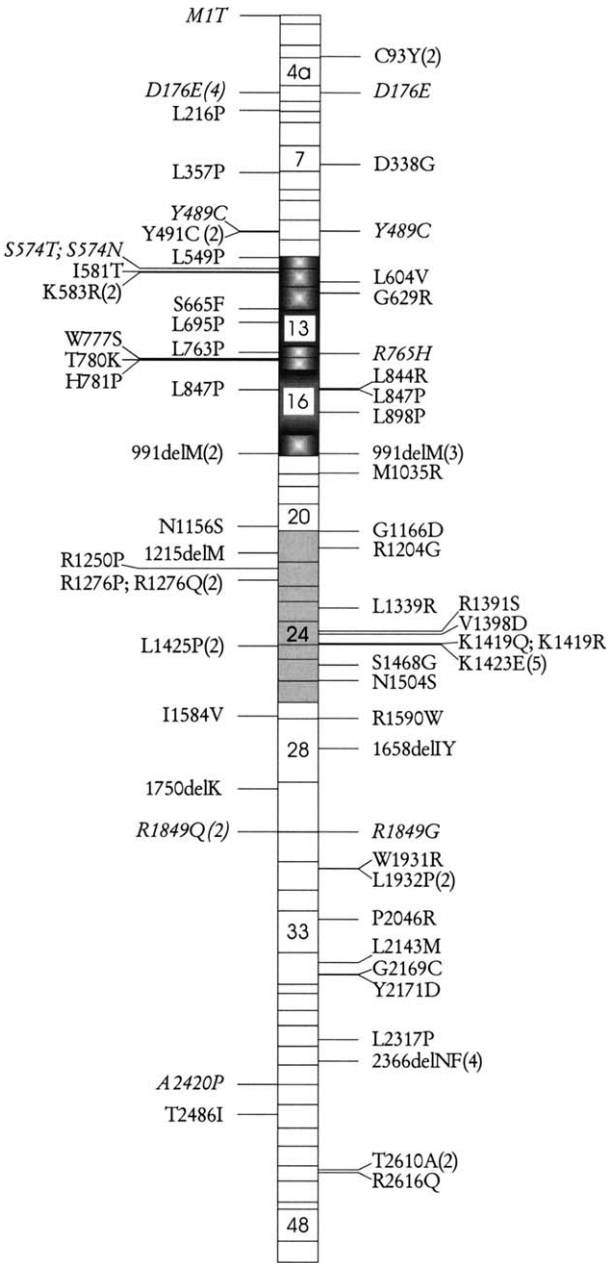

Figure 5 Synopsis of all known *NF1* missense mutations and deletions of 1 or 2 amino acids. Mutations on the left and right sides are data from this study and from the literature, respectively. Most published mutations have been reviewed in Upadhyaya and Cooper (1998). Some have been published very recently: R1204G (Krkljus et al. 1997); C39Y(1), Y489C, L847P, and 991delM(1) (Messiaen et al. 1998); and L2317P (Wu et al. 1999). Others have been submitted to the consortium but not published at this time. They are reported here with the consent of the consortium members who identified these mutations: 2366delNF(2) and R2616Q (L. Messiaen, personal communication); R1849G and L1932P (M. Upadhyaya, personal communication); 1658delIY and P2046R (D. Vidaud, personal communication). Mutations not representing genuine missense mutations including polymorphisms, splice mutations, or loss of the initiation codon are printed in italics. Number in parentheses after the mutation symbol indicates recurrent identifications. GRD region is shown in gray, whereas the exons 11–17, supposed to code for a new functional domain, are shown in black with a central light effect. To facilitate orientation, the numbers of some of the larger exons are given.

the worst-case scenario is operating: hundreds of private mutations for most of the families affected by NF1. Interestingly, all three alternatively spliced exons—9br, 23a, and 48a—seem to be irrelevant to mutation analysis. Likewise, two normally spliced exons—19b and 38—also failed to show a mutation in our study population, and other exons—such as 4a and 33—harbored only a single mutation. The reason for this underrepresentation in the compulsory exons is not clear and may be purely accidental. For exons 33 and 38, additional mutations have been reported to the consortium (Korf 1998).

In general, the mutational spectrum of the *NF1* gene seems to be very similar to that of other tumor-suppressor and mutator genes, which all seem to be characterized by a large proportion of truncating mutations—for example, nearly 100% for *APC* (Suzuki et al. 1998) and *TSC1* (Jones et al. 1999), >80% for *RB1* (Lohmann et al. 1996; 1997), ~80% for *BRCA1* (Miki et al. 1994) and *ATM* (Sandoval et al. 1999), and ~60% for *TSC2* (Jones et al. 1999), and all six *NBS1* gene mutations identified to date (Varon et al. 1998). Similarly, 5%–20% missense mutations, as well as whole-gene deletions, have been found in some of these genes (*RB1*, *ATM*, *TSC2*). In addition, the problem of unsuccessful mutation detection in many of the patients is common to all these genes. Little more than half of all the *NF1* alleles investigated in this study yielded a detectable mutation. It is true that the PTT protocol used here might have failed to detect missense as well as splicing-error mutations—especially those that result in in-frame skips of small exons— but, in most cases, all exons and adjacent intron regions of the *NF1* gene were sequenced. DGS, like TGGE, is commonly thought to provide a sensitivity close to 100% in the analyzed regions, and, although some problems with heterozygote detection in automated sequencing are known to impair the identification rate of point mutations, this alone is unlikely to account for missing >40% of the *NF1* mutations. Some of the unidentified mutations are definitely large deletions comprising the whole *NF1* gene or a major part of it. When analyzing 15 TGGE-negative cases by fluorescence in situ hybridization, we identified three *NF1* gene deletions (G. Thiel, unpublished data). Hence, we estimate the overall proportion of gross genomic deletions to be ~10%. Among the remaining 35% of undetected mutations, multiexon deletions may represent the largest group (15% of all mutations, according to the consortium data [Korf 1998]). Furthermore, large duplications or inversions would also have escaped our PCR-based mutation scanning (Naylor et al. 1993). Incomplete assessment of intronic and regulatory sequences probably accounts for other unidentified cases. However, *NF1* promoter mutations seem to be rare and the sequence variants identified so far are unlikely to cause the disease phenotype (Osborn and Upadhyaya 1998). For the *RB1* gene, silencing of the promoter by allele-specific hypermethylation of a CpG island in the 5′ region was shown in 10% of retinoblastomas (Sakai et al. 1991; Greger et al. 1994). Interestingly, a hypomethylated region near the transcription start site within the *NF1* CpG island could act as a target for silencing of the *NF1* gene by local hypermethylation (Rodenhiser et al. 1998). Thus, epigenetic and genetic mechanisms may cause inactivation of *NF1* transcription. Recent studies have shown that somatic mosaicism may be a frequent finding among sporadic cases of NF1 (Colman et al. 1996; Ainsworth et al. 1997; Tonsgard et al. 1997; Wu et al. 1997; Rasmussen et al. 1998). Provided the mutation was present in the tissues analyzed, the methods used for exon screening in this study are unlikely to have had sufficient sensitivity to detect low-level mosaicism. Unfortunately, we cannot exclude the possibility that patients who did not have NF1 were included in the screening, because some of the patients were diagnosed by others. Finally, the existence of genetic heterogeneity in NF1 is still an open discussion.

High Mutation Rate

The mutation rate for NF1 is one of the highest known for human disorders, estimated to be between 1×10^{-4} and 3.1×10^{-5} (Sergeyev 1975; Huson et al. 1989; Clementi et al. 1990). Thus, the *NF1* gene seems to mutate 10 times more often than other disease genes. Several reasons have been proposed to explain the high mutability of the *NF1* gene, including its relatively large size of ~350 kb, gene-conversion events via pseudogenes, and mutational hotspots. Acting on the results of our study, we can definitely exclude the many *NF1* pseudogenes as a major reason. Furthermore, pronounced hotspots of mutation have not yet been identified in the *NF1* gene. It is true that some of the recurrent mutations, such as R1513X and R1947X, affect CpG dinucleotides, but the overall proportion of C→T or G→A transitions within CpGs is as low as 19% of all mutations and 32% of all the single-base-pair substitutions. Many other genes show similar or even higher percentages of CpG mutations—for example, 46% of factor VIII point mutations in hemophilia A (Antonarakis et al. 1995), 45%–50% of *TP53* point mutations in colorectal cancer (Greenblatt et al. 1994), and 20%–25% of all *RB1* mutations (Cowell et al. 1994). Likewise, overlap between pseudogene sequence variants and *NF1* germline mutations as identified in this study is negligible. Therefore, we assume the large size of the *NF1* gene to be the major reason for the high mutation rate, which is in fact not considerably higher than that of other large genes. In Duchenne muscular dystrophy, which is caused by mutations in an even larger gene (79 exons in 2.5 Mb), a

similar high mutation rate is found (Vogel and Motulsky 1997). Interestingly, current estimates in Marfan syndrome place its prevalence at 1 per 3,000–5,000 people (Pyeritz 1996). This suggests that the *FBN1* gene (65 exons in 110 kb), which is very similar in size to the *NF1* gene, has a mutation rate nearly as high as in NF1.

Second Functional Domain

Our characterization of significant numbers of missense mutations and some small in-frame deletions is likely to be helpful in the investigation of putative functions of the *NF1* gene product. The RasGAP activity of the central GAP-related domain and the structure of the GRD from neurofibromin have already been well characterized (Kim and Tamanoi 1998; Scheffzek et al. 1998), in particular, the effects of mutations of the arginine finger (Arg 1276) were studied in detail (Ahmadian et al. 1997; Klose et al. 1998*a*). Clustering of missense mutations in the GRD, as observed in this and other studies (fig. 5), is what we could expect from its functional relevance. However, there is another segment in the *NF1* gene, upstream of the GRD, that harbors numerous missense mutations as well (see fig. 5). We assume this region defines a second functional domain of the neurofibromin molecule. Interestingly, this region coincides with the cysteine/serine-rich domain (CSRD) defined by Izawa et al. (1996). The CSRD comprises amino acid residues 543–909, in which three cysteine pairs (residues 622/632, 673/680, and 714/721) may be comparable to those that Maru et al. (1991) suggested form the ATP-binding domain of BCR protein. Furthermore, this sequence harbors three potential cAMP-dependent protein kinase A (PKA) recognition sites (Marchuk et al. 1991). These are, indeed, subject to phosphorylation by PKA (Izawa et al. 1996), and one is mutated in two of our NF1 families (mutation K583R in exon 12a). A second is situated in a small region (residues 815–834) of sequence similarity with two other proteins (MAP-2 and tau) that also associate with microtubules. It has been speculated that phosphorylation of this region might regulate the association of neurofibromin and microtubules (Gregory et al. 1993). The functional significance of the phosphorylation of neurofibromin by PKA is still unclear, but in view of the compelling evidence for the involvement of neurofibromin in cAMP-mediated signaling from *Drosophila* (Guo et al. 1997; The et al. 1997), it may explain the observed link between the second messenger cAMP and the Ras signaling pathway (Wu et al. 1993).

In summary, we have attributed functional relevance to a new region of the neurofibromin molecule on the basis of the missense mutations identified in a large cohort of NF1 patients. This protein segment was found upstream of the GRD and may be identical with the CSRD described elsewhere (Izawa et al. 1996). PKA phosphorylation sites within the domain suggest this region might be involved in cAMP-mediated signaling. However, further studies will be required to substantiate our hypothesis. To this end, the functional significance of the relevant missense mutations is currently being tested in the *Drosophila* model.

Acknowledgments

We thank the patients and their families for their willing cooperation, and we gratefully acknowledge the assistance of Peter N. Robinson, Annett Böddrich, Denise Horn, Fikret Erdogan, Mohammad R. Toliat, Anja Harder-Klose, Detlef Hess, Christiane Bielefeld, Andrea Lüder, Carmen Macsuga, Beatrice Heyne, and Kerstin Kamprath in the TGGE approach. We also thank Frances Hannan for his helpful comments on the manuscript. This work was supported in part by the Deutsche Krebshilfe.

Electronic-Database Information

Accession numbers and URLs for data in this article are as follows:

GenBank, http://www.ncbi.nlm.nih.gov/Genbank/index.html (for human and *Drosophila* neurofibromin protein sequences [accession numbers AAA59925 and AAB58976, respectively] and human *NF1* pseudogene sequences [accession numbers are listed in table 6])

International NF1 Genetic Analysis Consortium, http://www.nf.org/nf1gene/nf1gene.home.html (for unpublished *NF1* mutations)

Messiaen L, Callens T, Mortier G, van Roy N, Speleman F, de Pape A (1998) Identification of mutations in the *NF1* gene, including 3 different nonsense mutations and 1 missense mutation disrupting normal RNA splicing. (Abstract) http://nf.org/md1aspe1.htm

Online Mendelian Inheritance in Man (OMIM), http://www.ncbi.nlm.nih.gov/Omim/ (for *NF1* [162200])

References

Abernathy CR, Rasmussen SA, Stalker HJ, Zori R, Driscoll DJ, Williams CA, Kousseff BG, et al (1997) *NF1* mutation analysis using a combined heteroduplex/SSCP approach. Hum Mutat 9:548–554

Ahmadian MR, Stege P, Scheffzek K, Wittinghofer A (1997) Confirmation of the arginine-finger hypothesis for the GAP-stimulated GTP-hydrolysis reaction of Ras. Nat Struct Biol 4:686–689

Ainsworth PJ, Chakraborty PK, Weksberg R (1997) Example of somatic mosaicism in a series of de novo neurofibromatosis type 1 cases due to a maternally derived deletion. Hum Mutat 9:452–457

Andrews JD, Mancini DN, Singh SM, Rodenhiser DI (1996) Site and sequence specific DNA methylation in the neurofibromatosis (*NF1*) gene includes C5839T: the site of the

recurrent substitution mutation in exon 31. Hum Mol Genet 5:503–507

Antonarakis SE, Kazazian HH, Tuddenham EG (1995) Molecular etiology of factor VIII deficiency in hemophilia A. Hum Mutat 5:1–22

Böddrich A, Griesser J, Horn D, Kaufmann D, Krone W, Nürnberg P (1995) Reduced neurofibromin content but normal GAP activity in a patient with neurofibromatosis type 1 caused by a five base pair duplication in exon 12b of the *NF1* gene. Biochem Biophys Res Commun 214:895–904

Böddrich A, Robinson PN, Schülke M, Buske A, Tinschert S, Nürnberg P (1997) New evidence for a mutation hotspot in exon 37 of the *NF1* gene. Hum Mutat 9:374–377

Cawthon RM, Weiss R, Xu G, Viskochil D, Culver M, Stevens J, Robertson M, et al (1990) A major segment of the neurofibromatosis type 1 gene: cDNA sequence, genomic structure, and point mutations. Cell 62:193–201

Clark SJ, Harrison J, Frommer M (1995) CpNpG methylation in mammalian cells. Nat Genet 10:20–27

Clementi M, Barbujani G, Turolla L, Tenconi R (1990) Neurofibromatosis-1: a maximum likelihood estimation of mutation rate. Hum Genet 84:116–118

Colman SD, Rasmussen SA, Ho VT, Abernathy CR, Wallace MR (1996) Somatic mosaicism in a patient with neurofibromatosis type 1. Am J Hum Genet 58:484–490

Colman SD, Williams CA, Wallace MR (1995) Benign neurofibromas in type 1 neurofibromatosis (NF1) show somatic deletions on *NF1* gene. Nat Genet 11:90–92

Cooper DN, Krawczak M (1993) Human gene mutation. BIOS Scientific Publishers, Oxford

Cowell JK, Smith T, Bia B (1994) Frequent constitutional C to T mutations in CGA-arginine codons in the RB1 gene produce premature stop codons in patients with bilateral (hereditary) retinoblastoma. Eur J Hum Genet 2:281–290

Cummings LM, Glatefeller A, Marchuk DA (1993) *NF1* related loci on chromosomes 2, 12, 14, 15, 20, 21, and 22: a potential role for gene conversion in the high spontaneous mutation rate of NF1? Am J Hum Genet Suppl 53:A672

Danglot G, Régnier V, Fauvet D, Vassal G, Kujas M, Bernheim A (1995) Neurofibromatosis 1 (*NF1*) mRNAs expressed in the central nervous system are differentially spliced in the 5′ part of the gene. Hum Mol Genet 4:915–920

Däschner K, Assum G, Eisenbarth I, Krone W, Hoffmeyer S, Wortmann S, Heymer B, et al (1997) Clonal origin of tumor cells in a plexiform neurofibroma with LOH in *NF1* intron 38 and in dermal neurofibromas without LOH of the *NF1* gene. Biochem Biophys Res Commun 234:346–350

Easton DF, Ponder MA, Huson SM, Ponder BA (1993) An analysis of variation in expression of neurofibromatosis (NF) type 1 (*NF1*): evidence for modifying genes. Am J Hum Genet 53:305–313

Eikenboom JC, Vink T, Briet E, Sixma JJ, Reitsma PH (1994) Multiple substitutions in the von Willebrand factor gene that mimic the pseudogene sequence. Proc Natl Acad Sci USA 91:2221–2224

Friedman JM, Birch PH (1997) Type 1 neurofibromatosis: a descriptive analysis of the disorder in 1,728 patients. Am J Med Genet 70:138–143

Gasparini P, Grifa A, Origone P, Coviello D, Antonacci R, Rocchi M (1993) Detection of a neurofibromatosis type I (*NF1*) homologous sequence by PCR: implications for the diagnosis and screening of genetic diseases. Mol Cell Probes 7:415–418

Gille C, Gille A, Booms P, Robinson PN, Nürnberg P (1998) Bipolar clamping improves the sensitivity of mutation detection by temperature gradient gel electrophoresis. Electrophoresis 19:1347–1350

Greenblatt MS, Bennett WP, Hollstein M, Harris CC (1994) Mutations in the p53 tumor suppressor gene: clues to cancer etiology and molecular pathogenesis. Cancer Res 54: 4855–4878

Greger V, Debus N, Lohmann D, Hopping W, Passarge E, Horsthemke B (1994) Frequency and parental origin of hypermethylated RB1 alleles in retinoblastoma. Hum Genet 94:491–496

Gregory PE, Gutmann DH, Mitchell A, Park S, Boguski M, Jacks T, Wood DL, et al (1993) Neurofibromatosis type 1 gene product (neurofibromin) associates with microtubules. Somat Cell Mol Genet 19:265–274

Guha A, Lau N, Huvar I, Gutmann D, Provias J, Pawson T, Boss G (1996) Ras-GTP levels are elevated in human NF1 peripheral nerve tumors. Oncogene 12:507–513

Guo HF, The I, Hannan F, Bernards A, Zhong Y (1997) Requirement of *Drosophila* NF1 for activation of adenylyl cyclase by PACAP38-like neuropeptides. Science 276:795–798

Gutmann DH, Aylsworth A, Carey JC, Korf B, Marks J, Pyeritz RE, Rubenstein A, et al (1997) The diagnostic evaluation and multidisciplinary management of neurofibromatosis 1 and neurofibromatosis 2. JAMA 278:51–57

Harder A, Macsuga C, Tinschert S, Nürnberg P, Peters H (1999) A novel 5-bp deletion in exon 30 of the neurofibromatosis type 1 (*NF1*) gene. Hum Mutat 13:259

Heim RA, Kam-Morgan LNW, Binnie CG, Corns DD, Cayouette MC, Farber RA, Aylsworth AS, et al (1995) Distribution of 13 truncating mutations in the neurofibromatosis 1 gene. Hum Mol Genet 4:975–981

Hoffmeyer S, Assum G (1994) An RsaI polymorphism in the transcribed region of the neurofibromatosis (*NF1*)-gene. Hum Genet 93:481–482

Hoffmeyer S, Assum G, Griesser J, Kaufmann D, Nürnberg P, Krone W (1995) On unequal allelic expression of the neurofibromin gene in neurofibromatosis type 1. Hum Mol Genet 4:1267–1272

Hoffmeyer S, Nürnberg P, Ritter H, Fahsold R, Leistner W, Kaufmann D, Krone W (1998) Nearby stop codons in exons of the neurofibromatosis type 1 gene are disparate splice effectors. Am J Hum Genet 62:269–277

Horn D, Robinson PN, Böddrich A, Buske A, Tinschert S, Nürnberg P (1996) Three novel mutations of the *NF1* gene detected by temperature gradient gel electrophoresis of exons 5 and 8. Electrophoresis 17:1559–1563

Huson SM, Compston DA, Clark P, Harper PS (1989) A genetic study of von Recklinghausen neurofibromatosis in south east Wales. I. Prevalence, fitness, mutation rate, and effect of parental transmission on severity. J Med Genet 26: 704–711

Huson SM, Hughes RAC (1994) The neurofibromatoses: a clinical and pathogenetic overview. Chapman & Hall, London

Izawa I, Tamaki N, Saya H (1996) Phosphorylation of neu-

rofibromatosis type 1 gene product (neurofibromin) by cAMP-dependent protein kinase. FEBS Lett 382:53–59

Jones AC, Shyamsundar MM, Thomas MW, Maynard J, Idziaszczyk S, Tomkins S, Sampson JR, et al (1999) Comprehensive mutation analysis of TSC1 and TSC2—and phenotypic correlations in 150 families with tuberous sclerosis. Am J Hum Genet 64:1305–1315

Kehrer-Sawatzki H, Schwickardt T, Assum G, Rocchi M, Krone W (1997) A third neurofibromatosis type 1 (NF1) pseudogene at chromosome 15q11.2. Hum Genet 100: 595–600

Kim MR, Tamanoi F (1998) Neurofibromatosis 1 GTPase activating protein-related domain and its functional significance. In: Upadhyaya M, Cooper DN (eds) Neurofibromatosis type 1: from genotype to phenotype. BIOS Scientific Publishers, Oxford, pp 89–112

Klose A, Ahmadian MR, Schülke M, Scheffzek K, Hoffmeyer S, Gewies A, Schmitz F, et al (1998*a*) Selective disactivation of neurofibromin GAP activity in neurofibromatosis type 1 (NF1). Hum Mol Genet 7:1261–1268

Klose A, Nürnberg P, Tinschert S, Peters H (1998*b*) Recurrence of the neurofibromatosis type 1 (NF1) mutation R1276X probably due to interchromosomal gene conversion. Hum Mutat 12:291

Klose A, Peters H, Hoffmeyer S, Buske A, Lüder A, Hess D, Lehmann R, et al (1999) Two independent mutations in a family with neurofibromatosis type 1 (NF1). Am J Med Genet 83:6–12

Klose A, Robinson PN, Gewies A, Kluwe L, Kaufmann D, Buske A, Tinschert S, et al (1998*c*) Two novel mutations in exons 19a and 20 and a BsaBI [correction of BsaI] polymorphism in a newly characterized intron of the neurofibromatosis type 1 gene. Hum Genet 102:367–371

Korf BR (1998) The NF1 genetic analysis consortium. In: Upadhyaya M, Cooper DN (eds) Neurofibromatosis type 1: from genotype to phenotype. BIOS Scientific Publishers, Oxford, pp 57–63

Krawczak M, Reiss J, Cooper DN (1992) The mutational spectrum of single base-pair substitutions in mRNA splice junctions of human genes: causes and consequences. Hum Genet 90:41–54

Krkljus S, Abernathy CR, Johnson JS, Williams CA, Driscoll DJ, Zori R, Stalker HJ, et al (1998) Analysis of CpG C-to-T mutations in neurofibromatosis type 1. Hum Mutat 11: 411

Lázaro C, Kruyer H, Gaona A, Estivill X (1995) Screening for the neurofibromatosis type 1 recurrent mutation R1947X. Med Genetik 7:272 (Abstract)

Legius E, Marchuk DA, Collins FS, Glover TW (1993) Somatic deletion of the neurofibromatosis type 1 gene in a neurofibrosarcoma supports a tumour suppressor gene hypothesis. Nat Genet 3:122–126

Legius E, Marchuk DA, Hall BK, Andersen LB, Wallace MR, Collins FS, Glover TW (1992) *NF1*-related locus on chromosome 15. Genomics 13:1316–1318

Lerman LS, Silverstein K (1987) Computational simulation of DNA melting and its application to denaturing gradient gel electrophoresis. Methods Enzymol 155:482–501

Li Y, Bollag G, Clark R, Stevens J, Conroy L, Fults D, Ward K, et al (1992) Somatic mutations in the neurofibromatosis 1 gene in human tumors. Cell 69:275–281

Li Y, O'Connell P, Huntsman-Breidenbach H, Cawthon R, Stevens J, Xu G, Neil S, et al (1995) Genomic organization of the neurofibromatosis 1 gene (*NF1*). Genomics 25:9–18

Lohmann DR, Brandt B, Höpping W, Passarge E, Horsthemke B (1996) The spectrum of *RB1* germ-line mutations in hereditary retinoblastoma. Am J Hum Genet 58:940–949

Lohmann DR, Gerick M, Brandt B, Oelschläger U, Lorenz B, Passarge E, Horsthemke B (1997) Constitutional *RB1*-gene mutations in patients with isolated unilateral retinoblastoma. Am J Hum Genet 61:282–294

Marchuk DA, Saulino AM, Tavakkol R, Swaroop M, Wallace MR, Andersen LB, Mitchell AL, et al (1991) cDNA cloning of the type 1 neurofibromatosis gene: complete sequence of the *NF1* gene product. Genomics 11:931–940

Martin GA, Viskochil D, Bollag G, McCabe PC, Crosier WJ, Haubruck H, Conroy L, et al (1990) The GAP-related domain of the neurofibromatosis type 1 gene product interacts with ras p21. Cell 63:843–849

Maru Y, Witte ON (1991) The BCR gene encodes a novel serine/threonine kinase activity within a single exon. Cell 67:459–468

Maynard J, Krawczak M, Upadhyaya M (1997) Characterization and significance of nine novel mutations in exon 16 of the neurofibromatosis type 1 (*NF1*) gene. Hum Genet 99: 674–676

Messiaen L, Callens T, De Paepe A, Craen M, Mortier G (1997) Characterisation of two different nonsense mutations, C6792A and C6792G, causing skipping of exon 37 in the *NF1* gene. Hum Genet 101:75–80

Miki Y, Swensen J, Shattuck-Eidens D, Futreal PA, Harshman K, Tavtigian S, Liu Q, et al (1994) A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1. Science 266:66–71

Naylor J, Brinke A, Hassock S, Green PM, Giannelli F (1993) Characteristic mRNA abnormality found in half the patients with severe haemophilia A is due to large DNA inversions. Hum Mol Genet 2:1773–1778

Neote K, Brown CA, Mahuran DJ, Gravel RA (1990) Translation initiation in the HEXB gene encoding the β-subunit of human β-hexosaminidase. J Biol Chem 265: 20799–20806

Osborn M, Upadhyaya M (1998) Mutation analysis in the promoter and coding region of the *NF1* gene. Am J Hum Genet Suppl 63:A378

Patten JL, Johns DR, Valle D, Eil C, Gruppuso PA, Steele G, Smallwood PM, et al (1990) Mutation in the gene encoding the stimulatory G protein of adenylate cyclase in Albright's hereditary osteodystrophy. N Engl J Med 322:1412–1419

Peters H, Hess D, Fahsold R, Schülke M (1999*a*) A novel mutation L1425P in the GAP-region of the *NF1* gene detected by temperature gradient gel electrophoresis (TGGE). Hum Mutat 13:337

Peters H, Lüder A, Harder A, Schuelke M, Tinschert S (1999*b*) Mutation screening of neurofibromatosis type 1 (*NF1*) exons 28 and 29 with single strand conformation polymorphism (SSCP): five novel mutations, one recurrent transition and two polymorphisms in a panel of 118 unrelated NF1 patients. Hum Mutat 13:258

Purandare SM, Huntsman-Breidenbach H, Li Y, Lin Zhu X, Sawada S, Neil SM, Brothman A, et al (1995) Identification of neurofibromatosis 1 (*NF1*) homologous loci by direct sequencing, fluorescence in situ hybridization, and PCR amplification of somatic cell hybrids. Genomics 30:476–485

Purandare SM, Lanyon WG, Connor JM (1994) Characterisation of inherited and sporadic mutations in neurofibromatosis type-1. Hum Mol Genet 3:1109–1115

Pyeritz RE (1996) Disorders of fibrillins and microfibrillogenesis: Marfan syndrome and other disorders of fibrillin. In: Rimoin DL, Connor JM, Pyeritz RE (eds) Emery and Rimoin's principles and practice of medical genetics, 3rd ed. Churchill Livingstone, New York, pp 1027–1066

Rasmussen SA, Colman SD, Ho VT, Abernathy CR, Arn PH, Weiss L, Schwartz C, et al (1998) Constitutional and mosaic large *NF1* gene deletions in neurofibromatosis type 1. J Med Genet 35:468–471

Régnier V, Meddeb M, Lecointre G, Richard F, Duverger A, Nguyen VC, Dutrillaux B, et al (1997) Emergence and scattering of multiple neurofibromatosis (*NF1*)-related sequences during hominoid evolution suggests a process of pericentromeric interchromosomal transposition. Hum Mol Genet 6:9–16

Riccardi VM (1992) Neurofibromatosis: phenotype, natural history, and pathogenesis, 2nd ed. John Hopkins University, Baltimore

Riccardi VM (1993) Genotype, malleotype, phenotype, and randomness: lessons from neurofibromatosis-1 (NF1). Am J Hum Genet 53:301–304

Riesner D, Steger G, Zimmat R, Owens RA, Wagenhöfer M, Hillen W, Vollbach S, et al (1989) Temperature-gradient gel electrophoresis of nucleic acids: analysis of conformational transitions, sequence variations, and protein-nucleic acid interactions. Electrophoresis 10:377–389

Robinson PN, Böddrich A, Peters H, Tinschert S, Buske A, Kaufmann D, Nürnberg P (1995) Two recurrent nonsense mutations and a 4 bp deletion in a quasi-symmetric element in exon 37 of the *NF1* gene. Hum Genet 96:95–98

Robinson PN, Buske A, Neumann R, Tinschert S, Nürnberg P (1996) Recurrent 2-bp deletion in exon 10c of the *NF1* gene in two cases of von Recklinghausen neurofibromatosis. Hum Mutat 7:85–88

Rodenhiser DI, Coulter-Mackie MB, Singh SM (1993) Evidence of DNA methylation in the neurofibromatosis type 1 (*NF1*) gene region of 17q11.2. Hum Mol Genet 2:439–444

Rodenhiser D, Mancini DN, Singh SM, Archer TK (1998) Site specific DNA methylation in the neurofibromatosis (*NF1*) promoter interferes with binding of CREB and SP1 transcription factors. Am J Hum Genet Suppl 63:A190

Sakai T, Toguchida J, Ohtani N, Yandell DW, Rapaport JM, Dryja TP (1991) Allele-specific hypermethylation of the retinoblastoma tumor-suppressor gene. Am J Hum Genet 48: 880–888

Sandoval N, Platzer M, Rosenthal A, Dork T, Bendix R, Skawran B, Stuhrmann M, et al (1999) Characterization of ATM gene mutations in 66 ataxia telangiectasia families. Hum Mol Genet 8:69–79

Scheffzek K, Ahmadian MR, Wiesmuller L, Kabsch W, Stege P, Schmitz F, Wittinghofer A (1998) Structural analysis of the GAP-related domain from neurofibromin and its implications. EMBO J 17:4313–4327

Sergeyev AS (1975) On the mutation rate of neurofibromatosis. Humangenetik 28:129–138

Serra E, Puig S, Otero D, Gaona A, Kruyer H, Ars E, Estivill X, Lazaro C (1997) Confirmation of a double-hit model for the *NF1* gene in benign neurofibromas. Am J Hum Genet 61:512–519

Shannon KM, O'Connell P, Martin GA, Paderanga D, Olson K, Dinndorf P, McCormick F (1994) Loss of normal *NF1* allele from the bone marrow of children with type 1 neurofibromatosis and malignant myeloid disorders. N Engl J Med 330:597–601

Suzuki T, Ishioka C, Kato S, Mitachi Y, Shimodaira H, Sakayori M, Shimada A, et al (1998) Detection of APC mutations by a yeast-based protein truncation test (YPTT). Genes Chromosomes Cancer 21:290–297

The I, Hannigan GE, Cowley GS, Reginald S, Zhong Y, Gusella JF, Hariharan IK, et al (1997) Rescue of a *Drosophila Nf1* mutant phenotype by protein kinase A. Science 276: 791–794

Toliat MR, Erdogan F, Gewies A, Fahsold R, Buske A, Tinschert S, Nürnberg P (1999) Analysis of the *NF1* gene by temperature gradient gel electrophoresis (TGGE) reveals a high incidence of mutations in exon 4b. Electrophoresis 21: 541–544

Tonsgard JH, Yelavarthi KK, Cushner S, Short MP, Lindgren V (1997) Do *NF1* gene deletions result in a characteristic phenotype? Am J Med Genet 73:80–86

Upadhyaya M, Cooper DN (1998) The mutational spectrum in neurofibromatosis 1 and its underlying mechanisms. In: Upadhyaya M, Cooper DN (eds) Neurofibromatosis type 1: from genotype to phenotype. BIOS Scientific Publishers, Oxford, pp 65–88

Upadhyaya M, Osborn MJ, Maynard J, Kim MR, Tamanoi F, Cooper DN (1997) Mutational and functional analysis of the neurofibromatosis type 1 (*NF1*) gene. Hum Genet 99: 88–92

Valero MC, Velasco E, Moreno F, Hernandez-Chico C (1994) Characterization of four mutations in the neurofibromatosis type 1 gene by denaturing gradient gel electrophoresis (DGGE). Hum Mol Genet 3:639–641

Varon R, Vissinga C, Platzer M, Cerosaletti KM, Chrzanowska KH, Saar K, Beckmann G, et al (1998) Nibrin, a novel DNA double-strand break repair protein, is mutated in Nijmegen breakage syndrome. Cell 93:467–476

Vogel F, Motulsky AG (1997) Human genetics: problems and approaches, 3rd ed. Springer-Verlag, Berlin

Wartell RM, Hosseini SH, Moran CP (1990) Detecting base pair substitutions in DNA fragments by temperature-gradient gel electrophoresis. Nucleic Acids Res 18:2699–2705

White R, O'Connell P (1991) Identification and characterization of the gene for neurofibromatosis type 1. Curr Opin Genet Dev 1:15–19

Wu B-L, Boles RG, Yaari H, Weremowicz S, Schneider GH, Korf BR (1997) Somatic mosaicism for deletion of the entire *NF1* gene identified by FISH. Hum Genet 99:209–213

Wu J, Dent P, Jelinek T, Wolfman A, Weber MJ, Sturgill TW (1993) Inhibition of the EGF-activated MAP kinase signal-

ing pathway by adenosine 3′,5′-monophosphate. Science 262:1065–1069

Wu R, López-Correa C, Rutkowski JL, Baumbach LL, Glover TW, Legius E (1999) Germline mutations in NF1 patients with malignancies. Genes Chromosomes Cancer 26: 376–380

Xu G, O'Connell P, Viskochil D, Cawthon R, Robertson M, Culver M, Dunn D, et al (1990) The neurofibromatosis type 1 gene encodes a protein related to GAP. Cell 62:599–608