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ORIGINAL ARTICLE

Clinical application of array-based comparative genomic hybridization by two-stage screening for 536 patients with mental retardation and multiple congenital anomalies

Shin Hayashi[1,2], Issei Imoto[1,3], Yoshinori Aizu[4], Nobuhiko Okamoto[5], Seiji Mizuno[6], Kenji Kurosawa[7], Nana Okamoto[1,8], Shozo Honda[1], Satoshi Araki[9], Shuki Mizutani[9], Hironao Numabe[10], Shinji Saitoh[11], Tomoki Kosho[12], Yoshimitsu Fukushima[12], Hiroshi Mitsubuchi[13], Fumio Endo[13], Yasutsugu Chinen[14], Rika Kosaki[15], Torayuki Okuyama[15], Hirotaka Ohki[16], Hiroshi Yoshihashi[17], Masae Ono[18], Fumio Takada[19], Hiroaki Ono[20], Mariko Yagi[21], Hiroshi Matsumoto[22], Yoshio Makita[23], Akira Hata[24] and Johji Inazawa[1,25]

Recent advances in the analysis of patients with congenital abnormalities using array-based comparative genome hybridization (aCGH) have uncovered two types of genomic copy-number variants (CNVs); pathogenic CNVs (pCNVs) relevant to congenital disorders and benign CNVs observed also in healthy populations, complicating the screening of disease-associated alterations by aCGH. To apply the aCGH technique to the diagnosis as well as investigation of multiple congenital anomalies and mental retardation (MCA/MR), we constructed a consortium with 23 medical institutes and hospitals in Japan, and recruited 536 patients with clinically uncharacterized MCA/MR, whose karyotypes were normal according to conventional cytogenetics, for two-stage screening using two types of bacterial artificial chromosome-based microarray. The first screening using a targeted array detected pCNV in 54 of 536 cases (10.1%), whereas the second screening of the 349 cases negative in the first screening using a genome-wide high-density array at intervals of approximately 0.7 Mb detected pCNVs in 48 cases (13.8%), including pCNVs relevant to recently established microdeletion or microduplication syndromes, CNVs containing pathogenic genes and recurrent CNVs containing the same region among different patients. The results show the efficient application of aCGH in the clinical setting.
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INTRODUCTION

Mental retardation (MR) or developmental delay is estimated to affect 2–3% of the population.[1] However, in a significant proportion of cases, the etiology remains uncertain. Hunter[2] reviewed 411 clinical cases of MR and reported that a specific genetic/syndrome diagnosis was carried out in 19.9% of them. Patients with MR often have congenital anomalies, and more than three minor anomalies can be useful in the diagnosis of syndromic MR.[2,3] Although chromosomal aberrations are well-known causes of MR, their frequency determined by conventional karyotyping has been reported to range from 7.9 to 36% in patients with MR.[4–8] Although the diagnostic yield depends on the population of each study or clinical conditions, such studies

[1]Department of Molecular Cytogenetics, Medical Research Institute and School of Biomedical Science, Tokyo Medical and Dental University, Tokyo, Japan; [2]Hard Tissue Genome Research Center, Tokyo Medical and Dental University, Tokyo, Japan; [3]Department of Human Genetics and Public Health Graduate School of Medical Science, The University of Tokushima, Tokushima, Japan; [4]Division of Advanced Technology and Development, BML, Saitama, Japan; [5]Department of Medical Genetics, Osaka Medical Center and Research Institute for Maternal and Child Health, Osaka, Japan; [6]Department of Pediatrics, Central Hospital, Aichi Human Service Center, Kasugai, Japan; [7]Division of Medical Genetics, Kanagawa Children's Medical Center, Yokohama, Japan; [8]Department of Maxillofacial Orthognathics, Graduate School, Tokyo Medical and Dental University, Tokyo, Japan; [9]Department of Pediatrics and Developmental Biology, Tokyo Medical and Dental University Graduate School, Tokyo, Japan; [10]Department of Medical Genetics, Kyoto University Hospital, Kyoto, Japan; [11]Department of Pediatrics, Hokkaido University Graduate School of Medicine, Sapporo, Japan; [12]Department of Medical Genetics, Shinshu University School of Medicine, Matsumoto, Japan; [13]Department of Pediatrics, Kumamoto University Graduate School of Medical Science, Kumamoto, Japan; [14]Department of Pediatrics, University of the Ryukyu School of Medicine, Okinawa, Japan; [15]Department of Clinical Genetics and Molecular Medicine, National Center for Child Health and Development, Tokyo, Japan; [16]The Division of Cardiology, Tokyo Metropolitan Children's Medical Center, Tokyo, Japan; [17]The Division of Medical Genetics, Tokyo Metropolitan Children's Medical Center, Tokyo, Japan; [18]Department of Pediatrics, Tokyo Teishin Hospital, Tokyo, Japan; [19]Department of Medical Genetics, Kitasato University Graduate School of Medical Sciences, Sagamihara, Japan; [20]Department of Pediatrics, Hiroshima Prefectural Hospital, Hiroshima, Japan; [21]Department of Pediatrics, Kobe University Graduate School of Medicine, Kobe, Japan; [22]Department of Pediatrics, National Defense Medical College, Saitama, Japan; [23]Education Center, Asahikawa Medical College, Asahikawa, Japan; [24]Department of Public Health, Chiba University Graduate School of Medicine, Chiba, Japan and [25]Global Center of Excellence (GCOE) Program for 'International Research Center for Molecular Science in Tooth and Bone Diseases', Tokyo Medical and Dental University, Tokyo, Japan
Correspondence: Professor J Inazawa, Department of Molecular Cytogenetics, Medical Research Institute, Tokyo Medical and Dental University, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8510, Japan.
E-mail: johinaz.cgen@mri.tmd.ac.jp
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suggest that at least three quarters of patients with MR are undiagnosed by clinical dysmorphic features and karyotyping.

In the past two decades, a number of rapidly developed cytogenetic and molecular approaches have been applied to the screening or diagnosis of various congenital disorders including MR, congenital anomalies, recurrent abortion and cancer pathogenesis. Among them, array-based comparative genome hybridization (aCGH) is used to detect copy-number changes rapidly in a genome-wide manner and with high resolution. The target and resolution of aCGH depend on the type and/or design of mounted probes, and many types of microarray have been used for the screening of patients with MR and other congenital disorders: bacterial artificial chromosome (BAC)-based arrays covering whole genomes,[9,10] BAC arrays covering chromosome X,[11,12] a BAC array covering all subtelomeric regions,[13] oligonucleotide arrays covering whole genomes,[14,15] an oligonucleotide array for clinical diagnosis[16] and a single nucleotide polymorphism array covering the whole genome.[17] Because genome-wide aCGH has led to an appreciation of widespread copy-number variants (CNVs) not only in affected patients but also in healthy populations,[18–20] clinical cytogenetists need to discriminate between CNVs likely to be pathogenic (pathogenic CNVs, pCNVs) and CNVs less likely to be relevant to a patient's clinical phenotypes (benign CNVs, bCNVs).[21] The detection of more CNVs along with higher-resolution microarrays needs more chances to assess detected CNVs, resulting in more confusion in a clinical setting.

We have applied aCGH to the diagnosis and investigation of patients with multiple congenital anomalies and MR (MCA/MR) of unknown etiology. We constructed a consortium with 23 medical institutes and hospitals in Japan, and recruited 536 clinically uncharacterized patients with a normal karyotype in conventional cytogenetic tests. Two-stage screening of copy-number changes was performed using two types of BAC-based microarray. The first screening was performed by a targeted array and the second screening was performed by an array covering the whole genome. In this study, we diagnosed well-known genomic disorders effectively in the first screening, assessed the pathogenicity of detected CNVs to investigate an etiology in the second screening and discussed the clinical significance of aCGH in the screening of congenital disorders.

MATERIALS AND METHODS

Subjects

We constructed a consortium of 23 medical institutes and hospitals in Japan, and recruited 536 Japanese patients with MCA/MR of unknown etiology from July 2005 to January 2010. All the patients were physically examined by an expert in medical genetics or a dysmorphologist. All showed a normal karyotype by conventional approximately 400–550 bands-level G-banding karyotyping. Genomic DNA and metaphase chromosomes were prepared from peripheral blood lymphocytes using standard methods. Genomic DNA from a lymphoblastoid cell line of one healthy man and one healthy woman were used as a normal control for male and female cases, respectively. All samples were obtained with prior written informed consent from the parents and approval by the local ethics committee and all the institutions involved in this project. For subjects in whom CNV was detected in the first or second screening, we tried to analyze their parents as many as possible using aCGH or fluorescence *in situ* hybridization (FISH).

Array-CGH analysis

Among our recently constructed in-house BAC-based arrays,[22] we used two arrays for this two-stage survey. In the first screening we applied a targeting array, 'MCG Genome Disorder Array' (GDA). Initially GDA version 2, which contains 550 BACs corresponding to subtelomeric regions of all chromosomes except 13p, 14p, 15p, 21p and 22p and causative regions of about 30 diseases already reported, was applied for 396 cases and then GDA version 3, which contains 660 BACs corresponding to those of GDA version 2 and pericentromeric regions of all chromosomes, was applied for 140 cases. This means that a CNV detected by GDA is certainly relevant to the patient's phenotypes. Subsequently in the second screening we applied 'MCG Whole Genome Array-4500' (WGA-4500) that covers all 24 human chromosomes with 4523 BACs at intervals of approximately 0.7 Mb to analyze subjects in whom no CNV was detected in the first screening. WGA-4500 contains no BACs spotted on GDA. If necessary, we also used 'MCG X-tiling array' (X-array) containing 1001 BAC/PACs throughout X chromosome other than pseudoautosomal regions.[12] The array-CGH analysis was performed as previously described.[12,23]

For several subjects we applied an oligonucleotide array (Agilent Human Genome CGH Microarray 244K; Agilent Technologies, Santa Clara, CA, USA) to confirm the boundaries of CNV identified by our in-house BAC arrays. DNA labeling, hybridization and washing of the array were performed according to the directions provided by the manufacturer. The hybridized arrays were scanned using an Agilent scanner (G2565BA), and the CGH Analytics program version 3.4.40 (Agilent Technologies) was used to analyze copy-number alterations after data extraction, filtering and normalization by Feature Extraction software (Agilent Technologies).

Fluorescence *in situ* hybridization

Fluorescence *in situ* hybridization was performed as described elsewhere[23] using BACs located around the region of interest as probes.

RESULTS

CNVs detected in the first screening

In the first screening, of 536 cases subjected to our GDA analysis, 54 (10.1%) were determined to have CNV (Figure 1; Tables 1 and 2).

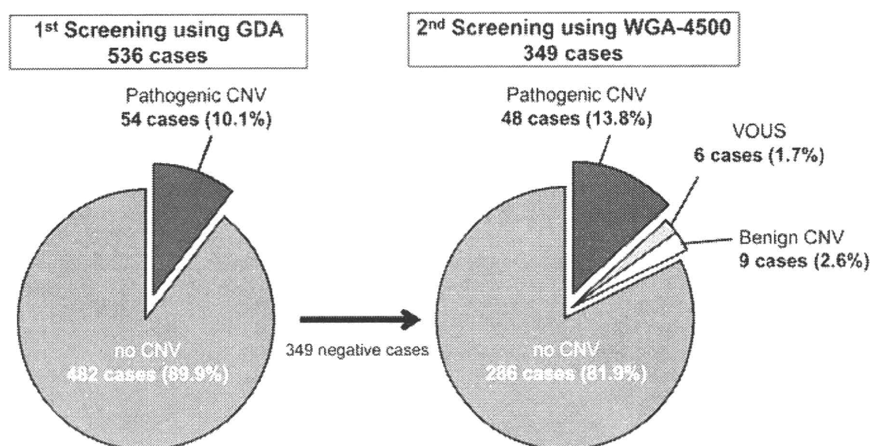

Figure 1 Percentages of each screening in the current study.

Table 1 A total of 40 cases with CNV at subtelomeric region(s) among 54 positive cases in the first screening

	Position where CNV detected				
Gender	*Loss*	*Gain*	*Corresponding disorder*[a]	*OMIM or citation*	*Parental analysis*[b]
M	1p36.33		Chromosome 1p36 deletion syndrome	#607872	
M	1p36.33p36.32		Chromosome 1p36 deletion syndrome	#607872	
M	1p36.33p36.32		Chromosome 1p36 deletion syndrome	#607872	
M	1p36.33p36.32		Chromosome 1p36 deletion syndrome	#607872	
M	1q44		Chromosome 1q43-q44 deletion syndrome	#612337	
F	2q37.3		2q37 monosomy[c]	Shrimpton *et al.*[24]	
F	2q37.3		2q37 monosomy[c]	Shrimpton *et al.*[24]	
M	3q29		Chromosome 3q29 deletion syndrome	#609425	
F	5p15.33p15.32		Cri-du-chat syndrome	#123450	
M	5q35.2q35.3		Chromosome 5q subtelomeric deletion syndrome	Rauch *et al.*[25]	
F	6p25.3		Chromosome 6pter-p24 deletion syndrome	#612582	
M	7q36.3		7q36 deletion syndrome[d]	Horn *et al.*[26]	
F	7q36.3		7q36 deletion syndrome[d]	Horn *et al.*[26]	
M	9p24.3p24.2		Chromosome 9p deletion syndrome	#158170	
F	9q34.3		Kleefstra syndrome	#610253	
F	10q26.3		Chromosome 10q26 deletion syndrome	#609625	
F	16p13.3		Chromosome 16p13.3 deletion syndrome	#610543	
F	22q13.31		Chromosome 22q13 deletion syndrome	#606232	
M	22q13.31q13.33		Chromosome 22q13 deletion syndrome	#606232	
M		15q26.3	15q overgrowth syndrome[c]	Tatton-Brown *et al.*[27]	
F		15q26.3	15q overgrowth syndrome[c]	Tatton-Brown *et al.*[27]	
M		21q22.13q22.3	Down's syndrome (partial trisomy 21)	#190685	
M		Xp22.33	A few cases have been reported; e.g. V5-130 in Lu *et al.*[28]		
M		Xq28	Chromosome Xq28 duplication syndrome	#300815	
F	1q44		Chromosome 1q43-q44 deletion syndrome	#612337	
		8p23.2p23.3			
M	3p26.3		3p deletion syndrome[d]	Fernandez *et al.*[29]	
		12p13.33p11.22			
F	3p26.3		3p deletion syndrome[d]	Fernandez *et al.*[29]	
		16p13.3	Chromosome 16p13.3 duplication syndrome	#613458	
F	4q35.2		4q− syndrome[d]	Jones *et al.*[30]	
		7q36.3			
M	5p15.33		Cri-du-chat syndrome	#123450	
		20p13			
M	5p15.33p15.32		Cri-du-chat syndrome	#123450	
		2p25.3			
F	6q27		6q terminal deletion syndrome[d]	Striano *et al.*[31]	
		11q25			
F	6q27		6q terminal deletion syndrome[d]	Striano *et al.*[31]	
		8q24.3			
M	7q36.3		7q36 deletion syndrome[d]	Horn *et al.*[26]	*dn*
		1q44			
M	9p24.3p24.2		Chromosome 9p deletion syndrome	#158170	
		7q36.3			
F	10p15.3p15.2		Chromosome 10p terminal deletion[d]	Lindstrand *et al.*[32]	*pat*
		7p22.3p22.2			
M	10p15.3		Chromosome 10p terminal deletion[d]	Lindstrand *et al.*[32]	
		2p25.3			
M	10q26.3		Chromosome 10q26 deletion syndrome	#609625	
		2q37.3	Distal trisomy 2q[d]	Elbracht *et al.*[33]	
M	18q23		Chromosome 18q deletion syndrome	#601808	
		7q36.3			
F	22q13.31q13.33		Chromosome 22q13.3 deletion syndrome	#606232	*pat*
		17q25.3	One case was reported	Lukusa *et al.*[34]	
M	Xp22.33/Yp11.32		Contiguous gene–deletion syndrome on Xp22.3[d]	Fukami *et al.*[35]	
		Xq27.3q28	Chromosome Xq28 duplication syndrome	#300815	

Abbreviations: F, female; CNV, copy-number variant; M, male; OMIM, Online Mendelian Inheritance in Man; *dn*, *de novo* CNV observed in neither of the parents.
[a]The name of disorder is based on entry names of OMIM, expect for entry names in DECIPHER and description in each cited article.
[b]*pat*, father had a balanced translocation involved in corresponding subtelomeric regions.
[c]Entry names in DECIPHER.
[d]Description in each cited article.

All the CNVs detected in the first screening were confirmed by FISH. Among the positive cases, in 24 cases one CNV was detected. All the CNVs corresponded to well-established syndromes or already described disorders (Table 1). In 16 cases two CNVs, one deletion and one duplication, were detected at two subtelomeric regions, indicating that one of parents might be a carrier with reciprocal translocation involved in corresponding subtelomeric regions, and at least either of the two CNVs corresponded to the disorders. We also performed parental analysis by FISH for three cases whose parental samples were available, and confirmed that in two cases the subtelomeric aberrations were inherited from paternal balanced translocation and in one case the subtelomeric aberrations were *de novo* (Table 1). In the other 14 cases, CNVs (25.9%) were detected in regions corresponding to known disorders (Table 2).

Table 2 Other cases among 54 positive cases in the first screening

	Position where CNV detected			
Gender	*Gain*	*Loss*	*Corresponding disorder*	*OMIM*
F		4p16.3 4q35.2	Ring chromosome	
M		3q22.323	BPES	#110100
M		2q22.3	ZFHX1B region	*605802
M		4q22.1	Synuclein (SNCA) region	*163890
F		7p21.1	Craniosynostosis, type 1	#123100
F		7q11.23	Williams syndrome	#194050
F		8q23.3q24.11	Langer–Giedion syndrome	#150230
M	15q11.2q13.1		Prader–Willi/Angelman	#176270/ #105830
F		17p11.2	Smith–Magenis syndrome	#182290
M		17q11.2	Neurofibromatosis, type I	+162200
M	22q11.21		DiGeorge syndrome	#188400
F		22q11.21	DiGeorge syndrome	#188400
F	Xp22.31		Kallmann syndrome 1	+308700
F	Whole X		Mosaicism	

Abbreviations: CNV, copy-number variant; F, female; M, male; OMIM, Online Mendelian Inheritance in Man.

CNVs detected in the second screening and assessment of the CNVs

Cases were subject to the second screening in the order of subjects detected no CNV in the first screening, and until now we have analyzed 349 of 482 negative cases in the first screening. In advance, we excluded highly frequent CNVs observed in healthy individuals and/or in multiple patients showing disparate phenotypes from the present results based on an internal database, which contained all results of aCGH analysis we have performed using WGA-4500, or other available online databases; for example, Database of Genomic Variant (http://projects.tcag.ca/variation/). As a result, we detected 66 CNVs in 63 cases (Figure 1; Table 3). Among them, three patients (cases 36, 42 and 44) showed two CNVs. All the CNVs detected in the second screening were confirmed by other cytogenetic methods including FISH and/or X-array. For 60 cases, we performed FISH for confirmation and to determine the size of each CNV. For five cases, cases 13, 36, 48, 57 and 63, with CNVs on the X chromosome, we used the X-array instead of FISH. For cases 4, 6, 16–19 and 34, we also used Agilent Human Genome CGH Microarray 244K to determine the refined sizes of CNVs. The maximum and minimum sizes of each CNV determined by these analyses are described in Table 3.

Well-documented pCNVs emerged in the second screening

CNVs identified for recently established syndromes. We assessed the pathogenicity of the detected CNVs in several aspects (Figure 2).[21,37,38] First, in nine cases, we identified well-documented pCNVs, which are responsible for syndromes recently established. A heterozygous deletion at 1q41–q42.11 in case 2 was identical to patients in the first report of 1q41q42 microdeletion syndrome.[39] Likewise a CNV in case 3 was identical to chromosome 1q43–q44 deletion syndrome (OMIM: #612337),[40] a CNV in case 4 was identical to 2q23.1 microdeletion syndrome,[41] a CNV in case 5 was identical to 14q12 microdeletion syndrome[42] and a CNV in case 6 was identical to chromosome 15q26-qter deletion syndrome (Drayer's syndrome) (OMIM: #612626).[43] Cases 7, 8 and 9 involved CNVs of different sizes at 16p12.1-p11.2, the region responsible for 16p11.2-p12.2 microdeletion syndrome.[44,45] Although an interstitial deletion at 1p36.23-p36.22 observed in case 1 partially overlapped with a causative region of chromosome 1p36 deletion syndrome (OMIM: #607872), the region deleted was identical to a proximal interstitial 1p36 deletion that was recently reported.[46] Because patients with the proximal 1p36 deletion including case 1 demonstrated different clinical characteristics from cases of typical chromosome 1p36 deletion syndrome, in the near term their clinical features should be redefined as an independent syndrome.[46]

CNVs containing pathogenic gene(s). In four cases we identified pCNVs that contained a gene(s) probably responsible for phenotypes. In case 10, the CNV had a deletion harboring *GLI3* (OMIM: *165240) accounting for Greig cephalopolysyndactyly syndrome (GCS; OMIM: 175700).[47] Although phenotypes of the patient, for example, pre-axial polydactyly of the hands and feet, were consistent with GCS, his severe and atypical features of GCS, for example, MR or microcephaly, might be affected by other contiguous genes contained in the deletion.[48] Heterozygous deletions of *BMP4* (OMIM: *112262) in case 11 and *CASK* (OMIM: *300172) in case 13 have been reported previously.[49,50] In case 12, the CNV contained *YWHAE* (OMIM: *605066) whose haploinsufficiency would be involved in MR and mild CNS dysmorphology of the patient because a previous report demonstrated that haploinsufficiency of *ywhae* caused a defect of neuronal migration in mice[51] and a recent report also described a microdeletion of *YWHAE* in a patient with brain malformation.[52]

Recurrent CNVs in the same regions. We also considered recurrent CNVs in the same region as pathogenic; three pairs of patients had overlapping CNVs, which have never been reported previously. Case 16 had a 3.3-Mb heterozygous deletion at 10q24.31–q25.1 and case 17 had a 2.0-Mb deletion at 10q24.32–q25.1. The clinical and genetic information will be reported elsewhere. Likewise, cases 14 and 15 also had an overlapping CNV at 6q12–q14.1 and 6q14.1, and cases 18 and 19 had an overlapping CNV at 10p12.1–p11.23. Hereafter, more additional cases with the recurrent CNV would assist in defining new syndromes.

CNVs reported as pathogenic in previous studies. Five cases were applicable to these criteria. A deletion at 3p21.2 in case 20 overlapped with that in one case recently reported.[53] The following four cases had CNVs reported as pathogenic in recent studies: a CNV at 7p22.1 in case 21 overlapped with that of patient 6545 in a study by Friedman *et al.*,[14] a CNV at 14q11.2 in case 22 overlapped with those of patients 8326 and 5566 in Friedman *et al.*,[14] a CNV at 17q24.1–q24.2 in case 23 overlapped with that in patient 99 in Buysse *et al.*[54] and a CNV at 19p13.2 in case 24 overlapped with case P11 in Fan *et al.*[55]

Large or gene-rich CNVs, or CNVs containing morbid OMIM genes. In cases inapplicable to the above criteria, we assessed CNVs

Table 3 Sixty-three cases with CNV in the 2nd screening

Case	Gender	Clinical diagnosis	Remarkable clinical features	CNV Position	WGA-4500[b]	FISH[b]	Base position and size of the identified CNV[a]: Start (max)	Start (min)	End (min)	End (max)	Size (min)	Size (max)	Parental analysis	Protein-coding genes[c]	CNV assessment[d]	Corresponding or candidate gene(s)
1	M	MCA/MR		del 1p36.23p36.22	arr cgh 1p36.23p36.22 (RP11-81J7→RP11-199O1)x1	ish del(1)(p36.23p36.22) (RP11-462M3+, RP11-106A3-, RP11-28P4+)dn	8 585 127	8 890 860	10 561 097	11 143 717	1 670 237	2 558 590	*dn*	32	P	
2	M	MCA/MR		del 1q41q42.11	arr cgh 1q41 (RP11-135J2→RP11-239E10)x1	ish del(1)(q41q42.11) (RP11-706L9+, RP11-224O19-, RP11-367O4-)dn	215 986 492	216 532 600	221 534 398	222 467 931	5 001 798	6 481 439	*dn*	35	P	
3	F	MCA/MR	Epilepsy	del 1q44	arr cgh 1q44 (RP11-156E8)x1	ish del(1)(q44) (RP11-56O19+, RP11-156E8-)	241 996 973	243 177 632	243 251 660	244 141 010	74 028	2 144 037		11	P	
4	F	MCA/MR		del 2q22	arr cgh 2q23.1 (RP11-72H23)x1	ish del(2)(q23.1) (RP11-375H16-)	147 651 472	147 688 255	149 855 826	149 879 891	2 167 571	2 228 419		7	P	
5	F	MCA/MR		del 14q12q13.2	arr cgh 14q12q13.2 (RP11-369O9→RP11-26M6)x1	ish del(14)(q13.2) (RP11-831F6-)	28 768 137	29 297 829	34 689 412	35 489 337	5 391 583	6 721 200		25	P	
6	M	MCA/MR	CHD	del 15q26.2	arr cgh 15q26.2q26.3 (RP11-79C10→RP11-80F4)x1	ish del(15)(q26.2) (RP11-308P12-)	93 199 415	93 214 053	96 928 421	96 942 334	3 714 368	3 742 919		6	P	
7	M	MCA/MR	CHD	del 16p12.1p11.2	arr cgh 16p12.1p11.2 (RP11-309I14→RP11-150K5)x1	ish del(16)(p11.2) (RP11-75J11-)dn	25 795 340	27 008 538	29 825 404	31 443 492	2 816 866	5 648 152	*dn*	138	P	
8	M	MCA/MR	CHD	del 16p11.2	arr cgh 16p12.1p11.2 (RP11-360L15→RP11-150K5)x1	ish del(16)(p11.2) (RP11-360L15-, RP11-388M20+, RP11-75J11+)dn	27 184 508	28 873 631	29 825 404	31 443 492	951 773	4 258 984	*dn*	134	P	
9	F	MCA/MR		del 16p11.2	arr cgh 16p11.2 (RP11-368N21→RP11-499D5)x1	ish del(16)(p11.2) (RP11-388M20-, RP11-75J11-)	28 873 841	29 408 698	32 773 200	34 476 095	3 364 502	5 602 254		125	P	
10	M	MCA/MR		del 7p14.2p13	arr cgh 7p14.2p13 (RP11-138E20→RP11-52M17)x1	ish del(7)(p14.1p13) (RP11-258I11+, RP11-2J17-, RP11-346F12-)dn	35 621 006	36 470 190	44 657 334	45 508 196	8 187 144	9 887 190	*dn*	70	P	*GLI3*
11	F	MCA/MR	Corneal opacity	del 14q22.1q22.3	arr cgh 14q22.1q22.3 (RP11-122A4→RP11-172G1)x1	ish del(14)(q22.1) (RP11-122A4-, RP11-316L15+)dn	51 964 774	51 983 834	54 730 496	55 054 754	2 746 662	3 089 980	*dn*	18	P	*BMP4*
12	M	MCA/MR	Idiopathic leukodystrophy	del 17q13.3	arr cgh 17p13.3 (RP11-294J5→RP11-357O7)x1	ish del(17)(p13.3) (RP11-4F24-, RP11-26N6+)dn	1 008 128	1 146 211	2 077 151	2 026 967	930 940	1 018 839	*dn*	22	P	*YWHAE*
13	M	MCA/MR		del Xp11.4p11.3	arr cgh Xp11.3p11.4 (RP11-1069J5→RP11-245M24)x1	ish del(X)(p11.4p11.3) (RP11-95C16-, RP11-829C10-)dn	41 392 291	41 385 453	45 419 624	45 495 709	4 034 171	4 103 418	*dn*	9	P	*CASK*

Table 3 Continued

Case	Gender	Clinical diagnosis	Remarkable clinical features	CNV Position	WGA-4500[b]	FISH[b]	Base position and size of the identified CNV[a] Start (max)	Start (min)	End (min)	End (max)	Size (min)	Size (max)	Parental analysis	Protein-coding genes[c]	CNV assessment[d]	Corresponding or candidate gene(s)
14	M	MCA/MR		del 6q12q14.1	arr cgh 6q12q14.2(RP11-502L6→ RP11-232L4)x1	ish del(6)(q13) (RP11-28P18-)dn	69 029 871	69 731 888	83 926 178	85 101 718	14 194 290	16 071 847	*dn*	56	P	
15	M	ZLS		del 6q14.1	arr cgh 6q14.1 (RP11-343P23→ RP11-217L13)x1	ish del(6)(q14.1) (RP11-5N7-,RP11-990K4-,RP11-1I6+)	75 484 004	76 145 436	79 474 428	79 851 528	3 328 992	4 367 524		10	P	
16	F	MCA/MR	CHD	del 10p12.1p11.23	arr cgh 10p12.1p11.23 (RP11-89D1→ 91A23)x1	ish del(10) (p12.1p11.23) (RP11-164A7-, RP11-110B21-)	27 045 285	27 054 002	29 057 401	29 088 950	2 003 399	2 043 665		18	P	
17	M	MCA/MR		del 10p12.1p11.23	arr cgh 10p12.1p11.23 (RP11-218D6→ RP11-RP11-181I11)x1	ish del(10)(p11.23) (RP11-15H10-)	28 121 596	28 131 608	30 559 024	30 577 807	2 427 416	2 456 211		12	P	
18	M	MCA/MR	CHD	del 10q24.31q25.1	arr cgh 10q24.31q25.1 (RP11-108L7→ RP11-108L7)x1	ish del(10)(q24.33) (RP11-416N2-)dn	102 560 783	102 568 462	105 914 057	105 929 608	3 345 595	3 368 825	*dn*	66	P	
19	M	MCA/MR		del 10q24.32q25.1	arr cgh 10q24.32q25.1 (RP11-21N23→ RP11-99N20)x1	ish del(10)(q24.33) (RP11-416N2-)dn	103 917 900	103 928 189	106 005 827	106 011 522	2 077 638	2 093 622	*dn*	41	P	
20	F	MCA/MR		del 3p21.31p21.2	arr cgh 3p21.31p21.2 (RP11-24F11→ RP11-89F17)x1	ish del(3)(p21.31) (RP11-3B7-)	46 150 261	46 359 965	51 390 597	52 571 544	5 030 632	6 421 283		175	P	
21	M	MCA/MR		del 7p22.1	arr cgh 7p22.1 (RP11-90J23→ RP11-2K20)x1	ish del(7)(p22.1) (RP11-2K20-)dn	3 185 609	5 892 225	6 233 987	6 409 277	341 762	3 223 668	*dn*	28	P	
22	F	MCA/MR	Corneal opacity, CHD	dup 14q11.2	arr cgh 14q11.2 (RP11-152G22→ RP11-84D12)x3	ish dup(14)(q11.2) (RP11-152G22++)	20 070 731	20 306 624	20 534 929	21 264 945	228 305	1 194 214		>30	P	
23	M	MCA/MR		del 17q24.1q24.2	arr cgh 17q24.1q24.2 (RP11-89L7→ RP11-79K13)x1	ish del(17) (q24.1q24.2) (RP11-93E5-, RP11-89L7-, RP11-79K13-)	60 576 365	60 936 391	64 592 701	64 587 782	3 656 310	4 011 417		29	P	
24	M	SMS susp.		del 19p13.2	arr cgh 19p13.2 (RP11-197O4→ RP11-164D24)x1	ish del(19)(p13.2) (91021-)	9 248 377	10 248 853	11 968 772	12 553 279	1 719 919	3 304 902	*dn*		P	
25	M	MCA/MR	Epilepsy	dup 2q11.2q13	arr cgh 2q11.2q13(RP11-90G13→ RP11-79K7)x3	ish dup(2)(q11.2) (RP11-542D13++)	88 273 220	91 696 986	109 869 691	112 714 666	18 172 705	24 441 446		>30	P	
26	M	MCA/MR	CHD	dup 4p16.1	arr cgh 4p16.1 (RP11-17I9)x3	ish dup(4)(p16.1) (RP11-301J10++)	8 202 790	8 520 479	9 793 705	10 638 054	1 273 226	2 435 264		17	P	

Table 3 Continued

Case	Gender	Clinical diagnosis	Remarkable clinical features	CNV	Position	WGA-4500[b]	FISH[b]	Base position and size of the identified CNV[a]: Start (max)	Start (min)	End (min)	End (max)	Size (min)	Size (max)	Parental analysis	Protein-coding genes[c]	CNV assessment[d]	Corresponding or candidate gene(s)
27	F	MCA/MR		del	7q22.1q22.2	arr cgh 7q22.1q22.2 (RP11-10D8→ RP11-72J24)x1	ish del(7)(q22.1q22.2) (RP11-124G15+,RP11-188E1-,RP11-95P19-)	97 314 215	98 261 079	105 604 920	106 451 506	7 343 841	9 137 291		135	P	
28	F	MCA/MR	Epilepsy	del	12q13.13	arr cgh 12q13.13 (RP11-74I8→ RP11-624J6)x1	ish del(12)(q13.13) (RP11-624J6-)	50 987 232	51 016 427	51 956 291	52 180 088	939 864	1 192 856		44	P	
29	M	MCA/MR		dup	16q22.3	arr cgh 16q22.3 (RP11-90L19→ RP11-89K4)x3	ish dup(16)(q22.3) (RP11-115E3++, RP11-90L19++)	70 355 260	70 848 592	72 328 913	73 785 124	1 480 321	3 429 864		25	P	
30	M	RTS susp.		dup	16q24.1	arr cgh 16q24.1 (RP11-140K16→ RP11-44201)x3	ish dup(16)(q24.1) (RP11-770B4++, RP11-140K16++)	82 699 729	82 797 548	83 749 375	84 123 857	951 827	1 424 128		16	P	
31	M	MCA/MR	Epilepsy	del	2q24.2q24.3	arr cgh 2q24.2 (RP11-89L13→ RP11-79L13)x1	ish del(2)(q24.2) (RP11-638N12-)	160 407 234	161 072 815	162 883 584	166 923 475	1 810 769	6 516 241		28	P	*TBR1*
32	M	MCA/MR		del	3p26.2	arr cgh 3p26.2 (RP11-32F23)x1	ish del(3)(p26.2) (RP11-32F23-)	3 943 353	4 016 797	4 198 468	4 329 970	181 671	386 617		2	P	*SUMF1*
33	M	MCA/MR	IgA deficiency	del	7q21.11	arr cgh 7q21.11 (RP11-22M18)x1	ish del(7)(q21.11) (RP11-115M2+, RP11-35304-, RP11-22M18-)	83 597 839	83 601 541	84 549 609	84 788 160	948 068	1 190 321		3	P	*SEMA3A*
34	M	MCA/MR		dup	14q32.2	arr cgh 14q32.2 (RP11-128L1)x3	ish dup(14)(q32.2) (RP11-177F8++)	99 330 486	99 337 358	99 841 558	99 845 472	504 200	514 986		7	P	*EML1, YY1*
35	M	MCA/MR	Epilepsy	dup	16p13.3	arr cgh 16p13.3 (RP11-349I11)x3	ish dup(16)(p13.3) (RP11-349I11++)	4 851 459	5 678 447	5 906 909	6 165 923	228 462	1 314 464		9	P	*A2BP1*
36	M	MCA/MR		dup	Xp22.2p22.13	arr cgh Xp22.2p22.13 (RP11-2K15→ RP11-115I10)x3	not performed (X-tiling array)	16 874 735	16 952 121	17 596 600	17 638 351	644 479	763 616		2	P	
				dup	Xp21.3	arr cgh Xp21.3 (RP11-438J7)x3	not performed (X-tiling array)	28 704 076	28 704 076	28 868 075	28 868 075	163 999	163 999		1	P	*IL1RAPL1*
37	F	MCA/MR		del	1p34.3	arr cgh 1p34.3 (RP11-89N10→ RP11-416A14)x1	ish del(1)(p34.2) (RP11-195A8+, RP11-166F21-)dn	37 830 131	38 338 265	39 466 349	39 583 645	1 128 084	1 753 514	*dn*	7	P	
38	M	MCA/MR	Hyper IgE	dup	1q25.2	arr cgh 1q25.2 (RP11-177A2→ RP11-152A16)x3	ish dup(1)(1q25.2) (RP11-177A2++, RP11-152A16++)	177 088 480	177 196 858	177 535 659	177 859 828	338 801	771 348	*dn*	9	P	
39	M	MCA/MR		del	2p24.1p23.3	arr cgh 2p24.1p23.3 (RP11-80H16→ RP11-88F6)x1	ish del(2)(p23.3) (RP11-88F6-, RP11-373D23+)dn	20 037 821	23 094 244	26 815 794	28 414 457	3 721 550	8 376 636	*dn*	86	P	
40	F	MCA/MR	CHD	del	3p26.1p25.3	arr cgh 3p26.1p25.3 (RP11-128A5→ RP11-402P11)x1	ish del(3)(p26.1p25.3) (RP11-936E1-, RP11-402P11-, RP11-1079H21+) dn	8 190 557	8 497 949	9 930 973	10 026 217	1 433 024	1 835 660	*dn*	18	P	

Table 3 Continued

Case	Gender	Clinical diagnosis	Remarkable clinical features	CNV Position	WGA-4500[b]	FISH[b]	Base position and size of the identified CNV[a]: Start (max)	Start (min)	End (min)	End (max)	Size (min)	Size (max)	Parental analysis	Protein-coding genes[c]	CNV assess-ment[d]	Corresponding or candidate gene(s)
41	M	MCA/MR		del 3p22.1p21.31	arr cgh 3p22.1p21.31 (RP11-241P3→RP11-88B8)x1	ish del(3)(p22.1) (RP11-61H16+, RP11-241P3-, RP11-78O10+)dn	41 365 663	42 284 365	48 177 538	49 198 542	5 893 173	7 832 879	*dn*	123	P	
42	M	MCA/MR	Corneal opacity	del 3p14.3p14.2	arr cgh 3p14.3p14.2 (RP11-80H18→RP11-79J9)x1	ish del(3)(p14.2) (RP11-79J19-, RP11-230A22+)mat	57 370 434	58 149 199	58 742 633	58 887 574	593 434	1 517 140	*mat*	11	B	
				del 8q21.11q21.13	arr cgh 8q21.11q21.13 (RP11-225J6→RP11-214E11)x1	ish del(8) (q21.11q21.13) (RP11-225J6-, RP11-48B3+)dn	75 722 961	75 821 163	81 110 557	81 493 446	5 289 394	5 770 485	*dn*	12	P	
43	M	MCA/MR		del 3q26.31q26.33	arr cgh 3q26.31-q26.33 (RP11-292L5→RP11-355N16)x1	ish del(3)(q26.32) (RP11-300L9+, RP11-105L6-)dn	175 650 310	176 531 688	180 613 203	181 653 281	4 081 515	6 002 971	*dn*	12	P	
44	M	MCA/MR	CHD	del 13q13.2q13.3	arr cgh 13q13.2 (RP11-269G10→90F5)x1	ish del(13)(q13.2) (RP11-142E9+, RP11-381E21-, RP11-98D3+)dn	33 451 136	33 895 560	34 813 379	34 909 905	917 819	1 458 769	*dn*	1	P	
				del 22q11.21	arr cgh 22q11.21 (RP11-155F20→54C2)x1	ish del(22)(q11.21) (RP11-155F20-, RP11-590C5-, RP11-54C2-)pat	19 310 307	19 310 307	19 590 642	19 590 642	280 335	280 335	*pat*	15	B	
45	F	aRS		del 18q21.2	arr cgh 18q21.2 (RP11-89B14)x1	ish del(18)(q21.2) (RP11-159D14+, RP11-186B13-, RP11-111C17-)dn	48 218 621	49 166 752	51 288 665	51 861 143	2 121 913	3 642 522	*dn*	9	P	
46	M	MCA/MR		dup 19p13.3	arr cgh 19p13.3 (RP11-49M3→RP11-268O21)x3		1 095 485	2 418 857	3 499 581	4 460 252	1 080 724	3 364 767	*dn*	113	P	
47	F	MCA/MR	Autism	del 19p13.3	arr cgh 19p13.3 (RP11-30F17→RP11-330I7)x1	ish del(19)(p13.3) (RP11-330I7-)dn	4 844 383	6 043 505	6 859 584	6 881 792	816 079	2 037 409	*dn*	23	P	
48	M	MCA/MR		del Xp11.3	arr cgh Xp11.3 (RP11-151G3→RP11-48J14)x0	ish del(X)(p11.3) (RP11-203D16-)mat	44 403 077	44 433 162	46 795 584	46 795 588	2 362 422	2 392 511	*mat*	18	P	
49	M	MCA/MR		dup 3p26.3	arr cgh 3p26.3 (RP11-63O1)x3	ish dup(3)(p26.3) (RP11-63O1++)pat	2 377 366	2 443 357	2 619 407	2 628 216	176 050	250 850	*pat*	1	B	
50	M	MCA/MR		dup 5p14.3	arr cgh 5p14.3 (RP11-91A5)x3	ish dup(5)(p14.3) (RP11-91A5++)pat	19 046 234	19 485 530	19 656 108	20 798 445	170 578	1 752 211	*pat*	1	B	
51	M	MCA/MR		dup 5q13.3	arr cgh 5q13.1 (RP11-40N8→RP11-91C10)x3	ish dup(5)(q13.1) (RP11-105A11++)mat	66 417 271	66 481 371	67 501 700	67 838 977	1 020 329	1 421 706	*mat*	3	B	

Table 3 Continued

Case	Gender	Clinical diagnosis	Remarkable clinical features	CNV Position	WGA-4500[b]	FISH[b]	Start (max)	Start (min)	End (min)	End (max)	Size (min)	Size (max)	Parental analysis	Protein-coding genes[c]	CNV assess-ment[d]	Corresponding or candidate gene(s)
							Base position and size of the identified CNV[a]									
52	M	MCA/MR		dup 7p22.3	arr cgh 7p22.3 (RP11-23D23)x3	ish dup(7)(p22.3) (RP11-23D23++, RP11-1133D5+)mat	1	954 016	954 584	1 101 944	568	1 101 943	*mat*	12	B	
53	F	MCA/MR		dup 8p23.2	arr cgh 8p23.2 (RP11-79I19→ RP11-89I12)x3	ish dup(8)(p23.2) (RP11-89I19++, RP11-89I12++)pat	3 324 954	3 726 061	4 564 671	5 973 493	838 610	2 648 539	*pat*	1	B	
54	M	MCA/MR		dup 9q33.1	arr cgh 9q33.1 (RP11-150L1)x3	ish dup(9)(q33.1) (RP11-150L1++)pat	118 980 752	119 452 372	119 614 984	120 011 559	162 612	1 030 807	*pat*	2	B	
55	F	MCA/MR		dup 10q22.3	arr cgh 10q22.3 (RP11-79M9)x3	ish dup(10)(q22.3) (RP11-79M9++)mat	77 356 915	77 718 484	77 873 148	78 230 039	154 664	873 124	*mat*	1	B	
56	M	MCA/MR	ELBW, hepato-blastoma	dup 12q21.31	arr cgh 12q21.31 (RP11-91C4)x3	ish dup(12)(q21.31) (RP11-91C4++, RP11-142L2+)pat	80 924 954	82 678 148	82 830 190	85 768 388	152 042	4 843 434	*pat*	3	B	
57	M	GS		del Xp11.23	arr cgh Xp11.23 (RP11-876B24) x0 mat	not performed (X-tiling array)	47 752 808	47 747 918	47 852 109	47 868 412	104 191	115 604	*mat*	3	B	
58	M	MCA/MR		dup 8q11.23	arr cgh 8q11.23 (RP11-221P7)x3	ish dup(8)(q11.23) (RP11-221P7++, RP11-26P22++)	53 665 974	53 717 675	54 235 229	54 576 654	517 554	910 680		3	VOUS	
59	F	MCA/MR	Micro-cephaly	dup 10q11.21	arr cgh 10q11.21 (RP11-178A10)x3	ish dup(10)(q11.21) (RP11-178A10++)	41 986 946	42 197 693	42 320 775	43 603 027	123 082	1 616 081		15	VOUS	
60	M	MCA/MR		dup 11p14.2p14.1	arr cgh 11p14.2p14.1 (RP11-1L12)x3	ish dup(11) (p14.2p14.1) (RP11-1L12++)	26 723 462	27 033 270	27 213 374	27 445 504	180 104	722 042		4	VOUS	
61	F	MCA/MR		dup 12p11.1	arr cgh 12p11.1 (RP11-88P4)x3	ish dup(12)(p11.1) (RP11-472A10++)	33 333 493	33 359 944	33 572 956	33 572 956	213 012	239 463		2	VOUS	
62	F	aRS		dup 12q21.31	arr cgh 12q21.31 (RP11-91I24→ RP11-91C4)x3	ish dup(12)(q21.31) (RP11-91C4++, RP11-142L2++)	79 949 648	82 172 368	83 968 319	85 768 388	1 795 951	5 818 740		12	VOUS	
63	F	MR	Congenital myopathy	dup Xq12	arr cgh Xq12 (RP11-90P17→ RP11-383C12)x3	Not performed (X-tiling array)	66 212 661	66 216 353	66 921 699	66 948 538	705 346	735 877		1	VOUS	

Abbreviations: aRS, atyplical Rett syndrome; B, benign; CNV, copy-number variant; *dn*: *de novo* CNV observed in neither of the parents; ELBW, extremely low birth weight; FISH, fluorescence *in situ* hybridization; GS, Gillespie syndrome; *mat*: CNV identified also in mother; P, pathogenic; *pat*: CNV identified also in father; RTS, Rubinstein–Taybi syndrome; SMS, Smith–Magenis syndrome; VOUS, variant of uncertain clinical significance; ZLS, Zimmermann–Laband syndrome.
[a]The sizes were estimated by WGA-4500, X-array, FISH or Agilent Human Genome CGH microarray 244K.
[b]The notation systems is based on ISCN2005.[36]
[c]The number of protein-coding genes contained in the respective CNVs.
[d]The result of CNV assessment.

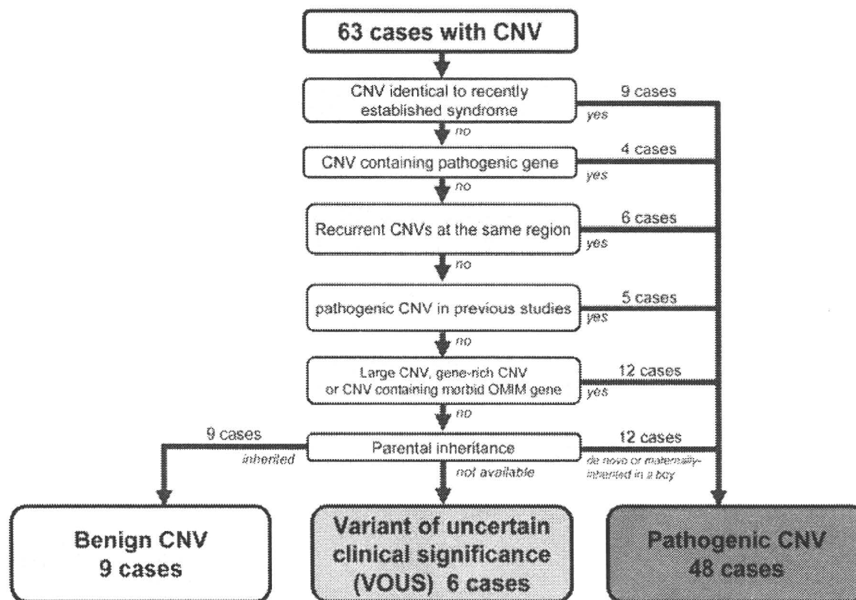

Figure 2 A flowchart of the assessment of CNVs detected in the second screening.

from several aspects. A CNV that contains abundant genes or is large (>3 Mb) has a high possibility to be pathogenic.[21] The CNVs in cases 25–30 probably correspond to such CNVs. Also, we judged a CNV containing a morbid OMIM gene as pathogenic:[21] *TBR1* (OMIM: *604616) in case 31,[56] *SUMF1* (OMIM: *607939) in case 32,[57,58] *SEMA3A* (OMIM: *603961) in case 33,[59] *EML1* (OMIM: *602033) and/or *YY1* (OMIM: *600013) in case 34,[60,61] *A2BP1* (OMIM: *605104) in case 35[62] and *IL1RAPL1* (OMIM: *300206) in case 36.[63] Several previous reports suggest that these genes are likely to be pathogenic, although at present no evidence of a direct association between these genes and phenotypes exists.

CNVs de novo or X maternally inherited. Among the remaining 27 cases, 12 cases had CNVs considered pathogenic as their CNVs were *de novo* (cases 37–47) or inherited del(X)(p11.3) from the mother (case 48). In the second screening we performed FISH for 36 CNVs of the 34 cases whose parental samples were available to confirm that 24 cases had *de novo* CNVs, which were probably pathogenic. A CNV in case 48, a boy with a nullizygous deletion at Xp11.3 inherited from his mother, was also probably relevant to his phenotype (Tables 3 and 4). Meanwhile, although case 57 was a boy with a deletion at Xp11.23 inherited from his mother, he was clinically diagnosed with Gillespie syndrome (OMIM: #206700) that was reported to show an autosomal dominant or recessive pattern,[64] thus we judged that the deletion was not relevant to his phenotype. As a result, cases 49–57 had only CNVs inherited from one of their parents which are likely to be unrelated to the phenotypes; that is, bCNV (Table 4).

As a result, we estimated that 48 cases among 349 analyzed (13.8%) had pCNV(s) in the second screening (Table 3; Figure 2). The CNVs of the remaining six cases, cases 58–63, were not associated with previously reported pathogenicity and their inheritance could not be evaluated, thus we estimated they were variants of uncertain clinical significance (VOUS).[38]

DISCUSSION

Because aCGH is a high-throughput technique to detect CNVs rapidly and comprehensively, this technique has been commonly used for analyses of patients with MCA and/or MR.[38,65–68] However, recent studies of human genomic variation have uncovered surprising properties of CNV, which covers 3.5–12% of the human genome even in healthy populations.[18–20,69] Thus analyses of patients with uncertain clinical phenotypes need to assess whether the CNV is pathogenic or unrelated to phenotypes.[21] However, such an assessment may diminish the rapidness or convenience of aCGH.

In this study, we evaluated whether our in-house GDA can work well as a diagnostic tool to detect CNVs responsible for well-established syndromes or those involved in subtelomeric aberrations in a clinical setting, and then explored candidate pCNVs in cases without any CNV in the first GDA screening. We recruited 536 cases that had been undiagnosed clinically and studied them in a two-stage screening using aCGH. In the first screening we detected CNVs in 54 cases (10.1%). Among them, 40 cases had CNV(s) at subtelomeric region(s) corresponding to the well-established syndromes or the already described disorders and the other 14 cases had CNVs in the regions corresponding to known disorders. Thus about three quarters of cases had genomic aberrations involved in subtelomeric regions. All the subtelomeric deletions and a part of the subtelomeric duplications corresponded to the disorders, indicating that especially subtelomeric deletions had more clinical significance compared to subtelomeric duplications, although the duplication might result in milder phenotypes and/or function as a modifier of phenotypes.[70] Moreover, parental analysis in three cases with two subtelomeric aberrations revealed that two of them were derived from the parental balanced translocations, indicating that such subtelomeric aberrations were potentially recurrent and parental analyses were worth performing. Recently several similar studies analyzed patients with MCA/MR or developmental delay using a targeted array for subtelomeric regions and/or known genomic disorders and detected clinically relevant CNVs in 4.4–17.1% of the patients.[28,65,70,71] Our detection rate in the first screening was equivalent to these reports. Although such detection rates depend on the type of microarray, patient selection criteria and/or number of subjects, these results suggest that at least 10% of cases with undiagnosed MCA/MR and a normal karyotype would be detectable by targeted array.

Table 4 Parental analysis of 34 cases in the second screening

Case	Gender	Clinical diagnosis	CNV		Size of CNV (bp)		Protein-coding genes	Parental analysis	Pathogenicity
			del/dup	Position	Min.	Max.			
1	M	MCA/MR	del	1p36.23p36.22	1670237	2558590	32	*de novo*	P
2	M	MCA/MR	del	1q41q42.11	5001798	6481439	35	*de novo*	P
7	M	MCA/MR	del	16p12.1p11.2	2816866	5648152	138	*de novo*	P
8	M	MCA/MR with CHD	del	16p11.2	951773	4258984	134	*de novo*	P
10	M	MCA/MR	del	7p14.2p13	8516513	9421233	70	*de novo*	P
11	F	MCA/MR	del	14q22.1q22.3	2746662	3089980	18	*de novo*	P
12	M	MCA/MR	del	17q13.3	930940	1018839	22	*de novo*	P
13	M	MCA/MR	del	Xp11.4p11.3	4034171	4103418	9	*de novo*	P
14	M	MCA/MR	del	6q12q14.1	14194290	16071847	56	*de novo*	P
18	M	MCA/MR	del	10q24.31q25.1	3345595	3368825	66	*de novo*	P
19	M	MCA/MR	del	10q24.32q25.1	2077638	2093622	41	*de novo*	P
21	M	MCA/MR	del	7p22.1	341762	3223668	28	*de novo*	P
24	M	SMS susp.	del	19p13.2	1719919	3304902	23	*de novo*	P
37	F	MCA/MR	del	1p34.3	1128084	1753514	7	*de novo*	P
38	M	MCA/MR	dup	1q25.2	338801	771348	9	*de novo*	P
39	M	MCA/MR	del	2p24.1p23.3	3721550	8376636	86	*de novo*	P
40	F	MCA/MR	del	3p26.1p25.3	1433024	1835660	18	*de novo*	P
41	M	MCA/MR	del	3p22.1p21.31	5893173	7832879	123	*de novo*	P
42[a]	M	MCA/MR	del	8q21.11q21.13	5289394	5770485	12	*de novo*	P
42[a]	M	MCA/MR	del	3p14.3p14.2	593434	1517140	11	Maternal	B
43	M	MCA/MR	del	3q26.31q26.33	4081515	6002971	12	*de novo*	P
44[b]	M	MCA/MR	del	13q13.2q13.3	917819	1458769	1	*de novo*	P
44[b]	M	MCA/MR	del	22q11.21	917819	1458769	15	Paternal	B
45	F	Rett syndrome	del	18q21.2	2121913	3642522	9	*de novo*	P
46	M	MCA/MR	dup	19p13.3	2041395	2404096	113	*de novo*	P
47	F	MCA/MR	del	19p13.3	816079	2037409	23	*de novo*	P
48[c]	M	MCA/MR	del	Xp11.3	2362422	2392511	18	Maternal	P
49	M	MCA/MR	dup	3p26.3	176050	250850	1	Paternal	B
50	M	MCA/MR	dup	5p14.3	170578	1752211	1	Paternal	B
51	M	MCA/MR	dup	5q13.3	1020329	1421706	3	Maternal	B
52	M	MCA/MR	dup	7p22.3	568	1101943	12	Maternal	B
53	F	MCA/MR	dup	8p23.2	838610	2648539	1	Paternal	B
54	M	MCA/MR	dup	9q33.1	162612	1030807	2	Paternal	B
55	F	MCA/MR	dup	10q22.3	154664	873124	1	Maternal	B
56	M	MCA/MR	dup	12q21.31	152042	4843434	3	Paternal	B
57	M	Gillespie syndrome	del	Xp11.23	104191	115604	3	Maternal	B

Abbreviations: B, benign; CNV, copy-number variant; F, female; M, male; MCA/MR, multiple congenital anomalies and mental retardation; P, pathogenic.
[a]Two CNVs were detected in case 42.
[b]Two CNVs were detected in case 44.
[c]Nullizygous deletion inherited from his mother probably affected the phenotype.

Another interesting observation in the first screening was that subtelomeric rearrangements frequently occurred even in patients with MCA/MR of uncertain whose karyotype had been diagnosed as normal. This result may be consistent with a property of subtelomeric regions whose rearrangements can be missed in conventional karyotyping,[72] and in fact other techniques involving subtelomeric FISH or MLPA also identified subtelomeric abnormalities in a number of patients with MCA and/or MR in previous reports.[70,73,74] Our result may support the availability of prompt screening of subtelomeric regions for cases with uncertain congenital disorders.

In the second screening we applied WGA-4500 to 349 cases to detect 66 candidate pCNVs in 63 cases (18.1%), and subsequently assessed the pathogenicity of these CNVs. The pCNVs included nine CNVs overlapping identical regions of recently recognized syndromes (cases 1–9; deletion at 1p36.23–p36.22, 1q41–q42.11, 1q43–q44, 2q23.1, 14q12, 15q26-qter and 16p11.2–p12.2, respectively), four CNVs containing disease-associated genes (cases 10–13; *GLI3*, *BMP4*, *YWHAE* and *CASK*, respectively), three pairs of CNVs of recurrent deletions (cases 14, 15: at 6q12–q14.1 and 6q14.1; case 16, 17: at 10p12.1–p11.23 and case 18, 19: at 10q24.31–q25.1 and 10q24.32–q25.1), five CNVs identical to pCNVs in previous studies (cases 20–24), six large and/or gene-rich CNVs (cases 25–30) and six CNVs containing a morbid OMIM gene (cases 31–36). For the remaining cases, we estimated the pathogenicity of the CNVs from a parental analysis (Table 4). We judged the 11 *de novo* CNVs (cases 37–47) and 1 CNV on chromosome Xp11.3 inherited from

the mother (case 48) as probably pathogenic. And nine inherited CNVs (cases 49–57) were probably benign. The clinical significance of CNVs in the other six cases, cases 58–63, remains uncertain (VOUS). As a result we estimated CNVs as pathogenic in 48 cases among 349 cases (13.8%) analyzed in the second screening. None of the pCNVs corresponded to loci of well-established syndromes. This may suggest that our two-stage screening achieved a good balance between rapid screening of known syndromes and investigation of CNV of uncertain pathogenicity.

Table 5 Summary of parental analyses

		Average size (bp)		The average number of protein-coding genes
		Min.	Max.	
Pathogenic CNVs[a]				
del	23	3 309 267	4 597 689	43
dup	2	1 190 098	1 587 722	61
Total	25	3 139 733	4 356 892	44
Benign CNVs[b]				
del	3	538 481	1 030 504	10
dup	8	334 432	1 740 327	3
Total	11	390 082	1 546 739	5

Abbreviation: CNV, copy-number variant.
[a]Twenty-four *de novo* CNVs and case 48.
[b]Eleven inherited CNVs other than case 48.

Among the cases with parental analyses, the 25 pCNVs had larger sizes and contained more protein-coding genes (average size, 3.1 Mb at minimum to 4.4 Mb at maximum; average number of genes, 44) as compared with the 11 inherited bCNVs that were probably unrelated to phenotypes (average size, 0.39 Mb at minimum to 1.5 Mb at maximum; average number of genes, 5) (Table 5). Although all of the 25 pCNVs except 2 were deletions, about three quarters (8 of 11 cases) of the inherited bCNVs were duplications (Table 5). These findings are consistent with previously reported features of pCNVs and bCNVs.[21,38]

We also compared our current study with recent aCGH studies meeting the following conditions: (1) a microarray targeted to whole genome was applied; (2) patients with MCA and/or MR of uncertain etiology, normal karyotype and the criteria for patients selection were clearly described; (3) pathogenicity of identified CNVs were assessed. On the basis of the above criteria, among studies reported in the past 5 years, we summarized 13 studies (Table 6).[10,14,15,17,54,55,75–81] Diagnostic yield of pCNVs in each study was 6.3–16.4%, and our current diagnostic yield of the second screening was 13.8%. Though cases with subtelomeric aberration detected in the first screening had been excluded, our diagnostic yield was comparable to those of the reported studies. It is not so important to make a simple comparison between diagnostic yields in different studies as they would depend on the conditions of each study, for example, sample size or array resolution,[38,82] however it seems interesting that the higher resolution of a microarray does not ensure an increase in the rate of detection of pCNVs. One recent study showed data that may explain the discrepancy between the resolution of microarray and diagnostic yield.[54,83] The authors analyzed 1001 patients with MCA and/or MR using one

Table 6 Previous studies of analyzing patients with MCA and/or MR using aCGH targeted to whole genome

	Applied array			Patients		Pathogenic CNV	
Author (year)	Type	Number[a]	Distribution[b]	Number	Type of disorders	Number	%
Schoumans *et al.*[75]	BAC	2600	1.0 Mb*	41	MCA and MR	4	9.8
de Vries *et al.*[76]	BAC	32 477	Tiling	100	MCA and/or MR	10	10.0
Rosenberg *et al.*[77]	BAC	3500	1.0 Mb*	81	MCA and MR	13	16.0
Krepischi-Santos *et al.*[78]	BAC	3500	1.0 Mb*	95	MCA and/or MR	15	15.8
Friedman *et al.*[14]	SNP	Affymetrix 100K	23.6 kb**	100	MR	11	11.0
Thuresson *et al.*[79]	BAC		1.0 Mb*	48	MCA and MR	3	6.3
Wagenstaller *et al.*[80]	SNP	Affymetrix 100K	23.6 kb**	67	MR	11	16.4
Fan *et al.*[55]	Oligo	Agilent 44K	24 kb–43 kb**	100[c]	MCA and MR, Autism	15[d]	15.0
Xiang *et al.*[15]	Oligo	Agilent 44K	24 kb–43 kb**	40[e]	MR, DD and autism	3	7.5
Pickering *et al.*[10]	BAC	2600	1 Mb*	354[f]	MCA and/or MR	36[g]	10.2
McMullan *et al.*[17]	SNP	Affymetrix 500K	2.5 kb–5.8 kb**	120	MCA and/or MR	18	15.0
Bruno *et al.*[81]	SNP	Affymetrix 250K	2.5 kb–5.8 kb**	117	MCA and/or MR	18	15.4
Buysse *et al.*[54]	BAC	3431	1 Mb*	298	MCA and/or MR	26	8.7
	Oligo	Agilent 44K	24 kb–43 kb**	703	MCA and/or MR	74	10.5
Our current study	BAC	4523	0.7 Mb	349	MCA and MR	48	13.8
Total				2613		305	11.7

Abbreviations: BAC, bacterial artificial chromosome; CNV, copy-number variant; DD, developmental delay; MCA, multiple congenital anomalies; MR, mental retardation; SNP, single nucleotide polymorphism.
[a]The number of clones or name of array is described.
[b]Each distribution referred to each article (*) or manual of each manufacturer (**).
[c]All cases were analyzed by both a targeted array and a genome-wide array.
[d]In five cases, CNVs were also identified by a targeted array.
[e]Ten cases with an abnormal karyotype were excluded.
[f]Only cases studied with an array throughout the genome are described. Ninety-eight cases were also analyzed by a targeted array.
[g]Seventeen cases with an abnormal karyotype were excluded.

of two types of microarray, BAC array and oligonucleotide array. The BAC array was applied for 298 patients to detect 58 CNVs in 47 patients, and among them 26 CNVs (8.7%) were determined to be causal (pathogenic). Conversely, the oligonucleotide arrays were applied for 703 patients to detect 1538 CNVs in 603 patients, and among them 74 CNVs (10.5%) were determined to be pathogenic. These results may lead to the following idea: a lower-resolution microarray detects a limited number of CNVs likely to be pathogenic, because such CNVs tend to be large, and a higher-resolution microarray detects an increasing number of bCNVs or VOUS.[38] Indeed, in studies using a high-resolution microarray, most of the CNVs detected were smaller than 500 kb but almost all pCNVs were relatively large.[54,81,83] Most of the small CNVs were judged not to be pathogenic, and the percentage of pCNVs stabilized at around 10%. This percentage may suggest a frequency of patients with MCA/MR caused by CNV affecting one or more genes, other than known syndromes and subtelomeric aberrations. The other patients may be affected by another cause undetectable by genomic microarray; for example a point mutation or microdeletion/duplication of a single gene, aberration of microRNA, aberration of methylation states, epigenetic aberration or partial uniparental disomy.

As recently hypothesized secondary insult, which is potentially another CNV, a mutation in a phenotypically related gene or an environmental event influencing the phenotype, may result in clinical manifestation.[84] Especially, in two-hit CNVs, two models have been hypothesized: (1) the additive model of two co-occurring CNVs affecting independent functional modules and (2) the epistatic model of two CNVs affecting the same functional module.[85] It also suggests difficulty in selecting an optimal platform in the clinical screening. Nevertheless, information on both pCNVs and bCNVs detected through studies using several types of microarrays is unambiguously significant because an accumulation of the CNVs will create a map of genotype–phenotype correlation that would determine the clinical significance of each CNV, illuminate gene function or establish a new syndrome.

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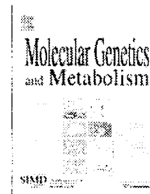

Japan Elaprase® Treatment (JET) study: Idursulfase enzyme replacement therapy in adult patients with attenuated Hunter syndrome (Mucopolysaccharidosis II, MPS II)

Torayuki Okuyama [a,*], Akemi Tanaka [b], Yasuyuki Suzuki [c], Hiroyuki Ida [d], Toju Tanaka [e], Gerald F. Cox [f,g], Yoshikatsu Eto [h], Tadao Orii [i]

[a] Department of Clinical Laboratory Medicine, National Center for Child Health and Development, 2-10-1 Okura, Setagaya-ku, Tokyo 157-8535, Japan
[b] Department of Pediatrics, Osaka City University Graduate School of Medicine, Osaka, Japan
[c] Medical Education Development Center, Gifu University School of Medicine, Gifu, Japan
[d] Department of Pediatrics, The Jikei University School of Medicine, Tokyo, Japan
[e] Department of Clinical Genetics and Molecular Medicine, National Center for Child Health and Development, Tokyo, Japan
[f] Genzyme Corporation, Cambridge, MA, USA
[g] Division of Genetics, Children's Hospital Boston and Department of Pediatrics, Harvard Medical School, Boston, MA, USA
[h] Lysosomal Disease Research Center/Institute for Genetic Disease, The Jikei University School of Medicine, Tokyo, Japan
[i] Emeritus Professor, Gifu University, Gifu, Japan

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ABSTRACT

This open-label clinical study enrolled 10 adults with attenuated Mucopolysaccharidosis II and advanced disease under the direction of the Japan Society for Research on Mucopolysaccharidosis Disorders prior to regulatory approval of idursulfase in Japan. Ten male patients, ages 21–53 years, received weekly intravenous infusions of 0.5 mg/kg idursulfase for 12 months. Significant reductions in lysosomal storage and several clinical improvements were observed during the study (mean changes below). Urinary glycosaminoglycan excretion decreased rapidly within the first three months of treatment and normalized in all patients by study completion (−79.9%). Liver and spleen volumes also showed rapid reductions that were maintained in all patients through study completion (−33.2% and −31.0%, respectively). Improvements were noted in the 6-Minute Walk Test (54.5 m), percent predicted forced vital capacity (3.8 percentage points), left ventricular mass index (−12.4%) and several joint range of motions (8.1–19.0 degrees). Ejection fraction and cardiac valve disease were stable. The sleep study oxygen desaturation index increased by 3.9 events/h, but was stable in 89% (8/9) of patients. Idursulfase was generally well-tolerated. Infusion-related reactions occurred in 50% of patients and were mostly mild with transient skin reactions that did not require medical intervention. Two infusion-related reactions were assessed as serious (urticaria and vasovagal syncope). One patient died of causes unrelated to idursulfase. Anti-idursulfase antibodies developed in 60% (6/10) of patients. In summary, idursulfase treatment appears to be safe and effective in adult Japanese patients with attenuated MPS II. These results are comparable to those of prior studies that enrolled predominantly pediatric, Caucasian, and less ill patients. No new safety risks were identified.

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Introduction

Mucopolysaccharidosis type II (MPS II, Hunter syndrome, OMIM #309900) is an X-linked recessive, lysosomal storage disorder caused by a deficiency of iduronate-2-sulfatase (IDS, EC3.1.6.13). This lysosomal enzyme catalyzes the first step in the degradation of the glycosaminoglycans (GAG), dermatan sulfate and heparan sulfate [1]. Iduronate-2-sulfatase deficiency leads to the accumulation of GAG within the lysosomes of virtually every cell in the body and is excreted in excessive amounts in the urine. MPS II encompasses a wide phenotypic spectrum that includes severe and attenuated forms. The severe form has onset of symptoms by 2–4 years old, progression of somatic symptoms and severe cognitive impairment during childhood, and death by 10–15 years of age. The attenuated form has a later onset in childhood, slower and milder progression of somatic disease, little to no cognitive impairment, and survival into adulthood. (Fig. 1) Common clinical features include coarse faces, upper airway obstruction, cardiac valve regurgitation, restrictive lung disease, hepatosplenomegaly, hernias, joint contractures, poor endurance, and reduced quality of life [2,3]. *IDS* gene mutations are heterogeneous, but some show genotype–phenotype correlations: deletions and gross rearrangements of the *IDS* gene are associated with the severe form, whereas missense

* Corresponding author. Fax: +81 3 3417 2238.
E-mail address: tora@nch.go.jp (T. Okuyama).

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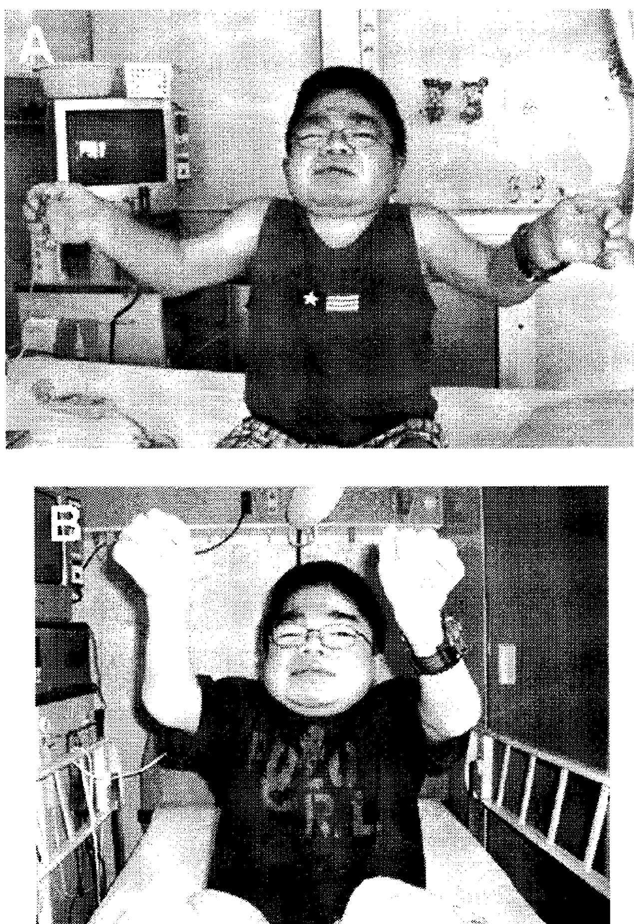

Fig. 1. A 23-year-old Japanese male study patient with MPS II. (A) Before treatment. (B) After 12 months of idursulfase treatment. Note the coarse facial features characteristic of MPS II. At baseline, the patient had severely limited shoulder range of motion (flexion and abduction), which improved following treatment.

mutations are more often associated with attenuated disease [4–10]. No racial or geographic differences have been observed. Females are only rarely affected, most often through skewed X-inactivation [1]. MPS II is the most prevalent MPS disorder in Asia, accounting for >50% of all MPS patients in Japan [10]. The annual incidence of all MPS disorders in Japan is estimated to be 1/50,000–1/60,000, and approximately half of the cases are due to MPS II. The estimated birth incidence of MPS II in Japan is, therefore, 1/90,000–1/100,000 [11], similar to the 1/92,000 to 1/162,000 incidences reported for predominantly Caucasian countries [12–15].

Until recently, treatment of MPS II was mainly palliative and focused on alleviating clinical symptoms through a variety of surgeries, medical devices, therapies, and medications. Several patients have undergone hematopoietic stem cell transplant (HSCT) as a source of iduronate-2-sulfatase, but unlike for MPS I, cognitive decline is not halted and the long-term effects on somatic disease are not well-documented [16,17]. Therefore, most centers consider the risk–benefit profile unfavorable and do not recommend HSCT for patients with MPS II.

Idursulfase (Elaprase®, Shire Human Genetic Therapies, Inc., Cambridge, MA, USA) is a recombinant human form of iduronate-2-sulfatase that is produced in a human cell line. Preclinical studies carried out in an MPS II knockout-mouse model [18] and in a Phase 1/2 dose-ranging study of MPS II patients [19] indicated that idursulfase was effective at reducing lysosomal GAG. The safety and efficacy of idursulfase was confirmed in a Phase 2/3 double-blind, placebo-controlled clinical study that randomized 96 MPS II patients to one of three treatment arms for 52 weeks: 0.5 mg/kg idursulfase weekly, 0.5 mg/kg idursulfase alternating with placebo every other week, or placebo weekly [20]. The primary efficacy endpoint was a composite of changes in percent predicted forced vital capacity (FVC) and the 6-Minute Walk Test (6MWT). Patients who received weekly idursulfase showed a greater difference in the composite endpoint compared to placebo ($p = 0.005$) than did the every other week idursulfase group ($p = 0.042$). The weekly idursulfase arm showed a mean 44.3 m increase in 6MWT distance (37 m difference from placebo, $p = 0.013$) and a mean 3.45 percentage point increase in percent predicted FVC (2.7 percentage point difference from placebo, $p = 0.065$). These clinical changes were associated with significant reductions versus placebo in urinary GAG level (−52.5%, $p < 0.0001$), liver volume (−25.3%, $p < 0.0001$), and spleen volume (−25.1%, $p < 0.0001$). Idursulfase was well-tolerated, with infusion-related reactions being the most common drug-related related adverse events, occurring in 69% (22/32) of patients in the weekly idursulfase arm.

Idursulfase was approved for the treatment of MPS II by the United States Food and Drug Administration (FDA) in July 2006 and by the European Medicines Agency (EMEA) in January 2007. Due to the life-threatening nature of the disease and the small number of patients, the Japanese Ministry of Health, Labour, and Welfare (MHLW) Committee for the Use of Unapproved Drugs recommended that idursulfase be approved based on ethical grounds and the results of overseas clinical trials, which included four Japanese patients. The committee also requested that idursulfase be made available to the most seriously ill MPS II patients prior to approval, which occurred in October 2007. Consequently, the Japan Elaprase Treatment (JET) study was initiated under the direction of the Japan Society for Research on MPS Disorders. Here, we present the results of this study.

Materials and methods

Patients

To be eligible for the study, patients had to meet all of the following inclusion criteria: (1) Documented deficiency of iduronate-2-sulfatase enzyme activity of <10% of the lower limit of normal with a normal enzyme activity level of one other sulfatase. (2) Male and above 20 years of age. (3) Clinically advanced disease status with <80% predicted FVC and New York Heart Association Class II–IV. (4) Capable of showing improved quality of life. (5) Able to complete study assessments.

Patient exclusion criteria included: (1) Previous bone marrow or cord blood transplant. (2) Known hypersensitivity to one of the components of idursulfase. (3) Previous treatment with idursulfase. (4) Unable to receive weekly infusions of idursulfase at the patient's local hospital. All patients provided signed informed consent prior to enrollment.

Study design

This was a multi-center, open-label study that enrolled 10 adult males with MPS II at 5 clinical sites in Japan. The study adhered to the guidelines set forth in the Declaration of Helsinki. Idursulfase was manufactured by Shire Human Genetic Therapies, Inc. and distributed by Genzyme Corporation (Cambridge, MA, USA). Genzyme Corporation performed all statistical analyses, and Genzyme Japan KK (Tokyo, Japan) provided data management support.

Idursulfase

Patients were administered 0.5 mg/kg idursulfase diluted in saline to a final volume of 100 cc intravenously over 3 h on a weekly

basis (±3 days) for up to 12 months. Infusions rates were ramped up over the first hour as described in the Phase 2/3 study [20]. Patients were monitored during each infusion and were discharged 1 h after completing the infusion, if clinically stable.

Efficacy assessments

Urinary GAG level was determined as the concentration of uronic acid normalized for creatinine (mg/g creatinine) and was measured using the carbazole reaction at a central laboratory (SRL Medisearch, Tokyo, Japan) or at Osaka City University Hospital. Liver and spleen volumes were quantitated by computerized tomography (CT), with the upper limits of normal being 2.5% and 0.2% of body weight, respectively. Percent predicted FVC and the 6MWT were performed according to American Thoracic Society guidelines [21,22]. Cardiac structure and function were evaluated by echocardiography (two-dimensional and M-mode). Left ventricular mass index (LVMI) was calculated as the left ventricular mass normalized for body surface area, with normal values defined as <131 g/m^2. Active joint range of motion was measured by goniometry, and included the shoulder (flexion, extension, and abduction), elbow (flexion and extension), hip (flexion and extension), and knee (flexion and extension). Left and right joint ranges of motion for each were averaged for each patient. The sleep study oxygen desaturation index (ODI) was assessed by pulse oximetry and defined as the number of desaturations (<89% oxygen saturation or $\geqslant$4% decrease in oxygen saturation from baseline lasting $\geqslant$ 10 s) per hour of sleep. A normal ODI was considered to be <5 events/h [23].

Safety assessments

Safety evaluation included continuous monitoring of adverse events and periodic clinical laboratory and physical examination evaluations. Adverse events were reported by severity (mild, moderate, severe, life-threatening) and by relatedness to idursulfase. An infusion-related reaction was defined as any adverse event occurring during or following an infusion (i.e., within 24 h of infusion initiation) that was reported by the investigator as related to idursulfase. Antibodies to idursulfase were measured by an enzyme-linked immunosorbant assay (ELISA; Shire Human Genetic Therapies).

Statistics

Efficacy results are reported as the mean ± standard error of the mean (SEM). For missing data at 12 months, the last observation carried forward method was used for values obtained at 6 months or later. The number of evaluable patients was at least nine for each endpoint, except for LVMI ($n = 6$, primarily due to missing baseline data) and the 6MWT ($n = 7$, primarily due to the inability to perform the test). The Wilcoxon signed rank test was used to evaluate changes in efficacy endpoint from baseline to 12 months, and p-values <0.05 were considered statistically significant. Percent change was tested for pharmacodynamic parameters (i.e., urinary GAG level and liver and spleen volumes), whereas absolute change was tested for clinical endpoints.

Results

Patient disposition

Ten adult Japanese males with attenuated MPS II were enrolled in the study and received idursulfase treatment. Nine patients completed the 12-month study; one patient died of causes unrelated to idursulfase after receiving 41 of 44 scheduled infusions (see Safety Section). Compliance with treatment was excellent, with all 10 patients receiving >93% of scheduled infusions; 80% (8/10) of patients did not miss a single scheduled infusion.

Patients

The mean patient age was 30.1 years (range 21.1–53.9). All patients had been diagnosed during mid-childhood or adolescence with MPS II (mean age 7.9 years), and all had advanced disease burden at the time of enrollment into the study. All patients had short stature (height <3rd percentile for Japanese adult males). Past medical history was significant for the following MPS II-related features (n = number of patients): valvular heart disease consisting mainly of aortic and/or mitral valve insufficiency (10), joint contractures (7), hepatomegaly (7), deafness (6), retinal degeneration (5), sleep apnea (5), otitis media

Table 1
Summary of efficacy changes after 12 months of treatment with idursulfase.

	N	Baseline	12 months	Change	% Change	p-Value
Urinary GAG (mg/g creatinine)	9	106.4 ± 7.8	21.2 ± 2.9	−85.2 ± 7.1	−79.9 ± 2.2	0.004†
Liver volume (cc)	10	1491.2 ± 92.9	993.2 ± 75.0	−498.0 ± 70.2	−33.2 ± 4.0	0.002†
Spleen volume (cc)	10	210.2 ± 22.5	138.1 ± 12.5	−72.1 ± 15.7	−31.0 ± 5.5	0.002†
6-Minute Walk Test (m)	7	286.0 ± 53.4	340.5 ± 49.6	54.5 ± 27.0	37.4 ± 18.1	0.109
Forced vital capacity (% predicted)	9	39.9 ± 6.6	43.7 ± 6.0	3.8 ± 2.8	15.0 ± 8.0	0.250
Forced vital capacity (L)	9	1.4 ± 0.3	1.5 ± 0.2	0.1 ± 0.1	16.3 ± 8.0	0.250
Left ventricular mass index (g/m^2)	6	139.9 ± 25.1	133.2 ± 38.9	−6.7 ± 15.5	−12.4 ± 11.1	0.563
Left ventricular ejection fraction (%)	10	67.0 ± 5.2	64.3 ± 6.0	−2.8 ± 2.5	−6.1 ± 5.7	0.244
Joint range of motion (degrees)					NA	
Shoulder flexion	10	93.8 ± 4.9	109.8 ± 7.1	15.0 ± 7.3		0.066
Shoulder extension	10	44.1 ± 4.1	43.8 ± 3.8	−0.3 ± 4.1		0.945
Shoulder abduction	10	76.3 ± 3.9	95.3 ± 8.1	19.0 ± 8.8		0.125
Knee flexion	9	103.7 ± 8.5	114.4 ± 5.2	10.7 ± 10.3		0.461
Knee extension	9	−11.1 ± 4.5	−10.3 ± 5.0	0.8 ± 2.5		0.875
Hip flexion	9	89.2 ± 8.1	103.3 ± 7.6	14.2 ± 5.1		0.031
Hip extension	9	3.1 ± 5.0	1.9 ± 6.7	−1.3 ± 1.8		0.750
Elbow flexion	10	120.9 ± 4.0	121.8 ± 3.7	0.9 ± 2.5		0.828
Elbow extension	10	−43.1 ± 4.2	−35.0 ± 4.2	8.1 ± 3.4		0.063
Oxygen desaturation index (events/h)	9	18.5 ± 6.1	22.3 ± 7.4	3.9 ± 3.5	NA	0.426

The last observation carried forward (LOCF) method was used to replace a missing value at the 12-month timepoint.
All values are the observed means ± SEM. All p-values are based on the Wilcoxon signed rank test for change from baseline to the 12-month timepoint.
NA, not applicable. Some patients had values of 0 at baseline that precluded calculation of percent change.
† The p-value is based on the Wilcoxon signed rank test for % change from baseline to the 12-month timepoint.

(4), macroglossia (3), umbilical hernia (2), carpal tunnel syndrome (2), heart failure (2), and left ventricular hypertrophy (1).

Urinary glycosaminoglycan (GAG)

All nine evaluable patients had elevated urinary GAG levels at baseline (mean 106.4 mg/g creatinine, approximately 8 times the upper limit of normal); one patient lacked an appropriate baseline value (Table 1). Following idursulfase treatment, urinary GAG levels decreased rapidly within the first three months of treatment and remained low for the remainder of the study (Fig. 2A). There was a statistically significant mean decrease in the urinary GAG level of −79.9 ± 2.2% from baseline to 12 months ($p = 0.004$). All nine evaluable patients showed a >70% decrease in urinary GAG levels and had normal values by the end of the study.

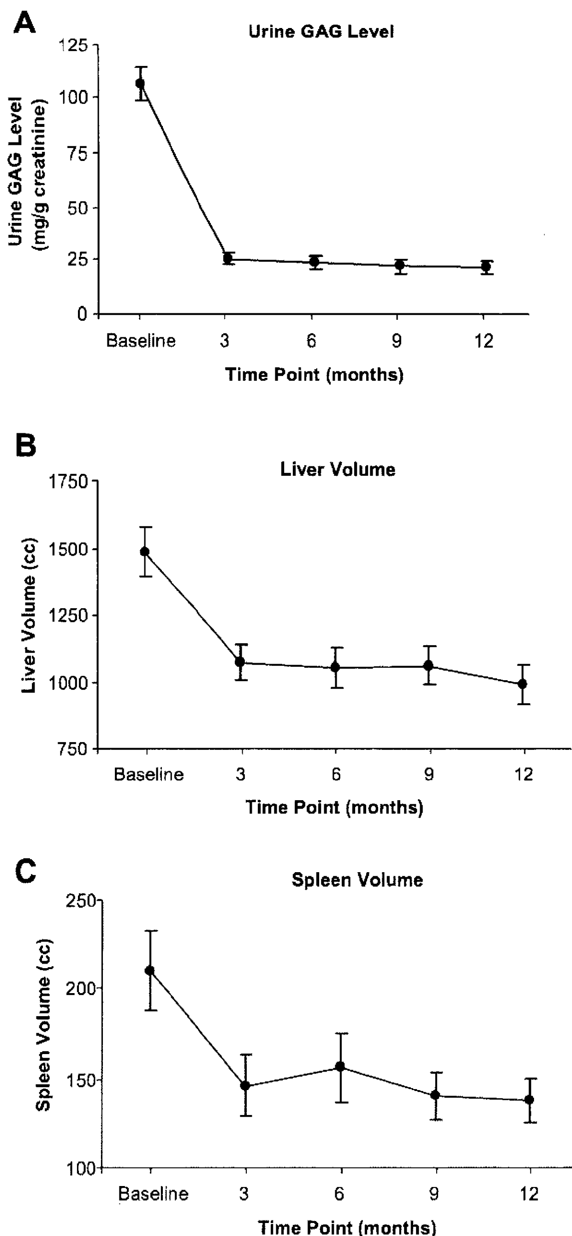

Fig. 2. The effects of idursulfase treatment on lysosomal storage over 12 months. (A) Urinary GAG level. (B) Liver volume. (C) Spleen volume. All changes are reported as mean ± SEM.

Liver and spleen volumes

At baseline, 9 (90%) patients had hepatomegaly (mean 1.3 MN, multiples of normal) and all 10 (100%) patients had splenomegaly (mean 2.4 MN) by CT. After 12 months of treatment, mean liver volume decreased by −33.2 ± 4.0% and mean spleen volume decreased by −31.0 ± 5.5% (Fig. 2B and C; Table 1), and both changes were statistically significant ($p = 0.002$). Most of the reductions occurred within the first three months of treatment. By the end of the study, all patients had liver volumes within the normal range and spleen volumes that were <2 MN, demonstrating efficient reduction of lysosomal GAG storage.

6-Minute Walk Test (6MWT)

At baseline, the mean 6MWT distance was 286.0 m for the seven patients who could perform the test (Table 1). All but one patient walked <399 m, the lower limit of normal for healthy adult men in the United States [24]. Three patients could not perform the 6MWT: one patient broke his leg just prior to the start of the study; one patient was wheelchair-bound secondary to shortness of breath and muscle weakness; and one patient was obese and could only walk a few steps with assistance. By the end of the study, the mean 6MWT distance had increased by 54.5 ± 27.0 m (Fig. 3A). This change represents a relative increase of 37.4%, and included one patient whose 6MWT distance increased by 131%. Four patients (57%) showed a clinically meaningful improvement of ⩾54 m [25], while the one patient with a normal 6MWT at baseline showed a decline (−71 m).

Percent predicted forced vital capacity (FVC)

Nine patients underwent spirometry at baseline and all showed a restrictive lung disease pattern: three were classified as having a severe defect (<50% predicted FVC) and five had a very severe defect (<34% predicted FVC) [26]. At baseline, mean percent predicted FVC was 39.9% (Table 1), and after 12 months it increased by 3.8 ± 2.8 percentage points (Fig. 3B). This improvement corresponds to a relative increase of 15.0% over baseline, which is considered clinically meaningful (⩾15% relative change) [25] and was achieved by four (44%) patients. Similarly, mean FVC increased by 16.3% over the baseline of 1.4 L. The mean forced expiratory volume in 1 s (FEV_1):FVC ratio remained unchanged at 0.70 during the study.

Cardiac

All patients had valve disease that remained stable during the study. The mean ejection fraction (EF) was normal at baseline and showed little change over 12 months (67.0–64.3%, change of −2.8 ± 2.5%) (Table 1). One patient with pre-existing cardiac failure showed gradual worsening during the study (EF 27–14%). At baseline, mean LVMI was slightly elevated at 139.9 g/m^2 (normal <131 g/m^2), and 50% (3/6) of evaluable patients had an elevated LVMI. After 12 months, mean LVMI decreased by −12.4%, with four patients showing a clinically meaningful improvement of >10% [27]. The patient with the largest LMVI at baseline showed a further increase (254.1–312.9 g/m^2).

Joint range of motion

Fig. 4 and Table 1 show the changes in joint range of motion observed during the study. At baseline, patients had significant joint contractures involving the shoulder (flexion, extension, and abduction), knee (flexion and extension), hip flexion and extension), and elbow (flexion and extension). Following 12 months of treatment, several joints showed increased range of motion, including mean

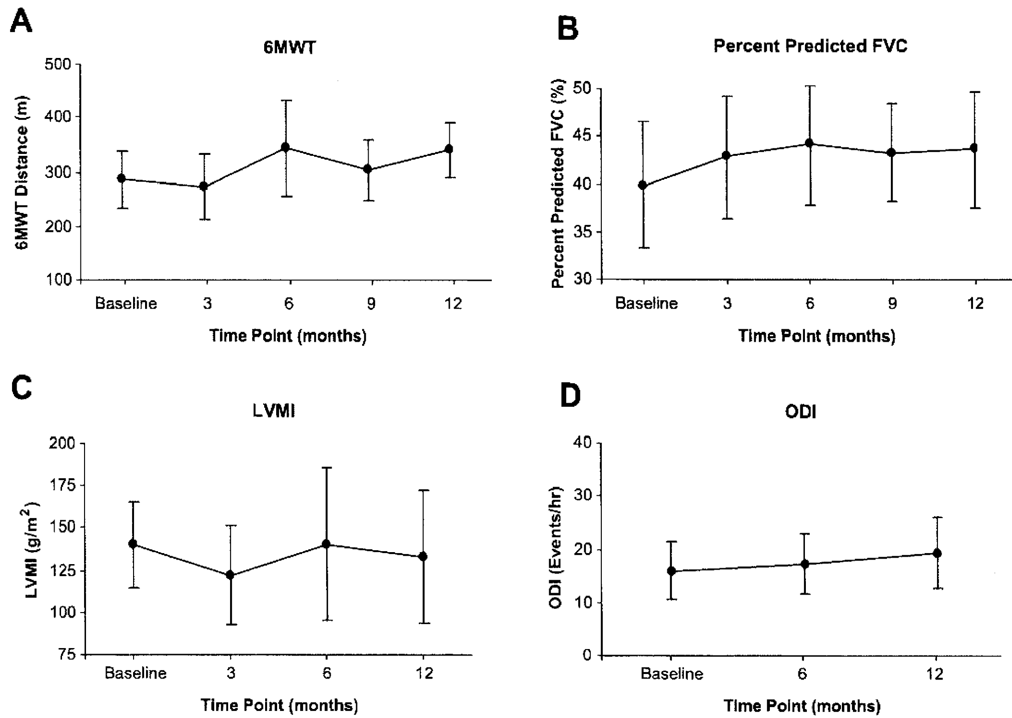

Fig. 3. The effects of idursulfase treatment on clinical endpoints over 12 months. (A) 6-Minute Walk Test. (B) % Predicted forced Vital Capacity. (C) Left Ventricular Mass Index. (D) Oxygen Desaturation Index. All changes are reported as mean ± SEM.

A Shoulder Flexion; B Shoulder Extension; C Shoulder Abduction; D Knee Flexion; E Knee Extension; F Hip Flexion; G Hip Extension; H Elbow Flexion; I Elbow Extension — Degrees vs. Time Point (months): Baseline, 6, 12

Fig. 4. The effects of idursulfase treatment on joint range of motion over 12 months. (A) Shoulder flexion. (B) Shoulder extension. (C) Shoulder abduction. (D) Knee flexion. (E) Knee extension. (F) Hip flexion. (G) Hip extension. (H) Elbow flexion. (I) Elbow extension. All changes are reported as mean ± SEM.