

Genomic Basis of Aromatase Excess Syndrome: Recombination- and Replication-Mediated Rearrangements Leading to *CYP19A1* Overexpression

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Context: Genomic rearrangements at 15q21 have been shown to cause overexpression of *CYP19A1* and resultant aromatase excess syndrome (AEXS). However, mutation spectrum, clinical consequences, and underlying mechanisms of these rearrangements remain to be elucidated.

Objective: The aim of the study was to clarify such unsolved matters.

Design, Setting, and Methods: We characterized six new rearrangements and investigated clinical outcome and local genomic environments of these rearrangements and of three previously reported duplications/deletions.

Results: Novel rearrangements included simple duplication involving exons 1–10 of *CYP19A1* and simple and complex rearrangements that presumably generated chimeric genes consisting of the coding region of *CYP19A1* and promoter-associated exons of neighboring genes. Clinical severities were primarily determined by the copy number of *CYP19A1* and the property of the fused promoters. Sequences at the fusion junctions suggested nonallelic homologous recombination, non-homologous end-joining, and replication-based errors as the underlying mechanisms. The breakpoint-flanking regions were not enriched with GC content, palindromes, noncanonical DNA structures, or known rearrangement-associated motifs. The rearrangements resided in early-replicating segments.

Conclusions: These results indicate that AEXS is caused by duplications involving *CYP19A1* and simple and complex rearrangements that presumably lead to the usage of cryptic promoters of several neighboring genes. Our data support the notion that phenotypes depend on the dosage of *CYP19A1* and the characteristics of the fused promoters. Furthermore, we show that the rearrangements in AEXS are generated by both recombination- and replication-mediated mechanisms, independent of the known rearrangement-inducing DNA features or late-replication timing. Thus, AEXS represents a unique model for human genomic disorders. (*J Clin Endocrinol Metab* 98: E2013–E2021, 2013)

Aromatase excess syndrome (AEXS; MIM no. 139300) is a rare autosomal dominant disorder that causes prepubertal- or peripubertal-onset gynecomastia, hypogonadotropic hypogonadism, advanced bone age, and short adult height in male patients (1, 2). Female patients are usually asymptomatic, although macromastia, irregular menses, and short stature have been reported in a few

individuals (2). AEXS results from excessive expression of the aromatase gene *CYP19A1* on chromosome 15q21.2 (NM_000103) (1). *CYP19A1* comprises 11 noncoding exons 1 that function as tissue-specific promoters (exons I.1, IIa, I.8, I.4, I.5, I.7, 1f, I.2, I.6, I.3, and PII), and nine coding exons (exons 2–10) (3, 4). We and other groups have identified various chromosomal rearrangements at

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Abbreviations: AEXS, aromatase excess syndrome; CGH, comparative genomic hybridization.

15q21 in patients with AEXS (1, 2, 5). These rearrangements included duplications that encompassed seven of the 11 non-coding exons 1 of *CYP19A1* and deletions and inversions that generated chimeric genes consisting of coding exons of *CYP19A1* and promoter-associated exons of neighboring genes. Genotype-phenotype analysis has indicated that clinical severities primarily depend on the functional properties of the fused promoters. These findings provide a novel example of gain-of-function mutations resulting from submicroscopic genomic rearrangements.

Rearrangements in the human genome are known to be generated by recombination-based mechanisms, namely, nonallelic homologous recombination and nonhomologous end-joining, and by replication-based mechanisms (6–9). Of these, nonallelic homologous recombination results from unequal crossover between two homologous sequences, usually on the same but sometimes on different chromosomes (10). Nonallelic homologous recombination accounts for most of the recurrent simple deletions and duplications in the human genome and represents the most common abnormality involved in human genomic disorders (9–11). Nonhomologous end-joining occurs as a result of double-strand DNA breakage and subsequent ligation of the two broken DNA ends (12). Nonhomologous end-joining often underlies nonrecurrent simple deletions associated with short nucleotide stretches at the fusion junctions (9–12). Replication-based mechanisms are caused by aberrant template switching during replication and can produce both simple and complex rearrangements that carry microhomologies at the fusion junctions (8, 9, 13). Previous studies have indicated that nonallelic homologous recombination, nonhomologous end-joining, and replication-based mechanisms are facilitated by various local DNA features including high GC content and palindromes (10, 14–16). Highly similar sequences widely spread in the genome (“repetitive elements”), such as *Alu*, *LINE1*, and *MIR*, can mediate the occurrence of genomic rearrangements (12). Non-B structures, ie, DNA conformations that differ from the canonical Watson-Crick right-handed double helix, and specific short sequence motifs and tri/tetranucleotides have also been suggested as local genomic stimulants (14–22). Furthermore, replication timing of each chromosomal region appears to determine the frequency of rearrangements; nonallelic homologous recombination preferentially occurs in DNA

segments that replicate in early S phase (early-replicating segments), whereas nonhomologous end-joining and replication-based errors frequently appear in late-replicating segments (23).

At present, the underlying mechanisms of the AEXS-associated rearrangements remain largely unknown. Although sequence analysis of the fusion junctions has indicated that nonallelic homologous recombination and nonhomologous end-joining—and possibly replication-based mechanisms as well—are involved in the formation of simple duplications and deletions in AEXS (5), the molecular basis of inversions remains to be determined. Here, we characterized the fine genomic structures of six rearrangements involved in AEXS. Furthermore, we investigated clinical consequences and local genomic environments of the six rearrangements and of three previously reported duplications/deletions.

Patients and Methods

Patients

This study consisted of six cases (cases 1–6) ascertained by prepubertal- or peripubertal-onset gynecomastia. Clinical findings of cases 1–6 are summarized in Table 1. Cases 1–4 are hitherto unreported. Cases 5 and 6 have been described previously, although the genomic structure remains to be determined (1, 2). Cases 1–3 and 5–6 had a 46,XY karyotype, whereas case 4 had a 46,XY inv (9) karyotype that is known as a normal variant. Case 2 had a brother with prepubertal-onset gynecomastia, a sister with premature thelarche, and a father and several paternal relatives with advanced bone age and/or short stature. Case 6 had a son with prepubertal-onset gynecomastia. There was no family history of AEXS in the remaining cases. This study was approved by the Institutional Review Board Committee at the National Center for Child Health and Development. Written informed consent was obtained from the patients and/or their parents.

Copy-number analyses

Leukocyte genomic DNA samples were obtained from cases 1–6, the parents and siblings of case 2, and the son of case 6. Genomic abnormalities involving *CYP19A1* exons and/or its flanking regions were examined by comparative genomic hybridization (CGH) using a custom-made oligoarray or a catalog human array (4 × 180K format, ID 030700 or G4449A; Agilent Technologies). The procedures were performed as described previously (5).

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Table 1. Phenotypic and Endocrine Findings of Cases 1–6

	Case 1	Case 2	Case 3	Case 4	Case 5	Case 6
Genomic rearrangement	Duplication	Deletion	Complex	Complex	Complex	Complex
Age at examination, y	10	8 (18) ^a	15	13	17	36
Phenotypic findings						
Gynecomastia (Tanner stage)	2–3	3	4–5	3–4	Severe	Severe
Onset of gynecomastia, y	7	Unknown	8	11	7	5
Mastectomy	No	Yes	Yes	No	Yes	Yes
Testis, mL	6	N.E.	15	12	Normal	Normal
Pubic hair (Tanner stage)	None	None	3–4	4	N.D.	Normal
Facial hair	None	None	None	Scarce	Scarce	None
Final height	Unknown	Unknown	–0.9 SD	Unknown	<1%ile	<1%ile
Bone age, y ^b	13.0	13.5	N.E.	18.0	N.E.	N.E.
Fertility (spermatogenesis)	Unknown	Unknown	Yes	Unknown	Unknown	Yes
Endocrine findings ^c						
At diagnosis						
LH, mIU/mL	<u><0.1</u> (0.4–1.6) → 0.4 (10.9–20.6) ^d		2.4 (1.6–3.5)	<u>1.3</u> (1.6–3.5) → 24.9 (21.7–39.5) ^d	4.3 (1.4–9.2)	1.7 (1.4–9.2)
FSH, mIU/mL	<u>0.3</u> (1.7–4.2) → <u>1.6</u> (4.6–10.8) ^d		< <u>1.0</u> (4.2–8.2)	<u>0.6</u> (4.2–8.2) → <u>2.1</u> (11.2–17.3) ^d	2.7 (2.0–8.3)	<u>1.5</u> (4.2–8.2)
T, ng/mL	<u>0.06</u> (0.4–1.1) → 3.6 (>2.0) ^e	<u>2.6</u> (2.8–7.0)	<u>0.7</u> (2.8–7.0)	<u>1.5</u> (2.8–7.0)	<u>2.3</u> (2.8–7.0)	<u>3.2</u> (2.8–7.0)
E ₁ , pg/mL				111 (14–50)	556 (15–32)	903 (15–32)
E ₂ , pg/mL	14 (<10)	65 (10–35)	406 (15–50)	43 (2–30)	392 (10–35)	223 (10–35)
On AI treatment						
LH, mIU/mL	0.5 (0.4–1.6) → <u>7.3</u> (10.9–20.6) ^d	44.8 (0.7–5.7) ^f	4.7 (1.6–3.5)		8.9 (1.4–9.2)	2.9 (1.4–9.2)
FSH, mIU/mL	1.7 (1.7–4.2) → <u>3.2</u> (4.6–10.8) ^d	34.9 (2.0–8.3) ^f	<u>2.5</u> (4.2–8.2)		5.6 (2.0–8.3)	5.6 (4.2–8.2)
T, ng/mL	0.9 (0.4–1.1)	8.6 (2.8–7.0)	6.9 (2.8–7.0)		5.3 (2.8–7.0)	10.7 (2.8–7.0)
E ₁ , pg/mL					89 (15–32)	27 (15–32)
E ₂ , pg/mL	<10 (<10)	<u>6</u> (10–35)	<u>13</u> (15–50)		59 (10–35)	68 (10–35)
Reference	Present study	Present study	Present study	Present study	Ref. 1	Ref. 1

Abbreviations: AI, aromatase inhibitor; E₁, estrone; E₂, estradiol; N.D., not described; N.E., not examined. Abnormal clinical findings are boldfaced. Hormone values below the reference range (shown in parentheses) are underlined, and those above the reference range are boldfaced. Conversion factors to the SI unit: LH, 1.0 (IU/L); FSH, 1.0 (IU/L); E₁, 3.699 (pmol/L); E₂, 3.671 (pmol/L); and T, 3.467 (nmol/L).

^a Physical examination and endocrine studies were carried out at 8 and 18 years of age, respectively.

^b Assessed by the Tanner-Whitehouse 2 method standardized for Japanese or by the Greulich-Pyle method constructed for Caucasians.

^c Evaluated by age-matched male reference data.

^d GnRH stimulation tests (100 μg/m², maximum 100 μg bolus iv; blood sampling at 0, 30, 60, 90, and 120 min).

^e Human chorionic gonadotropin stimulation tests (3000 IU/m², maximum 5000 IU im for 3 consecutive days; blood sampling on d 1 and 4).

^f Increased levels of LH and FSH during AI treatment may be associated with low E₂ levels (24).

Characterization of the genomic structures of rearrangements

Breakpoints of the rearrangements were determined by direct sequencing of the PCR-amplified DNA fragments harboring the fusion junctions. PCRs were carried out using a number of primer pairs for various genomic positions around *CYP19A1*. The sequences of the primers utilized in the present study are available upon request. To confirm the formation of a chimeric gene in a case with a complex rearrangement, we performed RT-PCR using leukocyte mRNA and primers annealing to exon 2 of *CYP19A1* and exons of neighboring genes. The presence or absence of promoter-associated histone marks in the fused exons was analyzed using the UCSC genome browser (<http://genome.ucsc.edu/>).

Genotype-phenotype analysis

We performed genotype-phenotype analyses in cases 1–6 and in 18 patients identified in our previous study (5).

DNA sequences at the fusion junctions

To clarify the underlying mechanisms of the rearrangements, we examined the presence or absence of microhomologies and short nucleotide stretches at the fusion junctions. In addition, we searched for repeat elements around the breakpoints using Repeatmasker (<http://www.repeatmasker.org>).

Genomic environments around the breakpoints

We studied the frequencies of known rearrangement-inducing DNA features in the breakpoint-flanking regions. In silico analyses were carried out in the 300-bp regions at the proximal and distal sides of each breakpoint. We also examined control regions (n = 53) randomly selected at an interval of 1.5 Mb from the entire 15q (Supplemental Table 1, published on The Endocrine Society's Journals Online web site at <http://jcem.endojournals.org>). We calculated the average GC content using GEECEE (<http://emboss.bioinformatics.nl/cgi-bin/emboss/geecee>) and searched for palindromes using PALINDROME (<http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::palindrome>) and Non-B structures using Non-B DB (<http://nonb.abcc.ncifcrf.gov>). Examined Non-B structures included direct repeats, inverted repeats (cruciforms), mirror repeats, A-phased repeats, G-quadruplex repeats, short tandem repeats, and Z-DNA motifs (17). The presence or absence of the 10 specific sequence motifs and two tri/tetranucleotides implicated in rearrangements in various chromosomal regions (14, 18–22) were analyzed using Fuzznuc (<http://emboss.bioinformatics.nl/cgi-bin/emboss/fuzznuc>).

Replication timing analysis

We analyzed whether the rearrangements at 15q21 have occurred at a specific timing of S phase (23). Replication timing profiles of the approximately 10-Mb genomic interval around *CYP19A1* were evaluated using 92 datasets currently available in

Table 2. Genomic Rearrangements in Cases 1–6

	Rearrangement	Genomic Abnormality	Affected Genes ^a
Case 1	Simple	Simple duplication	<i>CYP19A1</i> , <i>TNFAIP8L3</i> , <i>AP4E1</i>
Case 2	Simple	Simple deletion	<i>CYP19A1</i> , <i>GLDN</i> , <i>DMXL2</i>
Case 3 ^b	Complex	Multiple deletions?	<i>TMOD3</i> , <i>GLDN</i> , <i>DMXL2</i> ?
Case 4	Complex	Multiple duplications and inversion	<i>CYP19A1</i> , <i>GLDN</i> , <i>SEMA6D</i>
Case 5	Complex	Multiple duplications, deletion, and inversion	<i>TMOD3</i> , <i>DMXL2</i> , <i>TMOD2</i> , <i>LYSMD2</i> , <i>SCG3</i>
Case 6	Complex	Multiple deletions and inversion	<i>CGNL1</i> , <i>CYP19A1</i>

^a Genes involved in the deletion or duplication. Genes affected by copy-number-neutral inversions are not shown.

^b Genomic structure of the rearrangement in case 3 remains to be characterized.

the ReplicationDomain database (http://www.replicationdomain.com/replication_timing.php).

Statistical analyses

Statistical significance of the average GC content between the breakpoint-flanking and control regions was analyzed by Student's *t* test. Differences in the frequencies of other rearrangement-inducing DNA features were examined by Fisher's exact probability test. *P* < .05 was considered significant.

Results

Copy-number alterations in cases 1–6

CGH analyses indicated heterozygous genomic rearrangements involving *CYP19A1* and/or its neighboring genes; ie, an approximately 0.4-Mb duplication involving *CYP19A1*, *TNFAIP8L3*, and *AP4E1* in case 1; an approximately 0.3-Mb deletion affecting *DMXL2*, *CYP19A1*, and *GLDN* in case 2; an approximately 80-kb deletion involving *TMOD3* and an approximately 250-kb deletion involving *DMXL2* and *GLDN* in case 3; an approximately 130-kb duplication involving *GLDN* and *CYP19A1* and an approximately 340-kb duplication involving *SEMA6D* at a position of approximately 3.6 Mb distant from *CYP19A1* in case 4; an approximately 370-kb duplication involving *TMOD3*, *TMOD2*, *LYSMD2*, *SCG3*, and *DMXL2*, and a 3- to 35-kb deletion between *DMXL2* and *GLDN* in case 5; and an approximately 3.5-kb deletion in the promoter region of *CYP19A1* in case 6 (Table 2 and Figure 1). The deletion in case 5 could not be narrowed down because of the absence of CGH probes around the breakpoints. The father and siblings of case 2 and the son of case 6 carried the same abnormalities as the probands.

Genomic structures of six rearrangements

We were able to characterize all fusion junctions in cases 1, 2, and 6 and one of the multiple junctions in cases 4 and 5 (Table 3, Supplemental Table 2, and Figure 2). The remaining breakpoints could not be determined due to the low quality of the DNA samples, the presence of long repetitive sequences around the breakpoints, or the com-

plex structures of the rearrangements. In case 1, we identified a 387 622-bp tandem duplication involving six of the 11 exons 1 (exons I.7, 1f, I.2, I.6, I.3, and PII) and all coding exons of *CYP19A1*, together with all exons of *TNFAIP8L3* and *AP4E1*. In case 2, we detected a 303 624-bp deletion involving six of the *CYP19A1* exons 1 (exons I.1, IIa, I.8, I.4, I.5, and I.7), all exons of *GLDN*, and *DMXL2* exons 2–43. In case 4, we identified two duplications: an approximately 130-kb duplication encompassing all noncoding exons 1 and coding exons 2–3 of *CYP19A1* and *GLDN* exon 1, and an approximately 340-kb duplication involving *SEMA6D* exons 1–3. PCR products were obtained with a primer pair for *GLDN* intron 1 and *SEMA6D* intron 3 (P5 and P6 in Figure 2A), indicating that the approximately 3.6-Mb genomic interval harboring *GLDN* exon 1, all noncoding and coding exons of *CYP19A1*, and *SEMA6D* exons 4–20 was inverted. In addition, we analyzed mRNA of case 4 and detected a chimeric clone composed of *CYP19A1* exon 2 and *SEMA6D* noncoding exon 3 (Supplemental Figure 1). Thus, although we could not determine the fusion junctions of the duplication, these data imply that the rearrangement was caused by an inversion of an approximately 3.6-Mb region and a duplication of the telomeric part of the inverted DNA fragment. In case 5, we identified an approximately 370-kb duplication containing *TMOD3* exon 1, *DMXL2* exons 1–29, and all exons of *TMOD2*, *LYSMD2*, and *SCG3*. PCR products were obtained with a primer pair for *TMOD3* intron 1 and the downstream region of *GLDN* (P7 and P8), indicating that the approximately 370-kb region was duplicated and inserted into the genome in a reverse direction. The small deletion between *DMXL2* and *GLDN* detected by CGH could not be characterized because of the presence of long repetitive sequences around the breakpoints. In case 6, we identified a complex deletion–inversion–deletion rearrangement: a 202-bp deletion within *CGNL1* intron 1, an approximately 6.1-Mb inversion encompassing *CGNL1* exon 1, eight of the *CYP19A1* exons 1 (exons I.1, IIa, I.8, I.4, I.5, I.7, 1f, and I.2), and ≥ 25 genes, and a 3476-bp deletion within *CYP19A1* intron 1.

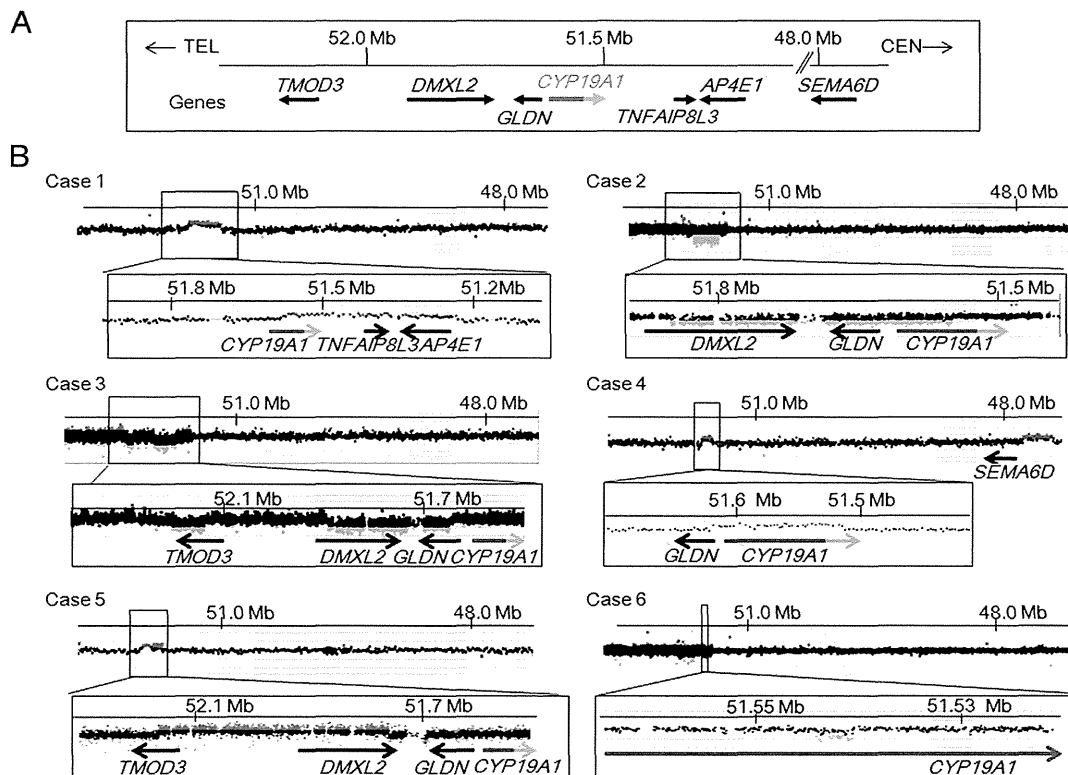


Figure 1. Copy-number analyses in cases 1–6. A, Schematic representation of the normal genomic structure around *CYP19A1*. The arrows indicate genomic positions and transcriptional direction of genes (5'→3'). For *CYP19A1*, the dark and light blue lines denote the genomic regions for noncoding exons 1 and coding exons 2–10, respectively. Genomic positions refer to Human Genome Database (hg19, build 37). Only genes around the fusion junctions are shown. B, CGH analyses in the six cases. The black, red, and green dots denote signals indicative of the normal, increased (>+0.5) and decreased (<-1.0) copy-numbers, respectively.

Phenotypic consequences of the six new and three previously reported rearrangements

We studied genotype-phenotype correlation in cases 1–6 and 18 previously reported patients (four patients from families A–B with simple duplications involving the *CYP19A1* promoter region, and 14 patients from families C–F with *DMXL2-CYP19A1* chimeric genes) (5). The re-

sults are summarized in Table 4. First, clinical severities were relatively mild in case 1 and patients from families A–B with simple duplications, obviously severe in cases 5 and 6 with complex rearrangements, and moderate in the remaining cases/patients with simple deletions or complex rearrangements. Second, among cases/patients with simple duplications, case 1 showed earlier onset of gynecol-

Table 3. Fusion Junctions in Cases 1–6

	No. of Fusion Junctions	No. of Fusion Junctions Characterized in This Study ^a	Sequences at the Fusion Junctions		
			Microhomology	Nucleotide Stretch	Predicted Mechanism
Case 1	1	1	Yes (4 bp)	Yes (2 bp)	RBM
Case 2	1	1	Yes (2 bp)	No	RBM
Case 3 ^b	2?	0	Unknown	Unknown	RBM?
Case 4	5	1	Yes (20 bp)	No	RBM
Case 5	3	1	Yes (3 bp)	Yes (5 bp)	RBM
Case 6	2	2	Yes (3 bp) ^c /No	No	RBM

Abbreviation: RBM, replication-based mechanism.

^a Several breakpoints could not be determined due to low quality of the DNA samples, the presence of long repetitive sequences around the breakpoints, or the complex structures of the rearrangements.

^b Genomic structure of the rearrangement in case 3 remains to be characterized.

^c Microhomology was observed at the telomeric junction.

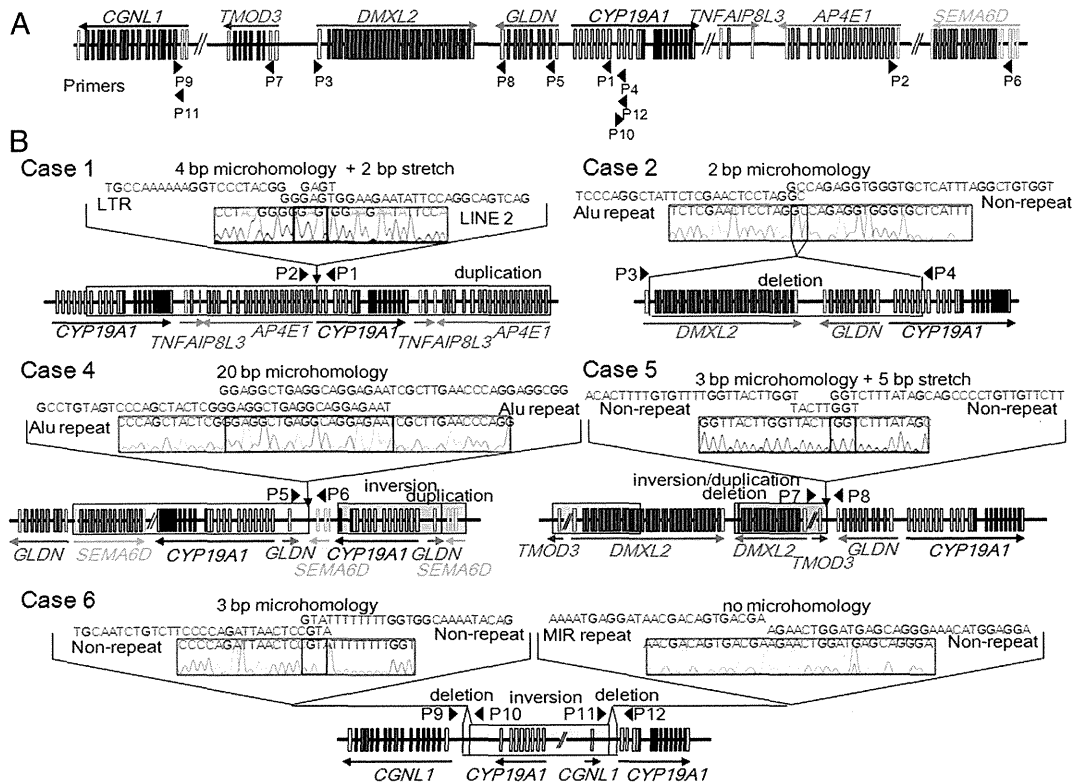


Figure 2. Fine genomic structures of the rearrangements. A, Schematic representation of the normal genomic structure. Arrowheads indicate the positions and the directions (5'→3') of PCR primers utilized in this study (P1–P12). The open and color-painted boxes denote noncoding and coding exons, respectively. The sizes of the exons, introns, and primers are not drawn to scale. B, Schematic representation of the rearrangements and the DNA sequences at the fusion junctions. The red, blue, and green areas indicate duplications, deletions, and inversions, respectively. P1–P12 indicate the same PCR primers as shown in panel A. The fusion junctions of case 3 were not characterized. For case 4, the precise genomic position of the duplication remains to be clarified.

mastia and more severely advanced bone age than patients from families A–B. Third, among cases/patients with deletions, case 2 manifested milder gynecomastia than case 3 and patients from families C–F. Lastly, among cases/patients with deletions or complex rearrangements, cases 2–4 and patients from families C–F showed milder phenotypes than cases 5 and 6.

DNA sequences at the fusion junctions

We characterized fusion junctions of the rearrangements in cases 1, 2, and 4–6 and in patients from families A–F (Table 3, Supplemental Table 2, and Figure 2). The results indicated the following: 1) nonallelic homologous recombination for the recurrent simple deletions in patients from families D–F that took place between two homologous sequences; 2) nonhomologous end-joining for the nonrecurrent simple deletions in patients from family C that were associated with short nucleotide stretches at the fusion junction; and 3) replication-based mechanisms for the simple and complex aberrations in cases 1, 2, and 4–6, and in patients from families A–B that were accompanied by microhomologies at the fusion junction. Nine of the 18 breakpoints resided within repetitive elements, such as LINE 1, LINE 2, *AluJo*, *AluY*, and *AluSx3*.

Genomic environments around the breakpoints

The average GC content was similar between the breakpoint-flanking and control regions (Supplemental Tables 2 and 3). Furthermore, the frequencies of known rearrangement-inducing DNA features (12, 14, 18–22) did not significantly differ between the breakpoint-flanking and control regions, except for some non-B structures enriched around the breakpoints of the deletions in patients from families D–F (Supplemental Tables 2 and 3).

Replication timing of the 15q21 region

Replication timing analysis indicated that in most cell lines examined, the genomic region around *CYP19A1* is replicated during early S phase (Supplemental Figure 2).

Discussion

We characterized six genomic rearrangements in patients with AEXS (Supplemental Figure 3). In case 1, the tandem duplication seems to have enhanced the transcriptional efficiency of *CYP19A1* in native *CYP19A1*-expressing tissues by increasing the number of transcription start sites. In cases 2–6, the rearrangements are predicted to have

Table 4. Genotype-Phenotype Correlation in Cases 1–6 and Families A–F

Cases/Families ^a	Case 1	Families A and B	Case 2	Case 3 ^b , Families C–F	Case 4	Case 5	Case 6
Molecular defects							
Predicted mechanism for <i>CYP19A1</i> overexpression	Duplication of <i>CYP19A1</i> coding exons	Duplication of <i>CYP19A1</i> promoters	Chimeric gene formation	Chimeric gene formation	Chimeric gene formation	Chimeric gene formation	Chimeric gene formation
Genes involved in chimeric gene formation	None	None	<i>DMXL2</i>	<i>DMXL2</i>	<i>SEMA6D</i>	<i>TMOD3</i>	<i>CGNL1</i>
Copy-number of the <i>CYP19A1</i> exon 1.4 ^c	Normal	Increased	Decreased	Normal	Increased ^d	Normal	Decreased
Clinical findings							
Onset of gynecomastia, y	7	10–13	Unknown	7–12	11	7	5
Gynecomastia (Tanner stage)	2–3	2–3	1–3 ^e	3–5	3–4	Severe	Severe
Advanced bone age	Mild	Subtle	Moderate	Mild/moderate	Severe	N.E.	N.E.

Abbreviation: N.E., not examined.

^a Cases 1–6 were present cases, whereas families A–F were reported previously (5).

^b Fine genomic structure of case 3 remains to be characterized.

^c Exon 1.4 functions as the major promoter in extragonadal tissues.

^d Duplicated exon 1.4 has been disconnected from the coding exons of *CYP19A1*.

^e The patient and his father had gynecomastia of Tanner stages 3 and 1, respectively.

created chimeric genes consisting of coding exons of *CYP19A1* and promoter-associated exons of neighboring genes. Actually, the deletions in cases 2 and 3 appear to have permitted splicing between *DMXL2* exon 1 and *CYP19A1* exon 2, as has been shown in the patients with similar deletions (5). Furthermore, the inversion in case 4 was found to produce a chimeric gene consisting of exon 3 of *SEMA6D* and exon 2 of *CYP19A1* (Supplemental Figure 1), and the inversions in cases 5 and 6 have previously been shown to form *TMOD3*- and *CGNL1-CYP19A1* chimeric genes, respectively (2). In this regard, the rearrangements in cases 2–6 have brought not only exons 1 of other genes, but also their flanking regions of >10 kb, to lie near the coding region of *CYP19A1*. Because these flanking regions harbor several enhancer- and promoter-associated histone marks (H3K4Me1 and H3K4Me3) (Supplemental Figure 4), they appear to contain most, if not all, components of cis-regulatory elements. Thus, although we can not examine the actual expression pattern of the chimeric genes, these genes seem to be expressed in a wide range of tissues where the original genes are expressed. These results argue for a broad mutation spectrum of AEXS.

Such diverse genetic basis of AEXS would be relevant to phenotypic variations (Table 4). First, cases/patients with copy-number gains of *CYP19A1* showed milder phenotypes than those with chimeric genes. This is consistent with the limited tissue expression pattern of *CYP19A1* and broad expression patterns of other genes involved in the chimeric gene formation (5, 25). Second, among cases/patients with simple duplications, case 1 showed a more

severe phenotype than patients from families A–B. This suggests that tandem duplications encompassing the transcriptional unit, ie, the promoter region plus the coding exons, permit more efficient aromatase protein production than tandem duplications encompassing the promoter region only. Third, among cases/patients with the same *DMXL2-CYP19A1* chimeric gene, case 2 manifested milder phenotypes than case 4 and patients from families C–F. These results can be explained by the difference in the number of *CYP19A1* exons 1, because six of *CYP19A1* exons 1 were deleted in case 2 and all exons 1 were preserved in the remaining cases/patients (Supplemental Figure 5). Fourth, case 4 with a *SEMA6D-CYP19A1* chimeric gene showed a milder phenotype than cases 5 and 6 with a *TMOD3*- and *CGNL1-CYP19A1* chimeric gene, respectively. This is consistent with a tissue expression pattern being broader in *TMOD3* and *CGNL1* than in *SEMA6D* (5, 25). Lastly, cases/patients with *DMXL2-CYP19A1* chimeric genes manifested milder phenotype than cases with a *TMOD3*- or *CGNL1-CYP19A1* chimeric gene. This would primarily be ascribed to the presence or absence of a translational start codon on the fused promoter-associated exons (Supplemental Figure 6). It is likely that *DMXL2-CYP19A1* chimeric mRNAs transcribed by the *DMXL2* promoter preferentially recognize the natural start codon on *DMXL2* exon 1 and undergo nonsense-mediated mRNA decay, and rather exceptional chimeric mRNAs utilize the start codon on *CYP19A1* exon 2 and produce the aromatase protein (5). Such a phenomenon would not be postulated for

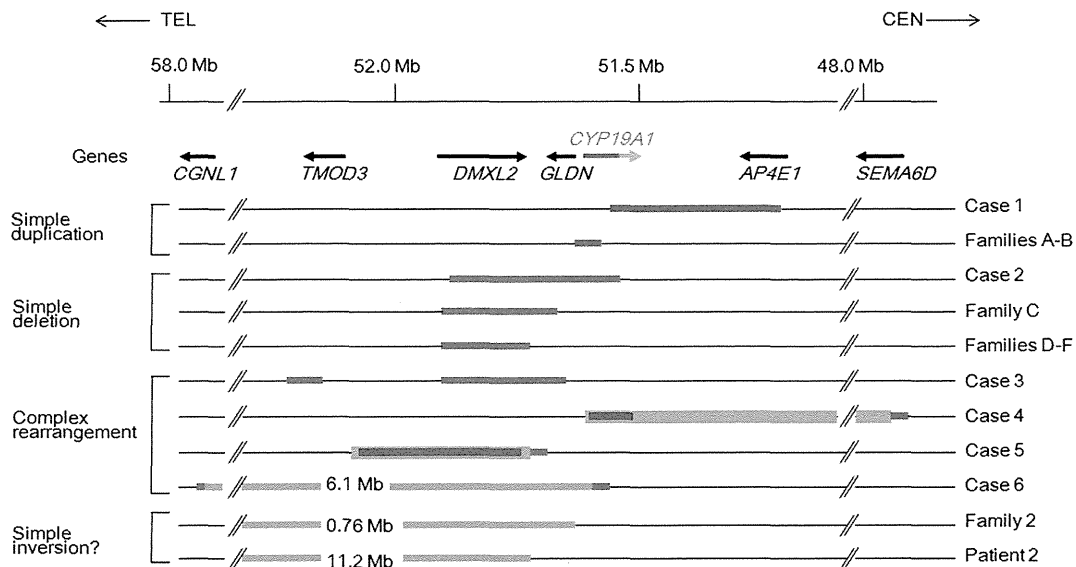


Figure 3. Schematic representation of the 11 rearrangements. Cases 1, 2, and 4–6 are from the present study, and patients from families A–F, patient 2, and patients from family 2 have been reported previously (1, 2, 5). The genomic abnormalities of case 3 were not characterized. The arrows indicate the positions and transcriptional direction of *CYP19A1* and its neighboring genes (5'→3'). Only genes around the fusion junctions are shown. The red, blue, and green lines indicate duplications, deletions, and inversions, respectively. For *CYP19A1*, the dark and light blue lines denote the genomic regions for the noncoding and coding exons, respectively. The inversions of family 2 and patient 2 may be complex rearrangements because copy-number analyses have not been performed in these cases.

the *TMOD3*- and *CGNL1-CYP19A1* chimeric mRNAs because of the absence of a translation start codon on exons 1 of *TMOD3* and *CGNL1*. Taken together, the present study suggests that phenotypic severity is primarily determined by the copy-number of *CYP19A1* and by the expression patterns and structural properties of the fused promoters. It should be pointed out, however, that this conclusion is based on the observation of only a limited number of patients. Phenotypic variation of the patients may be due to low penetrance of the clinical features.

To date, 11 genomic rearrangements have been identified in patients with AEXS (Figure 3). The 11 rearrangements are widely distributed on an approximately 9-Mb region and include simple duplications, deletions, and inversions, as well as complex rearrangements. Of these, the rearrangements in cases 1, 2, and 4–6 and in patients from families A–B are predicted to be replication-based errors (Supplemental Table 2 and Figure 2). Although the short nucleotide stretches at the fusion junctions in cases 1 and 5 may represent “information scars” characteristic of nonhomologous end-joining (9), the complex structures of the rearrangements would be consistent with replication-based mechanisms rather than end-joining (8). However, these rearrangements may result from microhomology-mediated end-joining (26). In contrast, the simple deletions in patients from family C and those in patients from families D–F are compatible with nonhomologous end-joining and nonallelic homologous recombination, respectively (Supplemental Table 2 and Figure 2). These re-

sults imply that the genomic region at 15q21 is vulnerable to both recombination- and replication-mediated errors.

In silico analyses revealed that deletions in families D–F due to nonallelic homologous recombination were associated with non-B structures and were located within an early-replicating segment of the genome, whereas the breakpoint-flanking regions of other rearrangements were independent of known rearrangement-inducing DNA features or late-replication timing. These data indicate that there are hitherto unidentified factors that facilitate nonhomologous end-joining and replication-based errors at 15q21. In this regard, it is noteworthy that nine of the 18 breakpoints resided within repetitive elements, and frequencies of *Alus* (16%) and *LINEs* (22%) in the breakpoint-flanking regions were slightly higher than expected from the draft human genome (*Alu*, 9.9%; and *LINE*, 16.1%) (27). An increased number of repetitive sequences was found around the breakpoints of various rearrangements (14, 18, 19, 21), and Boone et al (28) have reported that a high concentration of *Alu* elements may predispose replication-based errors. The presence of various *Alu* family members (*AluJo*, *AluY*, and *AluSx3*) at the fusion junction of our cases supports the notion that moderate sequence similarity between *Alu* elements would be sufficient to provide substrates for replication-based errors (28). Further studies are necessary to clarify the role of repetitive sequences in the formation of rearrangements.

In summary, the present study implies a broad mutation spectrum of AEXS and supports the previously proposed

notion that clinical severities of AEXS are determined by the dosage of the promoter and coding regions of *CYP19A1* and by characters of the fused promoters. We show that rearrangements involved in AEXS can be attributed to nonallelic homologous recombination that is induced by repeats and/or by early-replication timing, and to nonhomologous end-joining and replication-based mechanisms that occur independently of known rearrangement-inducing DNA features or a late-replicating timing. Thus, AEXS represents a unique model for human genomic disorders.

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Cryptic Genomic Rearrangements in Three Patients with 46,XY Disorders of Sex Development

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Abstract

Background: 46,XY disorders of sex development (46,XY DSD) are genetically heterogeneous conditions. Recently, a few submicroscopic genomic rearrangements have been reported as novel genetic causes of 46,XY DSD.

Methodology/Principal Findings: To clarify the role of cryptic rearrangements in the development of 46,XY DSD, we performed array-based comparative genomic hybridization analysis for 24 genetic males with genital abnormalities. Heterozygous submicroscopic deletions were identified in three cases (cases 1–3). A ~8.5 Mb terminal deletion at 9p24.1–24.3 was detected in case 1 that presented with complete female-type external genitalia and mental retardation; a ~2.0 Mb interstitial deletion at 20p13 was identified in case 2 with ambiguous external genitalia and short stature; and a ~18.0 Mb interstitial deletion at 2q31.1–32 was found in case 3 with ambiguous external genitalia, mental retardation and multiple anomalies. The genital abnormalities of case 1 could be ascribed to gonadal dysgenesis caused by haploinsufficiency of *DMRT1*, while those of case 3 were possibly associated with perturbed organogenesis due to a deletion of the *HOXD* cluster. The deletion in case 2 affected 36 genes, none of which have been previously implicated in sex development.

Conclusions/Significance: The results indicate that cryptic genomic rearrangements constitute an important part of the molecular bases of 46,XY DSD and that submicroscopic deletions can lead to various types of 46,XY DSD that occur as components of contiguous gene deletion syndromes. Most importantly, our data provide a novel candidate locus for 46,XY DSD at 20p13.

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Introduction

46,XY disorders of sex development (46,XY DSD) are genetically heterogeneous conditions that result from the impaired production or function of androgens, or from defective organogenesis of external genitalia [1]. To date, several genes such as *SRY*, *AR*, *SRD5A2*, and *SOX9* have been identified as causative genes for 46,XY DSD, although mutations in these genes account for only a minor fraction of the molecular causes of these conditions [1], [2].

Recent advances in microarray technology, including comparative genomic hybridization (CGH) analysis and single nucleotide polymorphism (SNP) genotyping, have enabled researchers to identify genomic rearrangements in individuals with apparently

normal karyotypes [3]. Cryptic genomic rearrangements can lead to developmental disorders, although they can also occur as benign polymorphisms [4]. To date, CGH analysis and SNP genotyping have been carried out for patients with 46,XY DSD, identifying multiple submicroscopic deletions and duplications [5], [6], [7]. Such rearrangements frequently affected coding exons or regulatory regions of known DSD-associated genes including *SF1*, *SOX9* and *DMRT1*, or exons of candidate genes including *KANK1* and *ZEB2* [5], [6], [7]. These data suggest that genomic abnormalities at various chromosomal loci may underlie 46,XY DSD.

To clarify the role of cryptic genomic rearrangements in the development of 46,XY DSD, we performed copy-number analyses

for 24 patients. The results provide novel insights into the molecular basis of 46,XY DSD.

Subjects and Methods

Ethics Statement

This study was approved by the Institutional Review Board Committee at the National Center for Child Health and Development. After obtaining written informed consent from the parents, peripheral blood samples were collected from the patients. When possible, blood samples were also obtained from the parents.

Patients

The study population comprised 24 patients with 46, XY DSD, including nine cases with complete female-type external genitalia, five with ambiguous genitalia and 10 with male-type external genitalia with hypospadias (Table 1). None of the 24 patients had a family history of DSD or a history of prenatal exposure to specific environmental pollutants. G-banding analysis showed a normal 46,XY karyotype in all patients. Mutations in the coding regions of known DSD-causative genes, *SRY*, *AR*, *SRD5A2*, *SFI*, *WNT4*, *SOX9*, *WT1*, *BNC2*, *DMRT1*, *HSD17B3*, and *MAP3K1*, were excluded by sequence analyses.

CGH Analysis

Genomic DNA samples were subjected to CGH analyses using a catalog human array (4×180 k format, Agilent Technologies, Palo Alto, CA), according to the manufacturer's instructions. The sizes and positions of the genomic rearrangements were analyzed using the UCSC genome browser (<http://genome.ucsc.edu/>; February 2009, hg19, build 37). In the present study, we focused on copy-number alterations with a physical size of more than 1.5 Mb, which have a higher probability of being associated with disease phenotypes [8]. Deletions and duplications registered in the database of genomic variants (<http://projects.tcag.ca/variation/>) were excluded as benign polymorphisms.

Results

CGH Analysis

We identified heterozygous submicroscopic deletions in three cases (cases 1–3; Fig. 1). The deletions affected several genes (Table 2). Case 1 harbored a ~8.5 Mb terminal deletion at 9p24.1–24.3 that encompassed *DMRT1*, in addition to 39 other genes. Case 2 carried a ~2.0 Mb interstitial deletion at 20p13 that included 36 genes. Case 3 had a ~18.0 Mb interstitial deletion at 2q31.1–32.1 that affected the entire *HOXD* cluster (*HOXD 1–13*), and 84 other genes. The parents of case 2 did not carry the deletion, whereas the parental samples of cases 1 and 3 were not available for genetic analyses.

Table 1. Patients analyzed in the present study.

Cases	Karyotype	Ethnic origin	External genitalia	Additional clinical features
1	46,XY	Japanese	Female	Mental retardation, schizophrenia
2	46,XY	Vietnamese	Ambiguous	Short stature
3	46,XY	Vietnamese	Ambiguous	Short stature, mental retardation, multiple anomalies
4	46,XY	Japanese	Female	
5	46,XY	Japanese	Female	Upper limb anomalies
6	46,XY	Japanese	Female	
7	46,XY	Japanese	Female	Short stature
8	46,XY	Japanese	Female	
9	46,XY	Japanese	Female	
10	46,XY	Japanese	Female	
11	46,XY	Japanese	Female	Agenesis of the corpus callosum, short palpebral fissures
12	46,XY	Japanese	Ambiguous	
13	46,XY	Japanese	Ambiguous	
14	46,XY	Indian	Ambiguous	
15	46,XY	Japanese	Male with HS	
16	46,XY	Japanese	Male with HS	
17	46,XY	Japanese	Male with HS	
18	46,XY	Japanese	Male with HS	
19	46,XY	Japanese	Male with HS	
20	46,XY	Japanese	Male with HS	
21	46,XY	Japanese	Male with HS	
22	46,XY	Japanese	Male with HS	
23	46,XY	Japanese	Male with HS	
24	46,XY	Vietnamese	Male with HS	

DSD, disorders of sex development; HS, hypospadias.
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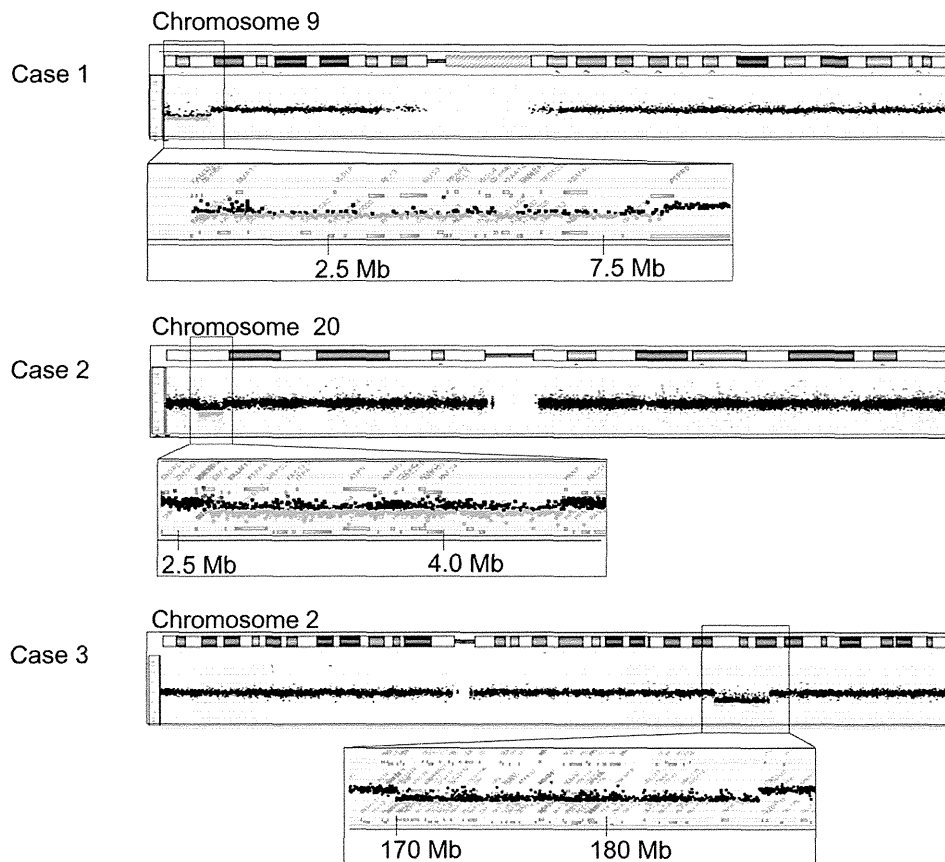


Figure 1. Cryptic heterozygous deletions in cases 1–3. CGH analysis identified heterozygous deletions in cases 1–3. The black, red, and green dots denote signals indicative of the normal, the increased ($> +0.5$) and the decreased (< -1.0) copy-numbers, respectively. Genomic positions correspond to the human genome reference assembly (UCSC Genome Browser, February 2009, hg19, build 37). The names of the genes affected by the deletions are shown in Table 2.
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Clinical Features of Deletion-positive Patients

Case 1 was a genetic male born to non-consanguineous Japanese parents. This patient had complete female-type external genitalia and was raised as a female. This patient exhibited mental retardation and behavioral problems and was diagnosed as having schizophrenia. At 17 years of age, this patient was referred to our clinic because of primary amenorrhea. Clinical analysis detected no dysmorphic facial features or cardiac/renal abnormalities. Abdominal ultrasonography delineated a uterus. Blood endocrine tests indicated primary hypogonadism (Table 3). At 17 years of age, the patient underwent gonadectomy. Histological analyses showed bilateral streak gonads with ovarian ducts. The parents were clinically normal.

Case 2 was a genetic male born to non-consanguineous Vietnamese parents. At birth, this patient exhibited a micropenis, cryptorchidism, and distal hypospadias. Abdominal ultrasonography detected bilateral testes (12×6 mm) in inguinal canals. The uterus and ovaries were absent. This patient was raised as a boy and underwent surgical intervention for hypospadias and cryptorchidism at 4 years and 2 months and at 4 years and 3 months of age, respectively. On his visit at 4.5 years of age, the patient showed a penis with a stretched length of 3 cm, and left testis (12×9 mm) in the scrotum and right testis (13×6 mm) in the inguinal canal (Fig. 2). He had no dysmorphic facial features (Fig. 2). He showed short stature (89 cm, -2.9 SD) and delayed bone age (equivalent to 2 years of age). His mental development

was normal. Blood endocrine tests at 4.5 years of age showed low levels of luteinizing hormone and testosterone (Table 3). His growth hormone levels were within the normal range at the baseline, but remained low after physical exercise. His parents were clinically normal and had normal statures.

Case 3 was born to non-consanguineous Vietnamese parents at 40 weeks of gestation with a birth weight of 2.0 kg (-3.7 SD). At birth, this patient manifested severe micropenis and hypospadias (Fig. 2). Bilateral testes were palpable in the scrotum, and uterus and ovaries were absent. Thus, this patient was raised as a boy. In addition to genital abnormalities, he exhibited multiple anomalies of the fingers and toes, i.e., camptodactyly and flexion contracture of the proximal interphalangeal joint of the right index and left ring fingers, cutaneous syndactyly of the 2nd and 3rd toes and medial deviation of the 4th toe in the right foot, lateral deviation of the 2nd toe and medial deviation of the 4th toe in the left foot, and overriding of the 4th toe on the third toe in both feet (Fig. 2). Furthermore, he showed dysmorphic facial features such as ptosis and micrognathia (Fig. 2). His blood testosterone level at birth was within the normal range (Table 3). On examination at 11 months of age, he showed obvious growth retardation (body weight; 6.0 kg, <-3.0 SD) and developmental delay (DQ <30). At one year of age, he presented with an episode of febrile convulsion. Brain magnetic resonance imaging detected delayed myelination, hypogenesis of the corpus callosum, and prominent ventricular and CSF spaces (Fig. 2). His parents were clinically normal.

Table 2. Genes affected by the cryptic deletions.

Case 1	Case 2	Case 3	
C9orf66	EBF4	BB55	CHN1
DOCK8	CPXM1	KBTBD10	ATF2
KANK1	C20orf141	FASTKD1	ATP5G3
DMRT1	FAM113A	PPIG	KIAA1715
DMRT3	TMEM239	CCDC173	EVX2
DMRT2	VPS16	SSB	HOXD1-13
SMARCA2	PTPRA	C2orf77	MTX2
FLJ35024	GNRH2	PHOSPHO2	LOC375295
VLDLR	MRPS26	KLHL23	HNRNPA3
KCNV2	OXT	METTL5	LOC100506866
KIAA0020	AVP	UBR3	NFE2L2
RFX3	LOC100134015	MYO3B	NR_026966
GLIS3	UBOX5	LOC440925	AGPS
C9orf68	FASTKD5	LOC285141	TTC30B
SLC1A1	SLC4A11	SP5	TTC30A
SPATA6L	C20orf194	NR_046248	PDE11A
AK3	DDRKG1	GAD1	SNORD77
CDC37L1	ITPA	GORASP2	OSBPL6
RCL1	SLC4A11	TLK1	DFNB59
C9orf46	C20orf194	METTL8	FKBP7
JAK2	ATRN	DCAF17	PLEKHA3
INSL6	GFRA4	CYBRD1	LOC100506866
INSL4	ADAM33	DYNC1I2	TTN
RLN2	SIGLEC1	SLC25A12	CCDC141
RLN1	HSPA12B	HAT1	SESTD1
C9orf46	C20orf27	METAP1D	ZNF385B
CD274	CDC25B	DLX1	CWC22
PDCD1LG2	C20orf29	DLX2	UBE2E3
KIAA1432	SPEF1	ITGA6	ITGA4
ERMP1	CENPB	PDK1	CERKL
MLANA	MAVS	RAPGEF4-AS1	NEUROD1
KIAA2026	PANK2	RAPGEF4	SSFA2
RANBP6	RNF24	ZAK	PPP1R1C
IL33	SMOX	MLK7-AS1	PDE1A
TPD52L3	LOC728228	CDCA7	DNAJC10
UHRF2	ADRA1D	SP3	FRZB
GLDC		OLA1	NCKAP1
KDM4C		LOC285084	PDE1A
C9orf123		CIR1	DUSP19
PTPRD		SCRN3	NUP35
		GPR155	ZNF804A
		WIPF1	FSIP2
		CHRNA1	

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Discussion

We identified cryptic heterozygous deletions with physical sizes of more than 1.5 Mb in three of the 24 patients with 46,XY DSD. The results support the notion that submicroscopic genomic rearrangements constitute a portion of causative mechanisms for

46,XY DSD [5], [6], [7]. Furthermore, molecular and clinical data of the three cases imply that cryptic deletions can cause DSD as components of contiguous gene deletion syndromes. Since array-based CGH analysis and SNP genotyping can detect copy-number alterations across the entire genome in a single assay,

Table 3. Clinical and laboratory findings of cases 1–3.

Cases	Case 1	Case 2	Case 3
Molecular analyses			
Karyotype (G-banding)	46,XY	46,XY	46,XY
Genomic rearrangement	Deletion	Deletion	Deletion
Genomic position of the deletion	9p24.1–24.3	20p13	2q31–32
Size of the deletion	~8.5 Mb	~2.0 Mb	~18.0 Mb
Parental origin of the deletion	Unknown	<i>de novo</i>	Unknown
Clinical features			
External genitalia	Female-type genitalia	Ambiguous	Ambiguous
Mental retardation	Yes	No	Yes
Growth failure/Short stature	No	Yes	Yes
Dysmorphic facial appearance	No	No	Yes
Additional features	Schizophrenia	Delayed bone age	Skeletal anomalies Brain anomalies Convulsion
Endocrine data^a			
Age at examination	17 y	4.5 y	at birth
LH (mIU/mL)	17.4 (0.2–2.2)	0.01 (0.2–1.9)	
FSH (mIU/mL)	101.1 (0.6–4.8)		
Testosterone (nmol/L)	0.71 (9–32)	0.01 (0.2–0.5)	4.9 (<12)
GH after physical exercise (ng/mL)		1.5 (3.0–28.3)	

DSD, disorders of sex development; MP, micropenis; HS, hypospadias; CO, cryptorchidism.

The hormone values below the reference range are boldfaced, and those above the reference range are italicized.

^aReference values of the age-matched control individuals are shown in the parenthesis.

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these methods should be considered for patients with 46,XY DSD, particularly for those with additional clinical manifestations.

Case 1 had a ~8.5 Mb heterozygous deletion at 9p involving 40 genes. Of the 40 genes, *DMRT1* is known to encode a male specific transcriptional regulator with a conserved zinc finger-like DNA-binding domain [9], [10]. Since mouse *Dmrt1* has been implicated in testicular differentiation [11], and intragenic deletions of human *DMRT1* have been identified in 46, XY patients with gonadal dysgenesis [6], [12], it appears that DSD in case 1 results from haploinsufficiency of *DMRT1*. These data argue for the assumption that heterozygous deletions involving the coding exons and/or the upstream region of *DMRT1* account for a substantial part of the etiology of complete and partial gonadal dysgenesis in individuals with 46, XY karyotype [6], [12], [13], [14]. Furthermore, our results provide additional information about other disease-associated loci. First, deletions at 9p22.3–23 are known to cause various malformations, such as craniofacial abnormalities, cardiac defects, and dysplastic kidneys, which are collectively referred to as the 9p- syndrome [13]. Lack of clinical manifestations of the 9p- syndrome in case 1 implies that the gene(s) responsible for this syndrome is not located in the ~8.5 Mb terminal region. This is consistent with previous studies which mapped the critical region of this syndrome to a genomic interval approximately 11–15 Mb from the telomere (Fig. 3A) [13]. Second, terminal deletions at 9p have previously been associated with mental retardation [13]. Our data suggest that a gene involved in brain development resides in the ~8.5 Mb terminal region that is deleted in case 1 (Fig. 3A).

Case 2 had a *de novo* ~2.0 Mb interstitial deletion at 20p13, which has not been identified previously in patients with DSD.

Furthermore, none of the 36 genes affected by the deletion have been associated with sex development. These results, in conjunction with previous reports of hypomaskulinized external genitalia in a patient with a ≥ 6 Mb deletion at 20p13-12.3 [15] and in a patient with a 20p11.2-pter deletion [16], indicate that the genomic interval spanning ~2.7–4.7 Mb from the telomere (deleted in case 2 and in the two aforementioned patients) encompasses a novel causative gene for DSD (Fig. 3B). However, the penetrance of DSD in males with 20p13 deletions appears to be low, because genital abnormalities have been described only in a small percentage of patients with such deletions [16], [17], [18], [19]. It might also be possible that the 20p13 and/or the 2q31.1–32 deletion has unmasked a recessive mutation of the testis development gene(s) on the structurally normal homologous chromosome, leading to DSD. In addition, the deletion of case 2 seems to harbor a gene that is indispensable for growth, because short stature was observed in case 2, as well as in most patients with partial monosomy of 20p [16], [17], [18], [19]. In this regard, although case 2 showed impaired growth hormone secretion after exercise, it remains to be clarified whether short stature in patients with 20p deletions is ascribed to growth hormone deficiency. Furthermore, unlike patients with terminal deletions of 20p [16], [17], [18], [19] case 2 showed no facial dysmorphism or mental retardation. These data indicate that a gene(s) involved in the development of the craniofacial region and brain resides within the 0–2.7 Mb interval from the telomere that is preserved in case 2. Consistent with this, facial abnormalities and developmental delay have been reported in two patients harboring 20p terminal deletions of less than 1.7 Mb [20] (Fig. 3B). Importantly, the deletion in case 2 includes *OXT* and *AVP* that are predicted to play

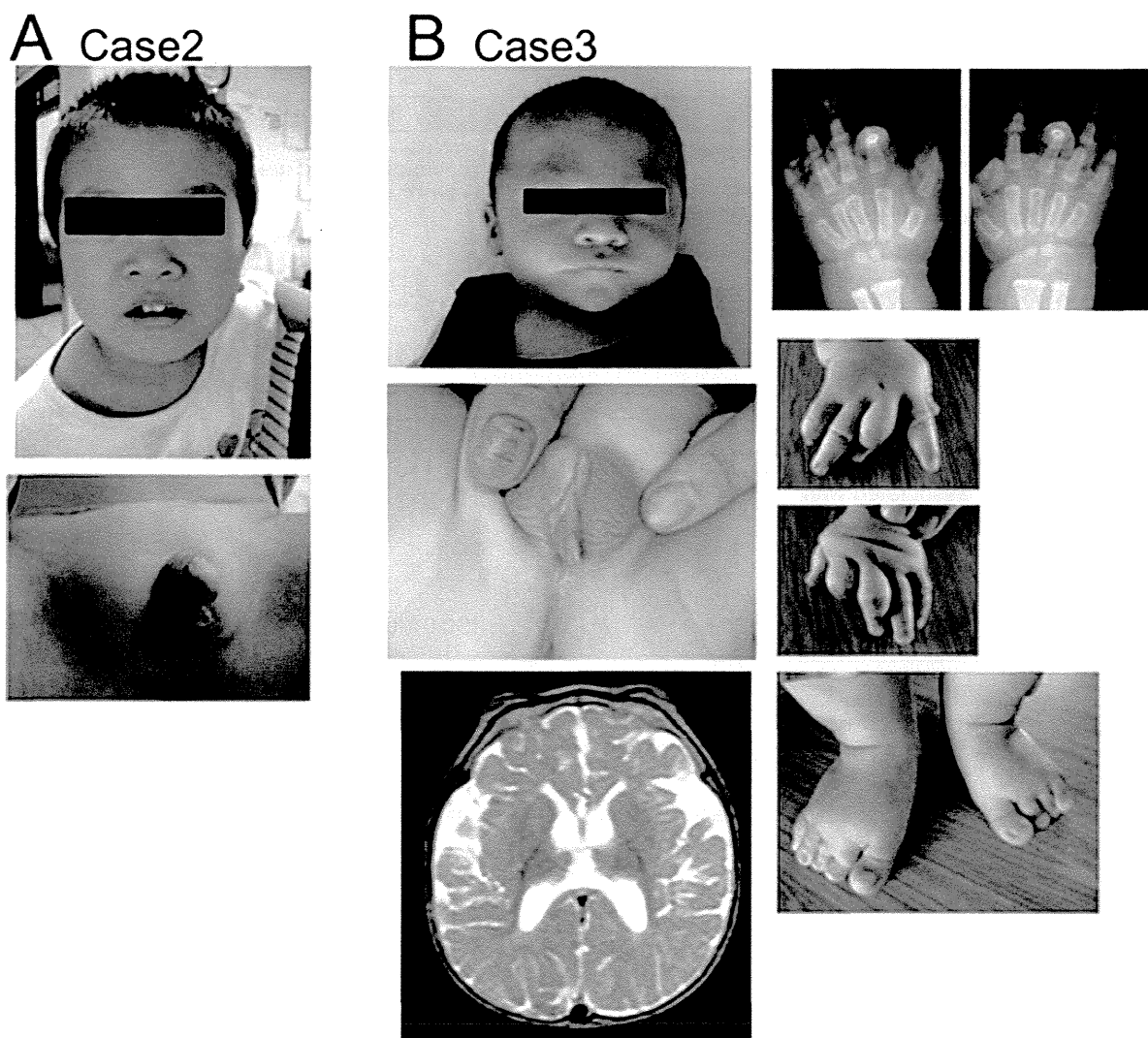


Figure 2. Clinical features of cases 2 and 3. A. Clinical findings of case 2 at 4.5 years of age. Images of the craniofacial region and external genitalia (after surgical intervention) are shown. B. Clinical findings of case 3 at 11 months of age. Multiple facial dysmorphisms and limb anomalies including syndactyly and camptodactyly are shown. Brain magnetic resonance imaging indicates delayed myelination, hypogenesis of the corpus callosum and prominent ventricular and CSF spaces. The parents of cases 2 and 3 have given written informed consent, as outlined in the PLOS consent form, to publication of the photographs of the patients.
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a role in social behavior [21]. Lack of social dysfunction in case 2 indicates that haploinsufficiency of *OXT* and *AVP* permits normal psychosocial development at least in childhood. However, this notion awaits further investigation.

Case 3 had a ~18.0 Mb interstitial deletion at 2q31.1–32.1. Clinical manifestations of case 3 including finger/toe anomalies, mental retardation and facial dysmorphism are compatible with the 2q31 microdeletion syndrome, a well-established contiguous gene deletion syndrome [22]. Notably, abnormal formation of the external genitalia has been reported in both male and female patients carrying 2q31 deletions [23], [24]. Previous studies have attributed the skeletal anomalies of 2q31 microdeletion syndrome to haploinsufficiency of the *HOXD* cluster [22], [25], and mental retardation and craniofacial abnormalities to deletions of certain genes located within the genomic interval spanning 174–175 Mb from the 2q telomere [22] (Fig. 3C). In this regard, while skeletal abnormalities are obviously milder in case 3 than the previously reported patients with deletions involving *HOXD* genes [25], this

would be consistent with the assumption that haploinsufficiency of developmental genes is frequently associated with a broad phenotypic spectrum [26]. Since mouse *Hoxd* genes have been shown to play a role in the formation of external genitalia by regulating multiple target genes, genital abnormalities of 2q31 microdeletion syndrome could be associated with haploinsufficiency of *HOXD* genes [25], [27]. Indeed, the phenotype of case 3, such as hypomaskulinized external genitalia without cryptorchidism and a normal blood testosterone value at birth, is indicative of perturbed organogenesis of the external genitalia rather than impaired hormone production in the gonads. However, since DSD has been described for only a small subset of males with 2q31 deletions [22], [23], [24], [25], impaired sex development in case 3 may be caused by other unknown genetic or environmental factors.

In summary, we identified cryptic genomic rearrangements in three of 24 individuals with 46,XY DSD. It appears that the genital abnormalities of case 1 result from gonadal dysgenesis due

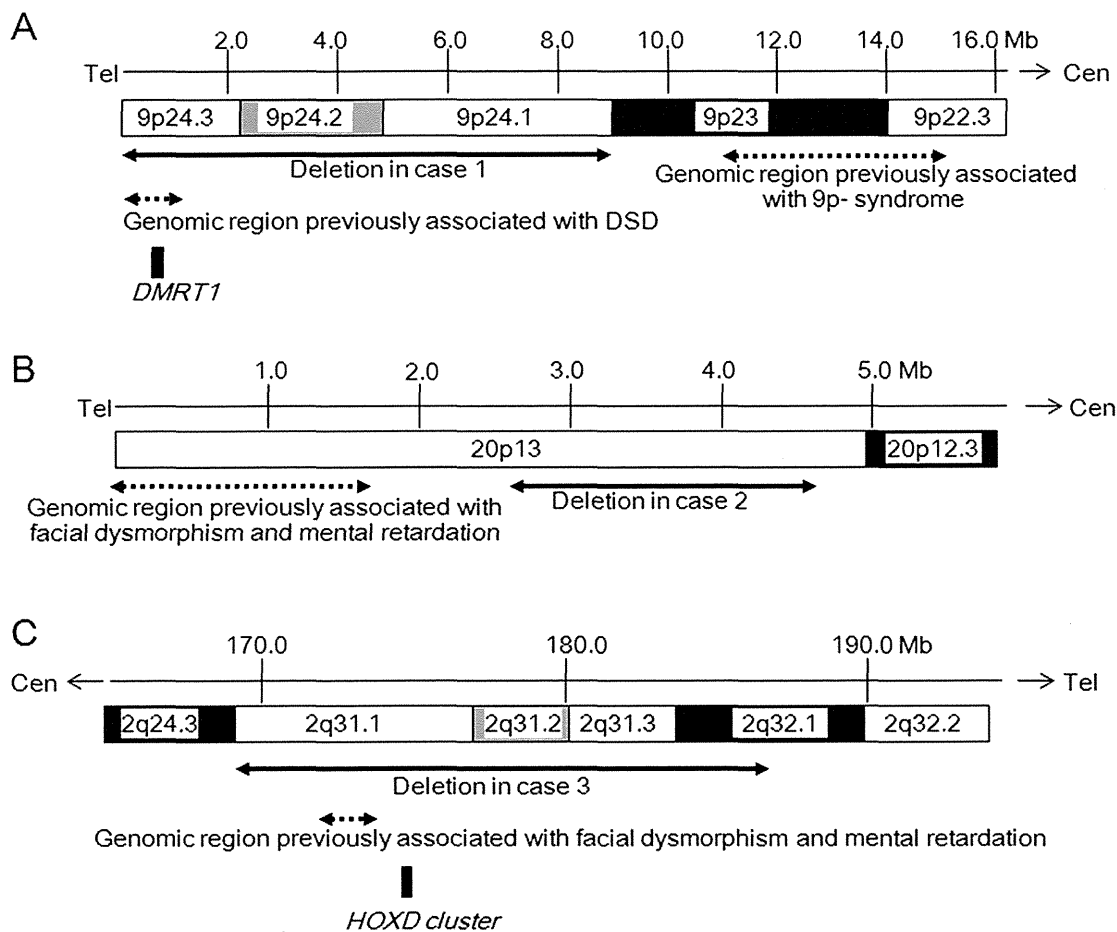


Figure 3. Schematic representation of the genomic regions around the deletions. A. Terminal part of the short arm of chromosome 9. The black arrow denotes the deletion identified in case 1. The dotted arrows indicate the genomic intervals associated with DSD and for 9p- syndrome [13]. The black box indicates the position of *DMRT1* that is likely to be associated with DSD in case 1. B. Terminal part of the short arm of chromosome 20. The black arrow denotes the deletion in case 2. The dotted arrow indicates the genomic region associated with facial dysmorphism and mental retardation [20]. C. The 2q24.3–2q32.2 region. The black arrow denotes the deletion in case 3. The dotted arrow indicates the genomic region associated with facial dysmorphism and mental retardation [22]. The black box indicates the position of the *HOXD* cluster possibly associated with DSD in case 3.

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to haploinsufficiency of *DMRT1*, while those of case 3 can be ascribed to perturbed organogenesis due to the deletion of the *HOXD* cluster. These data suggest that submicroscopic deletions can lead to various types of 46,XY DSD that occur as components of contiguous gene deletion syndromes. Moreover, the results obtained from case 2 provide a novel candidate locus for 46,XY DSD at 20p13. Further copy-number analyses on patients with 46,XY DSD and functional assays for genes involved in the

genomic rearrangements will help to clarify novel causative mechanisms for 46,XY DSD.

Author Contributions

Conceived and designed the experiments: VCD KK YK TO MF. Performed the experiments: MI ES KN. Analyzed the data: MI ES TO MF. Contributed reagents/materials/analysis tools: VCD SI MN KM YH KK YK. Wrote the paper: TO MF.

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In the United States the regulation of nonstandardized AEs presented some similarities with our approach. AEs were classified into 4 categories according to scientific data supporting their use in diagnosis and treatment, and the extracts were regularly evaluated by the regulatory agencies. The last update was conducted between 2003 and 2011, and the process was recently reviewed by Slater et al.¹ It was shown that for nearly half of nonstandardized AEs there were, in fact, little or no data to support their effectiveness. We had similar results: 66 of 84 AEs were validated for diagnosis, but only for 29 of 66 was there at least 1 published piece of data to support their effectiveness for immunotherapy (Table I). Among those 66 authorized AEs, approximately one third are standardized. There is no consensus about the standardization methods, and the European approaches present some differences compared with the US approach (see Table E1 in this article's Online Repository at www.jacionline.org). Briefly, in-house reference preparation (IHRP) AEs are standardized *in vivo* and *in vitro*. Each manufacturer has its own IHRP, and there is no national standard. Batch-to-batch standardization is performed *in vitro* through a comparison of the AEs with the IHRP.⁹

In the future, the NPP list will be updated every 5 years, and requests for MA will be made and processed for standardized AEs produced industrially and frequently used for immunotherapy.

In conclusion, for the first time in Europe, this work guarantees that available AEs are clinically relevant and safe. Moreover, it guarantees that all AEs comply with recent European guidelines on APs, including rare allergens for which it is not possible to obtain large clinical studies requested for MA. The process involved all the representatives of allergists and manufacturers and is still ongoing.

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Common variable immunodeficiency classification by quantifying T-cell receptor and immunoglobulin κ -deleting recombination excision circles

To the Editor:

Common variable immunodeficiency (CVID) is the most frequent primary immunodeficiency associated with hypogammaglobulinemia and other various clinical manifestations. CVID was originally reported to be a disease primarily caused by defective B-cell function, with defective terminal B-cell differentiation rendering B cells unable to produce immunoglobulin. However, combined immunodeficiency (CID) involving both defective B and T cells is often misdiagnosed as CVID.¹ Indeed, one study reported that CD4⁺ T-cell numbers were decreased in 29% of 473 patients with CVID²; similarly, another study found that naive T-cell numbers were markedly reduced in 44% (11/25) of patients with CVID.³ These observations indicated that a subgroup of patients with clinically diagnosed CVID is T-cell deficient. Consistently, some patients with CVID have complications that might be related to T-cell deficiency, including opportunistic infections, autoimmune diseases, and malignancies, which is similar to that observed in patients with CID.^{1,4} Therefore identifying novel markers to better classify CVID and distinguish CID from CVID will be required to best manage medical treatment for CVID.

We recently performed real-time PCR-based quantification of T-cell receptor excision circles (TREC) and signal joint immunoglobulin κ -deleting recombination excision circles (KREC) for mass screening of severe combined immunodeficiency (SCID)⁵ and B-lymphocyte deficiency⁶ in neonates. TREC and KREC are associated with T-cell and B-cell neogenesis, respectively.⁷ Here we retrospectively report that TREC and KREC are useful for classifying patients with clinically diagnosed CVID.

Hypogammaglobulinemic patients (n = 113) were referred to our hospital for immunodeficiency from 2005-2011, and the following patients were excluded from the CVID pool by estimating their SCID genes based on clinical manifestations and lymphocyte subset analysis: 18 patients with SCID diagnoses; 14 patients less than 2 years of age (transient infantile hypogammaglobulinemia); 10 patients with IgM levels of greater than 100 mg/dL (hyper-IgM syndrome); 26 patients with diseases other than CVID caused by known gene alterations (10 with X-linked agammaglobulinemia and 11 with hyper-IgM syndrome

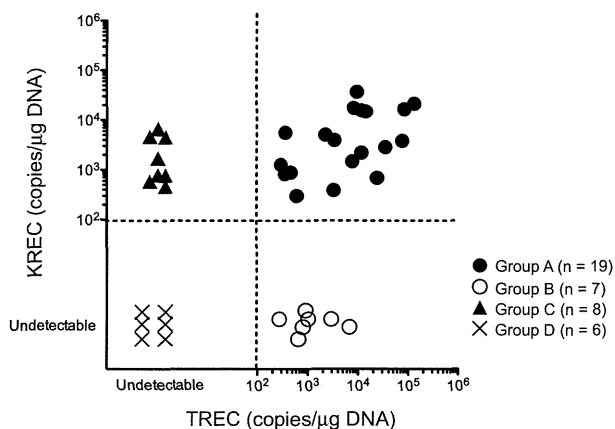


FIG 1. Quantifying TREC and KREC classifies patients with CVID into 4 groups. Patients with CVID were classified as follows: TREC(+)/KREC(+), group A (19 patients); TREC(+)/KREC(-), group B (7 patients); TREC(-)/KREC(+), group C (8 patients); and TREC(-)/KREC(-), group D (6 patients). Undetectable, Less than 100 copies/ μ g DNA.

[*CD40L* or *AICDA* mutated]), (2 with DiGeorge syndrome, and 3 with *FOXP3*, *IKBKKG*, or *6p* deletions); and 5 patients with drug-induced hypogammaglobulinemia. The remaining 40 patients with decreased IgG (≥ 2 SDs below the mean for age), IgM, and/or IgA levels, as well as absent isohemagglutinins, poor response to vaccines, or both were included in this study as patients with CVID and analyzed for TREC/KREC levels, retrospectively.

Ages of patients with CVID ranged from 2 to 52 years (median age, 15.5 years). The sex ratio of the patients was 21 male/19 female patients. Serum IgG, IgA, and IgM levels were 370 ± 33 mg/dL (0-716 mg/dL), 30 ± 7 mg/dL (1-196 mg/dL), and 40 ± 6 mg/dL (2-213 mg/dL), respectively. TREC and KREC quantification was performed by using DNA samples extracted from peripheral blood, as reported previously.^{5,6} Clinical symptoms were then assessed retrospectively. The study protocol was approved by the National Defense Medical College Institutional Review Board, and written informed consent was obtained from adult patients or parents of minor patients in accordance with the Declaration of Helsinki.

Based on TREC and KREC copy numbers, the 40 patients with CVID were classified into 4 groups (groups A, B, C, and D; Fig 1). Comparing lymphocyte subsets, $CD3^+$ T-cell numbers were similar among groups A, B, and D but were significantly lower in group C ($P < .05$; group A, 1806 ± 204 cells/ μ L; group B, 1665 ± 430 cells/ μ L; group C, 517 ± 124 cells/ μ L; and group D, 1425 ± 724 cells/ μ L; $P = .0019$, Tukey multiple comparison test based on 1-way ANOVA). $CD3^+CD4^+CD45RO^+$ memory T-lymphocyte percentages in groups B, C, and D were significantly higher than those in group A ($P < .0001$; group A, $37\% \pm 16\%$; group B, $67\% \pm 13\%$ [$P = .0006$]; group C, $92\% \pm 8.2\%$ [$P < .0001$]; and group D: $83\% \pm 14\%$ [$P < .0001$]; see Fig E1 in this article's Online Repository at www.jacionline.org); additionally, the percentages of these cells in groups C and D were higher than in group B ($P = .0115$). These results indicate that group C and D patients have markedly decreased $CD4^+CD45RA^+$ naive T-cell counts than group A patients and that counts in group B are also significantly decreased, although less so than in groups C or D, which is consistent with a report showing lower TREC copy numbers in $CD4^+CD45RO^+$ cells. Some patients in groups B, C, and D exhibited normal $CD4^+CD45RO^+$ percentages, although TREC

levels, KREC levels, or both decreased. This discrepancy indicates that TREC/KREC levels could be independent markers to determine the patient's immunologic status in addition to $CD4^+CD45RA^+$; the reasons underlying the discrepancy between $CD4^+CD45RA^+$ and TREC/KREC levels remain unsolved.

$CD19^+$ B-cell numbers in group A were significantly higher ($P < .05$) than those in groups B and D (group A, 269 ± 65 cells/ μ L; group B, 35 ± 16 cells/ μ L; group C, 60 ± 11 cells/ μ L; and group D, 29 ± 16 cells/ μ L; $P = .0001$). However, B-cell subpopulations, including $CD27^-$, IgD^+CD27^+ , and IgD^-CD27^+ cells, were not significantly different among the groups. Standardizing KREC copy numbers for each patient by dividing their $CD19^+$ by their $CD27^+$ percentages revealed the same patient classification as that shown in Fig 1 (data not shown), indicating that the original classification was independent of $CD19^+$ B-cell or $CD27^+$ memory B-cell percentages.

Because TREC and KREC levels decrease with age (see Fig E2 in this article's Online Repository at www.jacionline.org)^{5,6} and age distribution was wide in this study, we compared patients' ages among groups at the time of analysis to determine whether classification was associated with age. TREC/KREC-based classification was independent of both age and sex because age distribution was not significantly different among groups ($P > .05$; group A, 12.7 ± 2.3 years [2-30 years]; group B, 23.4 ± 4.2 years [6-39 years]; group C, 21.5 ± 6.1 years [4-52 years]; and group D, 25.5 ± 4.4 years [15-46 years]; data not shown) nor was male/female sex ratio (overall, 21/19; group A, 10/9; group B, 2/5; group C, 5/3; and group D, 4/2; $P = .4916$, χ^2 test; data not shown).

We next evaluated whether any correlation existed between TREC/KREC-based classification and clinical symptoms in each patient group. All patients in the study had been treated with intravenous immunoglobulin (IVIG) substitution at the time of analysis. We found that the cumulative events of complications (opportunistic infections, autoimmune diseases, and malignancies) per 10 patient-years were highest in group D (0.98 events/10 patient-years), followed by group C (0.63 events/10 patient-years), group B (0.30 events/10 patient-years), and group A (0.04 events/10 patient-years), where events in groups D and C were significantly higher than group A (group A vs group D, $P = .0022$; group A vs group C, $P = .0092$; group A vs group B, $P = .0692$; Fig 2). Furthermore, we found similar results when evaluating only patients 19 years old or older for group D (1.01 events/10 patient-years), group C (0.56 events/10 patient-years), group B (0.32 events/10 patient-years), and group A (0.06 events/10 patient-years; group A vs group D, $P = .0074$; group A vs group C, $P = .0407$; group A vs group B, $P = .1492$; data not shown). Categorizing patients by using several different previously reported CVID classifications (focused primarily on separating patients based on levels of circulating B-cell subsets), we found that no classification scheme showed any significant event increases in any particular group (see Fig E3 in this article's Online Repository at www.jacionline.org). Assessing longitudinal cumulative opportunistic infection incidence among the groups, group D and C values were significantly higher than in group A (see Fig E4, A, in this article's Online Repository at www.jacionline.org; $P = .0059$). Autoimmune and malignant diseases ($P = .5168$ and $P = .6900$, respectively) were observed in groups B and D but not in group A (see Fig E4, B and C). Cumulative events were significantly different between groups ($P = .0313$, log-rank test; group A, 5.3% and 5.3%; group B, 14.3% and

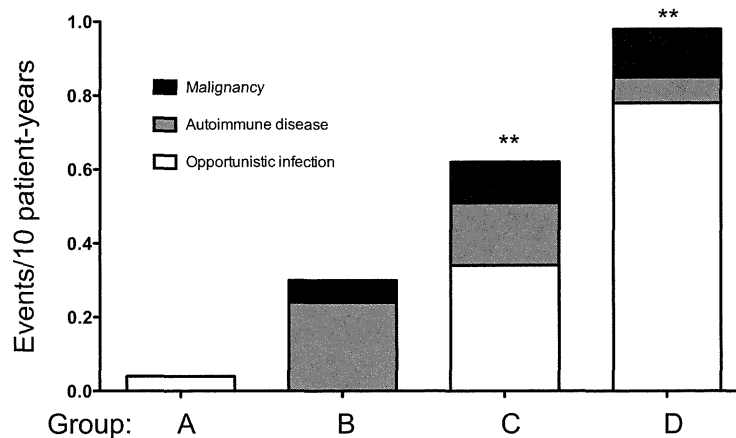


FIG 2. Cumulative incidence of complication events per 10 patient-years differs among groups. Opportunistic infections, autoimmune diseases, and malignancies were evaluated for each patient group. Complication incidences in group D (0.98 events/10 patient-years), group C (0.63 events/10 patient-years), and group B (0.30 events/10 patient-years) were higher than in group A (0.04 events/10 patient-years). Group A versus group D: $**P = .0022$; group A versus C: $**P = .0092$; group A versus B: $P = .0692$.

57.1%; group C, 27.1% and 63.5%; and group D, 33.3% and 83.3% at 10 and 30 years of age, respectively; see Fig E4, D). One patient in group D died of *Pneumocystis jirovecii* pneumonia, and 2 other patients in the same group received hematopoietic stem cell transplantation after complications caused by EBV-related lymphoproliferative disorder.

Assessing these data, TREC/KREC-based classification matches clinical outcomes. Because group D patients exhibited the most frequent complications (opportunistic infections, autoimmune diseases, and malignancies), they could receive a diagnosis of CID based on these symptoms. If they are indeed determined to have CID, then TREC/KREC analysis is helpful to distinguish between CID and CVID. Their TREC(-)/KREC(-) phenotype might relate to defective V(D)J recombination in T- and B-cell development⁸ because patients with B-negative SCID (*RAG1*, *RAG2*, *Artemis*, and *LIG4*), as well as patients with ataxia-telangiectasia (AT) and Nijmegen breakage syndrome (NBS; see Fig E5 in this article's Online Repository at www.jacionline.org),^{5,6} were also negative for both TREC and KREC; it is intriguing to speculate that an unknown V(D)J recombination gene or genes is responsible. As for treatment, hematopoietic stem cell transplantation should be considered the preferred treatment to "cure" group D patients, as reported in patients with severe CVID/CID, because event-free survival is poor.⁹

In contrast to group D patients, TREC(+)/KREC(+) group A patients treated with IVIG substitution therapy remained healthy. One possible explanation is that these patients harbor defects only in terminal B-cell differentiation, but not in T cells, and represent typical patients with CVID, as originally reported.

Group C patients had a high frequency of both opportunistic infections and malignancies, suggesting that these TREC(-) patients have T-cell defects. Although group C patients had a similar TREC/KREC pattern to patients with SCID with B cells (*IL2RG* and *JAK3*; see Fig E5, A), they do not fulfill the European Society for Immunodeficiencies criteria for SCID, and no mutation was identified in the SCID genes estimated from clinical manifestation and lymphocyte subset analysis. However, from our data, they would likely benefit from undergoing similar

treatment to patients with SCID or CID to prevent these complications.

Although opportunistic infections were rare in group B patients, autoimmune diseases were often observed. This is consistent with this group being TREC(+)/KREC(-) and the idea that balance between T and B cells is important to prevent autoimmune diseases in patients with CVID.¹ Intriguingly, a group of patients with AT and NBS were also TREC(+)/KREC(-) (see Fig E4, B), which is similar to group B patients. Additionally, CD45RA⁺CD4⁺ naive T-cell numbers were reduced in most group B patients, which is similar to the phenotype exhibited by patients with AT and NBS. This finding raises the possibility that although some group B patients are also T-cell deficient, as well as B-cell deficient, and should be treated similarly to patients with CID, other patients have only B-cell deficiency and are effectively treated with IVIG substitution therapy.

By analyzing a large CVID patient cohort, the overall survival rate of patients with more than 1 complication was worse than that for patients without other complications.⁴ Our findings indicate that low TREC levels, KREC levels, or both are useful markers that correlate well with the overall survival rate in patients with CVID. Therefore we conclude that TREC and KREC are useful markers to assess the clinical severity and pathogenesis of each patient with CVID and to distinguish CID from CVID. Thus patient classification based on TREC/KREC levels would provide a helpful tool for deciding on an effective treatment plan for each patient with CVID.

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