

ARTICLE

Combined array CGH plus SNP genome analyses in a single assay for optimized clinical testing

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In clinical diagnostics, both array comparative genomic hybridization (array CGH) and single nucleotide polymorphism (SNP) genotyping have proven to be powerful genomic technologies utilized for the evaluation of developmental delay, multiple congenital anomalies, and neuropsychiatric disorders. Differences in the ability to resolve genomic changes between these arrays may constitute an implementation challenge for clinicians: which platform (SNP vs array CGH) might best detect the underlying genetic cause for the disease in the patient? While only SNP arrays enable the detection of copy number neutral regions of absence of heterozygosity (AOH), they have limited ability to detect single-exon copy number variants (CNVs) due to the distribution of SNPs across the genome. To provide comprehensive clinical testing for both CNVs and copy-neutral AOH, we enhanced our custom-designed high-resolution oligonucleotide array that has exon-targeted coverage of 1860 genes with 60 000 SNP probes, referred to as Chromosomal Microarray Analysis – Comprehensive (CMA-COMP). Of the 3240 cases evaluated by this array, clinically significant CNVs were detected in 445 cases including 21 cases with exonic events. In addition, 162 cases (5.0%) showed at least one AOH region > 10 Mb. We demonstrate that even though this array has a lower density of SNP probes than other commercially available SNP arrays, it reliably detected AOH events > 10 Mb as well as exonic CNVs beyond the detection limitations of SNP genotyping. Thus, combining SNP probes and exon-targeted array CGH into one platform provides clinically useful genetic screening in an efficient manner.

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INTRODUCTION

Variation in the human genome consists of two major types: (1) single nucleotide variation, in the form of DNA base-pair substitutions and short indels, and (2) structural variation affecting many base pairs, including inversions, translocations, insertions, deletions, and duplications resulting in copy number variation (CNV).¹ Advances in genome-wide analytical techniques, such as array comparative genomic hybridization (array CGH) and single nucleotide polymorphism (SNP) genotyping, can be used to detect CNVs. The number of identified CNVs has increased dramatically as the resolution of the detection technologies has improved.^{2–7} Rapidly, CNV detection has become an integral part of genetic studies of disease susceptibility, delineation of novel genomic disorders,^{8–10} and analysis of data from genome-wide association studies.^{11,12}

Both array CGH and SNP genotyping are routinely utilized by clinicians for the evaluation of patients with developmental delay (DD)/intellectual disability (ID), multiple congenital anomalies (MCA),¹³ and neuropsychiatric disorders.¹⁴ Genomic resolution by both array platforms (SNP and array CGH) used in clinical

laboratories allows for the detection of genomic gains and losses of ~400 kb in size.¹⁵ Custom-designed oligonucleotide array CGH with greater resolution of the human genome, enabling detection of single-exon CNVs for clinically relevant genes, has also been implemented clinically.^{16,17} This approach increases diagnostic yield, but also increases the likelihood of detecting variants of uncertain clinical significance.

While single-exon resolution throughout the genome is not feasible for SNP arrays, SNP arrays show higher sensitivity for the detection of low-level mosaic aneuploidies and chimerism¹⁸ and offer the ability to detect copy number neutral regions of absence of heterozygosity (AOH).¹⁹ Consanguinity can be revealed by AOH, because multiple regions of AOH are expected to be present in individuals from inbred populations, representing chromosomal segments that are identical by descent after transmission through parental lineages. The size and number of AOH blocks correlate with the degree of parental relatedness.²⁰ Researchers and clinicians are also using the location of homozygous regions for mapping information in consanguineous families to identify autosomal recessive disease-causing genes.

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When confined to a single chromosome, AOH regions may indicate uniparental disomy (UPD).^{21,22} Several mechanisms can lead to UPD, resulting in isodisomy if both transmitted homologs are identical, heterodisomy if both homologs from one parent are present or segmental isodisomy if part of the chromosome is isodisomic and the other part is heterodisomic.^{23,24} Although the true prevalence of UPD is not known, it is expected to be at least ~1 in 3500 live births based upon information available in the 'pre-genome analyses era'.²⁵ UPD is a well-known mechanism leading to human disease if a chromosome containing imprinted genes is involved or if a recessive disease-causing mutation is present.^{25,26}

We now show that, by combining SNPs with our exon-targeted oligonucleotide array, detection for both copy number variation and copy-neutral AOH are optimized and enabled in a convenient, single genomic assay.

MATERIALS AND METHODS

Patients and sample preparation

A total of 3240 patient samples referred to the Medical Genetics Laboratory (<http://www.bcm.edu/geneticlabs/>) at Baylor College of Medicine from October 2010 to March 2012 were analyzed by the Chromosomal Microarray Analysis – Comprehensive (CMA-COMP) array. As an independent experimental SNP platform and quality assurance measure, 59 consecutive cases in which an AOH event (>10Mb) was identified by the CMA-COMP array were also analyzed on an Illumina SNP array (Illumina Inc., San Diego, CA, USA).

All studies were performed on patient DNA extracted from peripheral blood using the Puregene DNA blood kit (Gentra, Minneapolis, MN, USA) according to the manufacturer's instructions.

CMA-COMP

Microarray design. The custom-designed 400K CMA-COMP array used in this study was manufactured by Agilent Technologies, Inc. (Santa Clara, CA, USA), and contains ~280 000 oligonucleotide probes targeting 1860 genes at the exon level of genome resolution (<500bp), with an average backbone coverage of one probe per 30 kb, an improved design of a previously described version by Boone *et al*,¹⁶ and 60 000 SNP probes in duplicate.

Analysis. DNA was digested with *AluI* and *RsaI* in order to allow detection of the SNPs located at the enzymes' recognition sites. The remaining procedures of DNA labeling and hybridization were performed according to the manufacturers' instructions, with minor modifications.²⁷

For detailed array analysis, see Supplementary I.

Reporting. CNVs were reported and classified into three categories: (1) abnormal, (2) unclear clinical significance, and (3) likely benign. Abnormal CNVs include aneuploidy, known microdeletion/duplication syndromes, genomic imbalances larger than 2 Mb, other known genomic disorders (eg, the 1.5-Mb CMT1A duplication) and copy number changes involving pathogenic single genes. In cases where a pathogenic CNV is identified that may be associated with a presymptomatic condition, we report these incidental findings to the referring physician in order to facilitate adequate counseling and prompt medical attention as needed,²⁸ consistent with current ACMG recommendations. CNVs of unclear clinical significance include those smaller than 2 Mb in size that have not been correlated with a clinical phenotype. CNVs are classified as likely benign if they are polymorphic in the normal population as determined by reviews of recent literature. Evaluation of potential medically actionable variants includes careful consideration of the size of the CNV, variant allele frequency, gene(s) involved, whether it represents a *de novo* or inherited event, and the reported phenotypic clinical findings in the child or other relevant family members.^{29,30}

Additionally, AOH segments greater than 10 Mb in size were reported.

SNP genotyping platform. SNP array analysis was performed on the Illumina Infinium HD assay platform using HumanOmni1-Quad BeadChip (Illumina

Inc.) with 200 ng of genomic DNA according to the manufacturer's instructions. The GenomeStudio software (Illumina, Inc.) was used for data processing and analysis. AOH regions larger than 10 Mb were used for comparison to the CMA-COMP results.

RESULTS

Comparison of AOH calling by CMA-COMP and Illumina SNP array

Of the 3240 samples referred for the CMA-COMP array, 162 (5%) had at least one region of contiguous AOH larger than 10 Mb. A total of 59 consecutive cases with one or more AOH regions measuring >10 Mb in size as identified by the CMA-COMP array were also tested on the Illumina SNP array for quality control. Fifteen of these cases had interstitial, terminal, or centromeric AOH in single chromosomes (Table 1). The AOH regions were confirmed by the Illumina array in all 15 cases; however, the AOH calls in two cases were found to represent smaller-sized AOH regions by the higher-resolution Illumina SNP array. Twenty seven cases had AOH regions totaling 100 Mb or higher, which is suggestive of consanguinity. Such high levels of AOH were confirmed by the Illumina array for all these cases (Table 2). Therefore, the CMA-COMP platform, even though it has a lower density of SNP probes than the Illumina array, was able to reliably detect AOH events >10 Mb.

Uniparental disomy

Two cases were identified by CMA-COMP with AOH in a single chromosome within which all interrogated SNPs were homozygous, indicating the presence of uniparental isodisomy. One case showed isodisomy 1 and the other isodisomy 16. Maternal UPD16 has been associated with intrauterine growth restriction and fetal malformations.³¹ Additionally, 45 cases analyzed by CMA-COMP showed AOH regions exceeding 10 Mb involving one chromosome only, indicating possible uniparental heterodisomy for that particular chromosome. Twelve of these cases involved chromosomes that contain imprinted regions associated with a clinical phenotype [chromosomes 7 (three cases), 14 (seven cases), and 15 (two cases)]. Methylation-specific PCR was performed on two (Figures 1a and b) of the seven cases with AOH limited to chromosome 14; in both cases, there was no evidence of UPD. The B allele frequency plot for a case with AOH of ~61 Mb on chromosome 14 is shown in Figure 1c. Unfortunately, this case was lost to follow-up, so UPD could not be confirmed. For one case involving AOH on chromosome 15, an interstitial duplication of 15q11.2q13.1 and maternal uniparental trisomy was detected, genomic findings which are all consistent with a diagnosis of Prader-Willi syndrome. A detailed description of this clinical case is described elsewhere.³² All other remaining cases with AOH on imprinted chromosomes were lost to follow-up.

Of interest, one case had multiple AOH regions limited to chromosome 9 (Figure 2), which was confirmed by the Illumina SNP array. Analysis of the proband and parental genotypes indicated the presence of maternal heterodisomy 9.

Consanguinity

Multiple AOH regions >10 Mb involving two or more chromosomes were identified in 115 cases by CMA-COMP, of which 44 cases were also performed on the Illumina SNP array. As shown in Table 2, the AOH calls between the two arrays are comparable in the 27 cases with AOH regions totaling ≥100 Mb. For cases in which the degree of parental relatedness was provided by the referring center (Table 3), we compared the total length of AOH regions to that which is expected from the coefficient of inbreeding (*F*). Patients whose parents are first

Table 1 Comparison of the results of CMA-COMP and Illumina array for AOH regions greater than 10 Mb in size and limited to single chromosomes

Chromosome	CMA-COMP array		Illumina SNP array		Location	UPD confirmed
	Genomic interval	Size in Mb	Genomic interval	Size in Mb		
1	166 983 908–183 983 607	17.0	167 228 031–183 982 100	16.7	Interstitial	—
3	38 493 212–52 622 086	14.1	45 790 685–52 193 685	6.4	Interstitial	—
3	45 708 410–59 299 266	13.6	47 077 306–53 281 955 ^a	6.2	Interstitial	—
5	97 151 690–123 037 288	25.9	106 422 150–123 740 802	17.3	Interstitial	—
5	163 685 643–178 577 218	14.9	163 735 878–176 745 707	13.0	Interstitial	—
5	125 870 653–146 253 199	20.4	127 465 300–146 414 993	18.9	Interstitial	—
7	107 850 309–120 523 873	12.7	109 017 420–120 492 482	11.5	Interstitial	—
8	35 551 788–61 354 167	25.8	37 132 731–63 207 089	26.1	Centromeric	—
9	4 175 231–14 383 183	10.2	1 486 230–14 377 817	12.9	Interstitial	UPD
	88 061 835–128 350 612	40.3	66 587 429–126 250 362	59.7	Interstitial	—
12	1–22 919 015	22.9	1 607 841–22 154 162	20.5	Terminal	—
14	35 601 054–50 516 087	14.9	35 958 318–50 563 154	14.6	Interstitial	No UPD
14	33 803 584–70 306 504	36.5	33 742 889–70 200 059	36.4	Interstitial	No UPD
14	32 945 633–94 103 812	61.2	32 899 071–86 182 374	53.3	Interstitial	—
15	21 317 493–68 226 073	46.9	26 998 850–68 211 801	41.2	Interstitial	UPD
X	95 140 723–119 474 584	24.3	95 721 890–119 378 541	23.6	Interstitial	—

^aSmall non-contiguous segments of AOH were seen within the same AOH interval identified by the CMA-COMP.

Table 2 Comparison of the results of CMA-COMP and Illumina array for detection of AOH regions totaling 100 Mb or higher in size

Patients	CMA-COMP array			Illumina array
	AOH level (Mb)	Number of chromosomes involved	Number of blocks	AOH level (Mb)
Case 1	871	15	18	851
Case 2	863	20	25	787
Case 3	707	16	23	702
Case 4	678	18	20	681
Case 5	654	14	16	609
Case 6	514	10	14	529
Case 7	501	10	14	506
Case 8	352	8	8	354
Case 9	345	8	11	367
Case 10	332	7	9	310
Case 11	289	9	10	247
Case 12	276	8	8	244
Case 13	270	8	9	240
Case 14	252	8	9	245
Case 15	234	5	6	147
Case 16	223	8	8	228
Case 17	194	5	5	127
Case 18	187	7	7	150
Case 19	177	6	7	158
Case 20	158	6	7	152
Case 21	141	6	6	138
Case 22	138	6	7	130
Case 23	129	5	7	117
Case 24	122	3	4	90
Case 25	118	4	4	107
Case 26	110	3	3	108
Case 27	107	5	5	96

cousins (third degree of relationship) are expected to have 1/16 of their genome homozygous or ~179 Mb of total AOH regions. The total length of AOH regions observed was 225 Mb as shown in case 2. Consistent data were also observed in cases of fourth and sixth degree

of parental relationship [expected 90 Mb and observed 89 and 82 for fourth degree (cases 3 and 4), and expected 22.5 Mb and observed 58 for sixth degree (case 5)].

Notably, our analyses identified 10 cases in which the observed total length of AOH regions was consistent with that expected for a first degree relationship ($F = 1/4$ or ~716 Mb). In those cases, the total length of AOH ranged from ~506 Mb to 851 Mb, with a mean of 677 Mb. Amongst this group of subjects, consanguinity was confirmed in two patients, one of which was known to be the product of a sister–brother mating (Table 3, case 1).

Autosomal recessive disorders and AOH

We evaluated regions of AOH for gene content when the indication was a specific disease. In four patients with an autosomal recessive disorder, the associated gene localized within one of the AOH regions. Sequencing analysis performed elsewhere confirmed the presence of a homozygous mutation in two patients (Table 4).

One patient, the product of a consanguineous mating (second cousins once removed), presented with DD/ID and microcephaly, and MRI revealing a mild diffuse reduction in the volume of the cerebral hemispheric white matter with a borderline to increased size of the corpus callosum. CMA-COMP analysis showed AOH events larger than 10 Mb on chromosomes 8 and 14. The AOH event on chromosome 8 also harbored a homozygous deletion of ~52 kb involving exons 4–14 of the *VPS13B* (*vacuolar protein sorting 13 homolog B*) gene (Figures 3a and b), which is associated with Cohen syndrome (OMIM #216550) and consistent with the clinical phenotype of this patient.

Intragenic CNVs

An advantage of the CMA-COMP array platform is its ability to detect very small, single-exon copy number changes. Pathogenic genomic deletions and/or duplications were detected in 14% (445/3240) of the cases. CNVs of unclear clinical significance were detected in an additional 13% (421/3240). Intragenic pathogenic CNVs were detected in 21 cases (Table 5) with an average of 21 probes (range 4–90). The smallest CNV was confirmed by sequencing to be

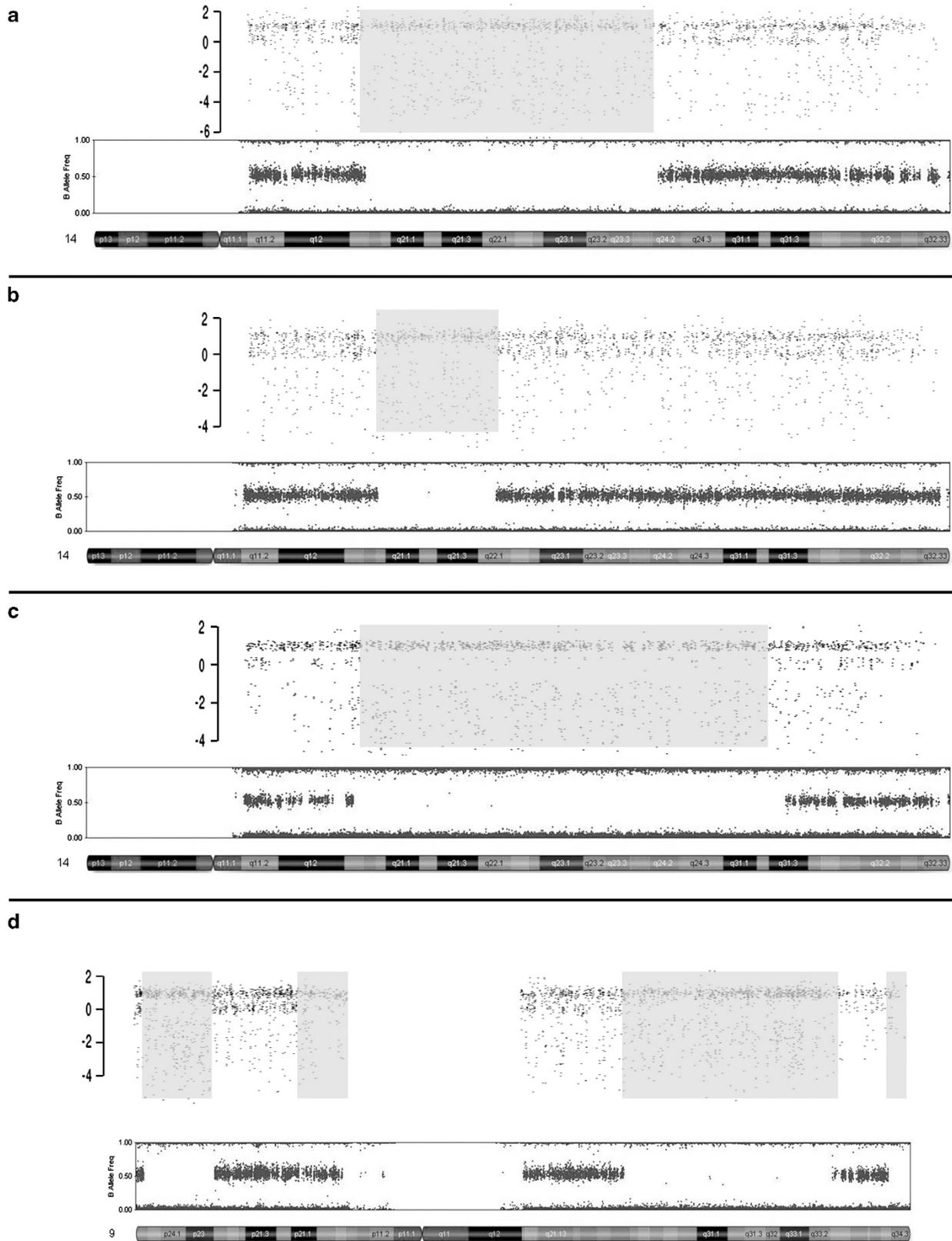


Figure 1 Large regions of AOH limited to single chromosomes suggestive of heterodisomy. Top panels – CMA-COMP SNP data. Bottom panels – corresponding Illumina B allele frequency data. (a–c) Chromosome 14. Follow-up studies by methylation specific PCR showed presence of both maternal and paternal bands, indicating biparental chromosome 14 inheritance for cases shown in panels (a) and (b). Methylation studies were not available for the case shown in panel (c). (d) Chromosome 9. Follow-up parental SNP array analyses confirmed presence of maternal heterodisomy in this patient.

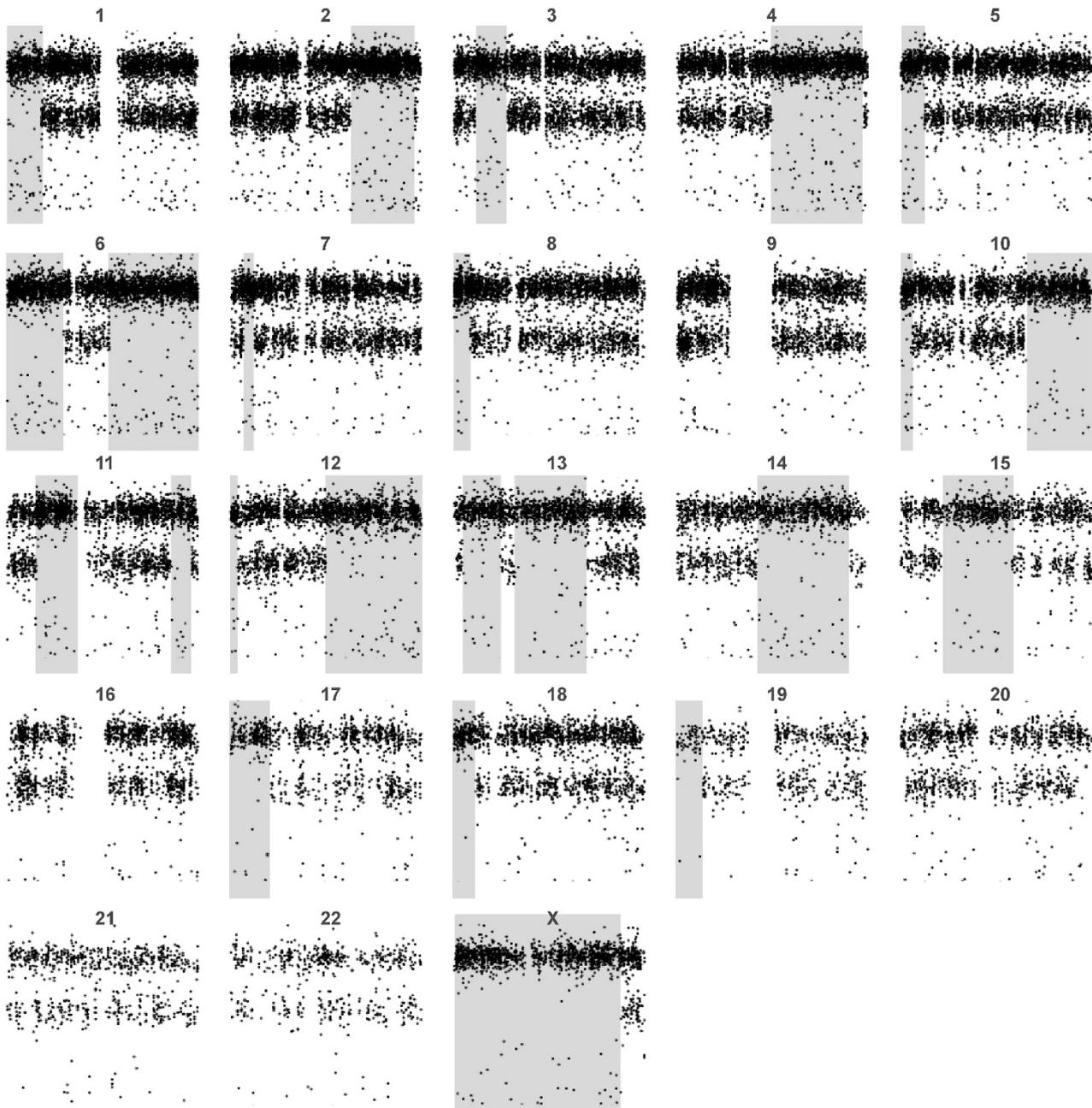


Figure 2 CMA-COMP array showing a patient with consanguinity as demonstrated by the multiple blocks of AOH (shaded) on numerous chromosomes.

500 bp. A comparison of the distribution of the probes of the CMA-COMP to two commercial SNP arrays for the intragenic deletions involving exons of the *VPS13B* gene (Table 5, cases 6 and 7) is provided in Figures 3c and d. In addition to the *VPS13B* gene, intragenic deletions of both *NRXN1* and *DMD* were detected in multiple patients as well as two cases involving genes that predispose to cancer.

DISCUSSION

With the addition of SNP probes to our exon coverage array, we provide a comprehensive approach for the identification of clinically relevant copy number neutral changes in addition to medically actionable CNVs in a single assay.

The principles used to guide this unique array design were to: (1) empirically select the best performing probes to maximize detection and signal to noise ratio, (2) detect CNVs known to be associated with diseases and target coverage of the exons of these known disease genes, (3) maintain 30 kb backbone coverage, and (4) exclude most of the known LCR regions. The rationale for our array design to maximize detection of clinically relevant genomic changes has been independently validated by the observations of Haraksingh *et al.*³³ They compared the CNVs observed in the 1000 Genomes Project with all the currently commercially available high-resolution array platforms and concluded that the sensitivity, total number, size range, and breakpoint resolution of CNV calls were highest for CNV focused arrays that did not compromise the backbone tiling

density of the rest of the genome. They also found that probe distribution greatly affected the performance of a platform. A disadvantage for SNP-only arrays is that the probe distribution is restricted by the non-uniform availability of informative SNPs throughout the genome. Additionally, probes that are optimized will provide maximum information for specific loci.

In this study, the CMA-COMP array, with only 60 000 SNP probes, was concordant with a high-density SNP array in detecting AOH events and is thus an excellent tool for genome-wide screening for AOH in order to identify UPD, consanguinity, and map genomic intervals containing potential recessive loci. The percent of the genome manifesting AOH for each case was calculated for both platforms (data not shown) and there was complete concordance between the two platforms within 1–2%. Because of the lower density of SNP probes in the CMA-COMP array, there may be an over-estimation of the genomic size of an AOH event, which occurred in two cases in Table 1. In one of these cases, the Illumina array revealed a smaller AOH (6 Mb) event, and in the other case, a series of smaller discrete AOH events interrupted by small regions of heterodisomy were seen in the Illumina array. The CMA-COMP did not resolve the discrete interval events; instead it showed a contiguous AOH event for this region. As both of these cases involved a non-imprinted chromosome, further studies were not recommended.

Added value to the genomic analysis provided by SNP probes is the detection of uniparental isodisomy without requiring analysis of parental samples, as it is with other conventional assays that utilize STR markers. In addition, UPD of virtually any chromosome can be detected in one assay. While SNP arrays will detect virtually 100% of isodisomies,²⁴ not all cases of uniparental heterodisomy may be detected by SNP arrays unless a heterodisomic chromosome underwent a recombination event during meiosis, resulting in

isodisomy interrupted by regions of heterozygosity, reflecting the presence of heterodisomy (hetero-isoUPD). In such cases, heterodisomy appears as a large block of AOH (isodisomic segment) confined to a single chromosome. Recently, Papenhausen *et al*²² found that their cohort of nine confirmed UPD cases all showed an AOH block within the affected chromosome. Similar findings were also observed in five confirmed UPD cases and an additional three were consistent with the phenotype by Bruno *et al*.³⁴ However, not all AOH regions confined to a single chromosome indicate the presence of heterodisomy, as shown in our patients with AOH on chromosome 14. Similar observations were reported by Papenhausen *et al*,²² who showed that only 29 out of 46 cases with a single segmental AOH event were confirmed to be UPD. Therefore, a single region of AOH could be a random finding representing a region of identity by descent or linkage disequilibrium (LD) because of a low recombination rate.

Detection of isodisomy has obvious clinical relevance for cases in which chromosomes bearing imprinted genomic regions are involved, but it is also relevant in the context of autosomal recessive (AR) disorders. Most of the non-imprinted UPD cases described so far were ascertained by detection of a homozygous mutation in autosomal recessive genes that did not follow the expected Mendelian allele transmission pattern.²⁶ From a genetic counseling perspective, detection of isodisomy or hetero-isoUPD modifies recurrence risk for AR disease from 25% to <1%. The importance of parental follow-up studies to confirm carrier status in cases in which a homozygous mutation was detected in the child cannot be underemphasized.

The identification of AOH has been previously employed for the determination of the genetic defects underlying genetically heterogeneous recessive disorders by a homozygosity mapping approach in a research setting. AOH regions determined by genome-wide SNPs analysis allows delineation of the critical disease-associated genomic interval and the number of potential candidate genes. Analysis of SNP data obtained for both affected and unaffected individuals enables further refinement of AOH regions and subsequent identification of candidate genes. Implementation of SNP arrays in clinical diagnostics allows the clinician to take advantage of this approach in their daily practice, especially because these data could be combined with clinically available whole-exome sequencing approaches. Clinicians can also utilize SNP genotyping information to devise a cost-effective strategy for determining the molecular etiology of genetically heterogeneous autosomal recessive diseases (e.g., deafness, retinitis pigmentosa, etc) by targeting sequence analysis for a suspected disease gene if it is located in an AOH block. Such was the case for the patients identified with SCID and Usher syndrome (Table 4).

The CMA-COMP array also has the advantage of detecting intragenic copy number changes. While intragenic deletions and duplications are known to account for a significant portion of disease-causing mutations for genes such as *DMD*, only more recently with the implementation of array CGH are intragenic deletions and duplications being detected for many other genes. Examples of

Table 3 Extent of AOH regions detected in patients from known consanguineous families

Patients	CMA-COMP array				Expected AOH
	AOH level (Mb)	Number of chromosomes involved	Number of blocks	Parental relationship	
Case 1 ^a	707	16	23	First-degree relatives	716 Mb ($F=1/4$)
Case 2	225	9	10	First cousins	179 Mb ($F=1/16$)
Case 3	89	4	4	First cousins once removed	90 Mb ($F=1/32$)
Case 4	82	3	3	First cousins once removed	90 Mb ($F=1/32$)
Case 5	58	3	3	Second cousins once removed	22.5 Mb ($F=1/128$)

^aSame as case 3 in Table 2.

Table 4 Correlation of AOH regions with autosomal recessive disorders

AR disorder	Genes related to diagnosis	Total AOH > 10 Mb	Gene within AOH block	AOH size (Mb)	Comment
Cohen syndrome	<i>VSP13B</i>	29	<i>VSP13B</i>	11	Homozygous exonic deletion detected
HHH syndrome	<i>SLC25A15</i>	270	<i>SLC25A15</i>	40	Homozygous mutation in <i>SLC25A15</i> detected
SCID	18 genes	332	<i>CD3D</i>	8	Homozygous mutation in <i>CD3D</i> detected
Usher syndrome	Dozens of genes	214	<i>USH2A</i>	18	

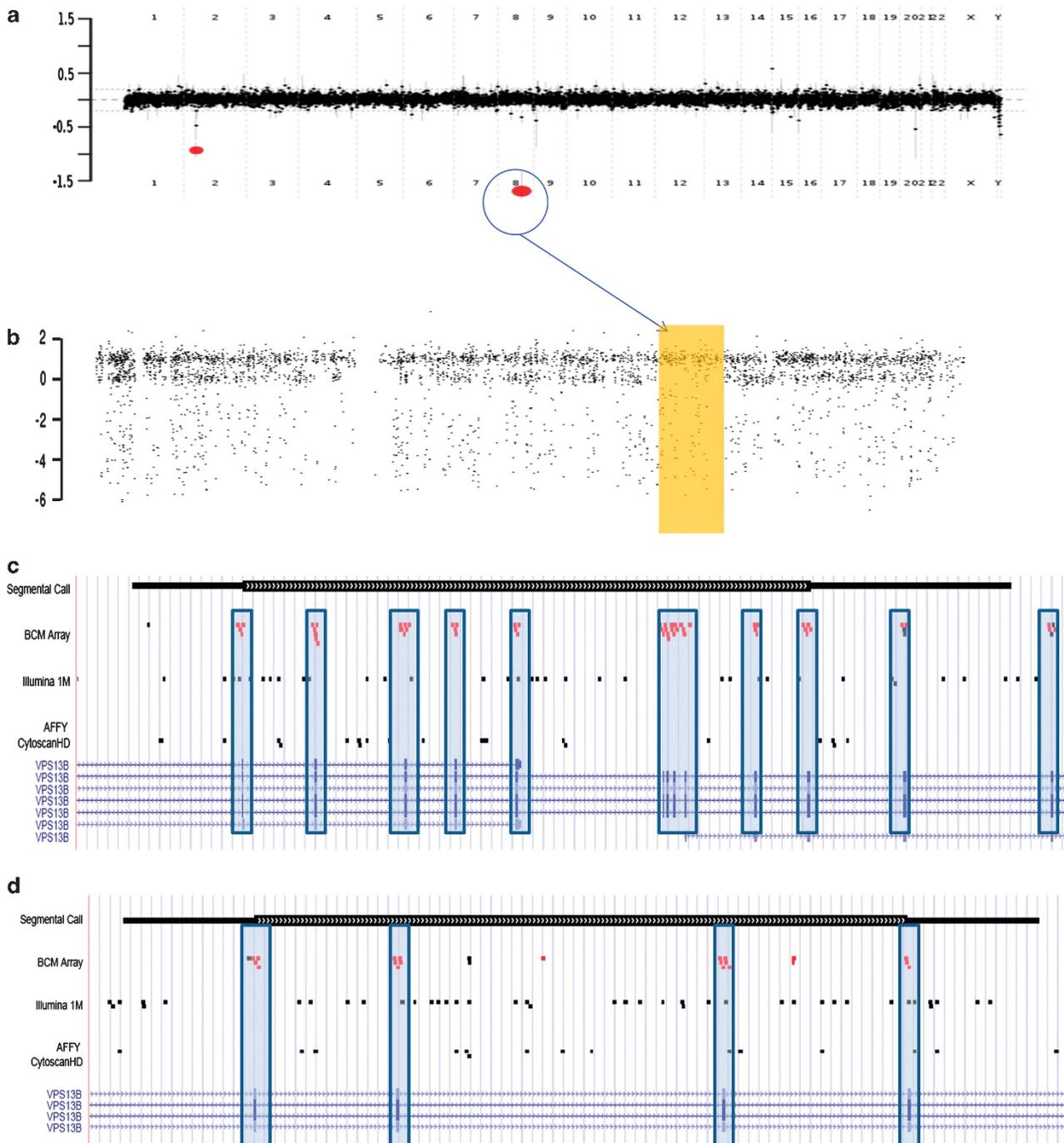


Figure 3 (a) A ~52-kb homozygous deletion involving exons 4–14 of the *VPS13B* gene in a patient with Cohen syndrome detected by CMA-COMP array. (b) shows the SNP data plot with an AOH region on chromosome 8, wherein the *VPS13B* gene is located. (c) and (d) Comparison of the probe distribution between the exon-targeted CMA-COMP array and two other commercial SNP arrays for the portion of the *VPS13B* gene deleted in cases 6 and 7 (Table 4) (c) Case 6 (same case as in (a)) with a deletion of exons 4–14 (red dots represent the deleted oligos in the exons). Note that the locations of the SNPs (black dots) are outside of almost all of the exons, and therefore single exon deletions would not be detectable by these SNP arrays. (d) Case 7 in Table 4 – red dots represent the deleted oligonucleotides corresponding to exons 22–25 (represented by the hatch marks at the bottom of the figure) as detected by the CMA-COMP array. The black dots represent the SNP distribution within the same region. Again, note that most SNP probes are located within introns.

haploinsufficient, intragenic deletions and the molecular mechanism and possible consequences of these intragenic CNVs have been previously reported.^{4,12,13,16,35,36} Detection of intragenic copy number changes also has a role in the diagnosis of autosomal recessive disease, as demonstrated by the case with an intragenic

heterozygous deletion of the *VPS13B* gene (case 7 in Table 4), which is associated with Cohen syndrome. Consistently, deletions have been reported as an important cause of Cohen syndrome.³⁷

Interestingly, genotype–phenotype correlations are being described for deletions occurring at different locations within a gene. For

Table 5 Pathogenic exonic CNVs detected by CMA-COMP array

Case	Gene	Disease association	Exon(s)	Copy number		Chromosome		
				change	Location	Inheritance	Gender	
1	<i>NRXN1</i>	Autism and developmental disorders	23	Loss	2p16.3	Unknown	F	
2	<i>NRXN1</i>	Autism and developmental disorders	3–5	Loss	2p16.3	Paternal	M	
3	<i>NRXN1</i>	Autism and developmental disorders	4–5	Loss	2p16.3	Unknown	M	
4	<i>MSH6</i>	Hereditary nonpolyposis colorectal cancer	5–6	Loss	2p16.3	Unknown	F	
5	<i>TGFB1</i>	Corneal dystrophy	8–10	Loss	5q31.1	Unknown	F	
6	<i>VPS13B</i>	Cohen syndrome	4–14	Homozygous loss	8q22.2	Unknown	F	
7	<i>VPS13B</i>	Cohen syndrome	22–25	Loss	8q22.2	Unknown	M	
8	<i>BRCA2</i>	Increased risk of cancer	13–14	Loss	13q13.1	Unknown	M	
9	<i>UBE3A</i>	Angelman syndrome	7–14	Loss	15q11.2	Maternal	F	
10	<i>CHRNA7</i>	Intellectual disability and seizures	Entire gene	Loss	15q13.3	Unknown	F	
11	<i>ANKRD11</i>	KBG syndrome	4–13	Loss	16q24.3	Unknown	F	
12	<i>ANKRD11</i>	KBG syndrome	2–3	Loss	16q24.3	Unknown	F	
13	<i>HNFB1</i>	Polycystic kidney disease, genital malformations, pancreatic atrophy and maturity-onset diabetes of the young type 5	7–8	Loss	17q12	Unknown	M	
14	<i>DMD</i>	Duchenne muscular dystrophy	15	Gain	Xp21.1	Unknown	M	
15	<i>DMD</i>	Duchenne muscular dystrophy	40–50	Loss	Xp21.1	Unknown	M	
16	<i>DMD</i>	Duchenne muscular dystrophy	63–64	Gain	Xp21.1	Unknown	M	
17	<i>DMD</i>	Duchenne muscular dystrophy	49–51	Loss	Xp21.1	Maternal	M	
18	<i>MED12</i>	FG syndrome and Lujan–Fryns syndrome	25–28	Gain	Xq13.1	<i>De novo</i>	M	
19	<i>GPC3</i>	Simpson–Golabi–Behmel syndrome	7	Gain	Xq26.2	Unknown	M	
20	<i>FMR1</i>	X-linked intellectual disability	Entire gene	Gain	Xq27.3	Unknown	M	
21	<i>L1CAM</i>	X-linked hydrocephalus	1–2	Loss	Xq28	Unknown	M	

example, the more C-terminal deletions, such as case 1 (Table 5), including those affecting the beta isoform of Neurexin-1, present with an increased head size and a high frequency of epilepsy (88%) when compared with more N-terminal deletions of *NRXN1*, as seen in cases 2 and 3 (Table 5). Therefore, increasingly specific genotype–phenotype predictions are becoming available to assist with the genetic counseling of the copy number changes identified by array studies.^{28,35}

However, genetic counseling can also become complicated by incidental findings, such as the intragenic deletions within *MSH6* in case 4 and *BRCA2* in case 8 (Table 5), which confers an increased lifetime susceptibility to cancer in a 13-year-old female and a 10-year-old male, respectively. These findings require careful counseling to address prognosis and surveillance. These findings also have obvious implications for other family members that may also have inherited the CNV. While unexpected, these findings can have a profound impact on optimizing medical management and prevention for the whole family. As intragenic deletions of these genes have been observed,^{36,38} it is expected that incidental findings such as these will occur as arrays with targeted exonic coverage are increasingly used in clinical practice.

In conclusion, combining both array CGH and SNP genotyping in a single platform optimizes the clinical diagnostic capability by offering the simultaneous detection of copy number neutral changes and small intragenic copy number changes.

CONFLICT OF INTEREST

Drs Wiszniewska, Bi, Shaw, Stankiewicz, Lalani, Probst, Scaglia, Beaudet, Lupski, Eng, Cheung, Bacino, Patel are the faculty of the Department of Molecular and Human Genetics at Baylor College of Medicine, which derives revenue from molecular genetic testing offered in the Medical Genetics Laboratory. Dr Lupski is a paid consultant for Athena Diagnostics, holds stock ownership in 23andMe, Inc. and Ion Torrent Systems, Inc., and is a co-inventor

on multiple United States and European patents related to molecular diagnostics. The remaining authors declare no conflict of interest.

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