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Phenotypic spectrum associated with de novo and inherited deletions and duplications at 16p11.2 in individuals ascertained for diagnosis of autism spectrum disorder

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ABSTRACT

Background Recurrent microdeletions and microduplications of ~555 kb at 16p11.2 confer susceptibility to autism spectrum disorder (ASD) in up to 1% of ASD patients. No physical or behavioural features have been identified that distinguish these individuals as having a distinct ASD subtype, but clinical data are limited.

Methods We report five autistic probands identified by microarray analysis with copy number variation (CNV) of 16p11.2 (three deletions, two duplications). Each patient was assessed for ASD and dysmorphic features. We also describe a deletion positive 26-month-old female who has developmental delay (DD) and autistic features.

Results Probands 1 (female with ASD, de novo deletion) is not dysmorphic. Probands 2 (male with autism, de novo deletion) and proband 3 and his brother (males with autism, inherited deletions) are dysmorphic, but the two probands do not resemble one another. The mother of proband 3 has mild mental retardation (MR), minor dysmorphism and meets the criteria for ASD. Probands 4 (dysmorphic autistic male, de novo duplication) had a congenital diaphragmatic hernia. Probands 5 (non-dysmorphic ASD female with a duplication) has two apparently healthy duplication positive relatives. Proband 1 and 2 have deletion negative siblings with ASD and Asperger syndrome, respectively. Probands 5 (female with DD and an inherited duplication) is dysmorphic, but has oligohydranios sequence.

Conclusions The phenotypic spectrum associated with CNV at 16p11.2 includes ASD, MR/DD and/or possibly other primary psychiatric disorders. Compared to the microduplications, the reciprocal microdeletions are more likely to be penetrant and to be associated with non-specific major or minor dysmorphism. There are deletion positive ASD probands with a less severe phenotype than deletion negative ASD siblings underscoring the significant phenotypic heterogeneity.

INTRODUCTION

Autism (OMIM 209850), typically apparent by the age of 3 years, is characterised by impaired communication, impaired reciprocal social interaction skills, and by restricted repetitive behaviours and interests. Autism spectrum disorder (ASD) is a broader phenotype, which includes autism as well as less severe conditions such as Asperger syndrome and pervasive developmental disorder—not otherwise specified (PDD-NOS). The prevalence of autism is 3 per 1000 and rises to 6 per 1000 when all forms of ASD are included. The male to female ratio is ~4:1 and after syndromic forms of ASD are excluded, it is associated with an empiric sibling recurrence risk of 5–10%.

The ASDs are aetiologically heterogeneous. About 10% are associated with a Mendelian syndrome (eg, fragile X syndrome and tuberous sclerosis complex). Another 5–7% are associated with a cytogenetically visible chromosome abnormality, the most frequently observed being a maternally derived duplication of 15q11-13. Teratogens, including in utero exposure to rubella and valproate, have also been implicated. The remainder of affected individuals are presumed to have multifactorial forms of ASD and linkage scans have mapped candidate risk loci. More recently, de novo copy number variations (CNVs) have been observed in 7–10% of sporadic ASD patients and in 2–5% of affected individuals from multiplex families.

Three studies have recently discovered recurrent microdeletions and microduplications at the 16p11.2 locus in ASD cohorts. This 555 kb CNV region, which is flanked by segmental duplications having >99% sequence identity, is presumed to have an elevated mutation rate due to its genomic architecture. In our previous study, we identified 4/27 (~1%) unrelated Canadian ASD patients who had chromosome 16p11.2 CNVs. The equivalent change was not observed in 1652 controls. Weiss and colleagues made a similar observation in 12 of 751 (1.6%) families having two or more ASD siblings (multiplex families) from the Autism Genetic Resource Exchange (AGRE) repository. Moreover, they found dosage changes at 16p11.2 in 5/512 (1%) children (~1%) who had either developmental delay (DD) or suspected ASD, in 3/299 (~1%) patients from an Icelandic ASD cohort, and in 2/1834 (0.01%) of Icelandic unscreened controls. Kumar et al found 16p11.2 CNVs in 5/712 (0.7%) unrelated autism probands comprised of 410 AGRE cases and 302 probands from the National Institutes of Mental Health Genetics Initiative (total of 87 simplex cases and 665 multiplex cases).

Four of the microdeletion patients reported by Weiss et al overlapped with the Kumar study (see...
Supplementary table 1). Subsequent exon sequencing of eight biological candidate genes within this locus failed to identify any variants associated with ASD.12

Bijlsma et al13 have now reported that 14/4284 (0.33%) individuals referred for mental retardation and/or multiple congenital anomalies carry the same 16p11.2 microdeletion. Only four of the probands were formally assessed for autism, with one receiving a diagnosis. Interestingly, three apparently normal transmitting parents (two mothers, one father) were identified. Here we present detailed genotype—phenotype correlation for six probands with CNV at 16p11.2, emphasising detailed assessment for ASD and dysmorphology in the index case and in the CNV/ASD positive family members. Coupled with a literature review, our findings reinforce the role of this 16p11.2 region in ASD, but reveal many complexities in interpreting clinical outcomes.

METHODS

Human subjects

ASD cases were collected through a multicentre Canadian research team using common ASD protocols approved by respective research ethics boards of the institutions where clinical evaluations were performed (the Provincial Medical Genetics Program, St John’s Newfoundland; the Hospital for Sick Children, Toronto; the Offord Center for Child Studies, Hamilton, Ontario). Informed consent including consent to publish photographs was obtained from each participant or legal guardian. Probands 1–5 met the criteria for ASD based on Autism Diagnostic Interview-Revised.14 Autism Diagnostic Observation Schedule (ADOS)15 and clinical history, with the exception of proband 5 who had a Childhood Autism Rating Scale16 rather than an ADOS. One of three medical geneticists (BF, RW, SM) reviewed the medical charts and performed physical examinations for dysmorphic features. Additional clinical evaluations included speech assessments (Oral Written and Language Scales, OWLs17) and Intelligence Quotient (IQ) testing. For the latter, Leiter International Performance scale18 was used for those who were young or significantly verbally impaired, and Wechsler Intelligence Scale19 was used for those who were able to complete the test.

Microarray analysis

DNA samples were genotyped using one or more of the Affymetrix 500K, Affymetrix 6.0, or Illumina 1M single nucleotide polymorphism arrays according to standard protocols (see table 1).5 For all microarray platforms, multiple calling algorithms were used to maximise CNV detection (sensitivity) and call accuracy (specificity). For the Affymetrix 500K array, the analysis tools dChip, CNAG, and GEMCA were used while Birdsuite, Partek Genomics Suite, and Affymetrix GTC were used for the analysis of the Affymetrix 6.0 arrays. For Illumina 1M arrays, the programs Quanti-SNP, PennCNV, and iPattern (unpublished) were employed for CNV detection. CNVs were merged if they were detected in the same individual by more than one algorithm using the outside probe boundaries. We have observed that those CNVs detected by more than one analysis tool validate at a rate of >95% using quantitative polymerase chain reaction (PCR) assays. All 16p11.2 CNVs were detected by all relevant algorithms. We used identical methods to examine 2387 population controls (but not assessed for autism) and found none with CNV of this region8 20, nor was the region identified as variable in the Database of Genomic Variants.21

For CNV validation, two independent SYBR Green based quantitative assays were used (primer sequences available upon request) to measure relative copy number in cases and controls between 16p11.2 and a control region (FOXP2). Standard fluorescent in situ hybridisation (FISH) techniques were also used for validation with RP11-114A14 (at 16p11.2) used as a test probe and RP11-55S3M22 (at 16q22.1) used as a control probe.

RESULTS

Table 1 and figures 1 and 2 summarise our original findings and table 2 integrates these results with the literature. Our results focus on genotype and phenotype correlations for 16p11.2 CNVs in ASD families. We also examined parents for potential inversions that might predispose to CNV events in children,22 but in those tested no inversion was detected (figure 2h,i).

Proband 1

This 18-year-old female has ASD and a de novo 16p11.2 microdeletion. While microarray analysis did not identify mosaicism, subsequent FISH testing showed 50% mosaicism for the deletion (figure 2e–g). Although not examined by a medical geneticist, no dysmorphic features were recorded in her medical chart. At 5 years, her head circumference was 51 cm (50th centile). Her younger brother was diagnosed with ASD at 10 years, but is microdeletion negative.

Proband 2

This 15-year-old male has autism and a de novo microdeletion. He was born to a 26-year-old G2P1 mother and a 29-year-old father. Pregnancy and delivery at term were uncomplicated. Birth weight was 2665 g (2nd–9th centile). At 14 months, eye contact deteriorated and he lost a four word vocabulary. By 4 years, he was obese. He was prescribed sertraline for anxiety at 7 years.

At 15 years (figure 3a,b), height was 157 cm (25th centile), weight was 104.75 kg (>97th centile), and head circumference was 59 cm (+5SDs). He had a low nuchal hairline, a short neck and a strikingly flat facial profile with low set ears. Palpebral fissures were narrow and long. Nose was short, with a flat broad nasal root/bridge and a delicate tip. Philtrum was smooth and mouth was downturned. Upper incisors were widely spaced and chin was pointed. Hand length was 17.2 cm (5rd–25th centile) with distally tapered fingers. Toes were short with 2/3 cutaneous syndactyly (extending half way up the interdigital space). Finger and toenails were thin and deep set. He had micropenis with testicles that were starting to enlarge.

His 15-year-old sister was diagnosed with Asperger syndrome at 12 years, but is microdeletion negative. She is not dysmorphic.

Proband 3

This 5-year-old male has autism and a microdeletion inherited from his mother who has mild mental retardation (MR) and ASD. He was born to a 29-year-old G2P1 mother and a 28-year-old father. Pregnancy was uncomplicated until mother was admitted with an antepartum bleed. He was born at 28+5 weeks and was extubated within the first 24 h of life. At 6 weeks, he was discharged from the neonatal intensive care unit (NICU) into foster care. At 14 months, extremities were hypertonic and he was diagnosed with spastic cerebral palsy. He walked at 27 months. At 5 years he had no speech, but had learned a few signs.

At 4.5 years, height was 99.5 cm (25th centile), weight was 16.5 kg (50th centile) and head circumference was 51.3 cm (50th centile). He had a frontal cowlick with a double hair whorl. He had a tall broad forehead with hypertelorism (inner canthal distance 3.4 cm, > +2SD). Midface was hypoplastic and nares were anteverted. Philtrum was smooth and measured 1.2 cm (3rd–25th centile). His mouth was wide and ears were...
Table 1  Phenotype of six probands with copy number variation (CNV) at 16p11.2

<table>
<thead>
<tr>
<th>Proband number, ID &amp; 16p11.2 CNV*</th>
<th>Sex</th>
<th>Diagnosis &amp; family history</th>
<th>ADOS†</th>
<th>ADI-R‡</th>
<th>IQ</th>
<th>Expressive speech testing</th>
<th>Receptive speech testing</th>
<th>Lang. regress</th>
<th>Adaptive functioning</th>
<th>Comorbid behaviour</th>
<th>Abnormal growth parameters &amp; dysmorphic features**</th>
<th>Other medical problems ††</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proband 1 MM0089-003</td>
<td>F</td>
<td>ASD with cognitive delay, deletion negative brother with ASD</td>
<td>ADOS-4 (12yr) Com 6 (cutoff 3) Soc 10 (cutoff 6) Play 2, SB 1</td>
<td>soc 19 (cutoff 10) com 12 (cutoff 7) behav 7 (cutoff 4) onset 2 (cutoff 1)</td>
<td>Leiter=87 WISC performance IQ=78</td>
<td>OWLS OE=6yr7mth (at 12y4mth)</td>
<td>OWLS LC=6yr1mth (12y4mth)</td>
<td>Unknown</td>
<td>VABS=4yr3mth (at 5y3mth)</td>
<td>None</td>
<td>N/A</td>
<td>Motor delay (walked 16mth)</td>
</tr>
<tr>
<td>Proband 2 SK0019-004</td>
<td>M</td>
<td>Autism with anxiety disorder, deletion negative sister with Asperger syndrome</td>
<td>ADOS-3 (7yr) Com 3 (cutoff 4) Soc 9 (cutoff 6) Play 1, SB 4</td>
<td>soc 27 (cutoff 10) com 22 (cutoff 7) behav 12 (cutoff 4) onset 5 (cutoff 1)</td>
<td>Leiter-R=93 (7yr5mth)</td>
<td>OWLS OE=6yr4mth (at 7yr4mth)</td>
<td>OWLS LC=7yr2mth (7yr4mth)</td>
<td>Yes</td>
<td>VBAS=6yr4mth</td>
<td>Hyperactivity</td>
<td>[+++]</td>
<td>Micropenis, hernia vertebra (110)</td>
</tr>
<tr>
<td>Proband 3 NA0269-000</td>
<td>M</td>
<td>Autism with cognitive delay, deletion positive mother (ASD) and brother (autism)</td>
<td>ADOS-1 (38mth) Com 5 (cutoff 4) Soc 10 (cutoff 4) Play 4, SB 5</td>
<td>soc 20 (cutoff 10) com 11 (cutoff 7) behav 8 (cutoff 3) onset 5 (cutoff 1)</td>
<td>Leiter (4yr8mth) not testable</td>
<td>OWLS (5yr) not testable</td>
<td>OWLS (5yr) not testable</td>
<td>N/A</td>
<td>Non-verbal</td>
<td>Not tested</td>
<td>Hyperactivity</td>
<td>None</td>
</tr>
<tr>
<td>Proband 4 SK0102-004</td>
<td>M</td>
<td>Autism with cognitive delay &amp; anxiety disorder, FH negative</td>
<td>ADOS-1 (9yr) Com 4 (cutoff 4) Soc 8 (cutoff 4) Play 2, SB 5</td>
<td>soc 26 (cutoff 10) com 8 (cutoff 7) behav 6 (cutoff 3) onset 4 (cutoff 1)</td>
<td>Leiter-R=74 (8yr7mth)</td>
<td>OWLS OE=1yr9mth (at 8yr7mth)</td>
<td>OWLS LC=1yr8mth (at 8yr7mth)</td>
<td>Yes</td>
<td>VBAS=2yr8mth (at 12yr8mth)</td>
<td>Anxiety</td>
<td>Short stature (H &amp; W &lt;5th). ++: Hypertelorism, smooth philtrum, posteriorly rotated ears</td>
<td></td>
</tr>
<tr>
<td>Proband 5 NA0133-000</td>
<td>F</td>
<td>ASD with cognitive delay, Healthy mother &amp; sister duplication positive</td>
<td>CAR 8yr2mth (mild-moderate autistic range)</td>
<td>soc 24 (cutoff 10) com 10 (cutoff 7) behav 7 (cutoff 3) onset 4 (cutoff 1)</td>
<td>WISC-III (8 yr) FSIQ=54(1%) PPVT=5 yr (at 9yr)</td>
<td>Not tested</td>
<td>Not tested</td>
<td>Yes</td>
<td>Not tested</td>
<td>None</td>
<td>Borderline short stature (H &amp; W &lt;5th). ++: Hypertelorism, smooth philtrum, reduced upper/lower segment ratio</td>
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<tr>
<td>Proband 6 TCAG0055</td>
<td>F</td>
<td>Developmental delay, Duplication positive father: bigdor disorder, academic difficulty</td>
<td>Carrying</td>
<td>Not performed</td>
<td>Not performed</td>
<td>Bayley Scales (21mth): low-average cognitive skills</td>
<td>First words 16mth, 15—20 single words at 26mth</td>
<td>Followed 1-step commands at 26mth</td>
<td>No</td>
<td>Not tested</td>
<td>Autistic features</td>
<td>Borderline short stature (H 3rd). ++: Frontal bossing, flat facies, varus, motor delay (walked 21mth)</td>
</tr>
</tbody>
</table>

*Primary array detection (subset array): Proband 1, 2, 4: Affymetrix 500 K (Illumina 1 M); Proband 3: BlueGene CytoChip (Affymetrix 6.0); Proband 5: Affymetrix 500 k; Proband 6: GenexDx 44k v1.0.
†Other genomic changes not seen in controls: Proband 1, 2, 3, 5, 6; none; Proband 4: two CNV gains (10q11.21).
‡ADOS, Autism Diagnostic Observation Schedule.
§ADI-R, Autism Diagnostic Interview-revised.
**Dysmorphism scale: ++ minor dysmorphism; +++ moderate dysmorphism; ++++ severe dysmorphism.
††Other normal medical tests: Proband 1: routine karyotype; Proband 2: Brain MRI, EEG, ophthalmology assessment, routine karyotype, FISH for Prader-Willi syndrome, methylation analysis of SNRPN; Proband 3: Brain MRI, EEG, ophthalmology assessment, FMR1 genetic testing, routine karyotype; Proband 4: routine karyotype; Proband 5: CT head, EEG, FMR1 genetic testing, routine karyotype; Proband 6: echocardiogram, abdominal ultrasound, ophthalmology assessment, routine karyotype.
†‡see figures 1 and 2e,f.
CARS, Childhood Autism Rating Scale; Carrying, communication score; OWLS LC, Oral and Written Language Scales, listening comprehension; OWLS OE, Oral and Written Language Scales, oral expression; Soc, social interaction score; SB, stereotypic behaviour; soc, social domain; com, communication domain; behav, repetitive behaviours domain; onset, domain for onset before age 16 months; VABS, Vineland Adaptive Behaviour scales 1984 (composite); PPVT, Peabody Picture Vocabulary test; mth, months; yr, years.
posteriorly rotated. He had fifth finger clinodactyly and a small umbilical hernia.

His autistic brother also carries the 16p11.2 microdeletion (see below).

**Patient 3b (brother of proband 3)**

This 4-year-old deletion positive boy also has autism. He is the second and only other child of the parents. Mother had threatened labour from 24 weeks and he was born vaginally at 36 weeks. Birth weight was 2800 g (50th centile), head circumference was 35.5 cm (90th centile). When examined at 13 years (50th centile), large ears (length 6.9 cm, +2SD) and unusually short 5th toes. She had an unexplained long-standing intention tremor.

When examined at 35.5 years (figure 3c,d), height was 157 cm (10th–25th centile), weight was 85.6 kg (>95th centile) and head circumference was 54.4 cm (50th centile). She was brachycephalic with a receding hairline. She had deep-set eyes with minor dysmorphism including a smooth philtrum (length 1.5 cm, 25th–50th centile), large ears (length 6.9 cm, >+2SD) and unusually short 5th toes. She had an unexplained long-standing intention tremor.

**Proband 4**

This 15.5-year-old male has autism (simplex case) and a de novo 16p11.2 microduplication. He had a repaired congenital diaphragmatic hernia (CDH). His other medical problems included epilepsy, an anxiety disorder with good response to fluvoxamine, and scoliosis. He has two other rare CNV gains (654 kb and 362 kb) affecting the congenital diaphragmatic hernia loci map to either of these CNVs. When examined at 15.5 years of age, height was 155 cm (<5th centile), weight was 38.1 kg (<5th centile) and head circumference was 54.5 cm (50th centile). He had hypertelorism with a smooth philtrum. Ears were small with curved pinnae. He had long slender fingers and toes. Hand length was 15.8 cm and foot length was 22.3 cm (both <5rd centile).

**Proband 5**

This 13-year-old girl has ASD and an inherited microduplication, which is also present in her healthy mother and sister. She was born to a 30-year-old GpP mother and a 32-year-old father. Delivery was induced for polyhydramnios at 38 weeks, and there were no neonatal complications. Birth weight was 3505 g (75th–90th centile), length 52 cm (90th centile) and head circumference 55.5 cm (90th centile). When examined at 13 years (figure 5e,f), eye contact was inconsistent. Height was 145.5 cm (5th centile) with an arm span of 144 cm. Weight was 29.3 kg.
Figure 1  Pedigrees of families with 16p11.2 copy number variants. Black symbols indicate a diagnosis of autism spectrum disorder (ASD) or autism, the grey symbol indicates Asperger syndrome, the symbol with hatched diagonal lines indicates developmental delay (DD), and the symbol with hatched vertical lines indicates bipolar disorder. Additional clinical details are provided in supplementary table 1. The proband was denoted by an arrow. The deletion in the MM0088 proband was determined to be mosaic (50:50) by fluorescent in situ hybridisation (FISH) analyses.

(<5th centile) and head circumference was 52 cm (50th centile). Upper to lower segment ratio was reduced (0.879). She was not dysmorphic, although mild synophrys and a smooth philtrum (a feature seen in her mother) were noted. Her duplication positive mother is a 44-year-old homemaker with a grade 9 education (figure 3g). Her 8-year-old sister (figure 3f), who also carries the duplication is healthy with no social or academic difficulties (negative Autism Screening Questionnaire23). Apart from a smooth philtrum in the mother, neither had dysmorphic features.

Proband 6
This 26-month-old girl has mild developmental delays and a microduplication inherited from her father who left vocational school in grade 11 and who was recently diagnosed with bipolar disorder. The proband was born to a 24-year-old G4P2A1 mother and a 29-year old father. Pregnancy was complicated by severe oligohydramnios, and maternal smoking and cannabis use. She was delivered vaginally at 38 weeks with a birth weight of 1145 g (50th centile) and head circumference was 46.5 cm (10th centile). Hypotonia and evidence of oligohydramnios sequence (Potters facies, left talipes varus) were noted at birth. She was ventilated for 3 weeks and discharged from hospital at age 78 days. She sat at 14 months, walked at 21 months and first spoke at 16 months. At 21 months, Bayley Infant Scale of Mental Development24 showed low-average cognitive skills, borderline-low motor skills and low-average language skills. Her hypotonia improved although she uses orthotics for walking.

When examined at 26 months, eye contact was inconsistent and play was mainly solitary. A formal assessment for autism is pending. Height was 82 cm (3rd centile), weight was 11.5 kg (25th centile) and head circumference was 46.5 cm (10th centile). She had distinctive facial features including frontal bossing with notably receding hairline, hypoplastic supraorbital ridges, sparse eyebrows and eyelashes, deep-set eyes, smooth philtrum, thin upper lip and a flat facial profile (figure 3h). She had single palmar creases and fifth finger clinodactyly (figure 3i).

DISCUSSION
Our collective analyses reveal extensive phenotypic heterogeneity in individuals with ASD and their relatives carrying microdeletion or microduplication of chromosome 16p11.2. In this case series and in several previous studies reporting indi-viduals with CNV at 16p11.2, patients were ascertained because of a diagnosis of ASD7 9 10 so that autistic individuals may be overrepresented in the literature to date. Nevertheless, a significant trend in the data is that 16p11.2 microdeletions are more penetrant with respect to ASD and dysmorphic features compared with the reciprocal microduplications.

Excluding probands 1 and 2 from this study (first published by Marshall et al in 20088), 40 microdeletion patients from 27 families have been reported7 9 10 13 25 (supplementary table 1). The breakdown of diagnoses is as follows: 10 patients had an ASD (table 2), four had DD with autistic features, 17 had DD/ MR without autistic features, three had speech disorders without MR, and two had attention deficit hyperactivity disorder (ADHD). One deletion positive female, who was developmentally normal at 3.5 years, had an array because of dysmorphic features and Wilms tumour (proband 25, supplementary table 1). This girl’s deletion positive father and two deletion positive mothers of females with MR were normal, but psychometric testing was not performed.13 Twenty-four of 27 microdeletion probands had parental testing and the origin was de novo in 16 and inherited in eight.

For 10 previously reported microdeletion patients with ASD7 9 10 13 (supplementary table 1), the lowest reported non-verbal IQ was 73 and two patients had Asperger syndrome. The three deletion patients characterised in this study had ASDs of variable severity (table 1). Proband 1 (ASD) and 2 (autism) are higher functioning while proband 3 and his deletion positive brother (both autism) are non-verbal, compared with a less severe form of ASD in their deletion positive mother. She has mild MR and was only diagnosed with ASD at age 35, after her micro-deletion was identified.

Dysmorphology was assessed in 22 of 40 previously reported deletion cases.10 13 25 The male MZ twins reported by Ghebranious had dysmorphism that was present in a deletion-negative sibling (supplementary table 1).25 Of the remaining 20 patients, nine were dysmorphic with no common appearance. Our data suggest that the deletion can be associated with variable dysmorphism. Proband 2 has very dysmorphic facial features, digit abnormalities, microopenis and a hemivertebra. Proband 3 and his deletion positive brother share the same dysmorphic facial features, but do not resemble proband 2. The brothers’ deletion positive mother has less striking dysmorphism than her sons.
We conclude that autistic individuals with microdeletion 16p11.2 often have a more complex phenotype than those with presumed multifactorial forms of ASD. They are more likely to have additional medical findings including congenital anomalies, dysmorphism, growth disturbance, motor delay and epilepsy. Within ASD research cohorts, there is a need to collect this type of data systematically.

Probands 1 and 2 (deletion positive) both have ASD siblings who are deletion negative (table 1). Four previously reported patients with deletion or duplication negative autistic sibs are summarised in supplementary table 2 (all pairs of brothers). In three of the four sib pairs, the deletion positive male had a less severe phenotype than his deletion negative brother. We add the first two sib pairs who are discordant for the 16p11.2 CNV and gender. Proband 1 (deletion positive female) and her deletion negative brother both have ASD. They have comparable IQs and language abilities, but she is higher functioning, with higher Vineland Adaptive Behavioural Scale scores. Proband 2 (deletion positive male) has autism and his deletion negative sister has Asperger syndrome. In both families, the females were less impaired than the males, suggesting that the sex difference that protects females against the development of ASD may also give them a relative advantage even when a rare CNV acts.

Table 2 summarises 18 ASD probands (including five from this report) with CNV at 16p11.2. In one exception, the 16p11.2 duplication positive mother from family AU0029 was not tested. Two hundred interphase nuclei were scored for each parent.
Excluding probands 4 and 5 first described by Marshall et al., 10 15 microduplication patients have been reported from 10 families9,10 28 (supplementary table 3). Eight had ASD (table 2), one had motor delay with autistic features, three had DD without autistic features, two had childhood onset schizophrenia, and one had psychiatric problems. IQs for seven patients ranged from 50–110. Probands 4 (autism) and 5 (ASD) have borderline and mild MR, respectively. Proband 6 is 26 months old and has developmental lags, with abnormal eye contact and play skills. She is relatively young and a formal assessment for autism is pending.

Four of 15 previously reported duplication patients were examined for dysmorphic features and none were identified 10 (supplementary table 3). Proband 4’s dysmorphism and diaphragmatic hernia may be related to the other rare CNVs identified. Proband 6 is also dysmorphic, but at least some of her features are related to in utero compression. Proband 5 and her duplication positive mother and sister were not dysmorphic.

The origin of the duplication was determined for six of 10 previously reported probands. One was de novo and five were inherited (supplementary table 3). Two of the three duplication patients from this report (probands 5 and 6) had inherited duplications. Proband 5’s mother and sister are both duplication positive with no overt health problems apart from academic challenges in the mother. This suggests that like microduplications of 22q11.2, 16p11.2 duplications can be associated with a normal phenotype.29 Genotype driven studies of general populations 30 or phenotype driven studies of non-ASD/MR phenotypes might yield more 16p11.2 duplications, with many being inherited because of less selective pressure.

In fact, 16p11.2 dosage changes may confer susceptibility to other psychiatric disorders including ADHD. Of 40 previously reported deletion patients (supplementary table 1), seven had aggression, over activity or ADHD.9 10 Of 15 previously reported duplication patients (supplementary table 3), two had childhood onset schizophrenia28 (which shares many features with ASD) and one had anxiety and depression.9 Weiss et al.10 screened other psychiatric cohorts and found the deletion in 1 of 648 patients with schizophrenia, 1 of 420 patients with bipolar disorder, and 1 of 205 patients with ADHD. In our data, probands 2 and 4 had anxiety disorders, proband 3 had hyperactivity, proband 3’s deletion positive mother had childhood onset depression, and proband 6’s duplication positive father had bipolar disorder.

Our data reconfirm our earlier recommendation 10 and that of others 31 to include chromosomal microarray in the assessment of autistic individuals. However, given the complexities of the genotype–phenotype correlations observed, we emphasise the importance of considering as much family information as possible when assessing the impact of the CNV on outcomes.27 As one example, by age 5 years, proband 5 was diagnosed with autism and cerebral palsy. If his mother had sought recurrence risk counselling at this stage, a microarray would not have been routinely ordered in our institution. A specific diagnosis would not have been made and the phenotypes of mother and son (minor dysmorphism with MR and major dysmorphism with autism) may not have been recognised as manifestations of the same genetic disorder. With microarray results now available, proband 3’s deletion positive mother has been counselled that each future child is at 50% risk of inheriting her deletion and that a deletion positive child is at risk for medical problems including, but not limited to, ASD.

As a second example, proband 1 carried a mosaic microdeletion, which likely contributed to her ASD. Nevertheless, her parents then had another more severely affected deletion negative son. We suggest that this couple’s future recurrence risk is lower than the 25–35% empiric risk figure given to parents who have two children with apparently multifactorial ASD, but cannot more precisely quantify this.32 33

Glessner et al.34 recently published a CNV study in which 1995 ASD cases and 2519 controls were screened using the Illumina HumanHap550 Beadchip. The frequency of 16p11.2 CNVs was reported to be similar in the cases and controls (seven deletions in ASD probands vs four in controls; five duplications in ASD probands vs four in controls). The authors screened two ASD cohorts: a discovery cohort of 859 children recruited from multiple US centres, and an AGRE cohort of 1336 cases. The four

Figure 3 Clinical photographs. (a and b) Proband 2 (de novo deletion 16p11.2). Note long narrow palpebral fissures, short delicate nose, short neck and brachydactyly with 2–3 cutaneous toe syndactyly. (c and d) Mother of proband 3 (both with deletions). Note her large ears, smooth philtrum and short fifth toes. (e) Proband 5 who has a maternally inherited duplication. (f) Proband 5 (note smooth philtrum) and her healthy duplication positive sister. (g) Duplication positive mother of proband 5, who also has a smooth philtrum. (h) Proband 6 (inherited duplication and oligohydramnios sequence). Note her frontal bossing, receding hairline, hypoplastic supraorbital ridges and smooth philtrum. (i) Proband 6’s right hand showing fifth finger clinodactyly. Written consent to publish these images has been obtained from each patient or legal guardian.
deletions and three duplications identified in the AGRE ASD probands have been reported previously.3 10 (supplementary tables 1 and 3). The three unique deletions and the two unique duplications in the discovery cohort are summarised in supplementary table 4.

The controls in this study were reportedly recruited through primary care clinics and ranged in age from 1–19 years. Each child’s history was negative for ASD, DD and chronic disease as determined by questionnaires and review of the electronic medical record. It is possible that at least some of the eight control CNVs were identified in young children (<age 2 years) when ASD and the other phenotypes discussed above may not be apparent. As evidenced by proband 3’s mother, higher functioning forms of ASD may not be diagnosed until adulthood. Also, the authors did not specify that the control group excluded siblings of the ASD cases. Finally, they reported CNV regions (CNVRs) and several cases and controls appear to have had very small CNVs that are not typical full length deletions or duplications.34

We failed to identify any 16p11.2 CNVs in 2587 population controls, perhaps because these individuals were older. Our controls included German adult blood donors and Canadians >60 years who were part of a coronary artery disease study. Our negative control results are in keeping with the identification of two deletions in 18,834 unscreened Icelandic population controls.10

The five deletion positive individuals in our case series all had abnormal phenotypes which we believe are at least partially attributable to the CNV; however, the seven apparently healthy deletion positive individuals reported by Glessner et al and Bijlsma et al15 34 suggest that 16p11.2 deletions (like the duplications) may be incompletely penetrant. Further studies are needed including formal psychometric assessments of apparently healthy individuals with 16p11.2 microdeletions.

Genetic counselling for parents at risk of having a child with a 16p11.2 CNV is challenging. The phenotypic spectrum includes ASD, MR/DD and/or possibly other primary psychiatric disorders, but a normal outcome is also possible. The latter appears more likely for duplications than for deletions. Deletions can also be associated with non-specific major or minor dysmorphism. Additional case reports as well as prospective cohort analyses of patients with ASD and other disorders will allow these interpretations to be refined.

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REFERENCES


