Copy Number Variation in Obsessive-Compulsive Disorder and Tourette Syndrome: A Cross-Disorder Study

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Objective: Obsessive-compulsive disorder (OCD) and Tourette syndrome (TS) are heritable neurodevelopmental disorders with a partially shared genetic etiology. This study represents the first genome-wide investigation of large (>500 kb), rare (<1%) copy number variants (CNVs) in OCD and the largest genome-wide CNV analysis in TS to date. **Method:** The primary analyses used a cross-disorder design for 2,699 case patients (1,613 ascertained for OCD, 1,086 ascertained for TS) and 1,789 controls. Parental data facilitated a de novo analysis in 348 OCD trios. **Results:** Although no global CNV burden was detected in the cross-disorder analysis or in secondary, disease-specific analyses, there was a 3.3-fold increased burden of large deletions previously associated with other neurodevelopmental disorders ($p = .09$). Half

Supplemental material cited in this article is available online.

of these neurodevelopmental deletions were located in a single locus, 16p13.11 (5 case patient deletions: 0 control deletions, $p = .08$ in the current study, $p = .025$ compared to published controls). Three 16p13.11 deletions were confirmed de novo, providing further support for the etiological significance of this region. The overall OCD de novo rate was 1.4%, which is intermediate between published rates in controls (0.7%) and in individuals with autism or schizophrenia (2-4%). **Conclusion:** Several converging lines of evidence implicate 16p13.11 deletions in OCD, with weaker evidence for a role in TS. The trend toward increased overall neurodevelopmental CNV burden in TS and OCD suggests that deletions previously associated with other neurodevelopmental disorders may also contribute to these phenotypes. J. Am. Acad. Child Adolesc. Psychiatry, 2014;53(8):910–919. **Key Words:** Tourette syndrome, obsessive-compulsive disorder, copy number variation, genetics, 16p13.11

Obsessive-compulsive disorder (OCD) and Tourette syndrome (TS) are neurodevelopmental disorders with significant phenotypic and genetic overlap.[1,2] One promising avenue for identifying cross-disorder genetic risk factors in neurodevelopmental disorders is the study of genomic copy number variants (CNVs), segments of DNA ranging from 1 kilobase to several megabases that show deletions or duplications compared to a reference.[3] The association of large rare CNVs with neurodevelopmental disorders including autism spectrum disorders (ASD), schizophrenia, and intellectual disability (ID) has been one of the most important recent advances in psychiatric genomics.[4] CNVs predisposing individuals to these disorders overlap substantially, highlighting the cross-disorder effects of this class of genetic variation.[5,6] Given this robust literature, an important, unanswered question is whether large rare CNVs are also relevant for the genetic architecture of OCD and TS.

Both OCD and TS are highly heritable and have long been suspected to share genetic liability, although specific gene variants have been difficult to identify.[7-9] Both disorders frequently co-occur in individuals,[10] and there is evidence for shared OCD/TS genetic risk from family studies,[9,11] with genetic correlation estimates ranging from 41% to 90%.[2,12] In OCD, locus-specific CNV analyses have been reported,[13,14] but no prior genome-wide CNV analysis has been performed. In TS, the 3 previous genome-wide surveys of CNVs have been limited by small sample sizes (<500 patients), and results differ with regard to whether there is an increased CNV burden in individuals with TS compared to controls.[15-17] No specific CNV region has received strong statistical support across studies, although exonic *NRXN1* deletions have been identified in 2 studies.[15,17]

Given the evidence for shared genetic underpinnings of OCD and TS and cross-disorder effects of specific neurodevelopmental CNVs, along with the need for large samples when investigating rare events, we chose a cross-disorder design that combined OCD and TS samples into a single case group, with follow-up analyses examining the individual disorders. This study is the first genome-wide CNV analysis in OCD and the largest to date in TS and addressed 3 key questions. First, is there an increased burden of large rare CNVs in OCD/TS? Second, are the recurrent and/or de novo CNVs implicated in other neurodevelopmental disorders also etiologically relevant for OCD/TS? Third, is there evidence of association between any specific genomic region and OCD/TS?

METHOD

Participants

Individuals with OCD or TS were recruited for a multicenter collaborative genome-wide association study (genome-wide association study [GWAS]; described by Scharf *et al.*[18] and Stewart *et al.*[19]). Participants aged 18 years and older provided written, voluntary informed consent for participation in genetic studies. Individuals aged less than 18 years provided assent; parents provided written consent. The study was approved by the Ethics Committees of all participating sites. Recruitment sites varied in screening and exclusions related to other neurodevelopmental disorders (see supplementary Tables S9, S10, and S11, available online, for available clinical information regarding ID, ASD, attention-deficit/hyperactivity disorder [ADHD], and seizures). OCD and TS samples were collected independently but were genotyped jointly to facilitate cross-disorder analyses. All patients were genotyped on the Illumina Human610-Quadv1_B platform.

OCD. The initial OCD sample consisted of 1,565 case patients and 437 parent–child trios (n = 406 independent families, 31 affected siblings) recruited from 22 sites in the United States, Canada, Europe, Latin America,

and South Africa, predominantly through OCD specialty clinics. In total, 1,971 independent case patients with OCD (including trio probands) were eligible for analysis. A total of 1,613 case patients with OCD (82%) survived quality control (QC), and were included in the final analyses. Mean age of OCD symptom onset was 13.8 years (SD = 9.1). In all, 327 patients and 21 affected siblings had parents available for de novo analysis (n = 348 total trios). TS or chronic tics (CT) were assessed in 57% of OCD probands using *DSM-IV-TR* criteria. Of those assessed, TS was present in 10% of case patients with OCD, and an additional 5% had CT.

TS. The initial TS sample consisted of 1,235 individuals recruited from 19 sites in the US, Canada, Europe, and Israel. Participants with *DSM-IV-TR*-diagnosed TS were recruited primarily from TS specialty clinics or from the Tourette Syndrome Association (TSA). A total of 1,086 individuals (88%) passed sample-level QC. The mean age of tic onset was 6.3 years (SD = 3.5 years). OCD as defined by *DSM-IV-TR* criteria was assessed in 88% of patients; OCD was present in 46% of assessed TS individuals.

Controls. Ancestry-matched controls (n = 720) were collected in parallel with their respective patients for the French-Canadian (n = 269), German (n = 224), South African (n = 188), and Dutch (n = 39) samples. These controls were screened for TS and OCD and genotyped with patients on the Illumina Human610-Quadv1_B[20,21] (referred to here as "Hap610 controls").

A total of 1,279 additional European-ancestry controls were obtained through the Database of Genotypes and Phenotypes (dbGaP) from the Studies of Addiction: Genetics and Environment (SAGE) cohort.[20] SAGE controls were excluded for lifetime substance dependence but were not screened for other psychopathology. The SAGE controls were genotyped on the Illumina HumanHap1Mv1_C (referred to here as "Hap1M controls").

CNV Calling and Quality Control

Data from the Hap610 (case patients and controls) and Hap1M (controls) platforms were processed and cleaned separately using standard procedures (see Supplementary Materials, available online). CNV calls were generated with PennCNV (version 2010-05-01)[21] and iPattern[22,23] using hg18 genomic coordinates. Analyses were limited to autosomal events. Trio analyses used the trio functions in PennCNV to improve calling accuracy and to estimate the likelihood of a de novo event.[21]

Both sample and CNV-specific QC was conducted by examining distributions of QC metrics informed by comparable published CNV analyses.[22,24,25] Because distributions were similar for calls from PennCNV and iPattern, the same QC thresholds were used for both algorithms to maximize comparability (see Supplementary Materials, available online). QC-filtered PennCNV and iPattern callsets were merged at the sample level using CNVision (http://futo.cs.yale.edu/mw/index.php/CNVision). Only calls with >50% overlap based on the union of the CNV region were included in the analysis. Overlap percentages were higher for the Hap1M (86%–98%) compared to the Hap610 chip (59%–82%; Table S1, available online). Because of the presence of a batch effect within the Hap610 samples, analyses were restricted to large (>500-kb) events, the size at which batch effects were no longer observed (Figure S1, Table S2, available online). All CNVs were also filtered for rare events (<1% frequency in the Database of Genomic Variants).

Ancestry Matching

The case patient–control sample was predominantly composed of individuals self-reporting European (EU) ancestry (n = 4,410), but did include a small number of individuals from Brazil, Mexico, and Costa Rica (n = 78) to maximize the power to detect rare events. However, a sensitivity analysis restricted to genetically defined EU ancestry (n = 4,276) via multidimensional scaling (Figures S2, S3, available online) confirmed that results were not biased by population stratification.

Statistical Analysis

CNV burden, region-specific analyses, and permutations were performed in PLINK using the rare CNV functions.[26] The primary case-control analyses grouped OCD and TS case patients versus Hap610 and Hap1M controls to maximize sample sizes. No additional covariates were included, although follow-up analyses were stratified by EU ancestry. To evaluate whether OCD and TS case patients harbored large pathogenic CNVs that have been repeatedly implicated in other neurodevelopmental disorders, we assembled a curated list of CNVs drawn from the ASD, schizophrenia, and ID literature, including 47 regions of interest (all >500-kb[22,24,27,28]; Table S3, available online).

Quantitative Polymerase Chain Reaction Validation

Validation of neurodevelopmental or putative de novo CNVs was performed with SYBR green quantitative polymerase chain reaction (qPCR). Two qPCR primers per CNV were designed against NCBI build hg18 sequence to obtain converging evidence for the called event. If 1 primer pair failed or gave ambiguous results, an additional primer pair was run to resolve the discrepancy (see Supplementary Materials, available online).

RESULTS

After filtering and QC, the final sample consisted of 2,699 case patients (1,086 ascertained for TS and 1,613 ascertained for OCD) and 1,789 controls.

Overall CNV Burden Analysis

There was no significant difference in burden of large rare CNVs between case patients with

TABLE 1 Global Burden Analysis of Large (>500 kb), Rare (<1%) Copy Number Variants (CNVs) in Patients Ascertained for Obsessive-Compulsive Disorder (OCD) or Tourette Syndrome (TS) Compared to Controls

Description		Combined OCD/TS n = 2,699	Hap610 Controls n = 561	Hap1M Controls n = 1,228	Case/Control Ratio	*p* Value[a]
All CNVs	No. of CNVs	186	39	111		
> 500 kb	Rate	0.069	0.070	0.090	0.82	.97
	Proportion	0.067	0.068	0.086	0.84	.95
	Gene rate	7.23	5.16	6.25	1.21	.19
Deletions	No. of CNVs	60	7	31		
> 500 kb	Rate	0.022	0.012	0.025	1.05	.45
	Proportion	0.022	0.012	0.025	1.03	.48
	Gene rate	6.29	4.00	4.39	1.46	.14
Duplications	No. of CNVs	126	32	80		
>500 kb	Rate	0.047	0.057	0.065	0.75	.99
	Proportion	0.046	0.055	0.063	0.75	.99
	Gene rate	7.63	5.42	6.75	1.20	.26

Note: gene rate = average number genes spanned by CNVs; proportion = proportion of samples with ≥1 CNV; rate = average number of CNVs per person.

[a]*One-sided, empirical p value.*

OCD/TS and controls for CNV rate (average number of CNVs per person), CNV proportion (proportion of samples carrying ≥1 CNV), gene rate (average number of genes spanned by a CNV), or by restricting to CNVs containing exons (Tables 1, S4, S5, S6; Tables S4–6 are available online). Similarly, no increased CNV burden was identified in secondary, disorder-specific analyses (OCD versus controls or TS versus controls; Tables S7, S8, available online).

Neurodevelopmental CNV Burden Analysis

Given that various neurodevelopmental disorders have previously been associated with large, rare, recurrent CNVs in specific regions of the genome,[4] we examined 47 known pathogenic neurodevelopmental loci for an excess of large rare CNVs in OCD/TS patients compared to controls (Tables 2, 3, S3, S9; Tables S3 and S9 are available online). We found a 3.3-fold trend-level increase in large deletions overlapping these loci for case patients with TS/OCD ($p = .09$; Table 2). In contrast, there was no enrichment of duplication events (case/control ratio 1.16, $p = .46$) and no difference in overall CNV size within these regions ($p = .31$).

In disorder-specific analyses, the neurodevelopmental deletion burden was larger in OCD (case/control ratio = 4.44, $p = .04$, 1-sided) than in TS (case/control ratio = 1.65, $p = .49$, 1-sided) (Tables S7, S8, available online). The most frequently observed neurodevelopmental CNVs were located at 16p13.11, 22q11, and *PARK2* (Figure 1, Tables 3, S4, S5; Tables S4, S5 are available online).

Laboratory Validation

We confirmed 10 of 11 neurodevelopmental deletion events (91%) with qPCR; the 1 unconfirmed deletion was near the 9q34 telomere and was excluded from the neurodevelopmental burden analysis (see Supplementary Materials, available online). We also confirmed 12 of 14 duplication events (86%) with 1 or 2 sets of primers. The 2 remaining duplications could not be confirmed but had qPCR results trending toward duplication. Of note, the LRR and BAF plots (Figure S6, available online) strongly supported all CNV events with the exception of the unconfirmed 9q34 deletion.

Region-specific Analyses

Half of the 10 large neurodevelopmental deletions were in the same genomic region on 16p13.11 (case:control ratio = 5:0, 1-sided Fisher's exact $p = .08$) (Figure 1, Table 3). Using previously published estimates to more accurately calculate the control rate for 16p13.11 deletions (3/8,329),[28] we found a statistically significant excess in the OCD/TS patients (1-sided Fisher's exact $p = .025$). Of note, the rate of 16p13.11 deletions in this sample (0.19%) was comparable to published rates from large samples of children with neurodevelopmental disorders (n = ~15,000) referred for genetic testing (0.11%–0.14%).[28,29] Interestingly, the clinical phenotype of the 5 cases with 16p13.11 deletions did not respect traditional diagnostic boundaries: 3 case patients had OCD without tics, 1 had TS without OCD, and 1 had OCD+CT.

TABLE 2 Neurodevelopmental Burden Analysis of Large Rare Copy Number Variants (CNVs) in Case Patients with Obsessive-Compulsive Disorder (OCD) or Tourette Syndrome (TS) Compared to Controls

Description		Combined OCD/TS n = 2,699	Hap610 Controls n = 561	Hap1M Controls n = 1,228	Case/Control Ratio	*p* Value[a]
All CNVs	No. of CNVs	24	2	8		
> 500 kb	Rate/proportion[b]	0.0089	0.0036	0.0065	1.59	.14
Deletions	No. of CNVs	10	0	2		
> 500 kb	Rate/proportion[b]	0.0037	0	0.0016	3.31	.09
Duplications	No. of CNVs	14	2	6		
>500 kb	Rate/proportion[b]	0.0052	0.0036	0.0049	1.16	.46

[a]*One-sided, empirical p value.*
[b]*Rate and proportion are identical because no samples had >1 large neurodevelopmental CNV.*

None of the case patients had ASD, ID, or a seizure disorder (Table S10, available online). All 16p13.11 deletions were validated with qPCR.

16p13.11 was also the top recurrent region in genome-wide, region-specific analyses combining deletions and duplications (case:control ratio = 7:1, 1-sided empirical $p = .13$; genome-wide permutation corrected $p = .86$). This region-specific effect was driven by deletions; no excess of 16p13.11 duplications was found in case patients with OCD/TS compared either to sample controls (case:control ratio = 2:1, 1-sided Fisher's exact $p = .65$) or to published controls (10/8,329)[28] (1-sided Fisher's exact $p = .83$).

We also examined genome-wide, region-specific associations in each disorder separately, combining deletions and duplications. In OCD, 16p13.11 again emerged as the locus with the most notable case:control excess (6:1; 1-sided empirical $p = .046$, genome-wide permutation-corrected $p = .35$). In TS, the 3p26.3 region had the largest case:control excess (7:2 ratio of duplications 50 kb upstream of *CNTN6*; 1-sided empirical $p = .018$, genome-wide permutation-corrected $p = .15$); exonic *CNTN6* regions had a more equivocal case:control ratio (8:6; 1-sided empirical $p = .11$, genome-wide permutation-corrected $p = .99$; see Figure S7, available online).

De Novo Analyses

The OCD parent–proband trios (total trios = 348) were examined for the presence of large (>500-kb), rare, de novo CNVs. We detected 5 high-confidence de novo CNVs at 4q24, 7p21.1-7p21.2, 16p13.11, 17q12, and 22q11.21, resulting in a de novo rate of 1.44% (Figure S8, available online). Three of these CNVs were in known pathogenic neurodevelopmental loci: 16p13.11, 17q12, 22q11.21 (Table S3, available online). All 5 events were validated in silico and by qPCR (Table S11, available online).

Given that 16p13.11 contained both a de novo CNV and the largest case patient/control difference across the genome, we undertook further investigation of the de novo status of other 16p13.11 case patient CNVs in our sample. Parental DNA was available for 1 of the 5 16p13.11 deletions (TS only), which we confirmed as de novo using qPCR. We also re-examined trios removed during QC for evidence of large 16p13.11 events, and found 1 additional deletion (OCD only) with a statistically significant in silico probability of being de novo ($p = 5.68 \times 10^{-14}$ that we subsequently validated using qPCR (Figure S8, available online). This increased the total number of 16p13.11 deletions from 5 to 6, 3 of which were de novo (2 OCD only, 1 TS only; see Table S10, available online). The de novo status of 2 16p13.11 deletions could not be determined because parental DNA was not available; 1 deletion was inherited.

DISCUSSION

In this GWAS of large rare CNVs in OCD and TS, although there was no global increase in CNV burden, we did find suggestive evidence for an increased burden of known pathogenic neurodevelopmental deletions in case patients with OCD/TS compared to controls. The 3.3-fold increased risk associated with this finding reached only trend-level significance, potentially due to the conservative bias toward the null introduced by having the majority of controls genotyped on a more sensitive, higher-density genotyping array than case patients.

Deletions at 16p13.11, which contributed disproportionately to the neurodevelopmental burden, have been implicated in a wide range of disorders, including ID/developmental delay,[28,29] seizures,[30,31] and, less strongly, ASD.[32] The

TABLE 3 Large Rare Copy Number Variants (CNVs) in Case Patients and Controls Overlapping Previously Identified Neurodevelopmental Loci

		Deletions			Duplications		
Chr	Region	Case Patients (OCD Only/TS Only/ OCD+TS/CT), n = 2,699	Controls n = 1,789	*p* Value[a]	Case Patients (OCD Only/TS Only/ OCD+TS/CT), n = 2,699	Controls n = 1,789	*p* Value[a]
2	2p15–16.1	0	0	—	0	1	1.00
2	2q11.2	1 (0/0/1)	0	.60	0	0	—
3	CNTN4	1 (0/0/1)	1	.84	1 (0/0/1)	0	.60
3	3q29	0	0	—	0	1	1.00
6	PARK2	1 (1/0/0)	0	.60	3 (2/0/1)	0	.22
7	7q11.23	0	0	—	1 (0/0/1)	0	.60
12	12q14	0	0	—	0	1	1.00
15	15q11–q13	0	0	—	2 (0/0/2)	0	.36
15	15q24	0	1	1.00	0	0	—
16	16p13.11	5 (3/1/1)	0	.08	2 (2/0/0)	1	.65
16	16p11.2	0	0	—	1 (1/0/0)	2	.94
17	NF1	0	0	—	1 (0/1/0)	0	.60
17	17q12	1 (1/0/0)	0	.60	0	1	1.00
22	22q11.21	1 (1/0/0)	0	.60	3 (2/0/1)	1	.48

Note: Chr = chromosome; CT = chronic tics; OCD = obsessive-compulsive disorder; TS = Tourette syndrome.
[a]*Fisher's exact 1-sided p value.*

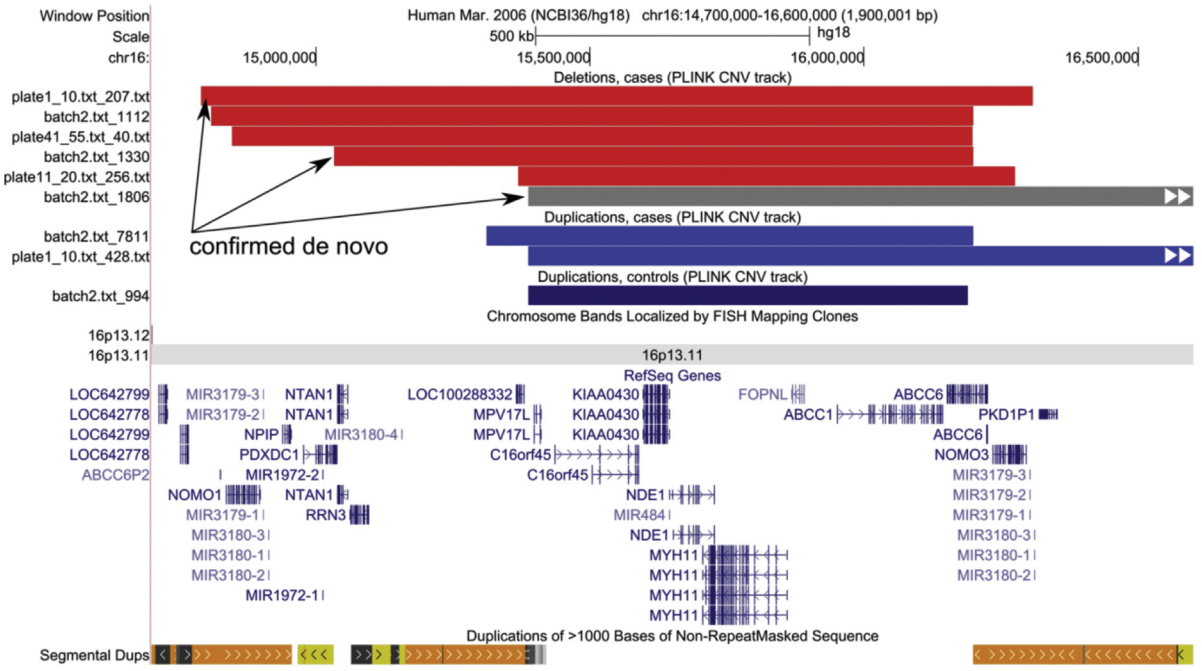
confirmation of 3 de novo events among our 6 case patients with OCD/TS 16p13.11 deletions, as well as the absence of comorbid ID, seizures, or ASD in the case patients assessed, suggests that these events may be pathogenic in our sample and that the phenotypic spectrum of 16p13.11 deletions should be expanded to include OCD and TS. Importantly, the phenotypic profiles indicate that 16p13.11 deletions are primarily associated with OCD (4 OCD only, 1 OCD+CT, 1 TS only). The presence of a case patient with TS but without OCD raises the possibility of a pleiotropic effect of this locus, although this hypothesis remains preliminary, as it is based only on a single case patient. It is also likely that additional genetic and environmental factors shape the ultimate phenotypic outcome of these CNV events, including patterns of comorbidity.

Three of the 5 large de novo CNVs reported in this study were located in regions previously associated with other neurodevelopmental disorders. The de novo events at 16p13.11 and 22q11 also had additional supporting case patient events in the same locus, whereas the deletion at 17q12 was a singleton event in a case patient with OCD. The final 2 de novo events were singleton deletions at novel loci: 4q24 and 7p21.1-7p21.2. The clinical significance of both events remains unclear, although pathogenic CNVs have been documented in both regions (www.iscaconsortium.org),[33] including a report of a patient with Saethre-Chotzen syndrome and co-occurring TS and OCD.[34]

The overall de novo rate in the OCD trio sample was 1.44% for large CNVs (>500 kb), which is intermediate between estimates in healthy controls (0.7%)[27] and estimates in ASD (1.8% multiplex, 3.9% simplex)[27] and schizophrenia (2%–3%).[35-37] Additional studies with larger samples and more sensitive CNV calling will be needed to refine this estimate.

Previous CNV studies have implicated *NRXN1* deletions in TS.[15,17] We detected one 600-kb *NRXN1* deletion in a case patient with OCD (TS status unknown) (chr2:50185814–50799877, hg18) that was called by iPattern and qPCR-validated, although it did not pass initial QC because <50% of the region was called by PennCNV. We also observed three 22q11 duplications, all case patients with OCD (2 OCD only, 1 OCD+CT), 1 de novo deletion (OCD only), and 1 control duplication (Figure S4, available online). The de novo 22q11 deletion was smaller (~700 kb) than the canonical 1.5 to 3-Mb 22q11 deletion associated with velocardiofacial and DiGeorge syndrome (OMIM 192430, 188400), whereas the duplications ranged in size from 700 kb to 2MB. Although the 3:1 22q11 CNV duplication excess in our sample is not significant, it is notable that 3 other 22q11 duplications, including 1 de novo event, have

FIGURE 1 16p13.11 Region with 8 case patient and 1 control copy number variants (CNVs). Note: red denotes deletions; blue, duplications. Gray denotes the de novo deletion that did not survive strict quality control filters but was validated in silico and by quantitative polymerase chain reaction.



previously been reported in TS patients,[16,17,38,39] and thus this region warrants further study.

The results of this study should be interpreted in the context of some limitations. First, the majority of controls were genotyped on a higher-resolution array (Hap1M) than were case patients (Hap610), resulting in a conservative bias toward the null hypothesis because of better CNV detection in controls than in case patients. This effect is evident when comparing the higher CNV rates in Hap610 controls to Hap1M controls (Table 1). However, a comparison of Hap610 patients to Hap610 controls did not reveal overall burden differences within the limits of this restricted sample size (Table S12, available online).

Second, we were unable to call CNVs smaller than 500 kb because of genotyping batch effects. Although previous research has shown that >500 kb events are most likely to be pathogenic,[22,25] we may have missed smaller pathogenic CNVs in this sample. Third, although it is the largest for OCD and TS to date, our sample is still small compared to large-scale investigations of CNVs in other disorders.[4,28,29] For this reason, and because the number of case patients with OCD/TS and rare pathogenic CNVs appears to be small, we recommend caution in interpreting these results, pending further studies in larger OCD/TS samples that can refine the global and neurodevelopmental CNV burden estimates.

Fourth, missing data on TS/CT and OCD comorbidity in some individuals prevented us from dividing case patients into mutually exclusive subgroups (TS only, OCD only, OCD+TS) for analysis. Instead, we identified CNVs in the combined OCD/TS sample and then reviewed the diagnostic profile of each research participant with a CNV. Moreover, TS and OCD participants were not universally screened for other neurodevelopmental disorders, although we documented this information when available (Tables S9, S10, S11, available online). Without comprehensive screening, we cannot exclude 2 possibilities regarding patients with neurodevelopmental CNVs: first, the primary TS/OCD diagnosis was misclassified (i.e., stereotypies or restricted interests/repetitive behaviors in the context of ASD were misdiagnosed as TS or OCD, respectively); and second, patients with complex comorbidities were more likely to harbor neurodevelopmental CNVs. All assessments were completed by internationally recognized expert clinicians, reducing the likelihood of

misclassification. However, some individuals with neurodevelopmental CNVs may have had subtle or unassessed ASD, ADHD, cognitive impairment, or psychotic symptoms.

These results suggest that deletions associated with other neurodevelopmental disorders may also contribute to OCD and TS. Converging lines of evidence specifically implicate 16p13.11 deletions, with stronger evidence for OCD than TS. Although it is premature to make clinical recommendations based on these observations, we note that tic and obsessive-compulsive symptoms often occur in the context of other neurodevelopmental disorders, such as ASD and ID, where practice parameters do recommend chromosomal microarray testing.[40] Future studies should help to refine clinical guidelines as to whether CNV testing might be indicated for children with TS and/or OCD in general or should be restricted to those with multiple co-occurring neurodevelopmental disorders. &

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