Excess of rare novel loss-of-function variants in synaptic genes in schizophrenia and autism spectrum disorders

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Schizophrenia (SZ) and autism spectrum disorders (ASDs) are complex neurodevelopmental disorders that may share an underlying pathology suggested by shared genetic risk variants. We sequenced the exonic regions of 215 genes in 147 ASD cases, 273 SZ cases and 287 controls, to identify rare risk mutations. Genes were primarily selected for their function in the synapse and were categorized as: (1) Neurexin and Neuroligin Interacting Proteins, (2) Post-synaptic Glutamate Receptor Complexes, (3) Neural Cell Adhesion Molecules, (4) DISC1 and Interactors and (5) Functional and Positional Candidates. Thirty-one novel loss-of-function (LoF) variants that are predicted to severely disrupt protein-coding sequence were detected among 2 861 rare variants. We found an excess of LoF variants in the combined cases compared with controls ($P = 0.02$). This effect was stronger when analysis was limited to singleton LoF variants ($P = 0.0007$) and the excess was present in both SZ ($P = 0.002$) and ASD ($P = 0.001$). As an individual gene category, Neurexin and Neuroligin Interacting Proteins carried an excess of LoF variants in cases compared with controls ($P = 0.05$). A *de novo* nonsense variant in *GRIN2B* was identified in an ASD case adding to the growing evidence that this is an important risk gene for the disorder. These data support synapse formation and maintenance as key molecular mechanisms for SZ and ASD.

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INTRODUCTION

Both schizophrenia (SZ) and autism spectrum disorders (ASDs) are neurodevelopmental in origin and are substantially heritable ($h^2 > 0.8$).[1,2] SZ is characterized by hallucinations, delusions, disordered thinking and cognitive and social deficits. The disorder affects ~1% of the population and causes considerable morbidity and mortality.[3] The onset of illness is typically in early adulthood, but the symptoms, severity and course of the disorder are variable. ASDs include autism, Asperger's syndrome and pervasive developmental disorder. They have an onset in childhood and are characterized by impairments in social interaction and communication and a pattern of repetitive behavior and restricted interests.[4,5] Prototypical ASD is diagnosed in 15–20 per 10 000 children,[6] with broader ASD affecting between 60 and 100 in 10 000.[7,8] Treatments for ASD include behavioral interventions and the use of psychotropic medications to treat comorbid conditions, but core symptoms persist.

SZ and ASD share some clinical features such as cognitive impairment and deficits in social functioning[9] and further support for biological overlap between the disorders comes from epidemiological[10] and neuroimaging studies.[11] The most recent evidence for shared aetiology comes from genetic studies, especially studies of rare copy number variants (CNVs). Many CNVs are common to both disorders, for example, 1q21.1,[12,13] 3q29,[14,15] 15q11.2,[16,17] 15q13.3,[12,18] 16p11.2,[19,20] 16p13.11,[21,22] and 17q12.[23,24] There is substantial heterogeneity at these sites in terms of type (deletion or duplication), penetrance and size, and these CNV loci are associated with multiple other neuropsychiatric, developmental and neurological phenotypes.[25,26] However, in certain instances, mutations in SZ and ASD cases only impact a single gene such as deletions at *NRXN1* suggesting a potential risk mechanism involving synapse function.[27–35] Additional evidence that abnormal synapse formation and maintenance is a part of the pathogenesis of both SZ and ASD comes from other CNV studies in SZ[32,36,37] and ASD,[21,38] single nucleotide polymorphism-based group/pathway analysis in SZ,[39,40] transcriptomic analysis of the brain in SZ[41] and ASD,[42] and protein interactome analysis in ASD.[43] Where SZ and ASD have been combined for CNV[44] or sequencing[45] analysis, the data support shared biological pathways for the disorders in synaptogenesis and glutamate neurotransmission.

On the basis of the emerging evidence that SZ and ASD share common pathogenic mechanisms, we have combined the two disorders in the present study. Here, we use next-generation sequencing to move beyond CNVs, to the remaining spectrum of potentially rare pathogenic mutations in the form of smaller indels and single nucleotide variants (SNVs). Initial next-generation sequencing studies in SZ and ASD took the form of whole exome studies of small number of trio samples to investigate *de novo* mutation,[46–48] family-based exome sequencing in ASD[49] or targeted association studies in SZ of small number of candidate genes in pooled DNA samples.[50] These studies indicate a role for rare sequence variation in risk of SZ and ASD. This has been extended by recent and larger exome sequencing studies in ASD[51–53] and SZ,[54] which confirmed the importance of *de novo* mutation and the paternal age effect, and for ASD identified new risk genes (for example, *CHD8*, *KATNAL2* and *SCN2A*) and provided new support for other strong candidate genes (for example, *GRIN2B*). Protein–protein interaction network analysis of genes

carrying severe *de novo* mutations indicates that a high proportion of these genes have a function in neuronal development.[51]

Using our Multiplex Target Enrichment method,[55] we adopted a focused approach and sequenced 215 candidate genes, selected primarily for their role in synaptic function and neurodevelopment, in a total sample of 743 individuals to detect rare sequence variations. Genes are grouped into five categories based on the biological basis for their selection, which briefly include (1) Neurexin and Neuroligin Interacting Proteins ($n=46$), (2) Post-synaptic Glutamate Receptor Complexes ($n=58$), (3) Neural Cell Adhesion Molecules ($n=61$), (4) DISC1 and Interacting Proteins ($n=23$) and (5) other Positional and Functional Candidates ($n=27$). Within these genes, our primary objective was to detect rare loss-of-function (LoF) variants that are predicted to severely disrupt protein-coding sequence. We tested for and found a significant excess of these disruptive mutations in our combined SZ and ASD case sample compared with controls, and for some ASD cases found that mutations were *de novo*. We brought these data forward to further experiments designed to elucidate the biological relevance of these variants in specific gene networks and intermediate cognitive and clinical phenotypes. In addition, we studied all rare missense variants for evidence that this class of mutation increases risk for these neurodevelopmental disorders in our selected networks and genes.

MATERIALS AND METHODS

Samples

SZ case samples ($n=297$) were recruited through community mental services and inpatient units in the Republic of Ireland with local ethics approval. All participants were interviewed using a structured clinical interview (Structured Clinical Interview for DSM-IV (SCID-P; ISBN:0880489324)). Diagnosis of a major psychotic disorder was made by the consensus lifetime best estimate method using DSM-IV criteria with all available information (interview, family or staff report and chart review). This sample is described in greater detail elsewhere.[56] The final sample ($n=273$) used for analysis was 65.2% male and had a mean age at collection of 47.1 years (s.d. = 19.4). In selecting the sample, we specifically wanted to include cases with low pre-morbid IQ ($n=110$ of 188 with available data) and cases that also had another recorded developmental disorders (epilepsy ($n=3$), speech delay ($n=8$)). Of the final 273 SZ cases, clinical data on symptom severity, collected using the SAPS and the SANS were available for 245 patients. Neuropsychological data were available for 188 SZ cases, collected using a battery of clinical and neuropsychological measures as previously reported.[57] ASD case samples ($n=152$) were recruited through schools, parent support groups and clinician referral with local ethics approval. Autism diagnoses were confirmed using the Autism Diagnostic Interview-Revised and the Autism Diagnostic Observation Schedule-Generic. This childhood sample is described in greater detail elsewhere.[58] The final sample used for analysis was 83.1% male. Control samples ($n=294$) were ascertained with informed consent from the Trinity Biobank and represent blood donors from the Irish Blood Transfusion Service recruited in the Republic of Ireland.[56] As the lifetime prevalence of SZ or autism is relatively low (<1%), there is no obvious reason for individuals with either disorder to be overrepresented in the controls. DNA for all samples was extracted from blood. The final sample used for analysis was 65.9% male and had a mean age at collection of 34.0 years (s.d. = 12.6).

Gene selection

Definitions of the five gene categories and the method of gene selection are described in full in Supplementary Information and the full list of gene IDs is detailed in Supplementary Table A along with the data source that underpinned each selection. In brief, the process involved extensive literature searches, with key references identified in the next sentence, and the use of KEGG (http://www.genome.jp/kegg/pathway.html) and online interaction databases HPRD (http://www.hprd.org/), String (http://string-db.org/), IntAct (http://www.ebi.ac.uk/intact/), BioGRID (http://thebiogrid.org/) and BOND (http://bond.unleashedinformatics.com/). The five gene categories were (1) Neurexin and Neuroligin Interacting Proteins,[27–35] (2) Post-synaptic Glutamate Receptor Complexes,[59,60] (3) Neural Cell Adhesion Molecules,[60] (4) DISC1 and Interacting Proteins[61] and (5) other Positional and Functional Candidates. The functional categories were used sequentially to select candidate genes. Therefore, 'Neurexin and Neuroligin Interacting Proteins' were selected first followed by genes that encoded 'Post-synaptic Glutamate Receptor Complexes' that were not already selected for the 'Neurexin and Neuroligin Interacting Proteins' category. We next moved to the third category 'Neural Cell Adhesion Molecules' and again selected genes not already picked for categories 1 and 2 and so on. Consequently, there are many instances of genes that could fit in multiple categories. These categories were maintained during association analysis as any re-categorization of genes after data generation could have biased analysis.

Targeted sequencing, quality control and variant annotation

The process of sequencing, QC and variant annotation are fully detailed in Supplementary Information. In brief, samples were indexed and multiplexed in groups of 24. The exons of 215 genes were targeted using the Agilent's SureSelect Target Enrichment system (Agilent Technologies, Santa Clara, CA, USA) (total target = 1 064 238 bp) and sequenced on an Illumina Genome Analyzer II (Illumina, San Diego, CA, USA). Sequence alignment and calling of both SNVs and indels was performed using GATK (v1.0.5506; ref. 62). The median coverage for all samples included in the final analysis was 41 × for SZ, 66 × for ASD and 52 × for controls (Supplementary Figure A). Following removal of poorly performing samples and low quality variant calls, variants were classified as rare if they had a minor allele frequency (MAF) of <0.01 in the combined case–control sample.[63,64] The average matching between available genome-wide association studies data and sequence data variant calls was >99%. All variants were functionally annotated using SNPeff (v2.0.5; http://snpeff.sourceforge.net/). Analysis of silent SNVs shows an average of 167 per SZ sample (s.d. = 12.6), 168 per ASD sample (s.d. = 12.3) and 167 variants per control sample (s.d. = 12.8), indicating an even rate of variant detection across each sample group. LoF variants are predicted to severely disrupt protein-coding sequence and we used the definition of LoF variants as suggested by MacArthur *et al.*[65]: nonsense SNVs that introduce stop codons, SNVs that disrupt canonical splice sites and indels that disrupt a transcript's open reading frame or a canonical splice site. We did not consider mutations as putative LoF variants in association analysis if they were located in the last 5% of coding sequence.[65] All rare missense SNVs were assigned a PolyPhen2[66] and SIFT[67] score.

Association analysis

Our primary analysis was to examine whether there is an excess of rare LoF variants in the combined SZ and ASD case sample versus controls using data from all genes together. This was done using a carrier-based association analysis where case and control samples were categorized as either carriers or non-carriers of at least one rare LoF variant and tested for association using a 2×2 contingency table. Results for χ^2 tests are reported except where indicated that a two-tailed Fisher's exact test was used because an expected cell count was <5. Where we achieved a nominally significant result ($P<0.05$), we (1) performed the same carrier-based analysis on SZ and ASD cases separately to observe the effect in the individual case groups and (2) tested within each of the gene categories. For the rare missense variants, we performed the same carrier-based association analysis for all genes in the combined case group and repeated this for the individual gene categories and the individual genes. We also tested for pairs of interacting genes that were hit by multiple rare missense variants in cases compared with controls.

RESULTS

Figure 1 provides a flowchart of the number of variants detected across all samples and how that number was reduced to a set of variants for inclusion in our association analysis. In total, we found 33 rare LoF variants in our sample. All variants were subjected to Sanger sequencing and 31 of 33 were confirmed by this method; 11 nonsense SNVs, 12 frameshift indels, 6 splice site SNVs, 1 splice site indel and 1 stop loss SNV (Table 1). All variants were novel of which 27 were singletons and 4 were found in more than one sample. Including data on all genes, we found an excess of individuals carrying LoF variants in our combined SZ and ASD case sample compared with controls (29 in 420 cases versus 8 in 287 controls; $P=0.02$) with the effect stronger for ASD (13 in 147

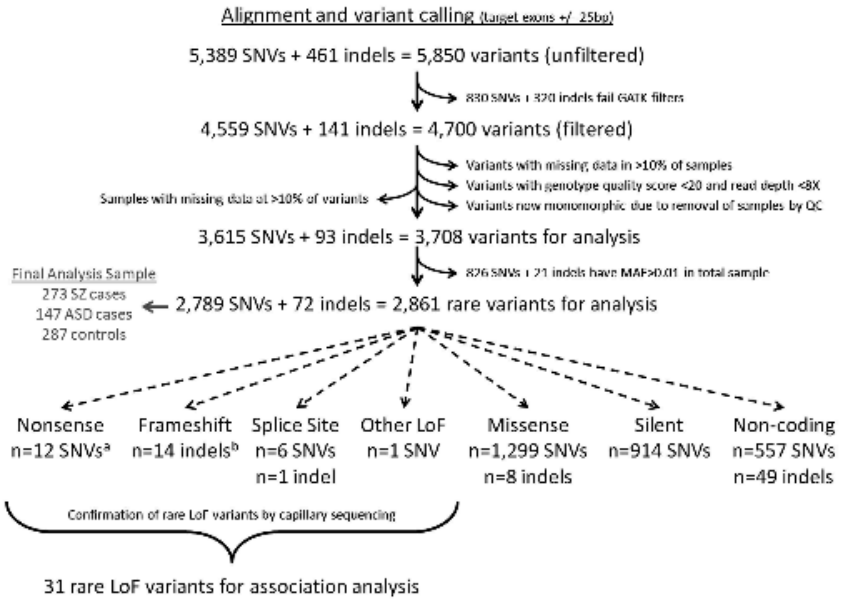

Figure 1. Flowchart displaying the number of variants and processes involved in reducing the total of 5 850 unfiltered variants to a set of 2 861 rare variants for analysis. [a]One nonsense single nucleotide variant (SNV) and one frameshift indel were called separately but were found to be in the same schizophrenia (SZ) case and located adjacent to each other in the *MACF1* gene. Following confirmation by Sanger sequencing, these two were combined, analyzed and reported as a single frameshift indel in MACF1 (see Table 1). Therefore, the total number of rare loss-of-function (LoF) variants detected was 33. [b]Two LoF indels were not confirmed by Sanger sequencing. The final number of LoF variants for association analysis was 31 (11 nonsense SNVs, 12 frameshift indels, 6 splice site SNVs, 1 splice site indel and 1 stop loss SNV; Table 1).

cases; $P = 0.005$) than for SZ (16 in 273 cases; $P = 0.07$; Table 2). To focus on variants that may be most deleterious, we dropped three low-frequency variants found in multiple samples that may represent benign variants circulating in the population. All three variants were found in both cases and controls. When the analysis is limited to variants that only occur in one individual (singleton variants), the data show a significant excess of LoF variants in the combined case sample versus controls (23 in 420 cases versus 2 in 287 controls; $P = 0.0007$) and the effect is similar for both ASD (9 in 147 cases; $P = 0.001$) and SZ (14 in 273 cases; $P = 0.002$; Table 2).

Following analysis of all genes combined, we next tested rare LoF variants in the individual gene categories. The Neurexin and Neuroligin Interacting Proteins grouping contained the highest number of these variants and a significant excess in cases (9 in cases (7xSZ and 2xASD) and 1 in controls, $P = 0.05$ for SZ + ASD; $P = 0.03$ for SZ; $P = 0.27$ for ASD (all Fisher's exact tests)). Results for all other gene categories were non-significant but the number of observations is small, for example, for Post-synaptic Glutamate Receptor Complexes there were 5 LoF variants in SZ + ASD cases and 0 in controls ($P = 0.08$; Fisher's exact test). At the level of individual genes, only *DST* had enough LoF variants to warrant a test (nine in cases (5xSZ and 4xASD) and three in controls, $P = 0.38$). The only other gene where we found more than two LoF variants was *INADL* ($n = 3$) and interestingly all were in cases. The effects of LoF mutations on cognitive and clinical intermediate phenotypes were assessed separately in SZ and ASD by comparing carriers versus non-carriers within each diagnostic group. Across both diagnostic groups little evidence was found to suggest that the LoF variant carriers differed significantly on clinical and cognitive metrics from non-carriers (see Supplementary Information).

Sanger sequencing of parental DNA that was available for the ASD samples revealed that the LoF variant at *GRIN2B* was *de novo*. The nonsense SNV (Q711*) at *GRIN2B* is located in exon 10 and parent of origin analysis indicated that it was on the maternal chromosome. The previously reported *de novo* LoF variants at *GRIN2B* in autism are a frameshift indel in exon 2, a nonsense SNV in exon 8 and a splice site SNV at exon 11.[51] Initial sequencing of parental samples for the *DISC1* variant indicated that it was *de novo*. This is a frameshift indel that affects transcript variant b (NM_001164538), which lacks two 3′ exons of longer transcripts but has an alternate 3′ segment. The frameshift occurs in this alternate segment and because of its position towards the end of the coding sequence, it was not included in our association analysis. Molecular analysis will be required to determine the functional impact of this variant. Parent of origin analysis indicated that this variant was on the paternal chromosome but closer study of the paternal DNA revealed evidence of the LoF allele, suggesting possible mosaicism in the father's blood cells and that the variant is not *de novo* in the proband.

Finally, we performed association analysis of the 1 299 rare missense SNVs identified in our sample of which 403 were classified as functional based on PolyPhen2/SIFT scores. Genes were grouped as follows: (1) All Genes, (2) Neurexin and Neuroligin Interacting Proteins, (3) Post-synaptic Glutamate Receptor Complexes, (4) Neural Cell Adhesion Molecules, (5) DISC1 and Interacting Proteins and (6) LoF-containing Genes ($n = 18$ genes that contained a rare LoF variant). For each gene group, we plotted the number of cases (SZ and ASD combined) and controls that carried 0, $\geqslant 1$, $\geqslant 2$, $\geqslant 3$, and so on rare functional missense SNVs (Figures 2a–f). We tested the number of samples that carried at least one rare functional missense SNV in cases versus controls and did not detect any significant differences for any of the gene categories. Similarly, when we plotted SZ and ASD separately, there were no significant differences between cases and controls. We also tested for a difference between cases and controls for the number of carriers of at least one rare functional missense SNV at each individual gene. Q-Q plots indicate a lesser number of nominally associated genes than would have been expected by chance, most likely reflecting the small number of variants included in the analysis of each gene (see Supplementary Information). None of the 18 genes containing LoF variants had a significant difference in carrier number of rare functional missense SNVs between cases and controls for either the combined or the individual disorders. In addition, within gene categories (2)–(5)

Table 1. Rare LoF variants in SZ, ASD and controls

Chr	Position (hg19)	Gene[a]	Gene category[b]	Ref allele	Alt allele	Type	SZ n = 273	ASD n = 147	CON n = 287	Singleton?	Effect[c]
1	62 321 741	INADL (1)	1	TC	T	Coding indel		1		Yes	Frameshift in exon 18 of 43, premature stop 2 codons downstream
1	62 349 979	INADL (2)	1	GC	G	Coding indel	1			Yes	Frameshift in exon 22 of 43, premature stop 44 codons downstream
1	62 456 007	INADL (3)	1	C	T	Nonsense SNV	1			Yes	R1280* in exon 28 of 43
1	208 216 512	PLXNA2	5	GT	G	Coding indel	1			Yes	Frameshift in exon 21 of 32, premature stop 37 codons downstream
1	39 788 292	MACF1	1	CAAC	TA	Coding indel	1			Yes	Frameshift in exon 32 of 102, premature stop 7 codons downstream
2	187 519 413	ITGAV	3	A	AG	Coding indel	1			Yes	Frameshift in exon 16 of 30, premature stop 7 codons downstream
2	239 257 490	TRAF3IP1	4	G	T	Splice site SNV		1		Yes	Donor site of exon 11 of 17, premature stop 30 codons downstream
3	57 282 220	APPL1	2	G	T	Splice site SNV		1		Yes	Acceptor site of exon 10 of 22, exon 10 skipped, transcript continues in frame
4	187 628 509	FAT1	2	C	A	Nonsense SNV	1			Yes	E825* in exon 2 of 27
6	56 358 939	DST (1)	3	TA	T	Coding indel	1			Yes	Frameshift in exon 83 of 102, immediate premature stop
6	56 472 474	DST (2)	3	G	A	Nonsense SNV	1			Yes	Q2285* in exon 39 of 102
6	56 479 284	DST (3)	3	T	C	Splice site SNV		1		Yes	Acceptor site of exon 36 of 102, exon 36 skipped, transcript continues in frame
6	56 482 783	DST (4)	3	C	CCT	Splice site indel		1		Yes	Donor site of exon 23 of 102, premature stop 23 codons downstream
6	56 483 170	DST (5)	3	C	A	Nonsense SNV	1			Yes	E1888* in exon 23 of 24
6	56 483 389	DST (6)	3	G	A	Nonsense SNV			1	Yes	Q1815* in exon 23 of 24
6	56 507 564	DST (7)	3	TA	T	Coding indel	2	2	2	No	Frameshift in exon 1 of 84, premature stop 33 codons downstream
6	112 025 283	FYN	1	G	A	Nonsense SNV	1			Yes	R156* in exon 7 of 14
8	27 463 990	CLU	3	CTG	C	Coding indel		1	1	No	Frameshift in exon 4 of 9, premature stop 4 codons downstream
10	79 584 235	DLG5	1	C	G	Splice site SNV			1	Yes	Acceptor site of exon 14 of 32, exon 14 skipped, transcript continues in frame
10	79 614 016	DLG5	1	C	A	Nonsense SNV	1			Yes	E217* in exon 4 of 32
12	13 724 778	GRIN2B	2	G	A	Nonsense SNV		1		Yes	Q711* in exon 10 of 13
12	66 765 472	GRIP1 (1)	2	A	T	Splice site SNV	1			Yes	Donor site of exon 23 of 25, premature stop 25 codons downstream
12	66 923 668	GRIP1 (2)	2	G	A	Nonsense SNV		1		Yes	R149* in exon 5 of 25
13	20 797 556	GJB6	3	TC	T	Coding indel		1	3[d]	No	Frameshift in exon 5 of 5, premature stop 11 codons downstream
13	109 610 055	MYO16	1	C	T	Nonsense SNV	1			Yes	Q627* in exon 16 of 34
17	40 844 654	CNTNAP1	1	C	T	Nonsense SNV		1		Yes	R890* in exon 17 of 24
X	32 429 867	DMD	4	G	A	Splice site SNV		1		Yes	Donor site of exon 30 of 79, premature stop 24 codon downstream
X	70 367 905	NLGN3	1	TC	T	Coding indel	1			Yes	Frameshift in exon 2 of 8, premature stop 42 codons downstream
						Total LoF variants	16	13	8		
						Total singleton LoF variants	14	9	2		
Other protein-truncating rare variants located in last 5% of coding sequence and not included in LoF-association analysis											
1	232 144 803	DISC1	4	CT	C	Coding indel		1		Yes	Frameshift in exon 11 of 11, premature stop 24 codons downstream
4	72 433 527	SLC4A4	2	G	GT	Coding indel			1	Yes	Frameshift in exon 25 of 25, premature stop 2 codons downstream
18	74 728 772	MBP	2	A	G	Stop loss SNV	1	1[d]		No	Stop codon lost, new stop 16 codons downstream

Abbreviations: ASD, autism spectrum disorder; LoF, loss-of-function; SNV, single nucleotide variant; SZ, schizophrenia.
[a]Numbers in parenthesis after gene names are to identify variants in phenotypic analyses (Supplementary Figures A–F). [b]1 = Neurexin and Neuroligin Interacting Proteins, 2 = Post-synaptic Glutamate Receptor Complexes, 3 = Neural Cell Adhesion Molecules, 4 = DISC1 and Interacting Proteins, 5 = Positional and Functional Candidates. [c]Position of variant is reported for largest protein-coding transcript containing that variant based on the Ensembl. [d]One sample is homozygous for this variant.

above, analysis of interacting gene pairs did not identify any pairs that were hit by mutations at a significantly different rate in cases compared with controls (see Supplementary Information).

DISCUSSION

By taking a targeted sequencing approach to the detection of rare variants, we add further support to the convergent evidence that synapse formation and maintenance are components of the pathophysiology of SZ and ASD. In our set of 215 candidate genes, we primarily focused on rare LoF variants that are likely to be most disruptive based on their predicted impact on protein-coding sequence. We find a significant excess of novel variants in our combined case sample and in ASD compared with controls. The selection of an MAF of <0.1 as a frequency cutoff for rare variants is arbitrary; not all variants above this threshold will be benign and not all variants below this threshold will be pathogenic. But highly pathogenic variants are likely to be rare or even unique. Therefore, to focus on variants that may be most deleterious, we performed an association analysis of singleton variants. There was a significant excess of singleton LoF variants in the combined case sample and for both ASD and SZ when analyzed separately.

When we tested the individual gene categories, we observed a significant excess of variants in Neurexin and Neuroligin

Table 2. Carrier-based association analysis of rare LoF variants in all genes

	SZ + ASD (n = 420)	*CON (n = 287)*	*P-value*	*OR (95% CI)*	*ASD (n = 147)*	*CON (n = 287)*	*P-value*	*OR (95% CI)*	*SZ (n = 273)*	*CON (n = 287)*	*P-value*	*OR (95% CI)*
# Of rare LoF variant carriers	29	8	0.02	2.59 (1.11, 6.24)	13	8	0.005	3.38 (1.27, 9.17)	16	8	0.07	2.17 (0.86, 5.64)
# Of singleton LoF variant carriers	23	2	0.0007	8.26 (1.87, 51.06)	9	2	0.001[a]	9.29 (1.85, 63.14)	14	2	0.002	7.70 (1.65, 49.53)

Abbreviations: ASD, autism spectrum disorder; CI, confidence interval; LoF, loss-of-function; OR, odd's ratio; SNV, single nucleotide variant; SZ, schizophrenia.
[a]Fisher's exact test.

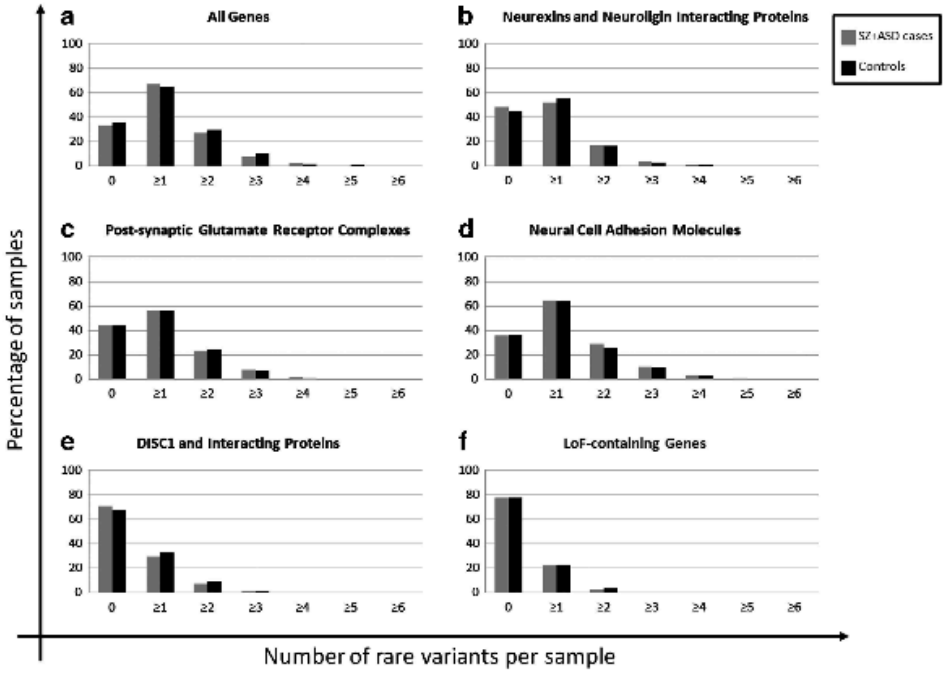

Figure 2. Data on rare functional missense variants (based on PolyPhen2 and SIFT scores) are plotted for the following groups of genes: (**a**) All Genes, (**b**) Neurexins and Interacting Proteins, (**c**) Post-synaptic Glutamate Receptor Complexes, (**d**) Neural Cell Adhesion Molecules, (**e**) DISC1 and Interacting Proteins and (**f**) Loss-of-Function (LoF)-containing Genes ($n = 18$ genes that contained a rare LoF variant). For each gene group, we plotted the percentage of cases (schizophrenia (SZ) and autism spectrum disorder (ASD) combined) and controls that carried 0, $\geqslant 1$, $\geqslant 2$, $\geqslant 3$ and so on variants. For example, for (**a**), across all genes 33.1% of cases had 0 rare functional missense single nucleotide variant (SNV) whereas 35.5% of controls had 0 SNV. Consequently, 66.9% of cases had $\geqslant 1$ SNV and 64.5% of controls had $\geqslant 1$ SNV. After that 26.7% of cases had $\geqslant 2$ SNVs and 29.3% of controls had $\geqslant 2$ SNVs and so on.

Interacting Proteins. Here, we found a variant in a male SZ case in the X-linked *NLGN3* gene, which had previously been reported to harbour rare risk variants in ASD.[68] In this category, we found three LoF variants in *INADL*, all in case samples (2xSZ and 1xASD). *INADL* functions to help anchor transmembrane proteins to the cytoskeleton and to organize signaling complexes. It interacts with neurexins and neuroligins and is important for cell polarity, migration and may have a role in neurite extension.[69,70] Also in the Neurexin category is *FYN* where we found an LoF variant in an SZ case that also had epilepsy. *FYN* is a Src family protein tyrosine kinase and is a key regulator of NR2B (encoded by *GRIN2B*) of the NMDA receptor.[71] Fyn-mutant mice exhibit blunting of long-term potentiation and impaired spatial learning plus other neurological defects including uncoordinated hippocampal architecture and reduced neural cell adhesion molecule-dependent neurite outgrowth.[72,73] Studies using Fyn-deficient mice support a role for *FYN* in the induction of epilepsy.[74] Our data further support *FYN* as a putative risk gene for SZ and/or epilepsy. Interesting, only two other SZ cases in the study had comorbid epilepsy and both were found to carry LoF variants, in *MACF1* (also in the neurexin category) and in *PLXNA2*. These samples were not included in previous SZ genome-wide association studies because of the comorbid epilepsy but highlight the value of taking an inclusive approach when selecting phenotype for rare variant studies.

After the Neurexin and Neuroligin Interacting Proteins gene category, no other categories had a significant excess of LoF variants but the number of observations is small, for example, for Post-synaptic Glutamate Receptor Complexes there were 5 LoF variants in SZ + ASD cases and 0 in controls. One of these variants was a *de novo* nonsense mutation in an ASD case at *GRIN2B*, which adds to the three recently reported *de novo* LoF mutations in other ASD samples[51] and supports *GRIN2B* as a risk gene for the disorder. Other data indicate that mutation at *GRIN2B* can contribute to various neurodevelopmental disorders. Endele *et al.*[75] identified *de novo* translocations with breakpoints disrupting *GRIN2B* in two individuals, one with mild mental retardation (MR)(46,XY,t(9;12)(p23;p13.1)) and another with severe MR (46,XY,t(10;12)(q21.1;p13)). Further screening of *GRIN2B* for

mutations in 468 individuals with MR and/or epilepsy identified four individuals with moderate MR and behavioral anomalies who had *de novo GRIN2B* mutations; a missense SNV, splice donor SNV, splice acceptor SNV and a 2-bp frameshift deletion. Talkowski *et al.*[76] characterized balanced chromosomal abnormalities in 38 subjects with neurodevelopmental abnormalities and identified a *de novo* translocation in an ASD case (46,XY,inv (12)(p13.1q21.31)dn) that disrupted *GRIN2B*. *GRIN2B* encodes the glutamate-binding NR2B subunit of the NMDA receptor and is important for channel function, organization of post-synaptic macromolecular complexes, dendritic spine formation or maintenance and regulation of the actin cytoskeleton.[77] Overexpression of the gene in animal models is associated with improved performance in learning and memory.[78,79] *GRIN2B* mutations in humans may affect brain function and cognition by disturbing the electrophysiological balance of the receptor during neurodevelopment.[75]

We detected two LoF variants in *GRIP1* (1xSZ and 1xASD). *GRIP1* is a member of the glutamate receptor interacting protein family and has a role in receptor trafficking, synaptic organization and transmission in glutamatergic and GABAergic synapses.[80] A recent study identified five rare missense variants in highly conserved regions of the gene in ASD cases only.[81] These variants were shown to be associated with altered *GRIP1* interaction with glutamate receptors, faster recycling and increased surface distribution of GluA2 in neurons *in vitro*, which supports a gain of *GRIP1* function in these variants. Knockout mouse studies demonstrated that *GRIP1* is essential for embryonic development and deficits in the protein lead to increased prepulse inhibition.[81]

Finally, the gene with the largest number of rare LoF variants was *DST* (Dystonin), a very large and transcriptionally complex gene that encodes multiple isoforms. It is a member of the plakin family of cytolinker proteins, which link cytoskeletal networks to each other and to junctional complexes. *DST* is expressed throughout mouse development and loss of its function results in neuromuscular dysfunction and early death in the mouse mutant *dystonia musculorum*.[82,83] Deleterious recessive mutations in *DST* have been identified as the likely cause of a lethal autonomic sensory neuropathy.[84] There is no additional evidence in the literature supporting rare variants at *DST* in SZ or ASD.

Phenotypic analysis of individual LoF carriers in the SZ and ASD samples did not identify any specific phenotypic characteristics. For SZ, it should be noted that when patients were originally chosen for inclusion in this study, we sought to include patients who showed deficits in cognitive performance. By definition, this lowered average cognitive performance scores for this group. Therefore, it is possible that our statistical approach was somewhat biased by comparison with a general SZ population. This reflects a broader issue in the study of symptom severity and cognitive function in rare variant carriers; that is how to classify the performance of individual carriers against an appropriate test group using appropriate statistical approaches. Investigators will want to move away from analysis of individual samples and instead study very large data sets where either multiple samples with rare variants in the same gene or ideally multiple samples with the same rare variant will be available for study.

In conclusion, we have used a focused targeted sequencing study of rare LoF variation to add to the growing volume of data supporting synapse formation and maintenance as key molecular mechanisms in the neurodevelopmental disorders SZ and ASD. We specifically find more evidence that rare variation in genes with Neurexin-related function increases the risk of SZ and ASD. The two disorders share some risk genes but there is not yet enough data to suggest that they share the same mutations. A major challenge for genetic analysis of both disorders will be to successfully understand the contribution and possible interaction of both common and rare variants. Synaptic function has been the focus of this rare variant study and an interesting example of how a common risk variant may impact the same molecular mechanisms has recently been reported in SZ. Knockdown of *ZNF804A*, site of the first genome-wide associated single nucleotide polymorphism for psychosis,[85] alters the expression of genes involved in cell adhesion, suggesting a role for *ZNF804A* in neural migration, neurite outgrowth and synapse formation.[86] In terms of specific genes, our work supports *GRIN2B* as a risk gene in ASD and adds further to data implicating *GRIP1* in ASD. We identify *FYN* as a putative risk gene for SZ and/or epilepsy and highlight multiple genes as potential susceptibility loci for these neurodevelopmental disorders that will require independent support from future sequencing studies.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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