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Gene constraint and genotype-phenotype correlations in neurodevelopmental disorders

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Abstract

With the advent and widespread adoption of high-throughput DNA sequencing, genetic discoveries in neurodevelopmental disorders are advancing very rapidly. Recent findings include the identification of previously unknown neurodevelopmental disorder genes, as well as multiple examples of rare, highly-penetrant variants in specific genes, which in turns is leading to improved understanding of genotype-phenotype correlations. Here we emphasize the importance of large-scale, reference databases such as gnomAD to determine gene and variant level constraints and facilitate gene discovery, variant interpretation, and genotype-phenotype correlations. While the majority of dominant NDD genes are highly intolerant to variation, some apparent exceptions in reference databases are related to the presence of variants in transcripts that are not brain expressed and/or genes that show acquired somatic mosaicism in blood. Multiple NDD genes are being identified where varying phenotypes depend on either the mode of inheritance (e.g., dominant or recessive), or the nature (e.g., missense or nonsense) and location of the mutation. Ongoing genome-wide analyses and targeted functional studies provide enhancements to the annotation of genes, gene products and variants, which will continue to facilitate gene and variant discovery and variant interpretation.

Keywords

autism; intellectual disability; mutation; constraint score; regional constrain

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Introduction

As clinical and research sequencing studies get ever larger, we are seeing unprecedented progress in gene discovery for a broad group of neurodevelopmental disorders (NDDs), including developmental delay (DD), intellectual disability (ID), autism spectrum disorder (ASD), and epilepsy. For all of these disorders, genes carrying highly penetrant rare variants are being identified, and these variants account for a significant proportion of the risk in the individual. Here we provide some background around gene discovery in these NDDs, with a focus on gene and variant level constraints and how they play out in the genetics of NDDs and then take examples from recent literature, focusing on informative genes as well as emerging genotype-phenotype correlations.

Gene and variant level constraints

No discussion of the genetics of NDDs can ignore the profound impact of large-scale population sequencing studies and the accumulation of these data in publicly available databases. The Genome Aggregation Database (gnomAD) is the best example of such an effort, and currently includes over 120,000 whole exome sequences and over 70,000 whole genome sequences [1]. Within gnomAD, which is a follow on of the Exome Aggregation Consortium (ExAC) [2], individuals with severe pediatric diseases and their first-degree relatives have been removed, and there are subsets of individuals who have been identified as free of neuropsychiatric disorders, so this cohort serves as a useful reference set of allele frequencies for NDDs, which in turn advancing gene discovery and facilitates the interpretation of variant pathogenicity in NDDs.

Some of the key parameters that can be derived from gnomAD are the (i) frequency of specific variants in controls, (ii) tolerance of a given gene to heterozygous protein truncating variants (PTVs) predicted to result in loss-of-function (although PTVs are often referred to as loss-of-function variants, the term ‘loss of function’ should be reserved to the function of the protein, as both PTVs and missense variants can result in loss of function), and (iii) tolerance of a gene to missense variation. The probability of being loss-of-function intolerant (pLI) is a metric that compares the expected number of PTVs in a given gene to the observed number of PTVs in gnomAD [2]. The closer pLI is to 1, the more intolerant a gene is to PTVs. Not surprisingly, the vast majority of the genes implicated in autosomal dominant and X-linked forms of NDDs have very high pLI (>0.9), reflecting selective pressure at these loci (Figure 1). In a first study of pLI in NDDs, Kosmicki et al. showed that individuals with ASD have a 3.24-fold increase in PTVs in genes that have high pLI (>0.9) and where PTVs are not seen in ExAC [3]. For individuals with ID/DD, this excess increases to 6.70, as compared to controls. There are, however, two caveats to the very high pLI finding in NDDs; first, we are most powered to identify highly penetrant genes and, second, some of the newest approaches to gene discovery focus on high pLI genes. But, while these points may bias the discovery to the genes with the highest pLI, there is no question that pLI is a very strong predictor of haploinsufficient genes that are likely to lead to severe, early-onset phenotypes when mutated with a PTV. On other hand, genes with many PTVs in controls are much less likely to be associated with phenotypes impacting development under a dominant mode of inheritance.

The gnomAD gene constraint metric for missense variants is the missense Z-score [2]. Here too, the comparison is made between the expected and the observed number of missense variants in a given gene. The expected number of missense variants is derived by sequence-specific mutational models with corrections using synonymous variation. A high missense Z-score (≥3.09) indicates that a gene is intolerant to missense variation, and is common in genes involved in autosomal dominant or X-linked NDDs, as opposed to recessive disorders (Figure 1).

Recent enhancements to the pLI and missense Z-score metrics include loss-of-function and missense observed/expected (o/e) scores, loss-of-function o/e upper bound fraction (LOEUF), as well as Missense badness, PolyPhen-2, Constraint (MPC) [1, 4]. Low values of the o/e and LOEUF metrics are indicative of strong intolerance. Importantly, the o/e metric includes estimates of confidence intervals, taking into account the gene size and numbers of samples, as well as providing a continuous measure across the constraint. LOEUF incorporates the upper bound of the confidence interval of the o/e ratio, and is thus a more reliable metric than pLI. MPC incorporates multiple metrics to better predict the impact of specific deleterious missense variants within a given gene, in contrast to missense Z-score, which looks at o/e for missense variation at the gene level. A recent study showed that the odds ratios associated with a de novo missense variant with high MPC were as high as the odds ratios associated with de novo PTVs in highly constrained genes (pLI > 0.9) [4]. Specifically, the study showed that there is a 5.79-fold increase in de novo variants with MPC > 2 in NDD cases, as compared to controls.

These constraint metrics are being used to facilitate gene discovery. For example, the most recent implementation of TADA (Transmitted and De Novo Association test), an approach to identify genes significantly associated with NDDs through ultra-rare variation, included pLI and MPC scores to greatly increase power to identify ASD genes [5, 6]. Since there is a strong bias for dominant highly penetrant NDD genes to have high pLI scores and/or to harbor missense variants with high MPC, incorporating these metrics enhances gene discovery [6].

Given the very strong association between autosomal dominant NDD genes with high constraint scores, great care should be taken before suggesting a causal implication of a heterozygous truncating or missense variant in a gene that is not constrained for that type of variant. To highlight just how powerful these approaches are, it is interesting to look at what appear to be exceptions to the above rules.

Transcript level constraints

Isoform diversity through alternative mRNA splicing across various tissues can sometimes explain the paradoxical finding of PTVs in known dosage-sensitive NDD genes in apparently healthy individuals in gnomAD [7]. *SHANK2*, encoding a synaptic scaffolding protein, is known to be involved in ID and ASD, based on both targeted and genome-wide studies [8, 9]. However, the gene has a pLI of 0 in gnomAD as of this writing, which is highly unusual for a dominant disease gene presumed to act through haploinsufficiency. A careful review of the data resolved this apparent conflict. gnomAD uses the longest

transcript in GENCODE as the canonical transcript (even when a different transcript is used as the reference sequence in medical genetics). However, when looking at the exon distribution of *SHANK2* in various tissues, there is little or no expression from over half the exons in this transcript in most tissues, including the brain, and the PTVs identified in gnomAD are primarily in these exons (Figure 2). Selecting the brain-specific transcript of *SHANK2* in gnomAD resulted in a pLI of 1. *MEF2C*, a gene encoding a transcription factor and involved in ID, ASD, epilepsy, and cerebral malformations, and responsible for the neurologic features of the 5q14.3 deletion syndrome [10], is another example, where the pLI for the default transcript in gnomAD, which is not expressed in the brain, is 0.02, but the pLI for the brain-expressed transcript is 0.97. For a more subtle example, *CAMK2B*, encoding a calcium/calmodulin-dependent protein kinase involved in ID [11], has a pLI of 0.74 for the reference transcript, but the truncating variants reported in gnomAD map to a small number of exons, which are not expressed in brain. pLI in the two brain-specific transcripts is 1.

Hence, careful attention needs to be paid to brain-expressed transcripts when attempting to assign clinical significance to a novel variant. In gene discovery studies, a focus on constraint scores from brain-expressed transcripts would enhance NDD gene discovery in genes where the constraint metrics of the reference sequence diverge significantly from those of the brain-expressed sequence. A recent ‘transcript-expression aware’ metric has been developed, called pext (proportion expressed across transcripts) [7]. Using pext it was observed that, for NDDs, *de novo* PTVs in low-expressed exons have effect sizes similar to those of synonymous variants (rate ratio ~1), while *de novo* PTVs in highly expressed exons have much larger effect sizes (rate ratio 4.64 for ID/DD and 2.11 for ASD). In addition, the metric proved useful for filtering PTVs in NDD genes.

Influence of somatic mosaicism on constraint metrics

Another explanation for the presence of potentially deleterious variants in NDD genes in population databases is somatic mosaicism. Although it is generally assumed that all variants present in ExAC and gnomAD are germline events, this is not always the case. *DNMT3A*, encoding a DNA methyltransferase involved in epigenetic regulation, is an interesting example. Germline mutations in *DNMT3A* result in Tatton-Brown-Rahman syndrome, an autosomal dominant disorder characterized by ID, tall stature, and a distinctive facies; many individuals also have ASD [12]. Missense and truncating variants, as well as whole gene deletions, have been reported, suggesting a loss-of-function mechanism. However, *DNMT3A* has dozens of PTVs reported in gnomAD and hence has a pLI of 0. The question then is how are the many PTVs in gnomAD consistent with the findings in Tatton-Brown-Rahman syndrome. While somatic mutations in *DNMT3A* are known to be common in acute myeloid leukemia [13], recent, large-scale, exome sequencing studies identified somatic mutations in this gene in tissue from older, healthy individuals [14]. Importantly, the mutations, although mosaic, are highly represented in the blood samples because of clonal hematopoiesis [15], a process where a substantial proportion of mature blood cells is derived from a single dominant hematopoietic stem cell lineage. Many of the *DNMT3A* truncating variants reported in ExAC and gnomAD exhibit allelic imbalance, consistent with somatic mosaicism [16]. In addition, numerous missense variants associated with Tatton-Brown-Rahman syndrome are present in gnomAD due to clonal hematopoiesis,

limiting the usefulness of population databases in the interpretation of *DNMT3A* variant pathogenicity [12, 16]. Interestingly, while germline loss-of-function variants in *DNMT3A* cause macrocephalic overgrowth in Tatton-Brown-Rahman syndrome, gain-of-function missense substitutions are associated with the reciprocal phenotype, microcephalic dwarfism (Heyn-Sproul-Jackson syndrome) [17]. Another autosomal dominant NDD gene that is frequently mutated in blood in older individuals is *ASXL1* [14]. *ASXL1* is associated with Bohring-Opitz syndrome and, like *DNMT3A*, encodes an epigenetic modifier [18]; it has a pLI of 0 in gnomAD because of the large number of cases with acquired hematopoietic mosaicism in the database [16]. *PPM1D*, involved in Jansen-de Vries syndrome [19] and encoding a protein phosphatase, is also enriched for truncating somatic mutations in the blood of cancer patients, asymptomatic individuals and the elderly [20–22], and has a pLI of 0. Of note, the majority of the somatic mutations occur in the C-terminal domain encoded by the two last exons, which is also the site of the truncating mutations reported in Jansen-de Vries syndrome; these PTVs escape nonsense-mediated decay and result in a truncated protein that retains the phosphatase domain [19, 20]. Taken together, these findings indicate that somatic mosaicism in blood should be considered to avoid misinterpreting the pathogenicity of germline variants or assume inaccurately that neurodevelopmental syndromes associated with genes affected by clonal hematopoiesis have reduced penetrance. Variant interpretation in clinical and research settings would be greatly facilitated by the systematic annotation in gnomAD of variants with decreased allele balance that are likely due to somatic mosaicism.

Complex genotype-phenotype correlations depending on mutation type and location

As the numbers of examples of mutations in NDD genes are increasing, we are beginning to find genes that show exclusively or primarily missense mutations, others that show primarily or exclusively truncating mutations, and others that show both types of variants. One gene with a preponderance of missense mutations is *DEAF1*. *De novo* heterozygous missense variants in *DEAF1,* encoding a transcription factor involved in embryonic and neuronal development, have been implicated in autosomal dominant ID and behavioral problems, including ASD [23]. Consistent with these findings, in a recent, large ASD study, five deleterious missense substitutions were observed in *DEAF1*, with no PTVs contributing to risk [6]. *DEAF1* shows a pLI of 0, and appears to be completely tolerant to truncating variation, hence the missense variants are likely acting through a dominant-negative or gain-of-function mechanism. In fact, deleterious missense variants cluster in the SAND domain, which is critical for dimerization and DNA binding , or the adjacent zinc binding motif [24, 25]. Of note, because only missense variants in specific functional domains are deleterious, the gene is not constrained for missense variants overall (Z-score=1.5). For some *de novo* missense variants in the SAND domain, it has been shown experimentally that they lead to a loss of transcriptional repression [23–25], suggesting a dominant-negative mechanism. Interestingly, biallelic recessive variants in *DEAF1* have been reported in several mostly consanguineous families with ID, ASD, epilepsy, microcephaly, and dyskinesia [25, 26]. The biallelic variants, inherited from unaffected parents, include nonsense, frameshift and splice variants predicted to result in loss of function due to nonsense mediated decay,

as well as three missense variants in the SAND domain. Functional analysis of these inherited missense variants showed that, in contrast to de novo variants, they do not affect transcriptional regulation or DNA binding affinity [24, 25]. While the pathobiology of recessive missense variants has not been elucidated, it is likely that they are hypomorphic compared to dominant alleles, and result in partial loss of function. Thus, these findings provide evidence for distinct underlying mechanisms in dominant and recessive *DEAF1*-associated NDDs.

Like *DEAF1*, an increasing number of NDD genes with autosomal dominant inheritance are being implicated in recessive disorders. For instance, *de novo* variants in *CAMK2A, GRIN1*, and *EEF1A2*, cause dominant forms of ID and epilepsy [11, 27, 28]. The variants reported are most often dominant-negative or gain-of-function missense variants, which tend to cluster in functionally important coding regions. Considering that these three genes are highly intolerant to variation, they are *a priori* not expected to be involved in recessive disorders. However, recent studies have reported novel recessive NDDs associated with homozygous missense variants in these genes resulting in hypomorphic alleles, which become pathogenic when recessively inherited [27, 29, 30]. Functional studies were necessary to demonstrate the pathogenicity of these variants. It is expected that as functional studies progress, it will be possible to categorize additional pathogenic variants as dominant-negative, gain-of-function and hypomorphic alleles, to improve our understanding of disease mechanisms, expand the disease spectrum, and better predict outcomes.

Many disease-associated genes (including *DEAF1* as noted above) show clustering of mutations within functional domains; these domain can also show evidence for regionalized constraint on deleterious variants [31–33]. Recent studies in ID, ASD and epilepsy identified deleterious, dominant missense variants in *KCNQ3*, a gene which encodes a subunit of the KV7potassium channel [6, 34–36]. The missense variants cluster in transmembrane regions involved in voltage sensing and appear to be gain-of-function affecting the neurophysiological properties of the channel. Similarly, NDD-associated mutations in *DDX3X* cluster around the helicase domain. DDX3X is emerging as the cause of 1–3% of unexplained ID and DD in girls and is implicated in ASD as well [37]. Dominant-negative missense mutations are associated with the most severe developmental and neurological phenotypes, while PTVs and hypomorphic missense alleles are associated with milder phenotypes [38]. Methods incorporating structural information and spatial constraints will enhance gene and variant discovery and variant interpretation.

Discovery of novel recessive NDD genes

For all of the success of genome-wide discovery for dominant NDD disorders, recessive variation still proves challenging in genome-wide analyses. Much of what we currently know about recessive genes is derived from traditional clinical genetic studies where multiply affected families were ascertained and sequenced. In large-scale, whole-exome and whole-genome sequencing studies, families typically have just one affected individual, or are case-control cohorts. The presence of heterozygous variants in unaffected individuals, and the relative paucity of *de novo* variation in recessive genes, decreases power to identify such NDD genes. A metric termed pREC, for probability of being recessive, which was

developed alongside pLI [2], has failed to gain traction because it is very hard to show convincing evidence of true recessive constraint (i.e., a specific deficit of individuals with biallelic variants, given the rates of heterozygous individuals) with sample sizes even at the level of gnomAD. In addition, phasing of rare variants (unless they are near each other) is very difficult with short read sequencing, hence distinguishing compound heterozygotes from two variants on a single haplotype is challenging. New approaches to address these issues are being developed now.

Conclusions

Large-scale sequence datasets from cohorts with and without NDDs are leading to enhanced gene discovery, variant interpretation, and etiologic diagnoses. Rates of different types of variation in such cohorts can also begin to illuminate mechanism and explain genotype-phenotype correlations. While interpretation of PTVs is most straightforward, careful attention to the localization and consequences of missense variation within genes can begin to shed light on hypomorphic, loss-of-function, gain-of-function, and dominant-negative alleles. The incorporation of improved annotation, as well as a focus on brain-expressed transcripts and critical domains within encoded proteins will enhance both gene discovery and variant interpretation.

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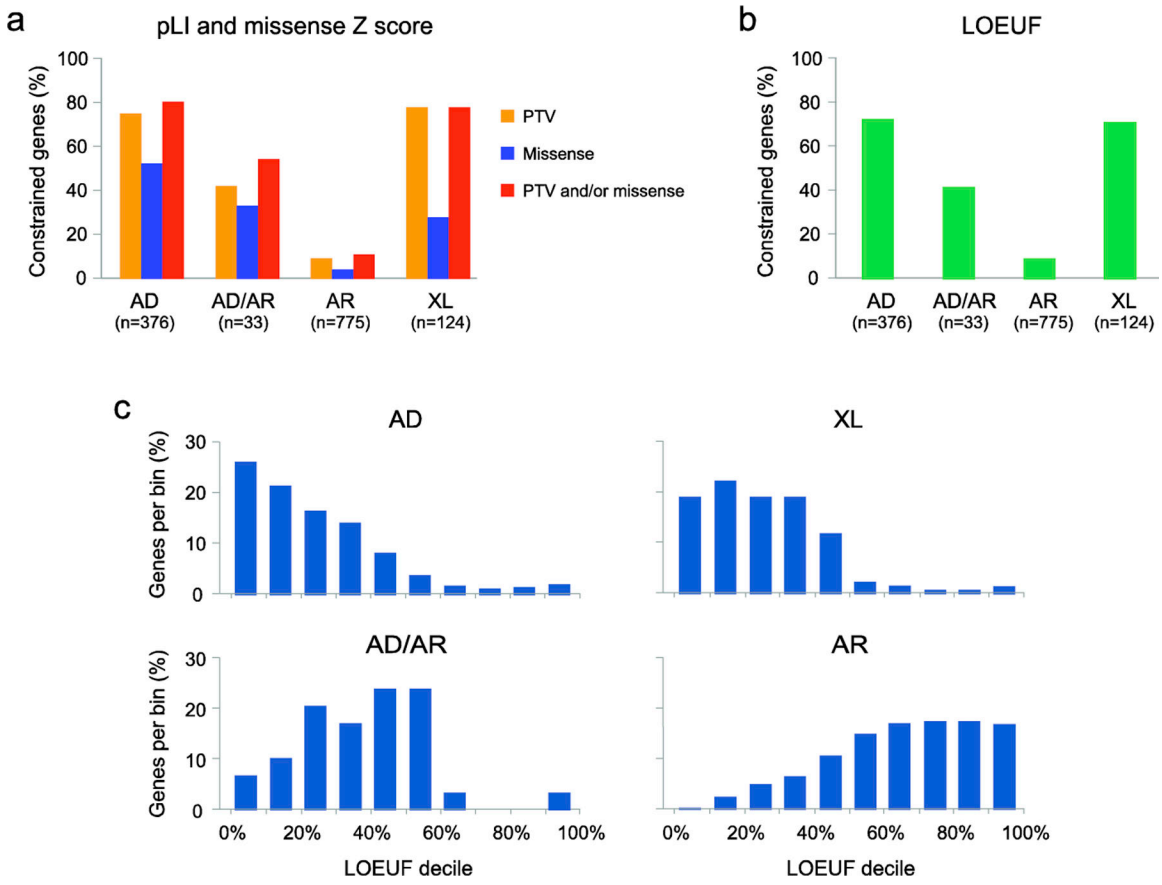

Figure 1. gnomAD constraint metrics of NDD genes.

The majority of the genes implicated in autosomal dominant (AD) and X-linked (XL) forms of NDDs are highly constrained for PTVs and/or missense variants. In contrast, genes involved in autosomal recessive (AR) disorders are usually not constrained. This is illustrated using curated sets of autosomal dominant, autosomal recessive, and X-linked genes, as well as autosomal genes showing NDD phenotypes with either monoallelic or biallelic mutations (AD/AR). **a,** The percentage of genes showing evidence of constraint for PTVs (pLI ≥0.9) and/or missense variants (missense Z score ≥3.09). **b,** The percentage of genes showing evidence of constraint for PTVs using the LOEUF metric (< 0.35). The proportion of constrained genes is similar to that obtained using the pLI score. **c**, The distribution of LOEUF scores is shown for each of the 4 gene sets. LOEUF, loss-of-function observed/expected upper bound fraction; pLI, probability of loss-of-function intolerant; PTV, protein truncating variant.

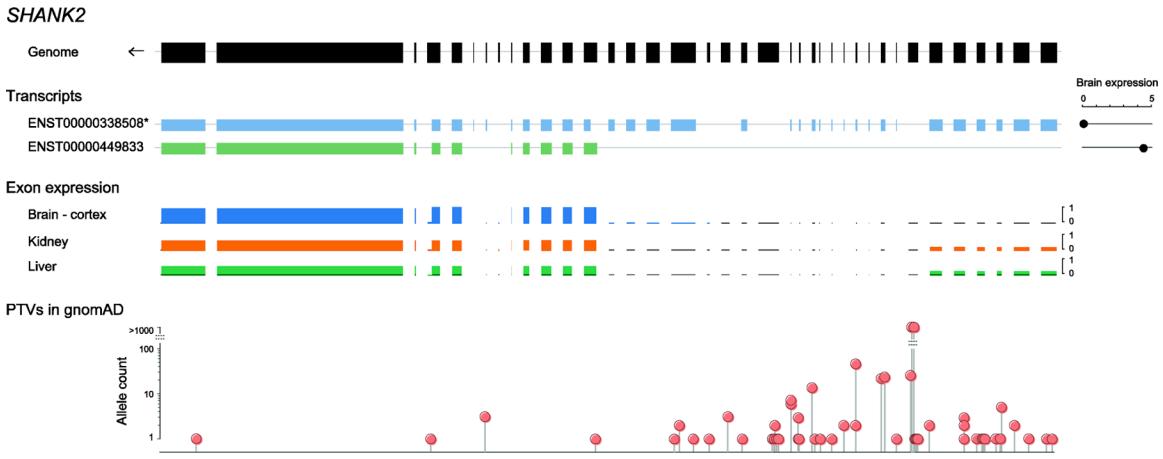

Figure 2. Distribution of truncating variants in gnomAD across *SHANK2* transcripts.

The figure shows (i) the genomic structure of *SHANK2*, (ii) two *SHANK2* transcripts, including the longest transcript selected as canonical in gnomAD ([1], noted with an asterisk), and the brain-specific transcript, with brain expression of the transcripts (read counts) shown on the right, based on the Genotype Tissue Expression (GTEx) dataset [39], (iii) ratios of exon expression in three example tissues, and (iv) the position and numbers of PTVs in gnomAD. There is no brain expression from over half the exons of *SHANK2* in the canonical transcript, where most of the PTVs are found. As a result, the pLI is 0 in the canonical transcript, but increases to 1 in the brain-specific transcript.