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# Low frequency of treatable pediatric disease alleles in gnomAD: An opportunity for future genomic screening of newborns

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**Data and Code Availability:** Source data for this study is available at gnomAD [https://gnomad.broadinstitute.org/]. This published article includes the filtered gnomAD dataset analyzed during this study.

Abstract: Hematopoietic stem cell transplants (HSCT) can prevent progression of several genetic disorders. Although a subset of these disorders are identified on newborn screening panels, others are not identified until irreversible symptoms develop. Genetic testing is an efficient methodology to ascertain pre-symptomatic children, but the penetrance of riskassociated variants in the general population is not well understood. We developed a list of 127 genes associated with disorders treatable with HSCT. We identified likely pathogenic or pathogenic (LP/P) and loss-of-function (LOF) variants in these genes in gnomAD, a dataset containing exome and genome sequencing data from 141,456 healthy adults. Within gnomAD, we identified 59 individuals with a LP/P or LOF variant in 15 genes. Genes were associated with bone marrow failure syndromes, bleeding disorders, primary immunodeficiencies, osteopetrosis, metabolic disorders, and epidermolysis bullosa. In conclusion, few ostensibly healthy adults had genotypes associated with pediatric disorders treatable with HSCT. Given that most of these disorders do not have biomarkers that could be cheaply and universally assessed on a standard newborn screen, our data suggest that genetic testing may be a complementary approach to traditional newborn screening methodology that has the potential to improve mortality and is not expected to lead to a high burden of false positive results.

Hematopoietic stem cell transplant (HSCT) and gene therapy prevent progression of symptoms in several severe childhood-onset monogenic diseases. These disorders include bone marrow failure syndromes, primary immunodeficiency disorders, inborn errors of metabolism, genetic forms of hemophagocytic lymphohistiocytosis, hemoglobinopathies and bleeding disorders, disorders of the skin (i.e. epidermolysis bullosa), and disorders of bone metabolism (i.e. osteopetrosis).<sup>1–8</sup> A genetic diagnosis of one of these conditions prior to the onset of symptoms provides an opportunity to initiate HSCT at an early stage of disease before neuroregression, potential life-threatening infections, or other sequelae occur.<sup>9,10</sup>

American newborn screening (NBS) protocols for some conditions treated with HSCT or gene therapy, such as various types of severe combined immunodeficiency, mucopolysaccharidosis type I (MPS1, MIM: 607014), and X-linked adrenoleukodystrophy (MIM: 300100), have been added to the Recommended Uniform Screening Panel (RUSP).<sup>11,12</sup> Krabbe disease (MIM: 606890), which is also treated with early HSCT, has also been added to NBS panels in 10 states within the United States.<sup>13</sup> Screening for these conditions includes biochemical or immunologic assays in combination with genetic testing. For example, MPS1 is screened using an enzymatic assay, but many states reflex to second-tier genetic testing for positive biochemical screening results. This second-tier testing greatly increases the positive predictive value of NBS for MPS1.<sup>14</sup> For actionable disorders that lack an efficient or accurate screening assay, such as spinal muscular atrophy, type I (MIM: 253300) quantitative polymerase chain reactions have been introduced as a first-tier test in state newborn screening laboratories.<sup>11</sup>

Genomic screening of newborns has the potential to capture infants with a wider range of actionable childhood-onset genetic disorders than those which are currently included on the RUSP. Recent studies have demonstrated, however, that both false positives and false negative

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results are identified via genomic screening compared with standard newborn screening practices.<sup>15–17</sup> A better understanding of the phenotypic spectrum and penetrance of pathogenic genotypes associated with these disorders is needed, particularly when the appropriate treatments, like HSCT, are invasive, costly, and pose major health risks.

In this study, we used the Genome Aggregation Database (gnomAD), an aggregated data set from unrelated individuals sequenced as part of various disease-specific and population genetic studies, to identify likely pathogenic or pathogenic (LP/P) and presumed loss-of-function (LOF) variants in genes associated with early-onset Mendelian diseases that are treatable with HSCT or gene therapy.<sup>18</sup> Given that gnomAD has been intentionally depleted of individuals with genetic disease, and that many individuals with severe forms of these disorders would not be expected to live until adulthood, these variants likely represent sequencing artifacts, non-penetrant alleles, or very attenuated phenotypes which may not require neonatal intervention.<sup>18</sup> In some cases, non-penetrant alleles may be due to mosaicism, as has been previously demonstrated in genes such as *NFKBIA*.<sup>19</sup> A higher than expected population frequency of disease variants could lead to low positive predictive value of screening and increase false positive rates of individuals for whom preventive treatment would be unnecessary.

The objectives of this study were to (1) identify a list of genes associated with Mendelian disorders that can be treated with HSCT or gene therapy and (2) assess of the number of individuals in gnomAD with disease-associated genotypes in these genes.

This study was exempt from review by the Institional Review Board. gnomAD is an aggregated data set of 125,748 exomes and 15,708 genomes from unrelated individuals sequenced as part of various disease-specific and population genetic studies.<sup>18</sup> The data in gnomAD were obtained primarily from the control groups of case–control studies of common

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adult-onset diseases, including cardiovascular disease, type 2 diabetes and psychiatric disorders. Samples with inadequate consent for the release of aggregate data have been removed.<sup>18</sup> Attempts have been made to deplete this data set of individuals known to be affected by severe pediatric disease, as well as their first-degree relatives.<sup>18</sup> Samples judged to have lower sequencing quality, as well as samples from first- or second-degree relatives, samples with inadequate consent for the release of aggregate data have also been excluded.<sup>18</sup>

We identified a preliminary list of childhood-onset diseases treated with HSCT and gene therapy using medical literature and a commercial genetic panel for primary immunodeficiency disorders.<sup>1–10</sup> After evaluating gene-disease association validity by reviewing the number of disease-causing variants reported in ClinVar and the Human Gene Mutation Database (HGMD), genes with insufficient evidence were removed.<sup>20,21</sup> This list of genes was then distributed to content-area experts, who modified the list based upon their clinical experience, and included only genes and disorders that were childhood-onset, severe, and current or future targets of HSCT or gene therapy.

All gnomAD variants (v2.1.1) that passed quality metrics from the selected genes were filtered to include only variants with implicated genotypes, i.e. for genes associated with an autosomal recessive disorder, only variants with  $\geq$ 1 homozygous counts were included, as the phase of heterozygous variants is unable to be determined. For genes associated with X-linked disorders, only variants with  $\geq$ 1 homozygous count or  $\geq$ 1 hemizygous count were included. This variant list was subsequently filtered to identify: (1) variants that have a minor allele frequency < 5.0% in gnomAD and have been classified as pathogenic or likely pathogenic from "single submitter, criteria provided" submitters in ClinVar; (2) predicted loss-of-function (LoF) variants (i.e. nonsense, frameshift, and +/-1,2 splice-site variants) with a minor allele frequency  $\leq$  1.0% in

gnomAD. Predicted LoF variants tagged as low-confidence (LC LoF) were removed from analysis.

We identified 127 high-evidence genes associated with childhood-onset Mendelian disorders treated by HSCT (Supplement 1). This list includes genes associated with primary immunodeficiencies (n = 61), bone marrow failure disorders (n = 34), inborn errors of metabolism (n = 19), hemophagocytic lymphohistiocytosis (n = 4), bleeding disorders and hemoglobinopathies (n = 3), osteopetrosis (n = 3), and epidermolysis bullosa (n = 3). The majority of these disorders are associated with autosomal recessive inheritance (n = 91), with a minority caused by autosomal dominant (n = 22) and X-linked recessive inheritance (n = 14).

Within gnomAD, we identified 59 individuals (0.04%) with 36 distinct LP/P variants. Assuming that no individuals within gnomAD have severe Mendelian childhood-onset disease, the false positive rate of genomic screening in this population would be 0.04%.

Variants were identified in 15 genes (Table 1). Associated genetic conditions included immunodeficiency disorders (n = 20), bone marrow failure syndromes (n = 18), hemoglobinopathies (n = 16), and inborn errors of metabolism (n = 5) (Figure 1). Most risk variants occurred in only one individual (n = 26), although several variants were identified in multiple individuals (n = 10). The highest number of individuals had variants in *ELANE* (n = 15), which is associated with AD congenital neutropenia (MIM: 202700).

Overall, individuals had variants that occurred predominantly in genes that confer disease in an AD pattern of inheritance (n = 24). A minority of individuals had homozygous variants in genes associated with AR (n = 6) and hemizygous variants associated with X-linked recessive conditions (n = 6). Within a large database of genome and exome sequence information, we identified only a small percentage of apparently healthy adults who harbor risk variants in a subset of genes associated with treatable Mendelian conditions. While issues regarding sensitivity of genomic sequencing versus traditional biochemical screening has been explored for inherited metabolic disorders, the reciprocal issue of specificity and positive predictive value of pathogenic genotypes has not been explored in as much detail. Incomplete penetrance or wide expressivity of childhood-onset conditions may lead to challenges in the screening and diagnosis of presymptomatic individuals. However, our data suggest that this issue is likely rare in the general population for the subset of genes assessed. Overall, assuming that the individuals within gnomAD are free from severe Mendelian childhood-onset disease, the false positive rate of genomic screening of newborns for diseases treatable with HSCT was calculated to be 0.04%, better than that of many enzymatic assays.<sup>15</sup>

At present, most Mendelian disorders treatable with HSCT are diagnosed after the onset of symptoms or due to the presence of a known affected family member. Pre-symptomatic screening for those with risk variants offers a potential opportunity to evaluate additional biomarkers of the related condition or initiate disease-modifying therapy prior to the emergence of symptoms. The individuals we identified with LP/P variants likely have non-penetrant alleles or highly attenuated symptoms of disease; alternatively, the variants are sequencing artifacts. While not all individuals with disease genotypes would immediately proceed to HSCT, early identification of genetic diagnoses would facilitate surveillance by appropriate clinicians and the opportunity to monitor early disease progression.

Our findings demonstrate that first-tier genomic screening for these disorders would not lead to a surplus of false positives, which could negatively impact patients and families or burden

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clinicians specializing in pediatric hematology-oncology, immunology, and other related specialties. We estimate that 0.04%, or 1 in 2500, individuals would be expected to have false positive genomic results, equal to approximately 1,500 of the 3,747,540 infants born in 2019.<sup>22</sup> Prior analyses of current newborn screening techniques for multiple inborn errors of metabolism (phenylketonuria, galactosemia, and biotinidase deficiency) and endocrinopathies (congenital hypothyroidism and congenital adrenal hyperplasia) have identified a positive predictive value of only 0.5-6.0%, generating more than 50 false positive results for every true positive result on newborn screening in the United States. For phenylketonuria alone, there were 8,867 false positive results generated during 1994.<sup>23</sup>

This study builds on previous analyses of the Exome Aggregation Consortium (ExAC) database that identified individuals with homozygous variants in genes associated with childhood-onset disease.<sup>24</sup> Other descriptive studies of large-scale exome datasets have identified healthy individuals with pathogenic and likely pathogenic genetic variants.<sup>24,25</sup> Our results reinforce prior observations regarding incomplete penetrance of some disease-related genotypes, although we found that in the genes of interest, incomplete penetrance or attenuated phenotypes were less common than previously reported.<sup>24,25</sup>

In general, the majority of disease-associated genotypes which we identified in ostensibly healthy adults were found in *ELANE*. A recent study utilizing CRISPR gene editing has found that variants in early exons of *ELANE* elicited nonsense-mediated decay, while terminal exon frameshift alleles escaped nonsense-mediated decay. Additionally, -1 frame insertions or deletions impeded neutrophil maturation and were associated with congenital neutropenia, whereas -2 frame late exon insertions and deletions supported neutrophil maturation.<sup>26</sup> It is likely that this more detailed information regarding the mechanisms underlying pathogenicity in

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*ELANE* will lead ClinVar submitters to reclassify many of the variants identified in gnomAD. Additionally, asymptomatic individuals harboring pathogenic *ELANE* variants exhibit mutant variant mosaicism in all examined cell types except neutrophils, which may provide the mechanism of decreased penetrance in the studied patient population.<sup>27</sup> For asymptomatic individuals with pathogenic variants in *ELANE*, there may be a need for the development of management guidelines to determine the frequency with which complete blood counts should be followed by a primary care doctor or hematologist.

This study provides a preliminary model for assessing the specificity of genomic screening, but has several limitations due to the constraints of the available data. First, we cannot rule out that the gnomAD variants have been identified in error or that prior variant classifications as recorded in ClinVar are flawed.<sup>28</sup> Next, we cannot be certain that the individuals whose data are included in gnomAD do not have manifestations of Mendelian disease and may benefit from appropriate treatment. Given the phenotypic heterogeneity of associated with some genes included in this study (i.e. hemoglobinopathies), it is also possible that some individuals may have mild or subclinical symptoms of disease, which would not require HSCT. Importantly, because biallelic variants cannot be ascertained in the gnomAD database, our analysis focused only on heterozygous and hemizygous variants associated with AD and X-linked disorders, as well as homozygous variants associated with AR conditions. We did not include compound heterozygotes, as these individuals cannot be definitively ascertained without parental data, and as such may increase rates of false positivity. Additionally, structural variants were not a target of this analysis and should be included in future work. This analysis could be replicated using other datasets such as dbGaP or genetic information aggregation tools such as AnVil.<sup>29,30</sup> Finally, while this analysis assesses the specificity of genomic sequencing,

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further investigations of the sensitivity of sequencing must be pursued to determine the suitability of this test for population-wide screening in newborns. Future analyses, including compound heterozygous variants and structural variants, should aim to improve the sensitivity of analyses.

Given these limitations, we suggest that identification of individuals with heterozygous and hemizygous LP/P variants associated with AD and XL disorders, as well as homozygous LP/P variants associated with AR conditions might be an initial target of genomic screening of newborns. A stepwise approach toward including biallelic should be considered in the future. However it should be noted that screening of biallelic variants may give rise to downstream bioethical challenges, as a newborn with two parents available for genetic testing stands to benefit from this screening information more than a newborn who only has one available parent. The overall clinical utility, costs, scalability, and equity of genomic screening are important future research directions.

New and effective therapies for Mendelian disorders are rapidly being developed. Many of these therapies are most efficacious if begun before clinical symptoms emerge. Our findings suggest that first-tier genomic screening for disorders treated with HSCT may be of value for affected newborns and in some circumstances would not lead to an undue burden of false positive results.

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# **Ethics declaration**

IRB/REC review was not required for this study as it was conducted using anonymous genotype and phenotype data.

# Data availability statement

While this manuscript analyzes anonymized data from a publicly available database (https://gnomad.broadinstitute.org/), any materials or data produced during this study will be made available upon request.

## **Author information**

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# Web resources

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# Tables

Table 1. Individuals (n = 59) with variants in genes associated with severe pediatric-onset disease treatable with HSCT or gene therapy identified in gnomAD.

Gene	Variant	Individuals with disease- associated genotypes	Phenotype
ABCD1	NM_000033.3:c.2106_2122del (p.Leu703AspfsTer25)		Adrenoleukodystrophy
CARD11	NM_032415.4:c.3261-2A>G	2	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.2704-1G>C	1	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.3260+1G>A	1	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.1518+1G>A	1	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.7+2T>G	1	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.2585delA (p.His862ProfsTer52)	1	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.2671C>T (p.Arg891Ter)	1	B-cell expansion with NKFB and T-cell anergy/Immunodeficiency 11B with atopic dermatitis
CARD11	NM_032415.4:c.1876G>T (p.Glu626Ter)	1	B-cell expansion with NKFB and T-cell

			anergy/Immunodeficiency
CADD11		1	11B with atopic dermatitis
CARDII	NM_032415.4:c.1156C>1 (p.Arg3861er)	1	B-cell expansion with
			NKFB and 1-cell
			11B with atopic dermatitis
CHD7	NM_017780.3:c.5051-2A>T	1	CHARGE syndrome
CHD7	NM 017780.3:c.401 402insAA	1	CHARGE syndrome
	(p.His134GlnfsTer78)	_	
CHD7	NM_017780.3:c.395_399delAGAGG	1	CHARGE syndrome
	(p.Glu132AlafsTer153)		
CHD7	NM_017780.3:c.8522C>A (p.Ser2841Ter)	1	CHARGE syndrome
CTLA4	NM_005214.4:c.255_256delTG	1	Autoimmune
	(p.Ala86GlyfsTer8)		lymphoproliferative
			syndrome, type V
ELANE	NM_001972.2:c.258_269dup	1	Neutropenia, severe
	(p.His87_Ser90dup)	$\mathbf{X}$	congenital 1
ELANE	NM_001972.2:c.427C>T (p.Arg143Cys)	5	Neutropenia, severe
			congenital 1
ELANE	NM_001972.2:c.573G>C (p.Arg191Ser)	2	Neutropenia, severe
			congenital 1
ELANE	NM_001972.2:c.659G>A (p.Arg220Gln)	1	Neutropenia, severe
			congenital 1
ELANE	NM_001972.2:c.628G>A (p.Gly210Arg)	6	Neutropenia, severe
E0	NNA 000122 2 C025 herT	1	
Fð	$NM_{000132.3}$ :c.0935dup1	1	Hemophilia A
F8	(p. val2313Ofy181Cf 72) NM 000132 3.c 6089G>A (p Ser2030A sp)	3	Hemophilia A
Г0 Г0	NM_000132.3.c.008/G/A (p.Sci2050ASii)	2	Hemophilia A
го	NM_000152.5:C.1854C>1 (p.Arg012Cys)	3	Hemophina A
F9	NM_000133.3:c.316G>A (p.Gly106Ser)	3	Hemophilia B
GAA	NM_001079803.1:c32-13T>G	1	Glycogen storage disease
			II
GATA2	NM_001145661.1:c.16_17insC	1	GATA2 syndromes
CD 4	(p.Glu6AlafsTer179)	2	
GBA	NM_001005741.2:c.1226A>G	3	Gaucher disease
	(p.Asn409Ser)	1	Data thalassamia maior
	NM_000518.4:C.19G>A (p.Glu7Lys)	1	Beta maiassenna major
НВВ	NM_000518.4:c.79G>A (p.Glu27Lys)	1	Beta thalassemia major
HBB	NM_000518.4:c.20A>T (p.Glu7Val)	4	Beta thalassemia major
NFKBIA	NM_020529.2:c.875_876delAG	1	Ectodermal dysplasia,
	(p.Glu292ValfsTer14)		anhidrotic, with T-cell
			immunodeficiency
NFKBIA	NM_020529.2:c.735_736delAG	1	Ectodermal dysplasia,

	(p.Arg245SerfsTer39)		anhidrotic, with T-cell
NEKBIA	NM 020529 2·c /38 /03del	1	Ectodermal dysplasia
MINDIA	(n Pro147ValfsTer43)	1	anhidrotic with T-cell
			immunodeficiency
RPS10	NM 001014.4:c.373 374delGA	1	Diamond-Blackfan
	(p.Asp125TyrfsTer34)		anemia
SBDS	NM_016038.2:c.258+2T>C	2	Shwachman-Diamond
			syndrome
XIAP	NM_001167.3:c.758C>G (p.Ser253Ter)	1	Lymphoproliferative
			syndrome, X-linked, 2

# **Figure legends**

Figure 1. Variants in genes associated with disorders treatable by HSCT in gnomAD.

# **Supplemental tables**

Supplemental table 1. Genes associated with severe pediatric-onset Mendelian disorders treatable with hematopoietic stem cell transplant or gene therapy (n = 127).

Johnsheren

Hematopoietic stem cell transplant can prevent progression of many genetic disorders. Penetrance of these disorders is unknown, however, limiting the application of early diagnosis. Among 141,456 healthy adults, only 59 had disease-associated variants, indicating that most of these disorders are highly penetrant. Genomic screening may facilitate early diagnosis and treatment.

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