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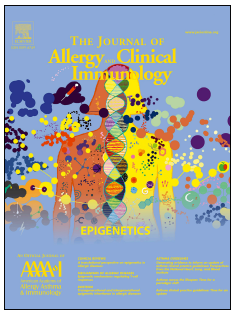

Diagnostic Interpretation of Genetic Studies in Patients with Primary Immunodeficiency Diseases: A Working Group Report of the Primary Immunodeficiency Diseases Committee of the American Academy of Allergy, Asthma, and Immunology

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Diagnostic Interpretation of Genetic Studies in Patients with Primary Immunodeficiency Diseases: A Working Group Report of the Primary Immunodeficiency Diseases Committee of the American Academy of Allergy, Asthma, and Immunology

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Abbreviations:
aCGH: array comparative genomic hybridization
ACMG: American College of Genetics and Genomics
AF: allele frequency
ALPS: autoimmune lymphoproliferative syndrome
AOH: absence of heterozygosity
bp: base pair
cDNA: complementary DNA
CADD: Combined Annotation-Dependent Depletion
CGD: chronic granulomatous disease
CLIA: Clinical Laboratory Improvement Amendments
CMA: chromosomal microarray analysis
CNV: copy number variant
CVID: common variable immunodeficiency disease
dbGaP: database of Genotypes and Phenotypes
ddNTP: dideoxynucleotide
DNA: deoxyribonucleic acid
eQTL: expression quantitative trait loci
ESP: Exome Sequencing Project
ExAC: Exome Aggregation Consortium
FISH: fluorescence *in situ* hybridization
FURID19: Facial dysmorphia, Urogenital malformation, growth and neurodevelopmental Retardation, ImmunoDeficiency, trisomy 19p13
G-C: guanosine-cytosine
GEO: Gene Expression Omnibus
gnomAD: genome Aggregation Database
GTEx: Genotype-Tissue Expression
GWAVA: Genome-Wide Annotation of VAriants
HGCS: Human Gene Connectome Server
HGMD: Human Gene Mutation Database
HGVS: Human Genome Variation Society
HPO: Human Phenotype Ontology
indel: small insertion or deletion
kb: kilobase pair

LOH: loss of heterozygosity
MAF: minor allele frequency
mRNA: messenger RNA
NCBI: National Center for Biotechnology Information
NGS: next generation sequencing
NHLBI: National Heart, Lung, and Blood Institute
NMD: nonsense-mediated decay
nt: nucleotide
OMIM: Online Mendelian Inheritance of Man
PCR: polymerase chain reaction
PIDD: primary immunodeficiency disease
pLoF: probability of loss of function intolerance
PolyPhen: Polymorphism Phenotyping
RNA: ribonucleic acid
RNA-Seq: RNA sequencing
SCID: severe combined immunodeficiency disease
SIFT: Sorting Intolerant From Tolerant
SNP: single nucleotide polymorphism
SNV: single nucleotide variant
SS: Sanger sequencing
TGP: targeted gene panel
UTR: untranslated region
VUS: variant of uncertain significance
WES: whole exome sequencing
WGS: whole genome sequencing

Abstract:
Genetic testing has become an integral component of the diagnostic evaluation of patients with suspected primary immunodeficiency diseases. Results of genetic testing can have profound impact on clinical management decisions. Clinical providers must therefore demonstrate proficiency in interpreting genetic data. Because of the need for increased knowledge regarding this practice, the American Academy of Allergy, Asthma, and Immunology Primary Immunodeficiency Diseases Committee established a Work Group that reviewed and summarized information concerning appropriate methods, tools, and resources for evaluating variants identified by genetic testing. Strengths and limitations of tests frequently ordered by clinicians were examined. Summary statements and tables were then developed to guide the interpretation process. Finally, the need for research and collaboration was emphasized. Greater understanding of these important concepts will improve the diagnosis and management of patients with suspected primary immunodeficiency diseases.

Definitions of terms, as used in this document (see also: Table 1):

- Absence of heterozygosity (AOH): lack of heterozygosity within a chromosomal region, sometimes used interchangeably with loss of heterozygosity (LOH), although the terms are not technically equivalent
- Allele: one of two or more variant forms of a gene
- Balanced translocation: structural variant in which DNA has been exchanged between 2 chromosomes with no loss of genetic material
- Canonical splice acceptor: conserved AG dinucleotide at the 3' end of an intron
- *Cis* configuration: occurrence of two or more variants on the same chromosome
- Compound heterozygous: present such that each variant within the same gene produces a different genetic change on opposite chromosomes of a homologous chromosome pair
- Consensus identity: nucleotide at a specific genomic coordinate chosen by consensus to represent the most common base present within the general population at that location
- Copy number variant (CNV): gain or loss of a region of DNA, resulting in deviation from the normal diploid state
- Coverage: percentage of targeted genomic regions sequenced to a minimum predefined read-depth
- Cryptic splice site: genomic sequence which, when transcribed into mRNA, contains the necessary elements for splicing, is not typically used as a splice site, but may become an active splice site due to a genetic change
- *De novo* genome assembly: creation of the genomic DNA sequence without use of a template
- *De novo* variant: a genetic change present in the sequenced individual but not observed in either parent
- Distal: located toward the 3' end of a DNA or mRNA sequence or toward the C-terminus of a peptide sequence
- Dominant: exhibiting a trait when only one allele is altered
- Dominant negative: encoding a mutated gene product that inhibits the activity of the wild-type gene product
- Enhancer: genomic region that is bound by proteins to increase transcription of a gene
- Exon: the protein-encoding portion of a gene
- Frameshift variant: an insertion or deletion that shifts the triplet codon reading frame by 1 or 2 bases
- Germline DNA: genetic material derived from gamete cells
- Haploinsufficient: producing an altered phenotype at 50% gene product function due to complete loss of gene product function from one allele
- Hemizygous: located within a single allele for which a second allele is missing or not present, *e.g.*, X chromosome loci in 46,XY males
- Heterozygous: present on one chromosome such that the genetic sequence differs from the sequence on the other chromosome of a homologous pair
- Homozygous: present such that the genetic change is identical for both chromosomes of a homologous pair

- Identity by descent: sharing of identical DNA sequences between individuals due to inheritance from a common ancestor without recombination
- Indel: a small insertion or deletion of DNA that results in a net change in the total number of nucleotides
- Initiation codon: messenger RNA sequence that signals beginning of translation
- Intron: intervening DNA sequence between exons
- Inversion: chromosomal defect in which a segment of DNA is present in reverse direction
- Locus heterogeneity: production of the same phenotype by pathogenic variants in different individual genes
- Mendelian inheritance: principle by which variation at a single genetic locus is tied to the trait of interest through Gregor Mendel's laws of segregation, independent assortment, and dominance
- Mosaicism: 2 or more cell lineages with differing genetic material derived from a single zygote
- Nonsense variant: a genetic change that causes the intended amino acid to be replaced with a premature stop codon, also known as a "stopgain" variant
- Nonsynonymous variant: a genetic change within a codon that substitutes one amino acid for another without altering the trinucleotide codon reading frame, also known as a "missense" variant
- Proximal: Located toward the 5' end of a DNA or mRNA sequence or toward the N-terminus of a peptide sequence
- Read-depth: number of sequences computationally aligned to a reference sequence at a given genomic coordinate
- Reading frame: schema in which a DNA or RNA sequence is divided into consecutive series of three-nucleotide segments
- Recessive: exhibiting a trait only when both alleles are altered
- Reversion: a change in the genetic material that further modifies or reverses the defect observed in a previously mutated gene product
- Silencer: genomic region that is bound by proteins to decrease transcription of a gene
- Single nucleotide variant (SNV): a genetic change in a single nucleotide
- Splice site variant: a genetic change that modifies splicing of the messenger RNA product
- Splicing branch point: conserved adenine near the 3' end of an intron that facilitates spliceosome component binding
- Structural variant: a large (greater than 50 bp) structural change in DNA that may be copy neutral (*e.g.*, an inversion) or a copy number variant (*e.g.*, deletion or duplication)
- Synonymous variant: a genetic change within a codon that does not alter the amino acid sequence or trinucleotide codon reading frame
- *Trans* configuration: occurrence of two or more variants on opposite chromosomes
- Uniparental disomy: inheritance of both copies of a chromosome from the same parent

- Variant: a genetic change from the reference or consensus sequence
- Variant calling: identification of the occurrence of a variant based upon a difference from the reference sequence
- Variant cosegregation: occurrence of a genetic condition, whether monoallelic or biallelic, with the phenotype of interest in different members of a family
- X-linked: exhibiting a trait associated with a genetic variant on the X chromosome

Introduction

Primary immunodeficiency diseases (PIDDs) arise from inherent defects in immunity, most of which result from inborn deviations in the genetic code. The term, PIDD, continues to evolve as a title and concept, as it has grown to encompass not only susceptibilities to infections, but also dysregulated inflammation and tolerance toward endogenous and exogenous antigens.[1, 2] Over 350 PIDDs have been recognized by the International Union of Immunological Societies, including over 340 caused by single-gene defects.[1, 3] Thus, genetic testing must be regarded as an indispensible part of the evaluation of patients with suspected PIDDs.[4-6] This process has been facilitated by the rapid evolution of molecular testing platforms. As advanced diagnostic modalities become applied more broadly, the information received must be interpreted appropriately in order to provide the best clinical care to patients.

Interpretation of genetic test results (see **Table 1**) can impact patients and families in three important ways. First, assignment of a genetic diagnosis to a patient can have significant ramifications for the advised therapeutic approach. In the short term, specific therapies may be immediately recommended based upon their efficacy in the identified disorder. As part of long-term management, prognostic awareness can allow families and medical care providers to make crucial decisions regarding surveillance or the use of higher risk therapies, such as hematopoietic stem cell transplantation. Second, attribution of a molecular diagnosis can have implications for family counseling regarding recurrence risk that impact parental decision making and may affect reproductive choices. Other family members may need to be alerted and tested. Lastly, identification of a putative molecular explanation and assignment of the corresponding genetic diagnosis can lead to diagnostic closure. If accurate, patients and families often receive appropriate treatment. If inaccurate, inappropriate testing or therapy may be performed that delay necessary treatment.

Genetic test results must therefore be considered carefully. Here, we review the genetic tests most commonly used by clinicians during the evaluation of patients with suspected PIDDs and then discuss various factors that merit consideration when assessing genetic variations in this unique patient population (see Appendix for suggested worksheet). It must be emphasized that the concepts are focused upon identification of rare genetic causes of PIDDs that follow Mendelian patterns of inheritance. Other genetic hypotheses that might influence disease susceptibility[7], such as epigenetics, major histocompatibility complex associations, and polygenic interactions, remain beyond the scope of this document. This report is also not intended to advocate for or against the use of specific genetic tests for certain conditions. For such recommendations, readers are referred to a separate document.[6]

Genetic Tests

Several options are available for clinical genetic testing, each of which bears its own set of advantages and limitations that should be considered when interpreting results. Tests most frequently used by clinicians include individual gene Sanger sequencing (SS), chromosomal microarray analyses (CMA), targeted gene panels (TGP), and

whole exome sequencing (WES). Whole genome sequencing (WGS) is included for discussion, as well. A summary of the differences between these genetic tests is provided in **Table 2**.

Individual Gene Sanger Sequencing

Background and Methodology

Sanger sequencing, developed by Frederick Sanger in the late 1970's, served as the most common method for genomic sequencing for more than 40 years.[8] The technique relies on selective incorporation of chain-terminating dideoxynucleotides (ddNTPs) by DNA polymerase during *in vitro* DNA replication. Initially, the region of DNA to be sequenced must be amplified. This amplification can be accomplished by two different methods: in the first, randomly fragmented DNA is cloned into a high copy number plasmid, which is then used to transform *E. coli*, where replication and amplification of the DNA fragment ensues; alternatively, amplification can be carried out using a method termed polymerase chain reaction (PCR). PCR amplification utilizes primers that flank the target region of DNA, facilitating replication of a specific DNA segment by DNA polymerase.[9] After amplification, the DNA is denatured to produce single stranded DNA. The single stranded DNA anneals to a sequencing primer, and reverse strand synthesis is performed using a mixture of deoxynucleotides and ddNTPs. When incorporated into a growing strand of DNA, a ddNTP prevents further addition of nucleotides, thus halting elongation of the DNA chain and further replication. This process ultimately leads to the generation of multiple DNA fragments of variable lengths. These fragments are then sorted by their molecular weight, historically by gel electrophoresis and more recently using capillary electrophoresis, and then analyzed.[10] After 3 decades of improved technology, SS can achieve read lengths of up to 1,000 base pairs (bp) with a nucleotide accuracy rate of over 99%.

Strengths

Because of its high accuracy, SS is typically recognized as the gold standard for validation of genetic variations.[11] The sensitivity and specificity of SS can surpass next generation sequencing (NGS) at some institutions, and the ability to analyze regions that NGS is not able to sufficiently cover increases the advantages and utility of SS.

Directed SS of one or more candidate genes often serves as a first-tier diagnostic approach in families with a known molecular defect. When applied in the proper clinical context, SS presents an effective, rapid, and cost-effective strategy for diagnosis.

Limitations

The most significant limitation of SS consists of the limited number of samples that can be analyzed in parallel, restricting the number of candidate genes that can be feasibly investigated. The poor efficiency of SS is exacerbated by the time and complexity involved in designing primers that will work as intended. Even in instances where a clear clinical phenotype exists, locus heterogeneity for a number of PIDD conditions (*e.g.*, $T^-B^-NK^+$ severe combined immunodeficiency [SCID]) requires consideration of multiple possible candidate genes (*e.g.*, *RAG1, RAG2, DCLRE1C, PRKDC, LIG4,* and *NHEJ1)*. In the more common clinical scenario in which the phenotype is less clear-cut,

an even larger number of gene targets require evaluation. Refinements in technology over the past several decades have led to development of capillary-based, semi-automated SS methods that allow for a limited degree of parallel analysis[9], but this methodology remains inferior to the capabilities of massively parallel DNA sequencing platforms.

SS carries several other limitations, as well. One lies in the maximum read length that can be sequenced, which is approximately 1,000 bp.[9, 12] This factor constrains the ability to efficiently analyze entire complex genes. Furthermore, although SS is traditionally regarded as having the highest sequencing fidelity of all platforms with an error rate of 1 in every 10,000 to 100,000 nucleotides (nt)[10], areas of guanine-cytosine (G-C) rich DNA are inaccurately sequenced by this method, as are DNA molecules with significant secondary structure.[12] SS also has limited sensitivity (estimated at 10-30%) for mosaicism, which may be insufficient for detecting clinically relevant mutant alleles, such as in the instance of tumor cell genetic changes.[13] Next, SS can miss variants in samples that are affected by allelic dropout.[14] Allelic dropout occurs when 1 of the 2 alleles fails to amplify during the PCR step. If the allele containing the variant is not amplified, only the wild-type sequence will be captured. Lastly, medical care providers should be aware that clinical laboratories sometimes sequence only a portion of the gene of interest and not the entire gene, allowing important novel or known pathogenic variants to be missed.

Chromosomal Microarray Analysis

Background

Chromosomal microarray analysis can be performed through the use of array comparative genomic hybridization (aCGH), single nucleotide polymorphism (SNP) array hybridization, or the combination of both techniques. aCGH testing allows for the detection of chromosomal losses and gains (copy number variants [CNVs]) throughout the genome[15] by comparing hybridization intensities of various probes between patient and control DNA samples.[16] SNP array testing can facilitate the analysis and filtering of WES data through its ability to detect regions of absence of heterozygosity (AOH). By using oligonucleotide platforms, CMA provides high analytical sensitivity compared to conventional cytogenetics.

CMA is useful as a genetic test when the clinical phenotype appears syndromic or too non-specific to identify a single candidate gene or narrow panel of genes for testing.[17, 18] CMA is the first-tier recommended genetic test for children with neurodevelopmental delay, multiple congenital anomalies, dysmorphism, autism spectrum disorders, neurobehavioral problems, and intellectual disabilities.[18-20]

CMA technology plays an essential role in the investigation of PIDDs. The 22q11 microdeletion in DiGeorge anomaly serves as a typical example of a PIDD that can be diagnosed using CMA. In addition, CMA has led to improved understanding of the underlying genetic abnormalities in several other PIDDs. For example, *DOCK8* was linked to genetic etiologies of autosomal recessive hyper-IgE syndrome through identification of large deletions in the gene by CMA.[21] CMA also helped to elucidate a

novel immunodeficiency syndrome associated with partial trisomy of 19p13 known as FURID19 (Facial dysmorphia, Urogenital malformation, growth and neurodevelopmental Retardation, ImmunoDeficiency, trisomy 19p13).[19] CNVs have been reported in some of the complement genes as well as other genes associated with PIDDs and autoimmunity.[19, 21-23] Importantly, CMA has been used successfully in conjunction with other technologies, such as WES, to further define disease-causing variants in PIDD patients for whom genetic etiologies were not previously identified and to identify CNVs that can be missed by WES.[23]

Method

CMA encompasses all types of array-based genomic copy number analyses, including aCGH and SNP arrays. aCGH is a probe-based hybridization platform in which thousands of short DNA probes that span the entire length of all human chromosomes are precisely arranged on a microchip. Patient and reference genomic DNA are enzymatically digested and labeled with different fluorescent dyes separately prior to being mixed together. Reference DNA may be derived from a single person or a pool of healthy control individuals who have no known genetic abnormalities. The mixed DNA is applied to the chip, where hybridization occurs. Afterwards, the chip is washed and read by a microarray scanner, which captures the fluorescence intensities of each DNA fragment binding to its cognate probe. The scanner, together with analytical software, calculates the ratio of fluorescence intensities of patient DNA binding relative to reference sample. For example, if the patient DNA is labeled with red dye, and the reference sample is marked with green dye, a yellow signal indicates comparable amounts of patient and reference DNA that have bound to a probe, a red signal indicates that the patient has more DNA (*i.e.*, potential duplication), and a green signal indicates less DNA (*i.e.*, possible deletion). SNP arrays, on the other hand, may be performed using either a microchip or a bead-based design. In both approaches, oligomerized patient DNA is hybridized to various probes that target hundreds of thousands of SNPs. These probes are fixed either to a microchip or to microscopic beads that become distributed within microwells. Presence or absence of binding to the probes is then detected in a similar fashion to aCGH.

Strengths

CMA facilitates the detection of CNVs, microdeletions, microduplications, and most unbalanced rearrangements of chromosome structure (translocations, etc.).[24] SNP arrays can also detect AOH, which could be caused by consanguinity, identity by descent, uniparental disomy, or hemizygous deletion of a portion of DNA. An additional advantage of CMA is that it enables the detection of losses and/or gains of chromosomal material that are submicroscopic and which can be missed by more traditional methods, such as fluorescence *in situ* hybridization (FISH). Moreover, because CMA analyzes DNA extracted from uncultured cells of all different types, it has fewer experimental requirements for sample quality, leading to shorter reporting time compared to traditional chromosomal analysis.[16]

Limitations

Because CMA is not fundamentally designed to be used as a sequencing platform, it does not replace SS, TGPs, or WES. CMA may not detect small changes in the sequence of single genes (*e.g.*, rare single nucleotide variants), very small (typically 2 to 16 bp)[25] duplications and deletions of DNA segments within a single gene (*e.g.*, small insertions or deletions [indels]), or chromosomal rearrangements that do not affect the nucleotide copy number (*e.g.*, balanced translocations, inversions).[26] Current oligonucleotide platforms can now detect genomic imbalances as small as 500 bp, allowing the resolution of copy number changes as small as 10 to 20 kb in many regions of the genome.[18, 27] Clinical arrays are typically designed to uncover gains or losses of chromosomal material ranging from 20 to 50 kb in targeted regions (*e.g.*, within known Mendelian genes) and 100 to 250 kb in non-targeted genomic regions.[27] CMA may poorly identify CNVs that are present due to mosaicism. It can also miss intermediate CNVs (250 to 500 bp) involving one to a few exons, which require a high-resolution CMA for detection that is not frequently used. Most current clinical CMA platforms can detect copy number changes with a lower limit of resolution approximating 400 kb throughout the genome.[27] Finally, CMA will identify copy number variants of uncertain significance, and determining the clinical significance of these genetic differences poses significant challenges to clinicians and genetic laboratories.[18, 28] As CMA probe density continues to increase, many CNVs are being observed in the general population, most of which are benign.

Targeted Gene Panels

Background

Targeted gene panels allow for the simultaneous examination of multiple genes in which variants are known to be associated with a specific PIDD or may more broadly encompass a large number of genes known to be associated with PIDDs affecting phagocytes, T cells, B cells, or innate immunity or causing either combined immune deficiency or autoinflammatory disease.[29] For example, when a specific immune defect is identified through a suggestive history and/or an abnormal functional assay (*e.g.*, a history of infection with a catalase positive organism and an abnormal neutrophil respiratory burst, suggesting chronic granulomatous disease [CGD]), TGPs are useful for confirming a specific molecular diagnosis and identifying the genotype. In many such cases, a clinical diagnosis may be suspected, but multiple genes are known to produce the disease (*e.g.*, *CYBA*, *CYBB*, *NCF1*, *NCF2*, and *NCF4*), and identification of the specific genetic defect can impact clinical care decisions. With the development of high throughput sequencing technology, the simultaneous examination of multiple genes permits a more rapid and often less expensive genetic examination compared to SS of single genes in a sequential manner.

Methods

At present, several methods are used for TGPs. These approaches include next generation sequencing of a large panel of genes and focused analysis of whole exome sequencing. For some specific phenotypes (*e.g.*, SCID or periodic fever syndrome panels), small lists of genes are being offered as SS panels. In the NGS-based large panel sequencing strategies, preselected exonic and even intronic regions known to cause the disorder of interest are enriched for sequencing. Older techniques, such as

multiplex PCR amplification, have been used to enrich for specific target regions.[30] Many of these approaches are nevertheless being replaced[31] clinically by hybridization-based methods using DNA or cDNA fragments captured by either a microchip or labeled beads.

In the NGS microchip assay, selected exonic and intronic regions of each targeted gene are screened using capture assays, either a microarray or other chip-based technique, followed by sequencing of the captured DNA. Briefly, human DNA or RNA is extracted from whole blood. If RNA extraction is performed, it is followed by cDNA synthesis. Genomic DNA or cDNA is sheared using restriction enzymes or sonication to create DNA fragments. The ends of the fragments are bound to a linker, which provides a priming site for PCR amplification. This pool of fragments is then hybridized to a microarray chip to enrich the sample for the desired gene regions. After the bound fragments are eluted from the chip, the oligonucleotides of interest are further enriched using ligation-mediated PCR.[32] Exons are amplified using a custom set of primers that cover the exonic region plus a set number of base pairs within the intronic regions bracketing each exon of interest. This custom design improves the sensitivity of the assay, particularly for known pathogenic intronic variants that have been established to cause PIDDs.[33] Various massively parallel sequencing methods may then be applied.

The second NGS method proceeds in similar fashion to the first except for the use of biotinylated beads with oligonucleotide probes that bind to the targets of interest. After selected DNA fragments bind to the beads, they are eluted using streptavidin-conjugated magnetic beads, thus enriching that DNA fragment mix for the regions of interest. The next steps are performed as for the first method, with PCR amplification of the fragments followed by sequencing.[34]

Methods for massively parallel sequencing are described in greater detail under *whole exome sequencing*. TGP arrays may target anywhere from 6 to over 400 different genes. After sequencing, the relevance of the identified variants to the underlying disease must be further assessed.[35-37]

Strengths

TGPs have an advantage over individual gene sequencing in expediting the simultaneous examination of all the known relevant genes for a particular disorder or group of disorders. This ability has been extended to the creation of panels that can examine hundreds of genes associated with PIDDs.[29, 35, 36] Such testing provides results in a more cost-effective, efficient, and timely fashion compared to sequential SS of single genes or to WES or WGS. Compared to WES or WGS, TGPs usually have a greater read depth and increased coverage, which enhances the sensitivity of the assay. Importantly, since only relevant genes are examined, results are less likely to include secondary findings. Thus, TGPs reduce the work of data analysis.

Limitations

The primary limitations for TGPs are inherent to weaknesses associated with NGS (excluding WGS, for the most part). They are linked to the number of genes included in

the panel as well as the limits of sequencing for genes that contain pseudogenes (duplicated nonfunctional sequences) or genes that contain long, repetitive sequences. For example, TGPs for CGD sometimes do not include *NCF1*, which causes one form of autosomal recessive CGD, due to at least 2 pseudogenes within the genome.[38] In addition, differences in PCR amplification efficiency and cross hybridization between primers and target DNA can result in false positive and false negative results. Large CNVs, such as deletions or duplications that result in the loss or gain of an entire exon, and structural variants, including large insertions, translocations, or inversions, may not be detected reliably by TGPs or WES.[39] On the other hand, the greater read depth of TGPs can allow bioinformatic algorithms to identify CNVs.[40, 41] These algorithms are still being validated for clinical use.[42] Finally, although gene panels can be designed to detect known intronic variants, they are not primarily used for such purposes. Thus, pathogenic intronic variants may still be missed.

TGPs typically restrict examination to exons in genes that are known to cause PIDDs. The identification of novel genetic defects or defects that may not have been previously associated with a particular clinical or immunologic phenotype therefore remains limited by these tests. When a clear diagnosis is not suggested by the clinical phenotype or laboratory testing, a narrow panel containing a limited number of genes may fail to identify any disease-causing variants. WES or WGS would be expected to have greater utility in such cases.

Whole Exome Sequencing

Background

Whole exome sequencing refers to the sequencing of the coding regions (exons) of all known genes that comprise the genome. The human exome accounts for 1.5% of the human genome. While current sequencing platforms are unable to sequence 100% of the exome, exome sequencing is nevertheless often known as ‘whole’ exome sequencing.

Methodology

WES requires the preparation of a DNA library that is enriched in coding sequences. The process begins with isolation and fragmentation of genomic DNA followed by the addition of oligonucleotide adaptors. Adaptors serve several purposes during PCR amplification-based enrichment of adaptor-ligated DNA, including binding of fragments to the sequencing flow cell and barcoding, which enables mixing samples from several subjects into a single sequencing lane.

To avoid off-target sequencing of non-coding regions of the genome, the fragmented, adaptor-ligated DNA libraries require an additional positive selection capture step. Modern capture platforms use biotinylated DNA or RNA baits, which hybridize to complementary sequences contained within the exome. Ideally, all parts of the exome are captured equally, but in reality, enrichment is uneven and depends upon which commercial capture platform is used.[43] Available products differ in their performance characteristics, including target-gene enrichment efficiency, single nucleotide variant (SNV) detection sensitivity, and insertion/deletion sensitivity.[44]

Massively parallel sequencing of bar-coded fragments proceeds identically in libraries prepared for WES or WGS. Sequencing reads are mapped to the human reference genome, and variants are called when the identity of a nucleotide differs from the consensus identity. The confidence that a variant has been correctly identified ultimately depends upon the number of overlapping sequencing reads at the variant-specific base position.[45] Read depth can also be used to approximate CNVs, although with less reliability compared to other methods.[46] Whenever possible, parental exomes should be analyzed alongside the exome of the index patient (creating a trio) to segregate the patterns of inheritance or alternatively to identify *de novo* variants.

Strengths

WES carries several distinct advantages as a genetic testing platform. First, some studies suggest that up to 85% of known genetic changes with large effects on disease-related traits exist within the exome.[47] Selectively sequencing the exome therefore represents a high-yield, more cost-efficient diagnostic opportunity in comparison to WGS. A sequenced exome results in a fraction of the sequencing reads, bioinformatic analysis time, and digital storage space relative to a sequenced genome. Accordingly, the cost of WES is significantly less than WGS and has decreased substantially since its introduction.[48] Next, for primary diseases of the immune system, the utilization of WES allows for hypothesis-free discovery of novel disease-associated genes, as well as detection of novel variants in known disease-associated genes.[49, 50] The ability to identify disease-causing variants in novel genes gives a clear advantage to WES over TGPs. In previously undiagnosed genetic disorders in a PIDD cohort, the WES approach can provide a genetic diagnosis in up to 40% of probands.[5] Third, the wide utility of WES in both research and commercial applications has resulted in improved methodology and confidence with reporting of results. Current WES platforms allow for deeper and broader coverage, which translates to increased confidence in variant calls. In addition, increased coverage and an expanded availability of 'normal' reference genomes for comparison improve the interpretation of large numbers of variants that may or may not have pathogenic potential. Finally, WES offers improved chances of diagnostic success in comparison to SS methods and TGP candidate gene approaches. If sequential SS of multiple genes is required, WES offers a significant savings of time, financial resources, and valuable genetic material from patients with potentially rare diseases.

Limitations

Clinical immunologists should be mindful that while WES has revolutionized the molecular genetics of Mendelian disorders, 50 to 75% of patients do not receive a genetic diagnosis after WES.[51] By design, WES covers only 1 to 2% of the genome, and while sequencing coverage of the exome continues to improve, coverage of coding regions of the genome through WES has not yet reached 100%. Early WES capture platforms lacked coverage of thousands of protein-coding exons, including dozens associated with monogenic disorders.[52] Although updated versions have demonstrated improved sensitivity, regions of uneven representation persist.[53] In addition to the bias introduced during exome capture platforms, additional distortions can be created by the

subsequent pre-sequencing DNA amplification steps that are related to typical PCR errors.[54] Accordingly, given the limitations of current technology, a "whole" exome should be considered only an approximate term.

Multiple reasons exist for poor sequencing coverage of areas throughout the exome and are shared with limitations inherent to SS and TGP tests (**Table 3**). These challenges include stretches of DNA with high G-C content, repetitive DNA regions (including trinucleotide repeats), and pseudogenes. Thus, presence of a strong correlation between a phenotype and specific known genetic disease but absence of a convincing genetic diagnosis by WES merits further evaluation of information concerning depth of coverage at a specific gene or locus, as well as variant quality scores. For example, PIDD genes known to have poor coverage in WES due to pseudogene interference include *IKBKG*, associated with nuclear factor-kappa B essential modulator deficiency, and *NCF1*, as previously discussed.[38, 55] If a specific gene generates strong suspicion as a molecular cause for the phenotype in a patient, sequencing coverage and read-depth may be improved through the use of a TGP or SS rather than WES.

Several other potential limitations of WES should be recognized. Coverage of exon-flanking intronic regions can vary by platform, and potential splice site and pathogenic intronic variants can be missed.[56] Sequencing errors in WES are also higher than other approaches. Furthermore, WES will not typically provide information about structural variants, such as large insertions or deletions, inversions, or translocations. CNVs may be inconsistently detected or reported. Other testing methods, such as CMA, should be used for detection of these defects.

Inherent to the WES approach, secondary findings and variants of uncertain significance (VUS) will be identified. The interpretation of VUS remains challenging and can raise ethical considerations regarding what and how results are reported to patients. As with all genetic techniques, the odds of diagnostic success using WES greatly improve if clinicians can provide upfront detailed reporting of the proband phenotype, phenotype the extended family members carefully, and then genotype each family member to determine if the variants cosegregate with the affected, rather than the unaffected, relatives.

Finally, the costs of WES are now largely incurred by time-intensive analysis of the many gene variants identified, and can be prohibitive. Nonetheless, in cases of diagnostic challenges and conditions with locus heterogeneity, WES often remains the sequencing modality of choice.

Whole Genome Sequencing

Background

WGS has the potential to identify known or novel variants in known or novel disease-associated genes in both exonic and intronic regions and has the ability to detect CNVs more reliably than WES.

Methods

The general principles of WGS are similar to WES with the exception of absence of an exome enrichment step. The process involves fragmenting genomic DNA, attaching linker sequences, and then massively parallel sequencing. The types of technologies used for WGS can be divided by their ability to read short (<1 kilobase pairs [kb]) versus long (>1 kb) sequences. The predominant platform for short-read sequencing uses sequence-by-synthesis, in which a polymerase is used to add nucleotides and generates a distinct signal with each nucleotide addition.[57] Pair-end sequences (*i.e.*, sequences from both ends of the template) are read, which increases the coverage. Platforms utilizing long-read sequencing can be divided into single molecule real-time sequencing and synthetic long-read sequencing. Single molecule real-time sequencing involves using either individual wells to detect incorporated nucleotides or measuring a change in an electrical current as the DNA passes through a pore.[58, 59] Amplification is not needed in single molecule real-time sequencing. Synthetic long-read sequencing is actually constructed from short-read sequences by using a barcoding system in the template preparation. Each of these technologies has its own advantages and disadvantages.

Strengths

A key strength of WGS involves its coverage of non-coding regions in addition to the coding regions that are obtained by WES. While the majority of disease-causing variants in PIDDs exist in coding regions, pathogenic intronic variants have been observed in PIDD-associated genes, such as *GATA2*, *IL7R*, *IL2RG*, *ZAP70, IKBKG*, and *DOCK8.*[56, 60-64] Structural variants, including the well-described inversion that disrupts *UNC13D*[65], can be missed by both WES and CMA but are detected by WGS. WGS may therefore reveal novel findings when WES is negative. Some PIDD patients with previously unknown defects have already been diagnosed using WGS. [66, 67]

WGS possesses several other important strengths. One is found in the lack of an enrichment step, which can introduce bias in the data. WGS data are more uniform across the whole genome and provide more consistent coverage of exonic sequences.[68, 69] Enhanced coverage with a uniform read-depth also improves the ability to detect CNVs, which is sometimes limited in WES. Furthermore, the long, continuous read sequences can allow for better resolution of difficult regions in the genome, such as repetitive sequences or copy-neutral structural variants, through *de novo* genome assembly. WGS also has a lower false-positive rate compared to WES.[52] Overall, WGS is suitable for Mendelian and complex trait identification, as well as sporadic phenotypes caused by *de novo* CNVs, single nucleotide variants (SNVs), or indels.[70]

Limitations

Cost presents a significant limitation of WGS. At this time, WGS is far more expensive than WES and TGPs. The cost of sequencing continues to decrease, and charges for WGS (excluding analysis) will likely become comparable to the technical fees for WES, especially since an additional cost for WES involves the enrichment kit. In fact, some institutions have reported the cost for WGS to be close to $1,000, and the goal of one company is to reduce it to $100 per genome.[71-74] Nonetheless, although these costs may decrease, the degree of third-party payor reimbursement for WGS remains

uncertain, and the out-of-pocket fees charged to families may vary widely. Furthermore, at this time, few options exist for obtaining clinical-grade WGS along with interpretation, but this barrier is anticipated to fade as the technology continues to improve.

Next, while WGS provides data concerning the entire genome, analyses of these data can be extremely time-consuming and difficult. Many identified variants have uncertain significance at this time, and bioinformatic tools and databases (*e.g.*, the genome Aggregation Database) are still being developed to assist with these analyses. Mechanistic and functional validation of potentially pathogenic variants remains necessary but may similarly prove resource intensive and technically challenging.

Finally, although WGS lacks an exon enrichment step, some bias can still be introduced in the different technologies used to generate WGS data. For example, the amplification step used in short-read sequencing (also used in WES) can generate bias in the data. On the other hand, single-molecule real-time sequencing lacks an amplification step. In all cases, bias can appear due to the fragmentation process of genomic DNA.

Interpretation Guidelines

Novel technologies, such as WES and WGS, are rapidly increasing the number of genes associated with PIDDs, and it has become clear that genetic testing should be used as an essential diagnostic tool in the evaluation of patients with suspected PIDDs.[1, 3, 23] Since an estimated 1 out of every 300 nucleotides on average within the human genome will be altered in any individual, the number of variants detected by genetic testing will increase proportionally with the number of bases sequenced. Most genetic variations do not produce a PIDD phenotype. Assessment of variant pathogenicity therefore becomes critical in order to formulate clinically actionable results. Despite advances in computing technology, this process still requires clinical expertise and judgment and cannot fully be automated at this time.

Criteria have been proposed for designation of pathogenicity of variants in single PIDD patients: (1) the variant must not occur in individuals who lack the clinical phenotype; (2) experimental studies must confirm that the variant (or 2 different variants within the same gene for compound heterozygosity) impairs, destroys, or alters the expression or function of the gene product; and (3) the causal relationship between the variant and clinical phenotype must be validated using a relevant biological tissue or animal model.[75] The first criterion continues to challenge clinical immunologists because genetic variations are known to exert incomplete penetrance in PIDDs. Moreover, fulfillment of the latter 2 criteria remains difficult for most clinicians or impractical for rapid medical decision-making.

The American College of Medical Genetics and Genomics (ACMG) has developed guidelines for the determination of pathogenicity of variants identified by genetic testing that may be more expeditiously applied.[76] In general, classification of variants occurs based upon several types of evidence, including collected population data, functional

and biological data, allelic distribution data, and variant-based computational data. All clinical genetics laboratories will have applied these guidelines in formulation of the clinical report. Even so, interpretation of the genetic data by the clinical provider often remains necessary, particularly concerning variants of uncertain significance. Overall, the ACMG guidelines may be difficult for clinical immunologists to apply and remain imperfect.[77] Thus, we provide focused concepts with relevance to patients with PIDDs in the following sections and in **Table 4** (worksheet provided in the Appendix).

Of note, the traditional terms, "mutation" and "polymorphism", are no longer recommended for descriptions of genetic changes, since they have no universally accepted definitions, and this outdated terminology can lead to incorrect assumptions about pathogenic and benign effects. Instead, both terms should be replaced by "variant" with the following modifiers: "pathogenic", "likely pathogenic", "uncertain significance", "likely benign", and "benign".[76] According to these guidelines, the descriptor "likely" means greater than 90% certainty, although a true quantitative assignment of variant certainty is usually not possible. Still, the expression, "mutation", often applies to changes to the actual protein molecules once they have been confirmed to affect function or expression.

Collected population data

Summary statement 1: *If the variant allele frequency in the general population is significantly higher than the prevalence of the PIDD, it is unlikely to represent the molecular etiology for the condition. A variant with a minor allele frequency ≥ 0.05 is likely to be benign.*

Summary statement 2: *Population and disease-specific databases should be used to provide evidence for or against pathogenicity for specific variants with recognition of the limitations of these databases.*

Summary statement 3: *Absence of a variant from population databases or a minor allele frequency below the expected carrier frequency for a recessive condition provides moderate evidence for pathogenicity of the variant. For most PIDDs, a minor allele frequency of 0.01 serves as an acceptable upper limit for consideration of pathogenicity.*

Clinicians must be familiar with two terms concerning associations between variant prevalence and pathogenicity. First, allele frequency (AF) is defined as the fraction of gene copies of a particular allele in a defined population (*e.g.*, AF = 0.01 indicates 1% of population dataset). Second, minor allele frequency (MAF) is defined as the incidence of less common alleles at a given locus. As an example, the report for the polymorphism "rs222" shows "MAF/MinorAlleleCount: G=0.249/542". This designation means that the minor allele with 'G' has a frequency of 24.9% in the database population and is observed 542 times.[5] MAF is used as a key factor within the ACMG classification scheme.[76]

Because PIDDs represent rare conditions, the phenotypes are more likely to be produced by rare variants than common variants within the general population.[75] An "allele frequency too high for the disorder" is considered strong evidence for a benign variant classification, yet no parameters exist to specify this upper limit.[76] Several

828 studies have tried to define MAF cutoffs for certain diseases.[78] This approach is less
829 feasible in PIDDs due to lack of population-based prevalences for most of the conditions
830 and the possibility of novel gene etiologies. Many variants can often be removed from
831 consideration by designating a MAF ≥ 0.05 as likely benign.[76, 79] Pathogenic variants
832 frequently exist at a MAF ≤ 0.01, aside from cases of well-defined founder variations
833 and one specific variant in *TYK2* (c.3310G>C:p.P1104A).[78, 80] This cutoff has been
834 used as a standard filter in several genetic testing studies in PIDD populations.[4, 23, 81-83]
835 A lower threshold can be achieved with an estimated disease prevalence. For example,
836 if autosomal recessive disease prevalence approximates 1 in 10^6, the disease-
837 associated variant of interest may be expected to carry a MAF ≤ 0.001 (*i.e.*, 10^{-3} x 10^{-3} =
838 10^{-6}).[83, 84]
839
840 Using a genetic hypothesis based on family history, clinical penetrance, and genetic
841 heterogeneity along with clinical and laboratory findings can help to further establish a
842 suitable MAF for variant pathogenicity.[83] For example, in autosomal dominant PIDDs
843 with high clinical penetrance, pathogenic variant MAFs should be very low or absent
844 within the general population.[75, 83] Meanwhile, MAFs for pathogenic variants in X-linked
845 or autosomal recessive PIDDs may be higher due to prevalence in unaffected
846 carriers.[75, 83]
847
848 Variant databases can be helpful for identifying MAFs in the general population or
849 underrepresented ethnicities, as well as in disease and non-disease states.[83] Multiple
850 public databases are available for assessing variant AFs.[75, 83] A list of commonly used
851 public databases is provided in **Table 5** (*n.b.*, this list is not exhaustive for all resources
852 available). Typically, 10,000 to 100,000 individuals are represented, depending upon
853 the database.[75] The genome Aggregation Database (gnomAD), National Heart, Lung,
854 and Blood Institute (NHLBI) Exome Sequencing Project (ESP), and Exome Aggregation
855 Consortium (ExAC) databases constitute the largest collections of data, consisting of
856 greater than 120,000, 100,000 and 60,000 individuals represented across multiple
857 ethnicities, respectively. Of note, public databases may not contain unique data: the
858 ExAC database, for example, contains some ESP data. The National Center for
859 Biotechnology Information (NCBI) offers the Variation Viewer (**Table 5**) to review MAFs
860 at a locus in ESP, ExAC, and 1000 Genomes project simultaneously. Population
861 databases are useful for assessing the frequencies of variants in large populations.
862 Disease-specific databases contain variants observed in patients with disease and an
863 assessment of the variant pathogenicity. Both types of databases should be used with
864 caution when gathering information.
865
866 A couple of caveats exist in the use of population databases. Depending on the source,
867 population databases reflect the frequencies of variants in not only healthy individuals
868 but also potentially affected cases. Because they can contain pathogenic variants, such
869 databases should be regarded for the patient population(s) sampled and whether
870 certain disease states are included. For example, the gnomAD database contains
871 cohorts of individuals with inflammatory bowel disease and malignancy, conditions that
872 can be associated with underlying PIDDs. Unfortunately, population databases do not
873 typically provide extensive clinical information. Furthermore, it remains important to

ensure that the ethnicity of the affected individual is well-represented within the queried population database. Advances in NGS have allowed for a variety of ethnicities to be represented in many databases, although some ethnicities may still be underrepresented. For example, the gnomAD database is enriched for data from Caucasian individuals. The Human Genome Variation Society (HGVS) lists multiple national databases (*e.g.*, UK10K [United Kingdom], deCODE [Iceland], African Genome Variation Project [sub-Saharan Africa], and so forth) but is not exhaustive for all NGS efforts (**Table 5**).[85] As an additional resource, some private databases generated from in-house data can be helpful for assessing ethnicities that are underrepresented in public databases.[23, 75]

Disease-specific databases must also be interrogated with caution. These databases can contain variants that are not classified correctly due to incorrect assumptions or assertions, since primary review of evidence may not occur.[23] One example is found in the HGMD database: a reported pathogenic *WAS* variant (exon 10 c.995T>C, NM_000377) with a low MAF is likely benign, since 115 hemizygous males carry this variant in the ExAC database.[23] Thus, it becomes important to consider how pathogenicity was ascertained. For instance, the ClinVar database permits tracking of review status and hence transparency in curation quality;[76] multiple clinical labs, such as GeneDx, Invitae, and Illumina, submit variants to this database. The Online Mendelian Inheritance of Man (OMIM) database (**Table 5**) links to various variant databases for a specific gene and is manually curated.[86] HGVS captures many locus-specific databases or disease-specific databases (*e.g.*, for C9 deficiency or periodic fever syndromes). HGMD is a manually curated database that has both public and professional access, with paid access disclosing at least 25% more pathogenic variants than the public version.[86]

Several factors should therefore be considered in gauging pathogenicity of variants based upon population data (**Table 4**).[76] As discussed, a MAF excessive for the disorder can be considered as stand-alone or strong evidence that the variant is benign. A MAF in controls inconsistent with disease penetrance also provides strong evidence that a variant is benign. For example, large numbers of individuals carrying a variant in the homozygous or hemizygous state (or heterozygous state, if dominant) would argue against pathogenicity for that variant, although a very low number of such individuals should not completely exclude the variant from consideration, especially if the condition is not fully penetrant at an early age or if the disease trait is sex-limited or sex-influenced (*e.g.*, reduced disease penetrance in males with pathogenic *COPA* variants). Absence of the variant from a population database or MAF below the expected carrier frequency, if recessive, provides moderate evidence for pathogenicity. It should be mentioned that the ACMG designates strong evidence for pathogenicity as prevalence in affected individuals increased over controls. Fulfillment of this criterion requires biostatistical analysis and comparison between an aggregated cohort of cases and appropriate controls. This measure is therefore generally not useful when individual PIDD patients are being examined. Finally, supporting evidence can be gathered from assertions from reputable sources, such as the disease-specific databases discussed.

Functional and biological data

Summary statement 4: *Functional validation should be used, when possible, to establish the pathogenicity of variants and their causal relationships with PIDDs.*

Summary statement 5: *Immunologic plausibility should be considered in determining variant pathogenicity and requires the expertise of a clinical immunologist.*

The ACMG has set parameters for the use of functional evidence to support pathogenicity.[76] For instance, well-established functional studies that demonstrate a deleterious effect of a variant toward the gene product provide strong evidence for pathogenicity, whereas absence of such an effect in similar studies strongly argues that the variant is benign. If the variant is a missense within a gene with a low frequency of benign missense variants or high frequency of pathologic missense variants, the evidence is considered supportive for pathogenicity. Indeed, ACMG recognition of the importance of functional validation aligns with the indispensable need for such studies to determine a causal relationship between a variant and PIDD, as proposed in the other PIDD-specific criteria.[75] In fact, it may be appropriate with functional validation within the context of these criteria to elevate the level of evidence for pathogenicity from "strong" to "very strong". Unfortunately, these necessary studies remain generally unavailable or impractical for expedient evaluation of most variants of uncertain significance.

Supportive evidence for pathogenicity of a variant as a potential explanation for PIDD should therefore be gained using the concept of immunologic plausibility. This approach incorporates what is known about the gene product and predicted impact of a variant upon its immunologic function. In fact, the ACMG guidelines already embrace the relevance of plausibility in stating that moderate evidence for pathogenicity is present if a variant is located within a mutational hot spot or a well-studied domain without benign variation.[76] Ability to interpret immunologic plausibility differs between various proprietary genotyping centers. Thus, clinical immunologists offer important expertise in this aspect of the analytic approach.

For example, one approach to evaluating variants uses a disease list based on known genes, networks of genes related to the immune system, or an extraction from a known database, such as OMIM. Most commercial pipelines for the interpretation of variants rely on the Human Phenotype Ontology (HPO)[87] to filter data based upon the phenotype of interest. HPO contains over 11,000 terms describing a key disease or condition phenotype. Over 1,000 terms are currently related to PIDDs. For comparison, nearly 5,000 terms have been applied to the musculoskeletal system. Thus, efforts to improve the HPO terms related to immune disorders are underway. The HPO terms are arranged in a hierarchical fashion such that more or less precision can be invoked. For instance, absence of respiratory burst is a subset of "Abnormality of the immune system". Each term is also assigned to one of the four ontologies: Phenotypic abnormality; Clinical modifier; Mortality/Aging; Frequency or Mode of inheritance. As an example of the importance of human expertise, a set of variants may be filtered on hypogammaglobulinemia and EBV infection as the key clinical features. Clinical immunologists have been trained to recognize that such a combination of features is

more central to *XIAP* deficiency, less common in *CTLA4* deficiency, and infrequent in CGD. Computer algorithms contain less ability to assess such likelihoods and typically score a gene as either associated or not with the phenotypic features. Using the current HPO scheme, X-linked lymphoproliferative disease and common variable immunodeficiency disease (CVID) would be associated with this duo of features; *CTLA4* deficiency does not yet appear. A clinical immunologist would recognize that *CTLA4* haploinsufficiency has been known to cause CVID and flag a *CTLA4* variant as potentially associated with the phenotype.[88] Thus, the use of HPO and similar filters can be useful for winnowing down the potential list of variants, but the best approaches still require a human to parse the list using knowledge of immunologic plausibility.

Several factors should be considered when evaluating immunologic plausibility of a variant. In general terms, the known function of the gene product in terms of cell biology, human physiology, and clinical disease must be understood. Many resources are publicly available for assisting with efforts to assemble and apprehend this information.

The first step involves gathering an understanding of the immunologic function of the gene product. This information is readily available from NCBI summaries (**Table 6**). Careful analysis of the published literature remains essential, and the NCBI PubMed database remains the largest publicly available compilation of indexed publication data. In addition, the Human Protein Atlas offers data concerning subcellular localization of the gene product, which can be particularly relevant to immune function.[89]

The next variable to consider in determining immunologic plausibility is the location of the variant within the gene and its subsequent likely effect on a specific domain or protein structure based on proximity. Domain-specific information remains essential, as disruption of critical motifs, such as nuclear localization signals or phosphorylation sites, can significantly alter protein function. For example, all pathogenic variants known to cause COPA syndrome are located within the WD40 domain of the coatomer protein complex subunit alpha protein, conferring plausibility for pathogenicity to unreported variants within the same region.[90] UniProt is the Universal Protein resource, which represents a central repository of protein data created by combining the Swiss-Prot, TrEMBL and PIR-PSD databases (**Table 6**).[91, 92] In addition to being a freely accessible database of protein sequences, it also provides biologic information about proteins derived from the published literature. UniProt is comprised of four major components, each optimized for different uses: UniProt Archive; UniProt Knowledgebase; UniProt Reference Clusters; and UniProt Metagenomic and Environmental Sequence Database. UniProt Knowledgebase is formed from two parts: 1) manually annotated records obtained from the literature and curator evaluated computational analysis (SwissProt) and 2) quality computationally analyzed but automatically annotated records (TrEMBL). The annotation consists of numerous categories of relevance, including function, taxonomy, subcellular location, pathology, biologically relevant domains, modifications, tissue specificity, expression, interaction, structure, sequence, and similarity to other proteins. UniProt has tools to help with analysis that include the basic local alignment search tool (BLAST), multiple sequence alignment tool (Align), retrieval and ID mapping

tool between databases (Retrieve/ID Mapping), and Peptide search that can be accessed through the various components described. Other helpful resources include the InterPro database and the Swiss-Model ExPASy webtool, which facilitates 3D predictive modeling (**Table 6**).

Another component of immunologic plausibility consists of assessing expression of the gene product within relevant tissues, especially immunologic cell types for patients with PIDDs. Multiple resources are available that provide information about tissue specific gene expression and how the gene variant of interest may affect this expression. These tools include the Genotype-Tissue Expression (GTEx) database, BioGPS portal, and Gene Expression Omnibus (GEO) repository (**Table 6**). The GTEx Project is composed of the GTEx database, the GTEx Portal, and dbGaP.[93] The database project studies genotypic variations and tissue gene expression of tissues collected from donors. GTEx has compiled data for about 50 types of tissues from a minimum of one donor each through low-post-mortem-interval autopsies or through transplant donors. The current database includes over 30,000 samples from 961 donors. GTEx raw data is available through the database of Genotypes and Phenotypes (dbGaP). Meanwhile, the GTEx Portal is an online interface that provides gene expression quantitative trait loci analysis (eQTL) for human genes. It also allows users to correlate genetic variations with gene expression. BioGPS is another tool that provides information about the tissue expression of the gene of interest. It is an online gene annotation portal that allows user customizability and extensibility. GEO is a separate database that archives and distributes gene expression data. Currently, the data are derived from a billion individual gene expression measurements from over 100 organisms. The data can be queried using NCBI Entrez GEO-Profiles, which yields a gene centric view of the data, or by using GEO BLAST. Finally, a number of resources have been developed to assist with integrated analysis of protein expression data in tissues, including the GeneCards Human Integrated Protein Expression Database and the Gene Expression Profiling Interactive Analysis web server[94] (**Table 6**).

Evidence for plausibility also comes from established associations between defects in the gene of interest and human disease conditions and from biochemical interactions between the affected molecule and products of known disease-causing genes. For example, a rare, novel VUS in *BTK* in a boy with agammaglobulinemia and no B cells has considerable evidence for pathogenic plausibility, since *BTK* deficiency is a recognized cause of X-linked agammaglobulinemia. Meanwhile, if a similar male patient is discovered to have an interesting VUS in *LYN* instead, although defects in this gene have not yet been demonstrated to cause human disease, support for immunologic plausibility for pathogenicity of the variant may come from the knowledge that Lyn interacts directly with Btk in B cells. In practice, a known connection between a gene of interest and human disease may lead to reporting of the VUS by the clinical genetics laboratory. The clinician must nevertheless determine whether the features of the patient sufficiently match the reported disease phenotype. Most associations between genetic conditions and human diseases are catalogued by OMIM. The PubMed database may need to be examined, as well, since curation of OMIM remains imperfect. For unknown or unreported human disease associations, comparison with

phenotypes in animal models may offer alternative evidence for immunologic plausibility. Resources include the Mouse Genome Informatics and Mutagenetix databases for mouse models (**Table 6**), whereas PubMed again carries the most extensive reporting of observations from experimental studies from a variety of organisms. Furthermore, interactions between the affected gene product and known disease-causing genes should be investigated in support of suspected pathogenicity. The Human Gene Connectome is a database that provides a set of shortest plausible biological proximities between all human genes.[95] The connectivity is described in terms of distance, route, and degree of separation between the genes. Each pair of genes may be connected directly or indirectly, or the genes may be entirely unconnected. The HGC server (HGCS) is an interactive, online interface that allows users to rank genes of interest in terms of biological proximity to core genes associated with a disease phenotype.[96] While HGCS is appropriate for monogenic diseases, other databases, such as STRING, FunCoup, and HumanNet, may be more appropriate for diseases where complex gene interactions are at play (**Table 6**).

These tools for assessment of immunologic plausibility are readily available to the clinician. They serve an integral role in facilitating rapid clinical decision making while awaiting collaborations with immunologic research laboratories to verify a deleterious effect of a variant through the necessary functional studies.

Allelic distribution data

Summary statement 6: *Pathogenic variants should cosegregate with an identified immunologic defect according to Mendelian patterns of inheritance.*

Summary statement 7: *Incomplete phenotypic penetrance may be considered when variant cosegregation with disease deviates from Mendelian expectations, but other potential genetic diagnoses must first be excluded. For PIDD-causing variants, the molecular and immunologic defect should be fully penetrant.*

Summary statement 8: *De novo variants should be examined closely for potential pathogenicity.*

Summary statement 9: *Biallelic pathogenic variants should be present in autosomal recessive conditions. A molecular diagnosis should not be assigned clinically if only a single heterozygous variant is identified in a gene for which PIDD solely occurs due to biallelic loss of function*.

Summary statement 10: *Digenic inheritance assertions remain hypothetical and should not be used to declare a genetic explanation in the absence of substantial functional evidence for pathogenicity*.

Mendelian patterns of inheritance govern most hereditary forms of PIDDs. These inheritance patterns are categorized as autosomal dominant, autosomal recessive, X-linked dominant, X-linked recessive, and mitochondrial.[23] Alleles refer to positions in a gene in which variations in genetic code may be present (wild type or variant). In autosomal dominant or X-linked dominant modes of inheritance, a single altered allele is disease causing. This phenotypic effect can be due to gene haploinsufficiency, gain-of-function, or dominant negative activity of the mutant gene product. Autosomal

recessive or X-linked recessive traits occur when both copies of a gene (or in the case of X-linked disease, the sole copy) are modified. Autosomal recessive disease is caused by homozygous or compound heterozygous pathogenic variants. In the setting of potential compound heterozygosity, in which both copies of a single gene harbor different pathogenic variants, it becomes imperative to confirm that the identified variants are *in trans* (on opposite chromosomes) rather than *in cis* (on the same chromosome).[97] *Cis* and *trans* configurations can sometimes be determined by identifying both variants on longer contiguous NGS reads, if the variants are closely spaced. Otherwise, assessment typically requires parental sequencing or sequencing of other family members. Importantly, although many forms of PIDD are familial, PIDDs caused by *de novo* pathogenic variants are also well described.[98-100] *De novo* variants can occur due to spontaneous genetic changes in either the parental ovum or sperm cell or in the subsequent fertilized egg. Identification of *de novo* variants requires parental sequencing. For all apparent *de novo* variants, the possibility of mosaicism must be considered.

Mosaicism results when 2 or more cell lineages with differing genetic material derived from a single zygote are present in an individual and can appear when either one of the distinct cell lineages carries a pathogenic variant or when an inherited variation is partially or fully corrected though reversion. Whereas parentally inherited variants will yield uniform results in sequencing of blood or tissue, the presence of mosaicism can result in an altered sequence in a minority of cells sequenced. Both types of mosaicism have the capacity to alter the phenotypes of PIDDs.[101-112] Somatic mosaicism may be challenging to identify in clinical sequencing assays alone and will not be detected if the mosaic cell population is not present in the sample tested.[113] In some cases, cell sorting may be necessary to detect and define a small mosaic cell population. Confirmation of somatic mosaicism in affected individuals has important implications for genetic counseling purposes, as *de novo* germline mutations can be potentially transmitted to offspring, whereas somatic variants can only be transmitted if they are present in the germline. Of note, gonadal mosaicism in a parent can explain the presence of an apparent *de novo* variant in multiple siblings but absence in either parental exome. An example of PIDD-causing somatic mosaicism includes *FAS* variants that produce autoimmune lymphoproliferative syndrome (ALPS).[114] Reversion variants, on the other hand, represent changes in genetic material that further modify a previously mutated gene product.[115] These variants can occur in the original altered codon, or they can emerge elsewhere in the affected gene and may take the form of a nucleotide replacement, indel, or a larger structural change in the gene.[116] Persistence and expansion of cells with reverted changes depends on the characteristics of the original revertant cell. Reversions in stem cells or early progenitor cells may be more likely to persist. Inherited pathogenic variants that impact the survival of lymphocytes tend to display greater selective pressure for revertant changes, as productive reversions often provide a survival advantage over diseased cells. In very rare cases, reversions in hematopoietic stem cells or early lymphocyte progenitors can be curative.[117]

Evaluation of allelic distribution constitutes a critical component of the determination of variant pathogenicity (**Table 4**). A careful family history must be obtained, and a pedigree should be constructed. Although a genetic hypothesis may be suspected from these exercises, all genetic hypotheses must still be considered and tested. Pathogenicity should be highly suspected for *de novo* variants: in the presence of confirmed paternity and maternity, evidence is considered strong, whereas absence of confirmation lowers the strength of evidence to "moderate". For potentially compound heterozygous variants, *trans* configuration should be regarded as moderate evidence for pathogenicity, while *cis* configuration argues that the variant may be benign. Appropriate genotypic cosegregation with disease phenotype lends support for pathogenicity. This support increases as the number of family members tested multiplies, especially if a rigorous statistical analysis (*e.g.*, Bayesian analysis) is performed.[118, 119] Distant relatives should be included as much as possible, as they are less likely to have both the disease and the variant by chance than first degree relatives. On the other hand, the ACMG guidelines state that "nonsegregation with disease" strongly argues that a variant is benign.[76] This assertion remains in place for absence of any genotype to phenotype correlation. For PIDDs, though, the molecular or immunologic defect must be considered separately from the clinical phenotype. For pathogenic variants, the molecular and immunologic defect should be fully penetrant.[75] In terms of clinical phenotype, on the other hand, the standard should be rephrased as "inappropriate segregation with disease", since incomplete penetrance is known to alter segregation patterns from Mendelian expectations in some PIDDs. Thus, although a pathogenic variant present in a single gene may be found in multiple family members or persons, expression of clinical disease can depend upon other genetic or external factors, leading to manifestation in only certain individuals. When some individuals who carry a pathogenic variant do not manifest signs or symptoms of a disease, incomplete penetrance is said to occur. Variations in penetrance can be more common in but are not limited to disorders of innate immunity (*e.g.*, defects in *IL12RB1*, *TLR3*, *UNC93B1*, *TIRAP*, *IFIH1*, and *IFNGR1*).[120-125] Altered penetrance is also prevalent in defects of immune dysregulation (*e.g.*, *FAS and CTLA4*)[126-128] and autoinflammation (*e.g.*, *COPA*).[90] Incomplete penetrance may be considered as an explanation in the absence of expected genotypic cosegregation with disease phenotype but should remain a hypothesis to be tested when other potential genetic diagnoses have been excluded.

Several factors can lead to incomplete penetrance of clinical disease. First, penetrance may be influenced by environmental circumstances (including range of encountered pathogens or use of prophylactic antimicrobials), co-inheritance of modifier genes, or epigenetic factors.[129, 130] Clinical testing for modifying and epigenetic elements is not currently recommended, as insufficient data exist to support broad interpretation. For PIDDs in particular, exposure to necessary pathogens or immune provoking conditions remains a vital element. For example, in X-linked lymphoproliferative disease type 1, males who carry a pathogenic variant in *SH2D1A* may not manifest signs of disease until they encounter EBV. Because of the unpredictable effect of modifying genetic factors, all apparently unaffected individuals who carry the variant of interest must be examined carefully for the presence of mild disease. Next, absence of disease may be due to age-related factors. For instance, a male infant with a pathogenic variant in *BTK*

may not exhibit infectious susceptibility immediately after birth due to maternally derived antibodies. Conversely, patients with *IRAK4* and *MYD88* deficiencies are known to improve after early childhood.[131] Finally, reversions can account for incomplete expression of disease.

Lastly, in terms of allelic distribution data, a molecular diagnosis should not be assigned clinically if only a single heterozygous variant is identified in a gene for which PIDD solely occurs due to biallelic loss of function. For example, a patient with recurrent infections and a single pathogenic or likely pathogenic variant in *LRBA* should not be labeled as having *LRBA* deficiency until either convincing biochemical evidence exists for absent LRBA protein function or a second pathogenic variant in the gene is identified. Similarly, digenic inheritance models have been proposed in which each parent exhibits haploinsufficiency for a different gene product and remains unaffected, yet the affected offspring develops disease due to combined inheritance of the two haploinsufficiencies.[132] These assertions remain hypothetical and should not be used to declare a genetic explanation in the absence of substantial functional evidence for digenic pathogenicity. For instance, in a patient with combined immune deficiency who possesses single allelic variants in *DOCK8* (maternally inherited) and *CARMIL2* (paternally derived), current lack of evidence that combined haploinsufficiencies of these 2 gene products results in PIDD mandates that a more appropriate or likely genetic explanation be pursued.

Variant-based computational data

Summary statement 11: *Variants that result in loss of gene product expression carry very strong potential for pathogenicity and should be considered further.*

Summary statement 12: *A number of computational tools have been developed to assist with predicting the potential for variants to alter the function of resulting gene products, but this determination remains imprecise.*

Variants can also be characterized based upon the type of sequence change and its computationally predicted functional relevance. These data remain essential in the assessment of variant pathogenicity (**Table 4**).

In terms of sequence change types, variants can be categorized several different ways. First, the majority of coding variants can be described as missense (also known as nonsynonymous), which leads to an amino acid change, or '*silent*' (synonymous), in which the amino acid sequence remains the same. Although synonymous variants do not modify the protein sequence, they can affect the RNA sequence and can cause changes in the efficiency of transcription or translation or in RNA conformation. Second, although 10% of published pathogenic variants alter splicing, various predictions suggest that perhaps a third or more of disease-causing variants cause errors in splicing.[133] The best understood splice site variants are canonical splice donor variants, in which the alteration disrupts the critical dinucleotide at the 5´ end of an intron, and splice acceptor variants that change the conserved dinucleotide at the 3' end of an intron. Other intronic splice region variants can occur due to a change within

either approximately 3 to 5 bases of the canonical donor splice site or about 3 to 10 bases proximal to the canonical acceptor site. These variations include rare but well-defined splicing sequence variants that are located in the polypyrimidine tract at the 3' end of introns and the conserved adenine at the branch point, impairing spliceosome assembly in both situations. It has been estimated that about 10% of exonic disease-associated single nucleotide variants alter splicing by disrupting spliceosome assembly.[134] Furthermore, *de novo* and cryptic splice site variants can produce novel splice sites and include missense, synonymous, and intronic variants. For example, a patient has been reported with SCID due to a synonymous *JAK3* variant that results in defective splicing.[135] Of note, although deep intronic variants can cause cryptic splicing defects and disease, these intronic sites further from the coding exons are often not sequenced (except by WGS). Changes to exonic and intronic splicing enhancers and silencers as well as splicing factors and spliceosome components can further influence splicing. Third, null variants include nonsense and frameshift changes, the canonical ±1 or 2 splice site variants, alteration of the initiation codon, and single exon or multiexon deletions. The truncating variants typically lead to complete absence of the gene product by nonsense-mediated decay (NMD) of the altered transcript. Fourth, large CNVs or structural variants can significantly perturb protein function or expression. For example, deletion or duplication of an exon can produce a null variation if the resulting reading frame is shifted. Alternately, if the deleted exon encodes an autoinhibitory domain, gain of protein function may be observed.[136] The functional consequences of these variants therefore require individual assessment. Meanwhile, the impact of small in-frame indel variants remains very difficult to predict. These changes can introduce or remove critical modification residues (*e.g.*, phosphorylation, methylation, or glycosylation sites), alter the three dimensional structure of the protein, or disrupt an important protein domain (*e.g.*, p.A58del in Janus kinase 3)[137], such as an enzymatic active site. Finally, non-coding variants consist of variants within the 5'-untranslated region (UTR), 3'-UTR, introns, intergenic regions, and polyadenylation domain. Technically-speaking, they also include the splice site variants. Variants can sometimes be annotated as upstream or downstream if they fall just outside a gene boundary. The intronic and intergenic regions can encode important regulatory and non-coding RNA elements that modulate gene expression. Importantly, a variant detected in the genomic DNA can be coding in one transcript and non-coding in another due to alternative splicing. Alternative transcripts can be tissue- or cell-type specific.

Evaluation of variant type plays an important role in determination of variant pathogenicity (**Table 4**). Identification of null variants remains essential, as the only "very strong" evidence for pathogenicity comes from a predicted null variant in a gene for which loss of function causes disease.[76] Still, variants that result in the production of a termination codon within the final exon or within the last 50 to 55 base pairs of the penultimate exon must be examined carefully. These transcription products have the capacity to escape NMD, resulting in a truncated gene product rather than absence of expression. Prediction software has been developed to identify these variants (**Table 7**). If a nonsynonymous nucleotide change produces the same amino acid change as a confirmed pathogenic variant, strong evidence for pathogenicity is present (**Table 4**). For example, evidence for pathogenicity is present with a change from AAA (lysine) to

AAT (asparagine) if a change from AAA to AAC (also asparagine) at the same residue is known to be pathogenic. Otherwise, a novel missense change that impacts a residue that is known to be altered by another confirmed pathogenic missense variant provides only moderate evidence for pathogenicity. For instance, if a change from TCT (serine) to TAT (tyrosine) has been shown to be pathogenic, a change from TCT to TTT (phenylalanine) at the same amino acid might be similarly pathogenic.

Other variant-based evidence for or against pathogenicity comes predominantly from computationally predicted functional relevance (**Table 4**). Functionally, pathogenic variants can generally be categorized as either "loss of function" or "altered function". Most classical PIDDs are caused by pathogenic loss of function variants, but an increasing number of more recently discovered dominantly inherited PIDDs are caused by variants that alter protein function, most notably by producing gain of functional activity. In one report, about 71% of PIDDs were autosomal recessive, 6% were X-linked, and 23% were autosomal dominant. Of the dominant cases, approximately 70% (44 of 61) were caused by loss of function, and about 30% were caused by gain of function.[138] In fact, most functionally altering variants are heterozygous, whereas loss of gene product function can be produced by homozygous, compound heterozygous, or hemizygous variants or by heterozygous variants. In biallelic conditions, both copies of the gene are typically inactivated to cause disease. Nonetheless, a genetic diagnosis should not necessarily be excluded if one of the variants is not computationally predicted to be damaging, as human disease is known to occur only with a combination of a null variant in one allele and a hypomorphic, even common, variant in the other allele.[139] Meanwhile, single heterozygous loss of function variants can cause disease through haploinsufficiency or a dominant negative effect. Haploinsufficiency refers to the mechanism in which loss of one copy of a gene results in a phenotype. These genes are usually referred to as dosage-sensitive. Dominant negative variants result in an altered protein that inhibits the function of the normal wild type protein expressed from the other gene copy. Clinical immunologists should be aware that some PIDD genes, such as *STAT1*, *CARD11*, and *IRF8*, are associated with both dominant and recessive inheritance of pathogenic variants and interpret the presence of one or multiple variants in such genes accordingly.[140-143] Furthermore, distinct heterozygous pathogenic variants within the same gene can also produce completely different PIDDs through either loss of function or altered function (e.g., *STAT3* variants that result in hyper-IgE syndrome versus gain-of-function disease; *WAS* variants that cause Wiskott-Aldrich syndrome versus X-linked neutropenia). OMIM serves as an excellent resource for examining different Mendelian patterns and phenotypic presentations for pathogenic variants within a single gene. In terms of pathogenicity criteria, then, variants that are predicted to alter the length of the gene product provide moderate evidence for pathogenicity. Often, the relevance of truncating variants with regard to loss of function or altered function cannot be interpreted without biological testing. Other computational evidence predicting the likelihood of a damaging effect of the variant lends support for or against pathogenicity. These prediction algorithms center chiefly upon splice site and missense variants.

Splicing of mRNA is a complex process and remains difficult to predict. Most splice site variants currently known to cause disease result in exon skipping, formation of new exon-intron boundaries, or generation of new cryptic exons as a result of alterations at donor or acceptor sites. Large numbers of computational tools have been developed to predict the creation or loss of splice sites at the exonic or intronic level.[144-146] Computational predictions remain inaccurate because of the degeneracy of sequence motifs regulating splicing. In general, splicing tools demonstrate high sensitivity (over 90%) but low specificity (below 80%) for prediction of functional damage. Some of the most commonly used programs are listed in **Table 7**. Importantly, many of the different software tools share similar underlying biological assumptions. The results of two software tools therefore cannot necessarily be used as independent lines of evidence. Thus, RNA or protein analysis must still be performed in many situations to confirm the presence of a splicing defect. Traditionally, minigene splicing assays[147, 148] have served as a common method for analyzing the effect of predicted splice site variants, but the emergence of technologies such as RNA sequencing (RNA-Seq), may provide additional tools in the near future.[149]

Prediction of the functional consequences of missense variants includes multiple considerations. Physicochemical comparison of missense variants remains an important factor: missense variants that change a hydrophobic amino acid into another hydrophobic residue within a transmembrane region may not affect function, whereas a change into a charged residue may cause functional interference. Phylogenetic conservation should also be considered: if a position is non-variable across species, it is more likely that a variant introduced at the position will lead to functional consequences. These considerations are typically included within *in silico* damage prediction algorithms.

Many such algorithms have been developed to predict the impact of genetic variants (**Table 7**). Polymorphism Phenotyping (Polyphen) and Sorting Intolerant From Tolerant (SIFT) are two widely used metrics that predict the effect of missense mutations based on sequence homology and protein structure.[150, 151] More recently developed programs utilize a multi-disciplinary approach that integrates biochemical data, phylogenetic conservation, population allele frequencies, and machine learning. For example, MutationTaster combines sequence homology information with data from public databases, such as the 1000 Genomes Project, ENCODE, and ClinVar, to predict variant impact.[152] Meanwhile, the Combined Annotation-Dependent Depletion (CADD) method predicts the effect of any type of single nucleotide variant or indel.[153] The scoring of CADD is based on data that include the degree of conservation at the nucleotide and amino acid levels, transcriptional and regulatory data (such as proximity to splice sites or transcription factor binding sites), and protein-level data (such as PolyPhen and SIFT). CADD scores range from the least deleterious score of 1 to the most deleterious score of 99; a score of 15, which indicates that the variant is in the most deleterious 3% of all variants in the human genome, has been proposed as a benchmark for a deleterious variant.[153]

To improve the predictive ability of *in silico* methods, integrative approaches have been developed. These tools include the mutation significance cutoff server. The mutation significance cutoff for a given gene is determined by the lower limit of the confidence interval for the CADD, PolyPhen-2, or SIFT score of deleterious variants in public databases.[154] Furthermore, one study has proposed a combination of MutationTaster, M-CAP[155], and CADD to identify pathogenic variants with a true concordance rate of 93.6% and false concordance rate of only 0.4% with the ClinVar database.[156] The same study found that a combination of VEST3[157], REVEL[158], and MetaSVM[159], on the other hand, was most useful for recognizing benign variants (true concordance rate of 81.3% and false concordance rate of 2.8%).

Finally, algorithms have been developed to examine the tolerance of specific genes to variation with the premise that genes under strong purifying selection will have fewer variants carried by the general population over time. Usually, the likelihood for pathogenicity decreases for a variant in a gene that is known to harbor a significant number of non-pathogenic variants, especially of the null type. The gene damage index, for example, is based on the assumption that highly polymorphic genes in healthy individuals are unlikely to be associated with disease and is a computational approach useful for distinguishing false from true positives.[160] As another tool, the ExAC and gnomAD databases report constraint metrics, including the probability of loss of function intolerance (pLoF), that statistically compare numbers of observed missense and loss of function variants to expected values to help gauge gene damage tolerance.

Nonetheless, due to the complexity of protein expression and function, no single tool or combination of *in silico* prediction algorithms can definitively predict the biologic effect of a given variant.[161, 162] For example, a gene with a proximal nonsense variant may still be expressed using a downstream alternative start codon, as has been reported in cases of *NFKBIA* gain of function disease.[163] Alternatively, truncated protein products can retain partial function, as evidenced by a variant in *CORO1A,* encoding the actin-binding protein coronin-1A, that results in hypomorphic combined immunodeficiency rather than SCID.[164] Although variants affecting non-coding regions of the genome cause disease,[165] these types of variants remain a significant challenge for all *in silico* prediction algorithms, since the function of many non-coding regions remains unknown.[166] A few computational programs, such as CADD and Genome-Wide Annotation of VAriants (GWAVA), attempt to predict the impact of variants in non-coding regions using a combination of public variant databases and transcriptional and regulatory data.[153, 167] Finally, prediction of gain of function or altered function (as opposed to loss of function) remains difficult for many computational algorithms.

Other evidence

Summary statement 13: *Although the presence of a probable genetic explanation may reduce the likelihood that other genetic changes are pathogenic, the presence of a dual molecular diagnosis must not be excluded.*

Summary statement 14: *A variant in a gene strongly associated with the immunodeficient phenotype in the patient should be viewed with increased suspicion for*

pathogenicity.

Two other factors must be weighed when judging the pathogenicity of a variant. First, the presence of an alternate explanation for the immunologic phenotype or disease is considered supporting evidence that the variant may be benign. Even so, this determination should be taken with caution, as over 5% of PIDD patients have been observed to carry dual molecular diagnoses that produce a blended phenotype.[23] In fact, this phenomenon argues that all variants with pathogenic potential must be fully considered as part of the genetic diagnosis and that analysis should not stop once a single pathogenic variant has been identified as a potential molecular explanation. As a footnote, in order to recognize phenotypic expansions, variants in genes associated with non-immunologic diseases should not be excluded unless the immunologic characteristics of patients with these diseases have been well-studied and determined to be normal. On the other hand, it has proven very difficult to establish the combinatorial effect of pathogenic variants in 2 separate genes, and substantial evidence should be acquired before multiple molecular diagnoses are conferred.[168] Second, the presence of a phenotype or family history highly specific for the gene affected by the variant is normally considered supporting evidence for pathogenicity. In PIDD patients, the greatly characteristic nature of some phenotypes may increase this evidence from supporting to moderate. For example, a novel variant in *CYBB* in a male patient with an absent neutrophil respiratory burst and history of recurrent staphylococcal abscesses should be judged with increased suspicion for pathogenicity.

Summary of interpretation guidelines for assessment of variant pathogenicity

According to the ACMG, variants can be classified as “pathogenic”, “likely pathogenic”, “benign”, and “likely benign” based upon the evidence gathered (**Table 4**, Classification Scheme). Using this scheme, a **pathogenic** designation requires the following:

(A) 1 very strong plus at least 1 strong, 2 moderate, 1 moderate and 1 supporting, or 2 supporting; or
(B) at least 2 strong; or
(C) 1 strong plus at least 3 moderate, 2 moderate and 2 supporting, or 1 moderate and 4 supporting pathogenic criteria.

For **likely pathogenic** classification, one or more of the following conditions should be met:

(A) 1 very strong and 1 moderate; or
(B) 1 strong and 1 moderate; or
(C) 1 strong and 2 supporting; or
(D) 3 moderate; or
(E) 2 moderate and 2 supporting; or
(F) 1 moderate and 4 supporting pathogenic criteria.

For variants designated as **benign**, they should (A) exist at a MAF over 5% for a rare Mendelian disorder; or (B) carry 2 strong criteria for a benign interpretation. Finally, **likely benign** variants are classified based upon (A) 1 strong and 1 supporting; or (B) 2 supporting criteria for a benign impact.

In PIDD patients, the ACMG criteria may be too stringent if strictly applied in a universal manner. Because individuals with PIDDs in many situations represent unique cases, appropriate judgment from experts in clinical immunology must be exercised regarding interpretation. As such, some flexibility has been incorporated into **Table 4**. Examples include consideration of immunologic plausibility and support for placement of greater weight on functional evidence for pathogenicity.

Development of a multidisciplinary team that includes a medical geneticist or genetic counselor provides essential opportunities for securing an accurate diagnosis and is strongly advised. Geneticists and genetic counselors often have access to databases and tools that may be otherwise unavailable to or poorly recognized by non-geneticists. Their formal training also facilitates discernment of specific genetic mechanisms that may be relevant to the patient. The expertise provided by medical geneticists therefore remains essential for guiding variant interpretation and for focusing clinical immunology providers toward appropriate diagnoses and potential further investigations.

Use of Research and Collaboration

Diagnostic yields of NGS in patients with PIDDs range from 15 to 40%, depending on the patient population studied and the sequencing technology utilized.[79] When NGS fails to identify a definitive genetic diagnosis, an important role exists for deeper investigation on a research basis. Research laboratories can 1) perform mechanistic studies necessary to determine the biological impact of candidate variants and 2) perform supplementary genetic analyses when no plausible candidate variants are identified. These approaches are particularly important for patients with rare diseases.

Use of research and collaboration to confirm or exclude candidate variants

Measurement of protein expression and functional assessment of immune pathways can confirm or exclude a candidate variant.[75] When possible, these studies should be performed in Clinical Laboratory Improvement Amendments (CLIA)-certified clinical laboratories so that results can be included in the medical record and used in medical decision-making. Clinical laboratories are unfortunately insufficiently equipped to evaluate all candidate variants because testing is limited to relatively common or well-described PIDDs, and variants may yield unexpected functional results.[79, 169] In many cases, definitive variant analysis requires detailed mechanistic studies available only in research laboratories.

Researchers have the flexibility to tailor functional analyses to the pathways potentially impacted by a candidate variant. Flow cytometry can be used for quantification of specific cell populations, measurement of protein expression at the cell surface or in intracellular compartments, and assessment of protein phosphorylation or cytokine production in response to stimulation.[170] A diverse range of techniques such as immunoblotting, enzyme-linked immunosorbent assays, quantitative PCR, and confocal microscopy aid in dissecting the complex and sometimes unpredictable manifestations

of variants.[79, 171] Given this potential for unpredictability, "unbiased functional analysis" has been proposed as a tool to be used alongside genetic approaches.[172]

Interpretation of functional data in patient cells may be complicated by genetic variants other than the one being studied.[75, 79] Transgenic mouse models of a candidate variant can circumvent this issue, as wildtype and mutant mice from the same strain have otherwise identical genetic backgrounds. Such models are particularly useful for defining the contribution of genes with poorly understood roles in human immunity or in cases of unexpected phenotypes. Such was the case for transferrin receptor 1 (TfR1), a ubiquitously expressed cell surface receptor known to be essential for erythropoiesis.[173] A homozygous missense variant that impaired TfR1 internalization was identified in multiple family members with an immunodeficiency associated with poor T and B cell proliferation and hypogammaglobulinemia but normal erythroid development.[173] A mouse model engineered with the same amino acid substitution fully recapitulated the human phenotype, validating pathogenicity of the candidate variant. Further studies revealed an erythroid cell-specific accessory pathway for TfR1 endocytosis, explaining the normal erythroid phenotype in affected family members.

Use of research and collaboration in "unsolved" cases

Research studies are also valuable in instances in which no strong candidate variants are identified after genetic analysis. RNA-Seq, proteomics, and metabolomics platforms, for example, offer the capability of pointing toward a genetic defect through downstream pathway analyses. Some of these tests are available clinically yet largely remain experimental through collaboration due to lack of third-party payor reimbursement. While absence of a molecular diagnosis could be due to non-coding variants, multi-genic contributions, poor quality sequencing data, or a variety of other factors, the possibility that a pathogenic variant that was inadvertently missed or filtered out also cannot be excluded.[79] In such cases, reanalysis of clinical exome data in a research setting can improve the diagnostic yield.[81] In a recent study, researchers reanalyzed clinical WES data from 74 probands for whom initial analyses did not produce a definitive diagnosis. Evaluation was supplemented with WES data from additional family members, use of additional bioinformatics filters, and alternative interpretive analyses and database resources. These studies led to a molecular diagnosis in 36% of previously unsolved cases and a candidate variant in an additional 15%.[81]

Internet-based repositories of phenotypic and genetic data have emerged as an additional tool for unsolved cases. Starting in the early 2010s, a number of platforms were created that use genotype/phenotype matching algorithms to identify cases with similar clinical details that share disrupted genes.[174] For example, GeneMatcher (https://genematcher.org/) offers a valuable collaborative tool for identifying other potential cases worldwide that may share a similar phenotype linked to a specific variant or gene of interest.[175] Matchmaker Exchange (http://www.matchmakerexchange.org/) was founded in 2013 to combine many of these databases into a network with a common interface.[174] Clinicians and researchers submit de-identified genetic and phenotypic data so that cases with similar profiles can be discovered, building evidence

for disease causality. Examples of discoveries made through use of "matchmaking services" should add further support for this approach to genetic analysis whose potential has not yet been realized, particularly in the diagnosis of PIDD.

Conclusions

Genetic testing remains an essential component of the evaluation of patients with PIDDs. Available diagnostic modalities continue to grow, each with its own inherent advantages and limitations that must be considered during the assessment of results. Importantly, for PIDDs, functional validation of potential disease-causing genetic candidates remains critical for pathogenic designation. As these necessary studies are being performed, a number of tools and guidelines can be used to assist with evaluation of pathogenicity or harmlessness of various genetic variations. While accepted criteria must be applied firmly in order to avert inappropriate diagnoses, PIDD patients represent an exceptional, well-studied population for which not only genetic principles but also immunologic and cell biologic expertise must also be incorporated into these determinations. Altogether, these concepts emphasize the need for greater availability of a broad array of specialized clinical immunologic tests and for collaborative research to expedite and facilitate diagnostic interpretation of genetic test results in patients with PIDDs.

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Table 1. Genetic Terms and Definitions

Genetic Term	Definition
Absence of heterozygosity (AOH)	Lack of heterozygosity within a chromosomal region, sometimes used interchangeably with loss of heterozygosity (LOH), although the terms are not technically equivalent
Allele	One of two or more variant forms of a gene
Balanced translocation	Structural variant in which DNA has been exchanged between 2 chromosomes with no loss of genetic material
Canonical splice acceptor	Conserved AG dinucleotide at the 3' end of an intron
Canonical splice donor	Conserved GU dinucleotide at the 5' end of an intron
Cis configuration	Occurrence of two or more variants on the same chromosome
Compound heterozygous	Present such that each variant within the same gene produces a different genetic change on opposite chromosomes of a homologous chromosome pair
Consensus identity	Nucleotide at a specific genomic coordinate chosen by consensus to represent the most common base present within the general population at that location
Copy number variant (CNV)	Gain or loss of a region of DNA, resulting in deviation from the normal diploid state
Coverage	Percentage of targeted genomic regions sequenced to a minimum predefined read-depth
Cryptic splice site	Genomic sequence which, when transcribed into mRNA, contains the necessary elements for splicing, is not typically used as a splice site, but may become an active splice site due to a genetic change
De novo genome assembly	Creation of the genomic DNA sequence without use of a template
De novo variant	A genetic change present in the sequenced individual but not observed in either parent
Distal	Located toward the 3' end of a DNA or mRNA sequence or toward the C-terminus of a peptide sequence
Dominant	Exhibiting a trait when only one allele is altered
Dominant negative	Encoding a mutated gene product that inhibits the activity of the wild-type gene product
Enhancer	Genomic region that is bound by proteins to increase transcription of a gene
Exon	The protein-encoding portion of a gene
Frameshift variant	An insertion or deletion that shifts the triplet codon reading frame by 1 or 2 bases
Germline DNA	Genetic material derived from gamete cells
Haploinsufficient	Producing an altered phenotype at 50% gene product function due to complete loss of gene product function from one allele
Hemizygous	Located within a single allele for which a second allele is missing or not present, *e.g.*, X chromosome loci in 46,XY males
Heterozygous	Present on one chromosome such that the genetic sequence differs from the sequence on the other chromosome of a homologous pair
Homozygous	Present such that the genetic change is identical for both chromosomes of a homologous pair
Identity by descent	Sharing of identical DNA sequences between individuals due to inheritance from a common ancestor without recombination
Indel	A small insertion or deletion of DNA that results in a net change in the total number of nucleotides
Initiation codon	Messenger RNA sequence that signals beginning of translation
Intron	Intervening DNA sequence between exons
Inversion	Chromosomal defect in which a segment of DNA is present in reverse direction
Locus heterogeneity	Production of the same phenotype by pathogenic variants in different individual genes

Mendelian inheritance	Principle by which variation at a single genetic locus is tied to the trait of interest through Gregor Mendel's laws of segregation, independent assortment, and dominance
Mosaicism	Two or more cell lineages with differing genetic material derived from a single zygote
Nonsense variant	A genetic change that causes the intended amino acid to be replaced with a premature stop codon, also known as a "stopgain" variant
Nonsynonymous variant	A genetic change within a codon that substitutes one amino acid for another without altering the trinucleotide codon reading frame, also known as a "missense" variant
Proximal	Located toward the 5' end of a DNA or mRNA sequence or toward the N-terminus of a peptide sequence
Read-depth	Number of sequences computationally aligned to a reference sequence at a given genomic coordinate
Reading frame	Schema in which a DNA or RNA sequence is divided into consecutive series of three-nucleotide segments
Recessive	Exhibiting a trait only when both alleles are altered
Reversion	A change in the genetic material that further modifies or reverses the defect observed in a previously mutated gene product
Silencer	Genomic region that is bound by proteins to decrease transcription of a gene
Single nucleotide variant (SNV)	A genetic change in a single nucleotide
Splice site variant	A genetic change that modifies splicing of the messenger RNA product
Splicing branch point	Conserved adenine near the 3' end of an intron that facilitates spliceosome component binding
Structural variant	A large (greater than 50 bp) structural change in DNA that may be copy neutral (*e.g.*, an inversion) or a copy number variant (*e.g.*, deletion or duplication)
Synonymous variant	A genetic change within a codon that does not alter the amino acid sequence or trinucleotide codon reading frame
Trans configuration	Occurrence of two or more variants on opposite chromosomes
Uniparental disomy	Inheritance of both copies of a chromosome from the same parent
Variant	A genetic change from the reference or consensus sequence
Variant calling	Identification of the occurrence of a variant based upon a difference from the reference sequence
Variant cosegregation	Occurrence of a genetic condition, whether monoallelic or biallelic, with the phenotype of interest in different members of a family
X-linked	Exhibiting a trait associated with a genetic variant on the X chromosome

Table 2. Comparisons between genetic testing methods

	Coverage	Strengths	Limitations
Sanger sequencing	Single candidate gene	• Low cost • Fast result time • >99% accuracy • Fewer variants of uncertain significance • No secondary findings	• Limited coverage of sequences shared with pseudogenes • Poor or no detection of: o Mosaicism o Copy number and structural variants o Portions of the gene not included in the assay • Requires well-defined diagnosis and limited number of candidate genes • Variants/genes need to be updated with new discoveries • Per gene cost of sequencing is higher than other methods
Chromosomal microarray	Array-dependent, but usually the entire genome	• Detection of copy number variants • Detection of absence of heterozygosity • Tolerance for lower quality samples • Fast result time	• Poor or no detection of: o Rare single nucleotide variants o Small duplications and deletions or chromosomal rearrangements that do not affect the nucleotide copy number o Low-level mosaicism • Detection of variants can depend upon resolution of the array • Copy number variants of uncertain significance
Targeted gene panel by next generation sequencing (NGS)	Multiple candidate genes via NGS	• Simultaneous sequencing of multiple genes • Detection of mosaicism • Lower overall cost than WES or WGS • Fast result time • Few variants of uncertain significance • No secondary findings	• Poor coverage of sequences shared with pseudogenes • Limited detection of: o Copy number and structural variants o Non-targeted noncoding variants o Defects in genes excluded from the panel • Requires well-defined diagnosis and candidate genes

			• Variants/genes need to be updated with new discoveries • Inability to detect novel disease-causing genes
Whole exome sequencing (WES)	Nearly all exons/coding sequences (about 21,000 genes, or 1.5 % of the entire genome)	• "Unbiased" sequencing of coding regions of >90% of known genes • Detection of mosaicism • Discovery of new genes that cause disease • Lower cost than WGS	• Poor or limited coverage of: o G-C rich regions o Sequences shared with pseudogenes o Noncoding regions • Limited detection of copy number and structural variants • Variants of uncertain significance • Secondary findings • Higher cost than Sanger sequencing or targeted gene panels • Sometimes slower result time than Sanger sequencing or targeted gene panels • Higher sequencing error rate than Sanger sequencing or targeted gene panels
Whole genome sequencing (WGS)	Nearly all coding and non-coding regions (3.2 billion base pairs)	• "Unbiased" approach • Uniform read-depth • Identification of variants in *coding and noncoding* regions, including G-C rich regions and sequences shared with pseudogenes • Ability to detect copy number and structural variants • Discovery of new genes that cause disease	• **Many** variants of uncertain significance, including non-coding variants • Secondary findings • Highest cost • Slowest result time • Difficult long-term storage of immense quantity of data • Higher sequencing error rate than Sanger sequencing or targeted gene panels

Table 3. PIDD genes that may require extra genetic testing consideration

Cause	International Union of Immunological Societies (IUIS) Primary Immunodeficiency Disease Gene(s)
Incomplete (less than 100%) exonic coverage by whole exome sequencing platforms at minimum read-depth of 10X	**A** *AIRE, AP3D1, ATP6AP1* **B** *BCL11B* **C** *C4A, C4B, CARMIL2, CD8A* **E** *ERCC6L2* **I** *IKBKG, IRAK1* **M** *MALT1* **N** *NCF1, NFAT5* **P** *PEPD, PRKDC* **R** *RBCK1, RMRP, RNU4ATAC* **S** *SLC29A3* **T** *TBX1, TPP2* **U** *UNC93B1, USP18*
Pathogenic intronic variants	*ATM, BTK, CYBB, DCLRE1C, DOCK8, GATA2, IL2RG, IKBKG, IRAK4, ITGB2, JAK3, LRBA, SKIV2L, UNC13D*
Pathogenic 5'-UTR variants	*RPSA*
Pathogenic 3'-UTR variants	*IL2RG, LAMTOR2*
Pathogenic polyadenylation signal variants	*FOXP3, WAS*

Table 4. Evidence and criteria for determination of variant pathogenicity

	Benign Evidence		**Pathogenic Evidence**			
Type of Criteria	Strong	Supporting	Supporting	Moderate	Strong	Very Strong
Collected population data	MAF exceeds disease prevalence MAF in controls inconsistent with disease penetrance	Reputable source suggests variant is benign	Reputable source suggests variant is pathogenic	Absent or appropriately rare in population databases	Statistically higher prevalence in cases compared to controls	
Functional and biological data	Functional studies demonstrate no deleterious effect		Missense in gene with many pathogenic missense variants Likely functional impact in immunologically plausible gene candidate[a]	In mutational hot spot or domain with no known benign variation	Functionally validated to produce a deleterious effect[b]	
Allelic distribution data	Nonsegregation with immunologic phenotype Inappropriate segregation with disease[c]	In *cis* with a pathogenic variant in the same gene	Cosegregation with disease in affected family members	Increased cosegregation with disease in family members *De novo* (parents unconfirmed) In *trans* with a pathogenic variant in the same gene	Even greater cosegregation with disease in family members *De novo* (parents confirmed)	
Variant-based computational data		Computational evidence argues against impact on gene product	Computational evidence supports a deleterious effect on gene product	Novel missense change at same residue known to be affected by pathogenic missense change(s) Predicted to alter protein length	Same amino acid change as confirmed pathogenic variant	Predicted null variant in gene for which loss of function causes disease
Other		Alternate cause detected	Phenotype or family history highly specific for gene[d]			
Classification Scheme[e]						
Pathogenic					1	1
				2		1
			1	1		1
			2			1
					2	
				3	1	
			2	2	1	
			4		1	
Likely pathogenic				1		1
				1	1	
			2		1	
				3		
			2	2		
			4	1		
Benign	1 or 2[f]					
Likely benign	1	1				
		2				

Adapted from Richards S et al. *Genet Med* 2015;17:405-24. A variant is assessed for evidence of benign or pathogenic impact within the 5 evidence type categories listed in the left-most column. The variant is then assigned a pathogenic, likely pathogenic, benign, or likely benign designation based upon the total quantity of criteria met within a given column. For example, a variant that fulfills the criterion for "very strong" pathogenic evidence and at least 1 "strong" pathogenic evidence criterion in any other evidence type categories should be considered "pathogenic".

Footnotes: [a] Not an ACMG criterion; [b] Consider elevation to "very strong" level of evidence for pathogenicity, especially within the context of Casanova JL, et al. *J Exp Med* 2014;211:2137-49; [c] Rather than "nonsegregation"; [d] Consider elevation to "moderate" level of evidence for pathogenicity; [e] Numbers in boxes refer to minimum total counts of criteria types fulfilled for each level of evidence within the same column; [f] 1 if stand-alone evidence, 2 if strong evidence

Table 5. Population Databases

Database Name	Website	Information
Population Based		
ExAC/gnomAD	http://exac.broadinstitute.org/ http://gnomad.broadinstitute.org/	>60,000 exomes (ExAC) and >120,000 exomes and >15,000 genomes (gnomAD) from unrelated individuals sequenced as part of various disease-specific and population genetic studies
NHLBI GO Exome Sequencing Project (ESP) Exome Variant Server	http://evs.gs.washington.edu/EVS/	Project evaluating heart, lung and blood disorders using NGS with over 200,000 individuals from multiple well-phenotyped cohorts
1000 Genomes Project	http://www.internationalgenome.org/data	2,504 samples, about 500 samples from each of five continental ancestry groups
NCBI Variation Viewer	https://www.ncbi.nlm.nih.gov/variation/view/?q=CFH	Viewer allows to view MAFs reported in ESP, ExAC, and 1000 Genomes databases
dbSNP	https://www.ncbi.nlm.nih.gov/snp	NCBI repository for sequence variations
HGVS (National Databases)	http://www.hgvs.org/national-ethnic-variation-databases	Arab, Cypriot, Finnish, Hellenic, Israeli, Iranian, Lebanese, Singaporian, and Turkish populations
ALFRED: the ALelle FREquency Database	https://alfred.med.yale.edu/	Kidd Lab maintained database of AF in >700 populations
FindBase	http://www.findbase.org/	100,000 individuals from 92 populations
Database of Genomic Variants	http://dgv.tcag.ca/v106/app/home?ref=	Collection of copy number and structural variations within healthy individuals
Disease Specific		
ClinVar	https://www.ncbi.nlm.nih.gov/clinvar/	Public archive of reports of relationships among human variations and phenotypes with supporting evidence
HGMD	http://www.hgmd.cf.ac.uk/ac/index.php	Collated archive of published genetic variants responsible for human inherited disease
OMIM	https://www.omim.org/	Database of human genes and genetic disorders
$Geno_2MP$	https://geno2mp.gs.washington.edu/Geno2MP/#/	Database of variants from exome sequencing data linked to phenotypic information from Mendelian gene discovery projects
HGVS (Disease Centered)	http://www.hgvs.org/disease-centered-central-mutation-databases	Listing of multiple disease specific registries [*e.g.*, INFEVERS (periodic fever syndromes registry)]
HGVS (Locus Specific)	http://www.hgvs.org/locus-specific-mutation-databases	Listing of multiple locus specific registries (e.g., *ADA* deficiency)
DECIPHER	https://decipher.sanger.ac.uk/	Public database of genomic information associated with specific patient data

Abbreviations: dbSNP: Single Nucleotide Polymorphism Database, ExAC: The Exome Aggregation Consortium, gnomAD: The Genome Aggregation Database, HGMD: Human Gene Mutation Database, HGVS: Human Genome Variation Society, NCBI: National Center for Biotechnology Information, OMIM: Online Mendelian Inheritance in Man.

Table 6. Resources for evaluating immunological plausibility

Resource	*Website*
Cell Biology	
Gene product function:	
NCBI	https://www.ncbi.nlm.nih.gov/gene/
PubMed	https://www.ncbi.nlm.nih.gov/pubmed/
GeneCards	http://www.genecards.org/
Human Protein Atlas	https://www.proteinatlas.org/
Domain-specific impact on gene product:	
Uniprot	http://www.uniprot.org/
InterPro	https://www.ebi.ac.uk/interpro/
Swiss-Model ExPASy	https://swissmodel.expasy.org/
Human Physiology	
Tissue expression:	
Genotype-Tissue Expression database	https://www.gtexportal.org/home/
BioGPS	http://biogps.org/#goto=welcome
Gene Expression Omnibus	https://www.ncbi.nlm.nih.gov/geo/
Human Integrated Protein Expression Database (GeneCards)	http://www.genecards.org/
Vertebrate Alternative Splicing and Transcription Data Base	http://vastdb.crg.eu/wiki/Main_Page
Gene Expression Profiling Interactive Analysis	http://gepia.cancer-pku.cn/
Clinical Disease Associations	
Known association with human disease:	
Online Mendelian Inheritance in Man	https://www.omim.org/
OMIM Explorer	https://omimexplorer.research.bcm.edu/
IUIS PIDD Catalogue	http://www.iuisonline.org/index.php?option=com_content&view=article&id=66&Itemid=71
Immunodeficiency Search	https://www.immunodeficiencysearch.com/
Mobile Resources	https://itunes.apple.com/us/app/pid-phenotypical-diagnosis/id1160729399?mt=8 https://play.google.com/store/apps/details?id=com.horiyasoft.pidclassification
Phenotype in animal models:	
Mouse Genome Informatics (mouse)	http://www.informatics.jax.org/
Mutagenetix (mouse)	https://mutagenetix.utsouthwestern.edu/
FlyBase (*Drosophila*)	http://flybase.org/
Model organism Aggregated Resources for Rare Variant ExpLoration	http://marrvel.org/
Interactions with known disease-causing genes:	
Human Gene Connectome Server	http://hgc.rockefeller.edu/index.php
String	https://string-db.org/
FunCoup	http://funcoup.sbc.su.se
HumanNet	http://www.functionalnet.org/humannet/

Table 7. Prediction algorithm resources for variant interpretation

Resource	Website
NMD Prediction	
NMD Prediction Tool	https://nmdpredictions.shinyapps.io/shiny/
Splicing Prediction	
FSPLICE	http://www.softberry.com/berry.phtml?topic=fsplice&group=programs&subgroup=gfind
GeneSplicer	http://www.cbcb.umd.edu/software/GeneSplicer/gene_spl.shtml
Human Splicing Finder	http://www.umd.be/HSF3/
MaxEntScan	http://genes.mit.edu/burgelab/maxent/Xmaxentscan_scoreseq.html
MutPred Splice	http://www.mutdb.org/mutpredsplice/submit.htm
NetGene2	http://www.cbs.dtu.dk/services/NetGene2
NNSplice	http://www.fruitfly.org/seq_tools/splice.html
PESX	http://cubio.biology.columbia.edu/pesx/pesx/
SKIPPY	https://research.nhgri.nih.gov/skippy/index.shtml
Spliceman	http://fairbrother.biomed.brown.edu/spliceman/index.cgi
Missense Prediction	
Align GVGD	http://agvgd.iarc.fr/agvgd_input.php
CADD	http://cadd.gs.washington.edu/
Condel	http://bg.upf.edu/fannsdb/help/condel.html
ConSurf	http://consurftest.tau.ac.il
DANN	https://cbcl.ics.uci.edu/public_data/DANN/
EA	http://mammoth.bcm.tmc.edu/uea/hEAt.html
Eigen	http://www.columbia.edu/~ii2135/eigen.html
FATHMM	http://fathmm.biocompute.org.uk/
GenoCanyon	http://genocanyon.med.yale.edu/GenoCanyon
GERP++	http://mendel.stanford.edu/SidowLab/downloads/gerp/
GWAVA	https://www.sanger.ac.uk/sanger/StatGen_Gwava
hEAt	http://mammoth.bcm.tmc.edu/uea/hEAt.html
integrated_fitCons	http://compgen.bscb.cornell.edu/fitCons/
LRT	http://www.genetics.wustl.edu/jflab/lrt_query.html
MAPP	http://mendel.stanford.edu/SidowLab/downloads/MAPP/index.html
M-CAP	http://bejerano.stanford.edu/mcap/
MetaLR	https://sites.google.com/site/jpopgen/dbNSFP
MetaSVM	https://sites.google.com/site/jpopgen/dbNSFP
MutationAssessor	http://mutationassessor.org/
MutationTaster	http://www.mutationtaster.org/
MutPred	http://mutpred1.mutdb.org/
nsSNPAnalyzer	http://snpanalyzer.uthsc.edu
PANTHER	http://www.pantherdb.org/tools/csnpScoreForm.jsp
phastCons100way	http://compgen.cshl.edu/phast/index.php
PhD-SNP	http://snps.biofold.org/phd-snp/phd-snp.html
phyloP100way	http://compgen.cshl.edu/phast/index.php
Polyphen2	http://genetics.bwh.harvard.edu/pph2/
PROVEAN	http://provean.jcvi.org/index.php
REVEL	https://sites.google.com/site/**revelgenomics**/about
SIFT	http://sift.bii.a-star.edu.sg/sift-bin/contact.pl
SiPhy	http://www.broadinstitute.org/mammals/2x/siphy_hg19/
SNPs&GO	http://snps-and-go.biocomp.unibo.it/snps-and-go
VEST3	http://karchinlab.org/apps/appVest.html
Other Prediction Tools:	
Mutation Significance Cut-off	http://pec630.rockefeller.edu:8080/MSC/
Gene Damage Index	http://pec630.rockefeller.edu:8080/GDI/
gnomAD pLoF	http://gnomad.broadinstitute.org/