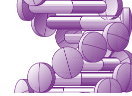

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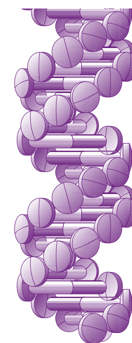

Sequencing the *CYP2D6* gene: from variant allele discovery to clinical pharmacogenetic testing

CYP2D6 is one of the most studied enzymes in the field of pharmacogenetics. The *CYP2D6* gene is highly polymorphic with over 100 catalogued star (*) alleles, and clinical *CYP2D6* testing is increasingly accessible and supported by practice guidelines. However, the degree of variation at the *CYP2D6* locus and homology with its pseudogenes make interrogating *CYP2D6* by short-read sequencing challenging. Moreover, accurate prediction of CYP2D6 metabolizer status necessitates analysis of duplicated alleles when an increased copy number is detected. These challenges have recently been overcome by long-read *CYP2D6* sequencing; however, such platforms are not widely available. This review highlights the genomic complexities of *CYP2D6*, current sequencing methods and the evolution of *CYP2D6* from allele discovery to clinical pharmacogenetic testing.

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CYP2D6: discovery & pharmacogenetic implications

The CYP450 superfamily of enzymes is directly involved in the oxidative metabolism of numerous drugs, xenobiotics and other endogenous substances. The subfamily member, CYP2D6 accounts for only approximately 1–4% of all hepatic CYP450 enzymes, yet it metabolizes approximately 25% of commonly prescribed drugs, making it one of the most studied enzymes in the field of pharmacogenetics [1–3]. Moreover, it is also implicated in approximately 25% of the medications currently listed on the US FDA pharmacogenomic biomarkers in drug-labeling table [4], including antiarrhythmics, anticancer agents, tricyclic antidepressants, serotonin-selective reuptake inhibitors, antiemetics, antihistamines, antipsychotics, antiviral agents, β-blockers and opioids.

The discovery of CYP2D6 began with the 1969 identification of the enzyme responsible for nortriptyline plasma concentration variability [5]. The gene was later cloned, including the discovery of its involvement in debrisoquine and sparteine metabolism and the roles of variant alleles on the recessive 'poor metabolizer' trait [6–8]. This enzyme was characterized as CYP2D6 and its gene localized to chromosome 22q13.1 [9–13], and sequencing studies later revealed the presence of two highly homologous neighboring pseudogenes (*CYP2D7* and *CYP2D8*) [12] (Figure 1). The *CYP2D6* gene is highly polymorphic, and its variant allele frequencies can vary among different ethnic and ancestral populations [1,14]. To date, there are more than 100 variant star (*) alleles catalogued by the Human CYP450 allele nomenclature database [15,16]. Based on an individual's *CYP2D6* genotype, four different CYP2D6

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metabolism phenotypes can be inferred: ultrarapid (UM), normal (previously referred to as 'extensive'), intermediate and poor (PM) metabolizer [1,17–18]. Importantly, individuals with the more extreme UM or PM phenotypes are at higher risks for increased toxicity or reduced efficacy depending on whether a drug is bioactivated or eliminated by CYP2D6.

The importance of *CYP2D6* in human drug metabolism and increasing evidence for potential clinical utility has prompted practice guidelines on *CYP2D6* for selected drugs by the Clinical Pharmacogenetics Implementation Consortium (CPIC) [19–22] and the Dutch Pharmacogenetics Working Group (DPWG) [23]. However, the *CYP2D6* gene is also notable for its complex molecular architecture and pseudogene homology, which together result in technical challenges with targeted genotyping, full gene sequencing and genotype interpretation. This review highlights the genomic complexities of *CYP2D6*, current genotyping and sequencing methods to interrogate *CYP2D6*, and the evolution of *CYP2D6* from allele discovery to phenotype prediction and clinical interpretation.

Genomic architecture of the *CYP2D6* locus

CYP2D6 gene locus & sequence variation

Capra *et al.* [24] estimate that CYP2D6 arose approximately 361.2 million years ago and that the *CYP2D* locus gene duplication event occurred in a common ancestor of Hominini and great apes [25]. The canonical RefSeq *CYP2D6* gene spans approximately 4400 nucleotides and includes 9 exons that are encoded on the minus strand at chromosome, 22q13.2. GENCODE release 25 recognizes three protein-coding transcript isoforms (ENST00000360608.5, ENST00000389970.3 and ENST00000359033.4) (Figure 2), one nonsense-mediated decay transcript (ENST00000360124.5), and one retained intron transcript (ENST00000488442.1). The 1000 Genomes Project identified more than 140 single-nucleotide variants and seven insertion/deletion variants in the *CYP2D6* exonic regions across approximately 2500 individuals from 26 different populations [26]. The high degree of variation in *CYP2D6* is further exemplified by the 680 PASS variants (i.e., those with a Variant Quality Score Recalibration score >99.95; 244 variants not passing quality filters) identified in >65,000 exomes by the Exome Aggregation Consortium (Supplementary Table 1) [27]. A number of repetitive and low-complexity sequences have also been annotated within and nearby *CYP2D6*, which give rise to the structural rearrangements characteristic of the *CYP2D* region, including the *CYP2D6* gene duplication [28].

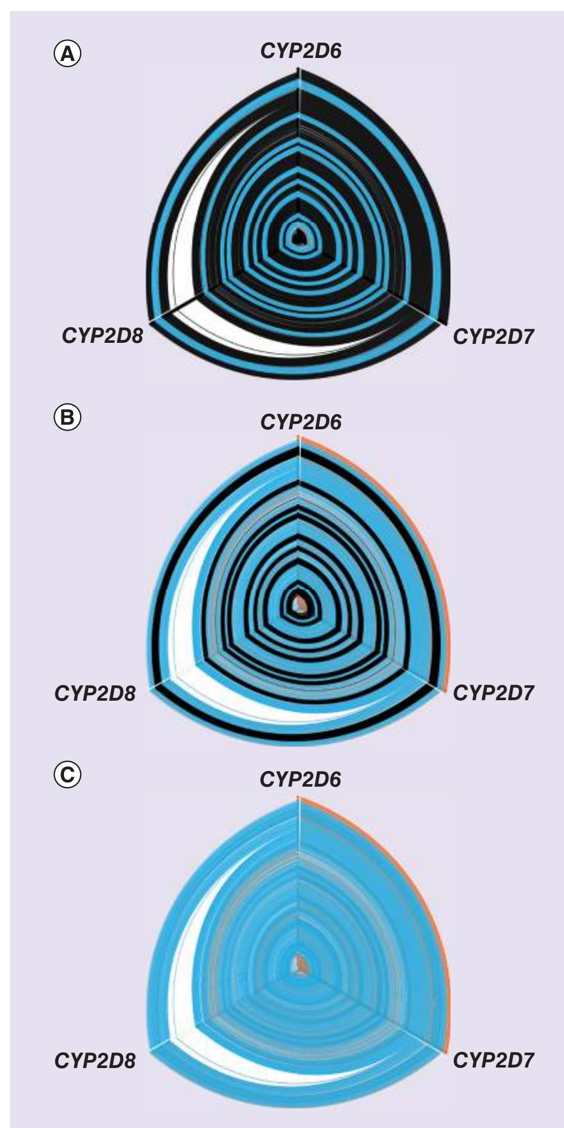

Figure 1. Hive panel displaying multiple sequence alignment of *CYP2D6*, *CYP2D7* and *CYP2D8*. The hive plot edges display sequence similarity between *CYP2D6*-*CYP2D7*, *CYP2D7*-*CYP2D8* and *CYP2D8*-*CYP2D6* (clockwise from top). Three principle axes (0, 120 and 240°) of the hive plots represent the nucleotide composition of the multiple sequence alignment for the indicated gene: **(A)** exonic sequences (intronic sequences shown in black), **(B)** intronic sequences (exonic sequences shown in black) and **(C)** exonic and intronic sequences. ClustalW was used to align the three genes (plus flanking 300 bp for each gene).
Blue: aligned sequence is identical across the three genes; orange: aligned sequences are identical between the labeled genes; white: sequence gaps created by inserted nucleotides unique to the principle axis colored white.For color figures please see http://www.futuremedicine.com/doi/full/10.2217/pgs-2017-0033

In addition to sequence variation in the *CYP2D6* coding region, noncoding regulatory variants have recently been studied in an effort to more

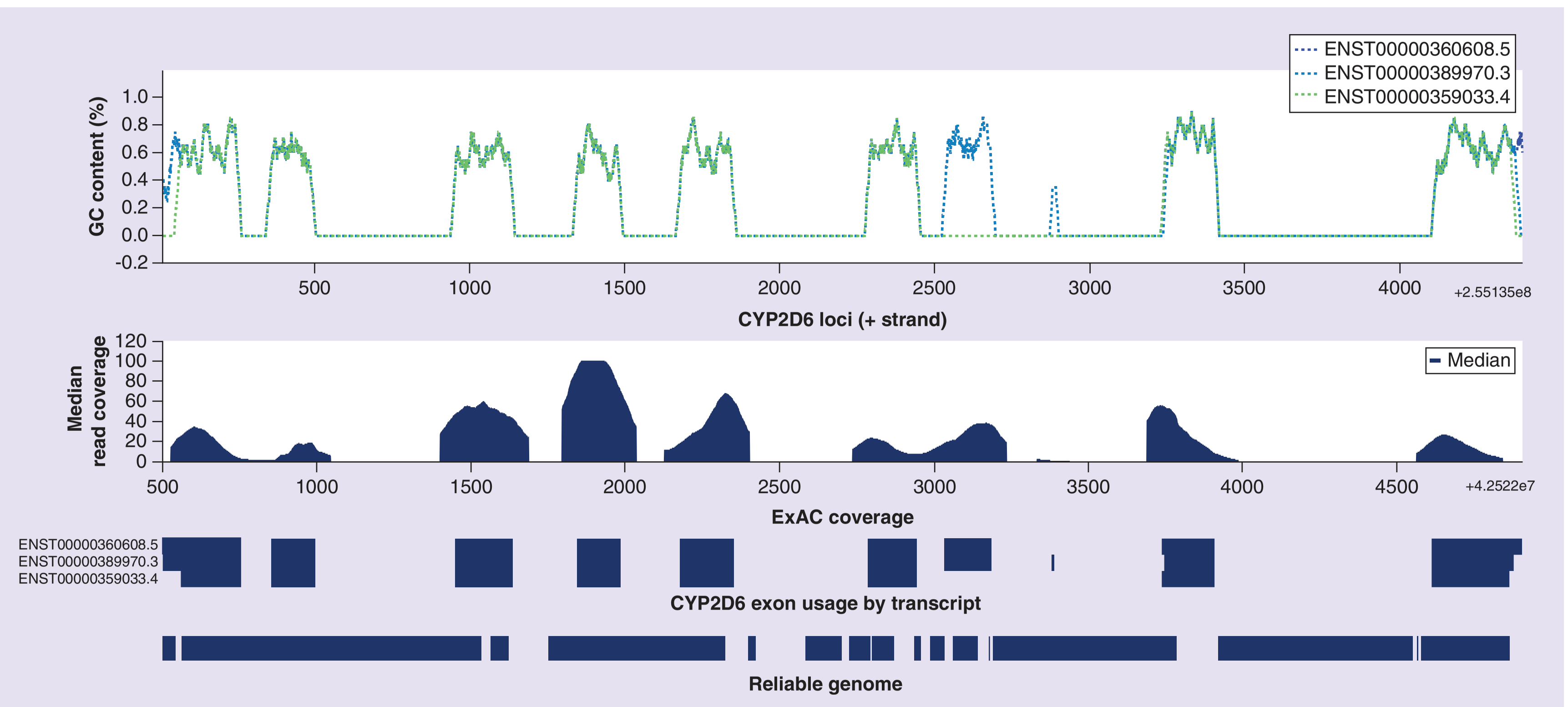

Figure 2. Illustration of the *CYP2D6* genomic region highlighting GC content across ten nucleotide-sliding windows of three functional *CYP2D6* transcript isoforms (*CYP2D6* loci: chr22, 42522500–42526907, GENCODE v19, hg19). Median read coverage of ExAC exomes; base pair resolution of three functional *CYP2D6* transcript isoforms; and base pair resolution of the intersection with 'reliable genome' intervals.
ExAc: Exome Aggregation Consortium.
Data taken from [29].

Table 1. Commercially available *CYP2D6* genotyping and sequencing tests.

Assay	Star (*) allele haplotypes interrogated	Company
xTAG CYP2D6 Kit v3	*2, *3, *4, *5, *6, *7, *8, *9, *10, *11, *15, *17, *29, *35, *41, *xN	Luminex[†]
Ion AmpliSeq Pharmacogenomics Research Panel	*2, *2A, *3, *4, *5, *6, *7, *8, *9, *10, *11, *12, *14, *15, *17, *20, *29, *35, *41, *29/*70, *xN	ThermoFisher/ Ion Torrent[‡]
DMET Plus	*2, *3, *4, *5, *6, *7, *8, *9, *10, *11, *12, 14A, *14B, *15, *17, *18, *19, *20, *21, *29, *38, *40, *41, *42, *44, *56A, *56B, *64	ThermoFisher/ Affymetrix
PharmacoScan	*2, *3, *4, *5, *6, *7, *8, *9, *10, *11, *12, *14A, *14B, *15, *17, *18, *19, *20, *21, *29, *38, *40, *41, *42, *44, *56A, *56B, *64, plus copy number variation	ThermoFisher/ Affymetrix
iPLEX CYP2D6 Panel	*1, (*2; *28; *32; *55; *59), (*2A; *31; *51), *2D, (*2L; *45B; *46), *2M, *3, *4, *4B, *4J, *4K, *4M, *4N;P, *53,*6, *6C, *7, *8, *9, (*10A; *37; *54), (*10B; *47; *49; *52; *72), *11, *12, *14A, *14B, *15, *17, *18, *19, *20, *21[a], *21B, *27, *29, *30, *34, *35, *36, *38, *39, *40, *41, *42, *44, *45A, *56A, *56B, *57, *58, *63, *64, *65, *68, *69, *70, *71, *82, *83, *84	Agena Bioscience
iPLEX PGx Pro Panel	*1A, (*2A; *31; *51), (*2L; *35; *71), *3, *4, *4M, *6, *7, *8, *9, (*10; *36; *37; *47; *49; *52; *54; *57; *65; *72), *11, *12, *14A, *14B, *15, *17, *18, *19, *20, *21A, *21B, *30, *40, *41, *42, *44, *56A, *56B, *58, *64, *69	Agena Bioscience
GenoChip Tamox	*3, *4, *5, *6, *7, *8, *9, *10, *11, *17, *29, *41, *xN	Akabiotech
INFINITI CYP450 2D6I	*2, *2A *3, *4, *5, *6, *7, *8, *9, *10, *12, *14, *17, *29, *41, *xN	AutoGenomics
VeraCode ADME Core Panel	*2A, *3, *4, *5, *6, *7, *8, *9, *10, *11, *12, *14, *15, *17, *18, *19, *20, *21, *38, *41, *42, *44, *56	Illumina
GenoChip CYP2D6	*3, *4, *5, *6, *7, *8, *9, *10, *11, *17, *29, *41, *xN	PharmGenomics

[†]The xTAG CYP2D6 Kit v3 assay is the only *CYP2D6* platform approved by the US FDA for *in vitro* diagnostic testing.
[‡]The Ion AmpliSeq Pharmacogenomics Research Panel is the only commercial sequencing assay presented in the table.

comprehensively inform CYP2D6 metabolism phenotype prediction. Genome-wide association studies have identified *cis*-regulation and more complex *trans*-regulation of CYP450 expression and activity, including noncoding variants implicated in CYP2D6 regulation [30]. In addition, the normal functional *CYP2D6*2* allele, which is largely believed to encode an enzyme with normal activity, has recently been scrutinized based on the identification of two linked variants within an enhancer region approximately 115 kb downstream from the gene that interact with the *CYP2D6* promoter through a long-range haplotype [31]. Although these regulatory variants require additional validation prior to incorporation into *CYP2D6* star (*) allele nomenclature, recent functional studies suggest that the rs5758550 enhancer variant is predictive of *CYP2D6* expression and may facilitate more precise CYP2D6 activity score and phenotype prediction, particularly among individuals who carry the common *CYP2D6*2* variants (i.e., rs16947 [2850C > T; p.Arg296Cys] and rs1135840 [4180G > C; p.Ser435Thr]) [31,32].

CYP2D6 copy number variation

It is estimated that approximately 12% of the human genome contains copy number variants (CNVs) ranging from <1 kb to several megabases [33], which are the result of either nonallelic homologous recombination, nonhomologous end joining, fork stalling and template switching, or microhomology-mediated break-induced replication [34]. *CYP2D6* CNVs include full-gene duplication and deletion, and complex rearrangements with *CYP2D7*, which can significantly influence the interpretation of *CYP2D6* genotyping, sequencing and phenotype prediction [35–38], particularly as not all duplication alleles encode functional enzymes (e.g., reduced function *CYP2D6*17xN* and **36xN*; no function *CYP2D6*4xN*). The frequencies of gene deletion (i.e., *CYP2D6*5*) and increased function duplication (e.g., **1xN*, **2xN*) alleles across worldwide populations range from approximately 2 to 6% and approximately 2 to 12%, respectively, with the *CYP2D6* duplication being more prevalent among individuals of Middle Eastern descent [14].

CYP2D6 gene conversion & tandem alleles

A common polymorphism in several *CYP2D6* star (*) alleles is an intron 1 *CYP2D7* gene conversion at nucleotide positions 214–245 of the M33388.1 GenBank reference sequence. Although this noncoding conversion does not affect *CYP2D6* transcription or translation, coding region conversion alleles have also been detected. Specifically, *CYP2D6*68A* is converted to *CYP2D7* from intron 1 onward, the **13* series all contain an exon 1 conversion [39], **82* contains an exon 2 conversion and the exon 9 conversion is found in **4N*, **36*, **57* and **83*.

Tandem *CYP2D6* alleles have two different copies of *CYP2D6* on a single chromosome, which interestingly are most commonly found together with *CYP2D6/2D7* conversion (or 'hybrid') alleles. These tandem alleles require thorough interrogation for proper detection, and the most notable example is the **36+*10* tandem allele that is prevalent among Asians [40]. The importance of detecting these reduced function alleles is underscored by the fact that nonspecific copy number assessment of these samples would identify a gene duplication; however, these tandem alleles are not consistent with the UM phenotype [41].

CYP2D6 interrogation & allele discovery

CYP2D6 Sanger sequencing & targeted genotyping

The *CYP2D6* gene and its pseudogenes were discovered by cloning and Sanger sequencing [12]; however, the subsequent availability of long-range PCR enabled Sanger sequencing of targeted exons across full-length *CYP2D6* amplicons (~2–7 kb) [42]. The long-range amplicon strategy can be coupled with nested mutation scanning techniques, such as, PCR-single strand conformation polymorphism (SSCP) and Sanger sequencing, which lead to the identification of many of the initial *CYP2D6* star (*) alleles [43]. Although still a gold-standard for many molecular genetics applications, Sanger sequencing is increasingly being replaced by high-throughput second-generation sequencing. However, the CYP Nomenclature Committee still requires that all novel *CYP2D6* variant alleles identified by high-throughput sequencing be confirmed by this classic technique.

Targeted genotyping is an inexpensive and common method to interrogate specific *CYP2D6* variants (Table 1 & Figure 3) [44]; however, the limitations include potentially missing clinically relevant variants that were not genotyped, structurally rearranged *CYP2D6* alleles and inaccurate star (*) allele haplotyping from the targeted variants. Although some *CYP2D6* star (*) alleles can be identified by a single functional variant (e.g., *CYP2D6*9* [2615_2617delAAG], rs5030656, p.Lys281del), many require more thorough haplotyping for identification. As noted, *CYP2D6* long-range amplicons can also be used as templates for multiplexed genotyping methods, such as, TaqMan, RFLP and high-resolution melting analyses and/or allele-specific primer extension bead arrays.

The detection of *CYP2D6* CNVs represents another challenge, but can be enabled by targeted genotyping using *CYP2D6*-specific quantitative real-time PCR. In addition, assessing copy number by targeted quantitative real-time PCR at both the 5′ and 3′ regions of *CYP2D6* can facilitate the identification of the *CYP2D6*36+*10* tandem allele, as the 3′′ *CYP2D7* gene conversion of **36* results in two detectable copies of the 5′ region (e.g., intron 2) and only one copy of the 3′ region (e.g., exon 9) on this chromosome [45].

CYP2D6 allele-specific interrogation

Allele-specific genotyping and sequencing techniques have been developed to more accurately characterize *CYP2D6* haplotypes by determining the *cis* and *trans* configurations of identified variants. For example, *CYP2D6*29* consists of four nonsynonymous variants in *cis* (1659G > A; 2850C > T; 3183G > A; 4180G > C), which encode an enzyme with reduced activity [46,47], one of these variants also occur on other star (*) allele haplotypes. In addition, individuals with a *CYP2D6*1/*4* diplotype (normal metabolizer phenotype) carry the defective 100C > T (p.Pro34Ser) and 1846G > A (c.506-1G > A) variants in *cis*; however, if these two variants are in *trans*, the diplotype would be *CYP2D6*4M/*10* (intermediate metabolizer phenotype) [48]. Allele-specific PCR directly amplifies specific haplotypes by anchoring PCR primers at specific variant nucleotides, which has been employed for both *CYP2D6* [49] and *CYP2C19* [50].

CYP2D6 second-generation short-read sequencing

Short-read sequencing produces read lengths of up to 300 bp and is predominantly derived from commercial platforms that use either light-based detection of fluorescently labeled nucleotides (Illumina) or electrical detection of proton release during nucleotide chain synthesis (Ion Torrent). Given the restrictions on read length for these platforms, the accuracy of short-read sequencing is reduced in genomic regions with low sequence complexity (e.g., tandem repeats, homopolymers), regions of dense polymorphism and/or repetitive elements (e.g., Alu, HERVs). Paired-end short-read sequencing, where reads are generated from both sides of a DNA fragment, can improve the accuracy of read mapping

and variant calling by increasing the uniqueness of sequence alignments. However, repetitive elements with lengths that exceed the mean length of the sequenced DNA fragments will compromise the accuracy and efficiency of the sequencing results. Current Illumina and Ion Torrent sequencing protocols yield read lengths of approximately 100 bp with per-base error rates <1% from 100 to 1000 bp DNA fragments [51].

The *CYP2D6* gene is a challenging region for short-read technologies due to repetitive elements, CNV, pseudogenes, and a high density of polymorphisms. A recent analysis of Illumina whole genome sequencing data partitioned the genome into regions of high and low reliability, which classified > 20% of *CYP2D6* as 'unreliable' (Figure 2) [29]. This is consistent with the 1000 Genomes Project assignment of the *CYP2D6* gene as 'inaccessible' [26]. Moreover, simulation studies using error-free standard paired-end *CYP2D6* reads, which are 100 bp from DNA fragments of 500 bp, have underscored the difficulty of uniquely assigning reads to exon two of *CYP2D6* versus *CYP2D7* or *CYP2D8* [52]. Longer read lengths and longer spacing resolve alignment ambiguity, but repetitive regions located at the upstream and downstream regions of *CYP2D6* still remain challenging. Single-end reads longer than 3 kb can eliminate multiple alignment, which indicates the potential advantage of long-read *CYP2D6* sequencing.

Both Illumina and Ion Torrent have high sequencing accuracy (>99 and >97%, respectively); however, the Ion Torrent chemistry has difficulty discriminating successive proton cleavage events in homopolymeric sequences [53], which are prevalent throughout *CYP2D6* (Supplementary Table 2). However, Ion Torrent does have a commercial amplicon short-read sequencing panel that includes *CYP2D6* (Table 1). As noted above, a principal issue for these short-read sequencing platforms when interrogated *CYP2D6* (and other genes with highly homologous pseudogenes) is the ability to specifically and accurately call variants in the targeted region. Commonly used target enrichment techniques (i.e., oligonucleotide capture, amplification) are likely not specific enough to anneal to *CYP2D6* and not *CYP2D7* or *CYP2D8*, and the subsequent short-read alignment, whether specifically enriched or not, may also misalign to *CYP2D7* and/or *CYP2D8*. In addition, the low-cycle amplification step commonly employed during Illumina sequencing library preparation may result in hybrid fragments between *CYP2D6* and *CYP2D7*/*CYP2D8*. All of these issues result in off-target short-read sequencing, which subsequently leads to skewed and potentially inaccurate *CYP2D6* variant calling. Illumina sequencing of the *CYP2D6* region by whole-genome, whole-exome, targeted capture using PGRNseq [54] and long-read Pacific Biosciences (PacBio) sequencing is illustrated in Figure 4.

CYP2D6 third-generation long-read sequencing

The difficulties with pseudogenes and CNVs that are inherent to short-read *CYP2D6* sequencing prompted the recent development of third-generation long-read *CYP2D6* sequencing using Oxford Nanopore and PacBio. Both platforms employ real-time sequencing but with different detection chemistries. The maximum read length recently achieved using Nanopore MinION was approximately 230 kb

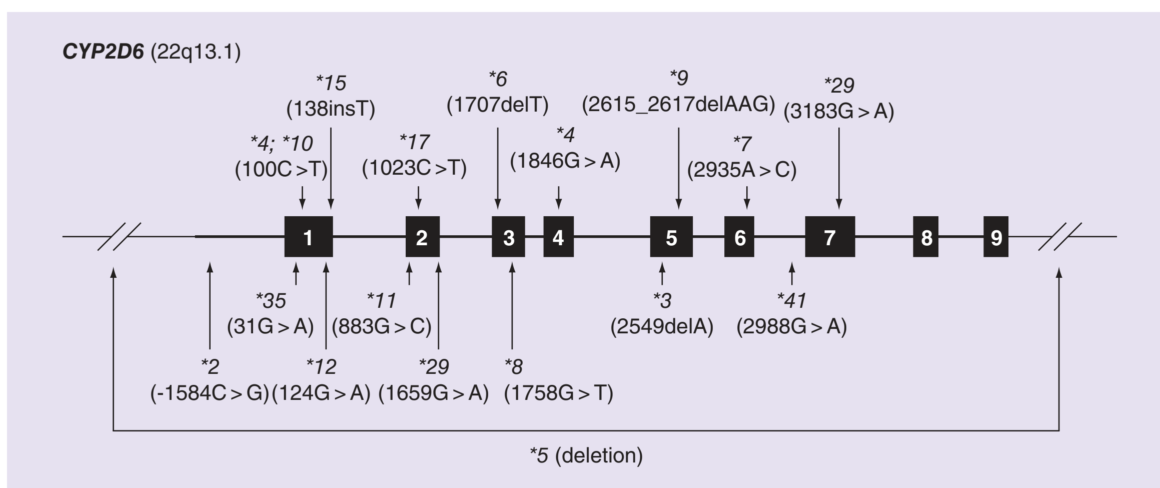

Figure 3. Gene diagram of *CYP2D6* (and chromosome cytoband location) highlighting the location of variant star (*) alleles that are commonly included in targeted genotyping assays, including the deletion allele (*5). Note that variants are denoted by their common nucleotide nomenclature from M33388.1 GenBank reference sequence.

Table 2. Example variant *CYP2D6* alleles and the 'activity score' framework. †

CYP2D6 diplotype		Total CYP2D6 activity score‡	Metabolizer phenotype§
Allele 1 (AS)	**Allele 2 (AS)**		
**1* (1)	**1xN* (2)	3	UM
**2* (1)†	**35* (1)	2	NM
**1* (1)	**4* (0)	1	NM
**4* (0)	**10* (0.5)	0.5	IM
**4* (0)	**7* (0)	0	PM

†Please note that the recently described *CYP2D6* upstream enhancer element may influence the expression of several star (*) allele haplotypes that include the common rs16947 (2850C > T) and rs1135840 (4180G > C) variants (e.g., **2, *41*), which could further refine the activity scores of these alleles.
‡The activity score values assigned to *CYP2D6* alleles are: 0 for **3, *4, *4xN, *5, *6, *7, *16, *36, *40, *42, *56B; 0.5 for *9, *10, *17, *29, *41, *45, *46; 1 for *1, *2, *35, *43, *45xN*; and 2 for **1xN, *2xN, *35xN.*
§The *CYP2D6* metabolizer phenotype classification based on the diplotype activity score is: >2 = UM, 1–2 = NM, 0.5 = IM and 0 = PM.
AS: Activity score; IM: Intermediate metabolizer; NM: Normal metabolizer; PM: Poor metabolizer; UM: Ultrarapid metabolizer.
Data taken from [31,32,66].

with an average of approximately 10.7 kb [55], and the latest P6-C4 chemistry from PacBio has a maximum read length of approximately 65 kb with an average of approximately 10–15 kb [56].

The recent Nanopore study sequenced approximately 5.0 kb *CYP2D6* amplicons on the MinION, and variant calling and haplotype determination using the 2D consensus reads [57]. The 1D reads were discarded due to their high error and short mapping rates. BLASR was used for alignment and variants were called if they were detected in a third of reads. *CYP2D6* haplotypes were inferred by interrogating nine targeted variants; however, the variant calling thresholds resulted in an ambiguous NA12878 *CYP2D6* diplotype with three distinct haplotypes (**2*, **3* and **4*), which the authors hypothesized was due to PCR template switching or sample contamination [57].

The recent PacBio study also sequenced approximately 5.0 kb *CYP2D6* amplicons using the RS II instrument, yet differed from the Nanopore study as it sequenced both 'downstream' and 'upstream' (i.e., duplicated) *CYP2D6* copies by the use of specific primer sets [45]. Circular consensus sequencing reads were aligned using BWA-MEM followed by a novel error correction procedure (ALEC [58]), and variants called using GATK HaplotypeCaller (Figure 4)[45]. Sequencing of previously genotyped controls identified expected star (*) alleles, but also enabled sub-allele resolution, diplotype refinement and discovery of novel *CYP2D6* alleles. Importantly, targeted PacBio sequencing of upstream and downstream *CYP2D6* gene copies characterized the duplicated allele in control samples with *CYP2D6* CNVs. This study concluded that PacBio *CYP2D6* sequencing has the capacity to interrogate the entire gene in a single sequencing read as well as specifically characterize duplicated alleles when present, which ultimately could facilitate improved *CYP2D6* metabolizer phenotype prediction for both research and clinical testing applications.

CYP2D6 phasing & star (*) allele haplotyping

Genetic phasing can be accomplished through analysis of parental genotypes (i.e., phasing by transmission), statistical comparison of observed variants with known haplotypes, statistical comparison of read sequences, analysis of RNAseq data and/or long-read DNA sequencing. Although phased *CYP2D6* haplotypes have traditionally been determined by manual interrogation, the recent availability of high-throughput sequencing has prompted the need for more robust and automated haplotype/diplotype inference tools with logic derived from *CYP2D6* star (*) allele definitions and translation tables. However, one of the current challenges is reconciling the historical star (*) allele nomenclature with current genome reference assemblies and a more informed understanding of the extent of variation in the genome [59]. In addition, a cumbersome informatics issue is converting identified *CYP2D6* variants from the genome assembly used for sequencing (e.g., GRCh37/hg19) to the M33388.1 GenBank reference sequence used to define *CYP2D6* star (*) alleles. This is typically accomplished by manual curation and/or with the *CYP2D6* haplotype tables at PharmGKB [60], but recently has been automated by the freely available *CYP2D6* VCF Translator [61]. Some of the currently available *CYP2D6* phasing and diplotyping tools are explained in the following sections (Cypiripi, Constellation/Astrolabe, PharmCAT).

Cypiripi

The Cypiripi algorithm infers *CYP2D6* diplotypes from short-read sequencing data, and is able to properly resolve complicated configurations, including *CYP2D6/2D7* hybrids as well as *CYP2D6* deletions and duplications [62]. The pipeline is composed of *CYP2D6* star (*) allele library preparation (extracted from the nomenclature database); read alignment to the *CYP2D* genes by BLAST-like alignment tool (BLAT) and custom multimapping tools; read, variation and allele filtering; and a combinatorial optimization step that infers *CYP2D6* genotype and copy numbers by integer linear programming [62].

Constellation/Astrolabe

Astrolabe (previously referred to as 'Constellation') was developed to impute diplotypes and assign metabolizer phenotypes for *CYP2D6* and *CYP2C19* from paired-end whole-genome sequencing data [52]. In the Astrolabe algorithm, identified variants are compared with all possible *CYP2D6* diplotypes, which were generated using the defining variants from 119 established *CYP2D6* star (*) alleles. A similarity coefficient is calculated for each possible diplotype, and the diplotype with the highest score is called for each sample. Astrolabe had a 97% sensitivity and 95% specificity and importantly, all extreme phenotypes (i.e., UM and PM) were accurately identified in the development cohort. In addition, simulation studies underscored the benefit of paired-end *CYP2D6* sequencing over single-end reads as well as the increased specificity observed with long-read (e.g., >1 kb) sequencing, particularly across the highly homologous exon 2 region [52].

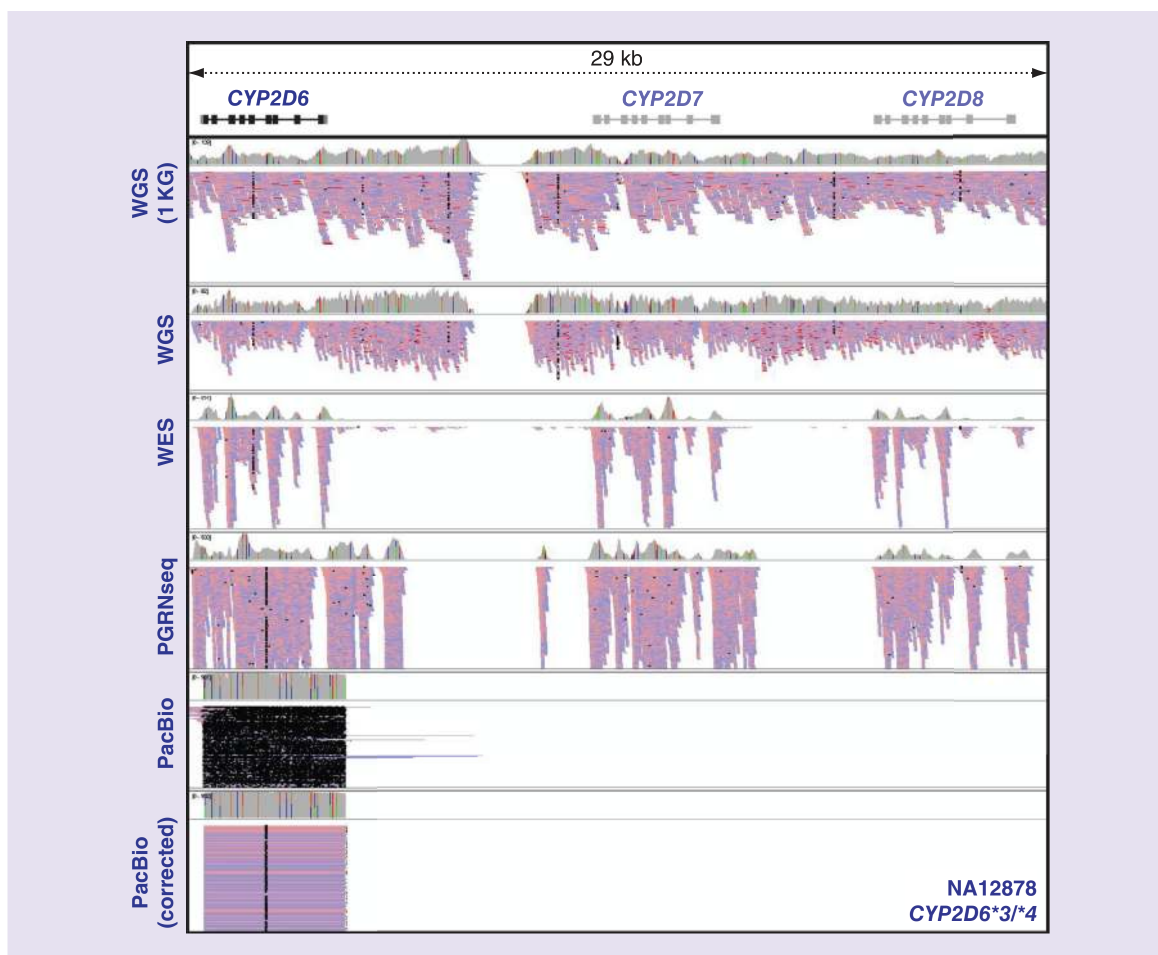

Figure 4. Paired-end short-read sequencing (Illumina) and long-read sequencing (Pacific Biosciences) of the *CYP2D6* gene region visualized with the Integrative Genomics Viewer. Results for NA12878 (*CYP2D6*3/*4*) are displayed from top to bottom panels for WGS from the 1000 Genomes Project, in-house WGS, WES, targeted capture with the PGRNseq platform, targeted PacBio *CYP2D6* sequencing, and ALEC-corrected targeted PacBio *CYP2D6* sequencing. Of note, discrepant and skewed allele frequencies in several loci from the WGS data indicate potential read misalignment errors. Moreover, the common *CYP2D6* capture strategies (e.g., WES, PGRNseq) coupled with short-read Illumina sequencing result in significant read assignment to the *CYP2D7* and *CYP2D8* pseudogenes. These reads indicate a lack of specificity for *CYP2D6* by these target enrichment approaches and/or informatic errors related to read misalignment. Targeted PacBio sequencing results in CYP2D6-specific sequencing and no misalignment to *CYP2D7* or *CYP2D8*, but random errors throughout the sequencing reads are characteristic to this technology. These random errors can be minimized by circular consensus sequencing read analysis; however, further correction prior to variant calling can also be accomplished by available informatics tools (e.g., Amplicon Long-read Error Correction [ALEC]).
1KG: 1000 Genomes Project; PacBio: Pacific Biosciences; WES: Whole-exome sequencing; WGS: Whole-genome sequencing.
Data taken from [26,45,54].

Pharmacogenomics Clinical Annotation Tool (PharmCAT)

The Pharmacogenomics Clinical Annotation Tool (PharmCAT) is a collaboration between the PGRN Statistical Analysis Resource, PharmGKB, the Clinical Genome Resource (ClinGen) and CPIC [63]. It extracts all CPIC level 'A' gene variants (except for *G6PD* and *HLA*) from a vcf file (including *CYP2D6*), interprets the variant alleles, infers diplotypes and generates an interpretation report based on CPIC guidelines [64]. The PharmCAT tool developers assemble and maintain the translation tables that underlie the tool, which could facilitate clinical implementation and more uniform pharmacogenetic sequencing interpretation.

CYP2D6 phenotype prediction & clinical pharmacogenetic testing

Predicting CYP2D6 metabolizer phenotype from diplotype is challenging and an imperfect inference [65]. Although there are over 100 variant *CYP2D6* star (*) alleles catalogued by the Nomenclature Committee, most targeted genotyping platforms employed by clinical laboratories only interrogate a small subset of variants with established functional effect (Figure 3). Consequently, the *CYP2D6*1* haplotype is assigned by default in the absence of any detected variant alleles. This commonly used system results in some alleles being incorrectly classified as *CYP2D6*1* when they actually carry a low-frequency functional variant allele that was not directly genotyped. Full-gene sequencing techniques, such as, *CYP2D6* SMRT sequencing [45] will result in the identification of more precise haplotypes and diplotypes, but the increased identification of rare and/or novel star (*) alleles could lead to an increased frequency of 'indeterminate' or 'unclear' CYP2D6 metabolizer phenotypes. As such, most clinical laboratories do not currently employ full-gene *CYP2D6* sequencing.

A related phenotype classification system has been proposed for CYP2D6 metabolizer phenotype prediction, which has been adopted by recent *CYP2D6* CPIC guidelines and is based on a continuum of 'activity scores' for different *CYP2D6* alleles [18,66]. All *CYP2D6* star (*) alleles are assigned an 'activity score' value when functional status is known (e.g., 0, 0.5, 1 and 2), and the sum of the maternal and paternal allele scores directly informs the CYP2D6 metabolizer phenotype (Table 2) [18]. Despite these advances in predicting CYP2D6 phenotype from genotype, some of the notable challenges still include interpreting reduced function and other low-frequency star (*) alleles with uncertain activities as well as determining which allele is duplicated when an increased *CYP2D6* copy number is detected.

Despite the role of CYP2D6 in the metabolism of numerous medications, a clinically relevant effect of increased or decreased CYP2D6 activity has only been actualized in a subset of medications and drug classes. Clinical utility, cost–effectiveness and third-party reimbursement issues for *CYP2D6* pharmacogenetic testing are beyond the scope of this review; however, clinical *CYP2D6* testing is increasingly accessible and being adopted by clinicians to inform pharmacotherapy. Proficiency testing for *CYP2D6* is available by the College of American Pathologists [67], and Coriell Institute Biorepository reference materials for *CYP2D6* test validation have been developed by the CDC-based Genetic Testing Reference Material Coordination Program [68]. Clinical laboratory guidelines for *CYP2D6* genotyping in the context of tamoxifen response testing have been published by the American College of Medical Genetics and Genomics [48], and support for healthcare practitioners on how to interpret clinical *CYP2D6* diplotype and CYP2D6 metabolizer phenotype results can be found in the practice guidelines published by the CPIC [19–22] and DPWG [23].

Conclusion

Since the discovery of the polymorphic *CYP2D6* gene, it has been one of the most widely studied genes in the field of pharmacogenetics due to its direct role in the metabolism of many commonly prescribed medications. Despite this extensive body of research over the past 25 years, interrogating *CYP2D6* has proven challenging due to its pseudogene homology and the extent of structural variation that eventually was discovered at this locus. As such, it is likely that many early clinical research studies that only genotyped isolated *CYP2D6* variants and limited star (*) alleles did not thoroughly capture the true diversity of *CYP2D6* variation in their cohorts, which ultimately could have confounded result interpretation and study conclusions. Long-range PCR facilitated more accurate assessment of the *CYP2D6* gene sequence; however, it has become clear that parallel copy number and sequence interrogation is necessary to properly define *CYP2D6* diplotype and predicted metabolizer phenotype in any one individual. As third-generation long-read *CYP2D6* sequencing becomes more commonly used by both research and clinical laboratories, it is likely that these platforms will facilitate a more precise and informed ability to infer interindividual CYP2D6-mediated drug response. These technical advancements will complement the refinement of phenotype prediction, which ultimately could further enable the reporting and implementation of clinical *CYP2D6*-based practice guidelines.

Future perspective

The accessibility of clinical *CYP2D6* pharmacogenetic testing and interpretation practice guidelines coupled with the growing evidence for clinical validity and utility of *CYP2D6* genotype-directed pharmacotherapy indicate that clinical genetic testing for this important pharmacogene will increasingly be incorporated into routine clinical care. This is further supported by the deployment of pre-emptive pharmacogenetic testing programs at selected academic medical centers [69] and the continued federal support for genomic medicine research aimed at returning 'actionable' sequence variants to study participants. Although *CYP2D6* is an ideal gene for clinical implementation in all of these contexts, thorough full-gene sequencing and structural characterization is necessary for accurate metabolizer phenotype prediction. Long-read full-gene *CYP2D6* sequencing platforms, including both allele- and duplication-specific assays, are available; however, most platforms used for clinical *CYP2D6* testing are limited to only a small number of targeted *CYP2D6* variants with known functional effect. As such, in order to facilitate the clinical implementation of more thorough *CYP2D6* sequencing strategies, it will be imperative to develop rapid functional assays that assess novel and rare *CYP2D6* variants as they are identified. In addition to facilitating more accurate metabolizer phenotype prediction for *CYP2D6*, a strategy of coupling long-read full-gene sequencing with functional assays is likely to have utility for other genes involved in interindividual drug response variability as well as other clinically actionable traits and Mendelian disorders.

Supplementary data

To view the supplementary data that accompany this paper please visit the journal website at: www.futuremedicine.com/doi/full/10.2217/pgs-2017-0033

Executive summary

CYP450-2D6: discovery & pharmacogenetic implications

- The CYP2D6 subfamily member accounts for only approximately 1–4% all hepatic CYP450 enzymes, yet it metabolizes approximately 25% of commonly prescribed drugs.
- The *CYP2D6* gene is implicated in approximately 25% of the medications currently listed on the US FDA pharmacogenomic biomarkers in drug-labeling table.

Genomic architecture of the *CYP2D6* locus

- The *CYP2D6* gene is highly polymorphic with more than 100 variant star (*) alleles catalogued by the Human CYP450 Allele Nomenclature Database; however, *CYP2D6* is challenging to interrogate due to highly homologous pseudogenes (*CYP2D7* and *CYP2D8*).
- Noncoding variants have recently been implicated in the regulation of *CYP2D6* expression, and other important structural variants include *CYP2D6* deletions and duplications as well as gene conversion alleles and tandem allele configurations.

***CYP2D6* interrogation & allele discovery**

- The earliest *CYP2D6* variant alleles were discovered by cloning and/or Sanger sequencing; however, the availability of long-range PCR subsequently enabled the use of multiplexed targeted genotyping across full-length *CYP2D6* gene amplicons.
- Short-read sequencing of *CYP2D6* (including exome sequencing) is challenging due to nonspecific target enrichment and/or misalignment as a result of the homologous pseudogenes.
- Long-read sequencing has recently been successfully applied to full-gene *CYP2D6* amplicons, including long-range haplotyping, duplication-specific sequencing and novel allele characterization.

***CYP2D6* phasing & star (*) allele haplotyping**

- Many *CYP2D6* sequence variants are found in multiple star (*) allele haplotypes, underscoring the need for proper variant phasing, which recently has been enabled by automated software tools (Cypiripi, Astrolabe and Pharmacogenomics Clinical Annotation Tool).

***CYP2D6* phenotype prediction & clinical pharmacogenetic testing**

- CYP2D6 metabolizer phenotype prediction infers four different categories (ultrarapid, normal, intermediate and poor metabolizer) based on the available genotype or sequencing data; however, the *CYP2D6*1* haplotype is assigned by default in the absence of detected variant alleles, which can lead to inaccurate phenotype prediction.
- An 'activity score' phenotype prediction system has been developed to facilitate more uniform *CYP2D6* diplotype interpretations, and practice guidelines and resources are increasingly available for clinical laboratories and practitioners to enable *CYP2D6* testing and pharmacogenetic-guided medical management.

Future perspective

- To facilitate the clinical implementation of more thorough *CYP2D6* sequencing strategies, it will be imperative to develop rapid functional assays that assess novel and rare *CYP2D6* variants as they are identified.

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