Genetic Test of Cytochrome P450 2C19 (CYP2C19) for Drug Metabolism

Background
Cytochrome P450 (CYP) enzymes, largely present in the liver, regulate the metabolism of several prescription drugs. CYP2C19 is an isoenzyme that mediates the metabolic activation and elimination, and hence the therapeutic effect of a variety of drugs including antiplatelet agents, anticonvulsants, antidepressants, antineoplastic drugs, antiretroviral/antifungal drugs, antimalarial drugs, antithrombotics, antilulcer drugs, beta blockers and proton pump inhibitors. Drugs metabolized through CYP2C19 are listed in Table 1.

The ability to metabolize drugs that are CYP2C19 substrates differs among patients resulting in wide variability in their response to specific drug therapy. A major cause of such interindividual variability is associated with variations in CYP2C19 gene encoding CYP2C19 enzyme. Prevalence of a specific genetic variant is dependent on racial and ethnic background. Over 25 variants have been identified for the CYP2C19 gene, and about a dozen variants, which are functionally impaired, can lead to the production of CYP2C19 with high, low or no enzyme activity causing abnormal levels of drugs and their derivatives. This can result in adverse events including toxicity, sub-therapeutic effect or non-responsiveness.

On the basis of CYP2C19 metabolic ability, individuals can be broadly classified into four phenotypes: normal (extensive), intermediate, poor and ultra metabolizers. Since the therapeutic effect of a specific drug is dependant on whether it is metabolically activated or cleared/inactivated by CYP2C19, determining the phenotype of patients from their genotype may help to manage individualized therapy and limit adverse events.

Clinical Significance of Genetic Testing
The CYP2C19 isoenzyme metabolizes about 5-10% of all prescription drugs, and poor metabolizers taking those drugs may be predisposed to adverse events due to underdosing or overdosing, depending on whether it is a pro-drug or active drug, respectively. It is estimated that about 2-14% of the U.S. population are poor metabolizers. Pharmacokinetics of drugs and consequent therapeutic efficacy depend on the metabolic rate of activation or elimination. Poor metabolizers are likely to have markedly reduced or no conversion rate of pro-drugs (examples: clopidogrel; tamoxifen) to active drugs resulting in either sub-therapeutic effect or non-responsiveness (underdosing), which eventually require alternative treatment or increased dosage. Poor metabolizers may also have a reduced capacity to eliminate active drugs (examples: Prilosec, generic name – omeprazole; Valium, generic name – diazepam) leading to accumulation and resulting in toxicity and life-threatening side effects (overdosing).

Such adverse effects can be predicted by determining the genotype-phenotype associations (Figure 1). The homozygous wild type allele of CYP2C19, designated CYP2C19*1, is defined as an extensive metabolizer (EM). Nine common variants of CYP2C19 gene associated with impaired drug metabolism include *2 to *10. While the wild-type form of the CYP2C19 gene (*1) encodes an enzyme with normal functional activity, genetic variants (*2 to *8) encode enzymes with non-functional activity and two other variants (*9 and *10) have decreased functional activity. The most common poor metabolizer (PM) phenotypes are from CYP2C19 with homozygous *2 and *3 alleles. Homozygous *4 to *8 alleles are less common PM. One of the variants (*17) confers augmented enzyme activity, leading to an ultra metabolizer (UM) phenotype. Inheritance of one normal allele and one non-function allele can result in intermediate metabolizer (IM) phenotype.

This genetic test is used to identify patients at risk for adverse events due to impaired metabolism by:

Detecting 6 variants of CYP2C19 gene responsible for non-functional metabolic activity:

Detecting 2 variants of CYP2C19 gene responsible for decreased functional metabolic activity:
- CYP2C19*9 and *10

Detecting one variant of CYP2C19 gene responsible for increased functional metabolic activity:
- CYP2C19*17

Interpretation
Interpretation of the assay is based on the presence of specific genetic variants of CYP2C19 (Table 2).
1. Individuals with CYP2C19 variant alleles designated *2, *3, *4, *6, *7 and *8 have non-functional activity compared to *1 (wild-type) individuals. Administration of pro-drug such as clopidogrel can result in a markedly reduced or no conversion to their active metabolite, and sub-therapeutic effect or non-responsiveness, which require alternative treatment or increased dosage. Conversely, administration of active drugs, such as diazepam and omeprazole, may result in impaired elimination, and potential risk of drug toxicity and life-threatening side effect, which requires alternative treatment or reduced dosage.

2. Individuals with CYP2C19 variant alleles designated *9 and *10 have decreased functional activity. Such individuals may have sub-therapeutic effect for pro-drugs. Conversely, administration of active drugs may result in impaired elimination, and potential risk of drug toxicity.

3. Individuals with CYP2C19 variant alleles designated *17 have augmented enzyme activity compared to *1 (wildtype) individuals, leading to increased conversion of pro-drugs to active metabolites with potential risk for toxicity requiring reduced dosage. Conversely, it may also lead to rapid elimination of active drugs and sub-therapeutic effect.

4. Individuals with a CYP2C19 genotype comprised of one of the non-function alleles (*2, *3, *4, *6, *7 or *8) and *17 have an unknown metabolizer phenotype. Due to the low population frequency of these alleles, the level of CYP2C19 activity cannot be predicted based on genotype.

5. Individuals with a CYP2C19 genotype comprised of one of the reduced function alleles (*9 or *10) and *17 have an unknown metabolizer phenotype. Due to the low population frequency of these alleles, the level of CYP2C19 activity cannot be predicted based on genotype.

6. Prevalence of CYP2C19 gene variants differs depending on ethnic background. The frequency of allele CYP2C19*2 has been reported as approximately 30-35% of Asians, and 15-26% of Caucasian and African Americans. The frequency of allele CYP2C19*3 has been reported as approximately 10% of Asians, and less than 2% of Caucasian and African Americans.

7. Genotype-phenotype interpretation should be made in the context of a patient's clinical condition and concomitant medications, which may be substrates, inhibitors and inducers of CYP2C19.

**Methodology**

An array-based test kit employing Infiniti analyzer (Auto-Genomics Inc., CA) is used for genotyping CYP2C19 variants. The assay involves a multiplex PCR amplification of genomic DNA followed by allele-specific primer extension using fluorescently labeled dCTP and hybridization on to a microarray.
Table 2. CYToChroMe P450 2C19 GenoTYPe and PhenoTYPe For druG MeTabolISM

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Allele</th>
<th>Phenotype / Enzyme Activity</th>
</tr>
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<tbody>
<tr>
<td>CYP2C19*1</td>
<td>wild type</td>
<td>EM / Normal function</td>
</tr>
<tr>
<td>CYP2C19*2</td>
<td>681 G&gt;A</td>
<td>PM / Non-function</td>
</tr>
<tr>
<td>CYP2C19*3</td>
<td>636 G&gt;A</td>
<td>PM / Non-function</td>
</tr>
<tr>
<td>CYP2C19*4</td>
<td>1 A&gt;G</td>
<td>PM / Non-function</td>
</tr>
<tr>
<td>CYP2C19*6</td>
<td>395 G&gt;A</td>
<td>PM / Non-function</td>
</tr>
<tr>
<td>CYP2C19*7</td>
<td>IVS 5+2T&gt;A</td>
<td>PM / Non-function</td>
</tr>
<tr>
<td>CYP2C19*8</td>
<td>358 T&gt;C</td>
<td>PM / Non-function</td>
</tr>
<tr>
<td>CYP2C19*9</td>
<td>431 G&gt;A</td>
<td>IM / Decreased function</td>
</tr>
<tr>
<td>CYP2C19*10</td>
<td>680 C&gt;T</td>
<td>IM / Decreased function</td>
</tr>
<tr>
<td>CYP2C19*17</td>
<td>-806 C&gt;T</td>
<td>UM / Increased function</td>
</tr>
</tbody>
</table>

Abbreviations: EM (Extensive Metabolizer); IM (Intermediate Metabolizer); PM (Poor Metabolizer); UM (Ultra Metabolizer)
Test Name: Genetic Test of Cytochrome P450 2C19 (CYP2C19) for Drug Metabolism

Methodology: Multiplex PCR and array hybridization assay

Reference Range: An interpretive report will be provided.

Specimen Requirements:
- Testing Volume/Size: 3 mL
- Type: Whole blood
- Tube/Container: EDTA (Lavender)
- Collection Temperature: Refrigerated

Ordering Mnemonic: 2C19PL

Billing Code: 88307

CPT Codes: 83891, 83900, 83901 x4, 83914 x18, 83912

References:
4. US Food and Drug Administration. Table of Pharmacogenomic Biomarkers in Drug Labels http://www.fda.gov/Drugs/ScienceResearch/ResearchAreas/Pharmacogenetics/ucm083378.htm

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