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## **Pharmacogenomics of Anti-platelet and Anti-coagulation Therapy**

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## **Abstract**

Arterial thrombosis is a major component of vascular disease, especially myocardial infarction (MI) and stroke. Current anti-thrombotic therapies such as warfarin and clopidogrel are effective in inhibiting cardiovascular events; however, there is great inter-individual variability in response to these medications. In recent years, it has been recognized that genetic factors play a significant role in drug response, and, subsequently, common variants in genes responsible for metabolism and drug action have been identified. These discoveries along with the new diagnostic targets and therapeutic strategies on the horizon hold promise for more effective individualized anticoagulation and anti-platelet therapy.

#### **Keywords**

Pharmacogenomics; Personalized medicine; Anti-platelet therapy; Clopidogrel; Plavix; Warfarin; Coumadin; CYP2C19; CYP2C9; VKORC1; Platelet function; Cardiovascular disease; Thrombosis; Coronary artery disease; Percutaneous coronary intervention; Anti-coagulation

## **Introduction**

Anti-coagulant and anti-platelet medications are widely prescribed drugs used for the primary and secondary treatment of a variety of pathological thrombotic processes such as thrombotic cerebrovascular and cardiovascular diseases, atrial fibrillation, pulmonary embolism, deep vein thrombosis and genetic or acquired hypercoagulability. Warfarin is the most commonly used oral anti-coagulant, whereas the most commonly used anti-platelet

#### **Conflict of Interest**

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medications include aspirin and clopidogrel, each of which influences blood hemostasis through different mechanisms. Marked inter-individual variation in response to these commonly prescribed medications have been well-documented and represent a significant challenge to medical practice [1•]. Warfarin has a relatively narrow therapeutic index around which under-dosing may result in recurrent thrombosis and over-dosing may result in severe and life-threatening bleeding. While newer agents such as dabigatran and rivaroxaban are now available, physicians' familiarity with warfarin, its effectiveness when dosed properly, and its low cost continue to make it the anti-coagulant treatment of choice. Likewise, clopidogrel continues to be widely prescribed due to its efficacy in the majority of patients as well as its relatively low price, while newer anti-platelet medications such as prasugrel and ticagrelor often function as alternative anti-platelet agents offered to patients for whom clopidogrel is not effective. Understanding factors that influence response to these agents offers practical opportunities for more individualized and effective therapy.

Several gene polymorphisms have been found that reproducibly contribute to interindividual response variability to warfarin and clopidogrel. The aim of this review is to familiarize the reader with the gene polymorphisms found thus far that most significantly contribute to a given individual's response to either of these two medications; because of the lack of genetic polymorphisms reproducibly associated with aspirin response, aspirin pharmacogenomics will not be discussed in this review, though others have covered the issue very well [2-4]. With bona fide common polymorphisms that can predict one's response to warfarin and clopidogrel now in hand, the next challenge and active area of investigation is the development of strategies to implement these discoveries into clinical practice.

## **Warfarin**

In 1948, warfarin was introduced as a pesticide against rodents. Recognizing its potent anticoagulant action and potential efficacy for thrombotic disease, warfarin was approved for use in humans in 1954 and remains among the most commonly prescribed drugs today. It is derived from dicoumarol, a natural product initially isolated from sweet clover. Its synthetic form consists of both R and S enantiomers of which the S form is more active. Each form is metabolized through a different mechanism, with S-warfarin metabolized primarily by cytochrome P450 2C9 (CYP2C9) and R-warfarin metabolized predominantly by CYP3A4 [5]. Warfarin acts by inhibiting the vitamin K epoxide reductase complex by binding to the VKORC1 subunit, thus preventing reduced vitamin K-dependent gamma-carboxylation of clotting factors II, VII, IX and X, as well as proteins C and S, resulting in a potent anticoagulant effect [6].

Dosing of warfarin typically involves a loading dose followed by daily maintenance therapy. Its therapeutic dosing is monitored by measuring activity of the extrinsic coagulation pathway using the standardized international normalized ratio (INR). There is wide interindividual variation in the warfarin dose required to reach a therapeutic INR. Factors that markedly affect the anti-coagulant effect of warfarin include diet, particularly foods high in vitamin K, smoking, certain drugs and botanicals that affect warfarin metabolism, alcohol, body weight, and age [7]. Based upon knowledge of the mechanism of action and metabolism of warfarin, candidate gene studies have identified three genes whose common variation explains ~40%, and up to 54% of inter-individual response to warfarin dose, depending on the ancestry of the population studied. More recent genome-wide association studies (GWAS) have provided additional insights into warfarin pharmacogenomics.

## **CYP2C9**

The CYP2C9\*1 allele encodes a fully active enzyme, has the highest frequency of the 30 different alleles discovered to date, and is considered the wild-type allele. Although frequencies vary across ethnic populations, the most common decreased function alleles are  $CYP2C9*2$  (C430T; rs1799853) and  $*3$  (A1075C; rs1057910) alleles, which encode enzymes with 70% and 20% of wild-type enzyme activity, respectively. Multiple studies now show that patients with CYP2C9\*2 and \*3 alleles have greater sensitivity to warfarin, requiring lower doses to achieve a therapeutic INR [8, 9]. Among the initial important studies, Higashi and colleagues performed a retrospective study of 185 largely Caucasian patients followed in two Seattle area anticoagulation clinics, and found that compared to the  $*1/*1$  genotype, patients with one or two copies of the  $*2$  or  $*3$  variant required significantly lower daily doses of warfarin [8]. Gage and colleagues examined the effect of the CYP2C9 variants in 369 patients who were taking maintenance doses of warfarin and found that the presence of the \*2 or \*3 variant was strongly associated with lower warfarin dose necessity; the maintenance dose was decreased by 19% per \*2 allele and by 30% per \*3 allele [9]. From these and other studies, it has become clear that about 13% of the variability in warfarin dose can be explained by CYP2C9 polymorphisms.

As might be expected of patients who have increased sensitivity to warfarin, several studies indicate that CYP2C9 decreased function allele carriers are at increased risk of over-anticoagulation and bleeding events [10-12]. Higashi found that patients carrying \*2 or \*3 alleles experienced a bleeding rate of 10.92 per 100 patient-years, which was significantly higher than the 4.89 per 100 patient-years experienced in the \*1/\*1 homozygotes [8].

Some uncommon CYP2C9 decreased function alleles include \*5, \*6, \*8, and \*11. These alleles have not been studied as thoroughly but would be predicted to have similar effects as the more common CYP2C9 decreased functional alleles [13]. The allele frequencies vary noticeably among ethnic groups; for example, the frequencies of CYP2C9\*2 and \*3 are higher in Asian populations than Caucasian populations, which have higher frequencies of the alleles than African-American populations [12, 13]. Importantly, the allele frequency of CYP2C9\*8 among African-Americans is approximately 9%, suggesting that this allele should be measured and considered in warfarin dosing algorithms [14].

## **VKORC1**

The VKORC1 G-1639A (rs9923231) variant is located in the promoter region and results in decreased transcription as well as lower levels of VKORC1 messenger RNA (mRNA) [1•, 15]. Another VKORC1 variant, C1173T (rs9934438), is in complete linkage disequilibrium with G-1639A [16]. Decreased *VKORC1* expression is associated with increased warfarin sensitivity and thus patients heterozygous (G/A) and homozygous (A/A) for the VKORC1 G-1639A variant require lower doses of warfarin compared to individuals homozygous for the wild-type *VKORC1* genotype  $(G/G)$  [17]. The early important study demonstrating the potent effect of VKORC1 variants on warfarin dose was carried out by Rieder and colleagues with the same Seattle area cohort discussed above. They found that compared to those patients homozygous for the wild-type *VKORC1* allele, having one of five highly correlated variants predicted an approximately 25% variance in warfarin dose. The effect of the *VKORC1* variants on warfarin dose in this study was more potent than the CYP2C9 variants and accounted for 10% of the variance in warfarin dose. With respect to Rieder's findings, it is currently estimated that the VKORC1 G-1639A variant accounts for 24% of the variation in warfarin dose [16]. The frequency of the *VKORC1* -1639A allele is approximately 40% in Caucasians, 20% in African-Americans, and 85% in Asians [16, 18]. As might be expected, the *VKORC1* -1639A allele has been shown to be associated with increased bleeding events and over-anti-coagulation [18, 19]. In a randomized trial of

genotype-guided versus standard warfarin dosing, Anderson et al. [19] found that patients who carry variants in both CYP2C9 and *VKORC1* were at a significantly increased risk of an elevated INR (INR>4) compared to all other patients.

#### **CYP4F2**

After vitamin K is reduced by the vitamin K epoxide reductase complex, the reduced form of vitamin K can used in the synthesis of coagulation factors or it can be converted into hydroxyl-vitamin K1 by the enzyme CYP4F2, encoded by the CYP4F2 gene [20]. The rs2108622 variant in CYP4F2 is a C>T nucleotide substitution that introduces a V433M missense mutation resulting in a CYP4F2 enzyme with decreased function [21]. Patients with the *CYP4F2* decreased function T allele require 4-12% more warfarin per allele compared to CC homozygotes [22], accounting for approximately 1.1-7% of the interpatient variability in warfarin dose requirement [23, 24]. The frequency of rs2108622 T alleles is approximately 25% among Caucasians and Asians, with a lower frequency of 7% observed among African-Americans [22]. Moreover, dosing models designed to include rs2108622 along with *CYP2C9* and *VKORC1* variants resulted in improved overall warfarin dose predictability [25]. Two GWAS identified the same three variants as being significantly associated with warfarin response [26, 27]; other genome-wide significant associations were not detected, suggesting that it is unlikely that there are other common variants that exert as large an effect.

#### **Translation of Warfarin Pharmacogenomics into Patient Care—**CYP2C9,

VKORC1, and CYP4F2 genotyping is likely to have clinical utility, allowing clinicians to better individualize warfarin dosing to enhance efficacy and decrease adverse events such as bleeding. In 2007, the FDA modified the package insert of warfarin to reflect the clinical utility of *VKORC1* and *CYP2C9* genotype to include the statement, "lower initiation doses should be considered for patients with certain genetic variations in CYP2C9 and VKORC1 enzymes" [28]. The package insert was later modified in 2010 to include a table containing recommended daily warfarin doses for patients with various CYP2C9 and VKORC1 haplotypes [7]. There are currently several trials examining application of genetics in warfarin therapy, including the Warfarin Adverse Event Reduction For Adults Receiving Genetic Testing at Therapy Initiation (WARFARIN, 2011-2014) Trial, and the Clarification of Optimal Anticoagulation Through Genetics (COAG, 2009-2013) Trial. Both of these are NIH-funded prospective randomized clinical trials designed to determine if a dosing algorithm that includes genotypes for warfarin-response genes, such as CYP2C9 and VKORC1, can result in a greater proportion of time within the therapeutic INR range, as well as decreased warfarin-related clinical events, compared to standard dosing practices that do not include genotypes. A number of warfarin dosing algorithms and tables, such as those found at<http://www.warfarindosing.org>[29], have been developed that incorporate genotype to estimate warfarin dose. In addition, the Pharmacogenomics Research Network Clinical Pharmacology Implementation Committee recently published guidelines for warfarin dosing recommending that pharmacogenetic algorithm-based dosing be used when possible, and if electronic means for dosing are not available, the table-based dosing approaches are suggested [7].

## **Clopidogrel**

Clopidogrel is an oral second-generation thienopyridine that prevents platelet activation and aggregation by irreversibly inhibiting the  $P2Y_{12}$  ADP receptors on the surfaces of platelets [30]. Upon ingestion, clopidogrel is absorbed by duodenal enterocytes and moves through these cells into the bloodstream. Once in circulation, approximately 85% of the clopidogrel is hydrolyzed into inactive metabolites by carboxylesterases, primarily carboxylesterase 1

 $(CES1)$ , in the liver during first-pass metabolism [31]. The remainder of the drug undergoes biotransformation from an inactive pro-drug into the unstable active metabolite. This process requires two steps that involve several CYP enzymes also found in the liver. Two important CYP enzymes involved in this activation step include CYP2C19 and CYP2B6, as well as other potential enzymes including CYP1A2, CYP2C9, CYP3A4/5, and PON1 [32-34]. The active metabolite then circulates through the bloodstream, oxidizing cysteine residues and irreversibly blocking platelet P2Y<sub>12</sub> ADP receptors. Without functional P2Y<sub>12</sub> receptors, the G<sub>i</sub> proteins associated with the receptors are unable to inhibit adenylyl cyclase. This causes an increase in cAMP, followed by the lack of activation of phosphoinositide 3-kinase (PI3K) and decreased expression of glycoprotein IIb/IIIa (GpIIb/ IIIa). The ultimate result of this pathway is a slow-starting, long-term activation and aggregation of platelets, which clopidogrel effectively blocks [35].

Clopidogrel response variability is well established [36-41]. Patients treated with clopidogrel who demonstrate higher *ex vivo* platelet reactivity are at increased risk of ischemic events [42-48]. For example, Matezky and coworkers [49] found that up to 25% of subjects who received PCI with stenting for acute MI and who were placed on aspirin and clopidogrel were resistant to clopidogrel when ADP-induced platelet aggregation was assessed at day 6 of therapy. Recurrence rates for a cardiovascular event were 40% in the lowest quartile of clopidogrel response compared to only 6.7% in the upper quartile of responders. Factors that may influence variation in platelet function in response to clopidogrel include use of lipophilic statins, calcium channel blockers, proton pump inhibitors, St. John's Wort, and smoking [50-52]. However, these factors account for only a small fraction of the variation in response.

Genetic factors have also been found to play a role in clopidogrel resistance. The Amish Pharmacogenomics of Anti-Platelet (PAPI) Study found that in healthy subjects the heritability of clopidogrel response, as measured by post-exposure ADP-stimulated platelet aggregation, was 70%. In search of specific genetic variants that influence clopidogrel response, a number of candidate gene studies and, to date, one GWAS has been performed. Following is a summary of the most salient findings.

#### **CYP2C19**

Common loss-of-function (LOF) variants in CYP2C19 are the most well-established genetic determinants of clopidogrel responsiveness. Its most common LOF variant is \*2 (rs4244285), with allele frequencies of 29% in Asians, and 15% in Caucasians and Africans. Other LOF alleles include \*3-\*8, which are all considered rare. Those with one and two CYP2C19 LOF alleles are considered intermediate metabolizers (IM) and poor metabolizers (PM), respectively. Multiple studies have demonstrated that CYP2C19 LOF variants are associated with lower clopidogrel active metabolite concentrations [53-55], greater ontreatment residual platelet function [54-57] and poorer cardiovascular outcomes in PCI patients treated with clopidogrel [53, 58-63]; other excellent reviews have also covered much of the literature surrounding CYP2C19 [1•, 64-69]. Other studies in coronary artery disease populations with lower rates of stent placement or in patient populations with other indications for anti-platelet therapy have not shown significant effects of CYP2C19LOF variants on clopidogrel response [70, 71]. Meta-analyses provide supporting evidence for a clinically important role of CYP2C19 LOF variants [72, 73]. For example, Jang et al. [72] estimated that carriers of one or more CYP2C19 LOF alleles had an increased risk of cardiovascular death (OR 2.18, 95% CI 1.37 to 3.47), MI (OR 1.42, 95% CI 1.12 to 1.81), and stent thrombosis (OR 2.41, 95% CI 1.76 to 3.30). These effects appear to be qualitatively consistent across ethnic populations [74-76]. By contrast, a recent metaanalysis by Holmes and coworkers [77] concluded that CYP2C19 LOF variants are not clinically significant contributors to clopidogrel response, citing issues with "treatment

only" study designs and small study bias as the reasons for positive findings of other metaanalyses. We [78] and others [79, 80] suggest that a more likely explanation is that CYP2C19 genotype is an important determinant of patients' responses to clopidogrel after receiving PCI, but possibly not in patients treated with clopidogrel for other indications [78, 81].

The burden of evidence led the FDA in March 2010 to mandate the addition of a boxed warning to clopidogrel's label informing physicians that patients carrying CYP2C19LOF variants may be less responsive to clopidogrel, that tests are available to assess CYP2C19\*2 status, and that alternative drugs or doses are recommended in poor metabolizers [82]. The label was silent regarding *CYP2C19* intermediate metabolizers and fell short of stronger language regarding use of alternative therapy. A consensus report by the American College of Cardiology Foundation Task Force on Clinical Expert Consensus Documents and the American Heart Association (ACCF/AHA) published in June 2010 recommends against routine testing for *CYP2C19* LOF variants, citing that these variants only explain approximately 12% of the variation in clopidogrel response and have low positive predictive value [83]. Furthermore, at the time of its writing, prospective randomized clinical trials showing that genotype-directed therapy improves clinical outcomes had not been performed. Subsequently, in the RAPID GENE Study, 200 PCI patients were randomized to standard treatment with clopidogrel versus genotype-directed therapy in which CYP2C19\*2 carriers received prasugrel. None of the 23 CYP2C19\*2 carriers in the genotype-directed group had high on-treatment platelet reactivity while 7 of the 23 CYP2C19<sup>\*</sup>2 carriers in the standard care group, a significantly higher number of individuals, had high on-treatment platelet reactivity [84].

At the time of this writing, no prospective randomized trials of genotype-directed therapy and clinical outcomes have been reported. The ACCF/AHA consensus statement stressed the importance of clinical judgment in choice of anti-platelet therapy, and we and others have suggested that *CYP2C19* genotype may be useful in context with clinical and other factors in choosing anti-platelet therapy [85]. The Pharmacogenomics Research Network (PGRN) Clinical Pharmacogenomics Implementation Consortium (CPIC) published guidelines for CYP2C19 testing and interpretation, and a suggested algorithm for treatment (Fig. 1) [86••]. These guidelines may be useful in select patients, at least until results of properly designed and powered randomized clinical trials are available.

In addition to LOF variants in *CYP2C19*, there is a gain-of-function (GOF) variant, CYP2C19\*17 (rs12248560), residing in the 5' regulatory region of the gene. This common variant, with minor allele frequencies of 21% and 16% in individuals of European and African ancestry, respectively, [87] is associated with increased transcriptional activity [63, 88]. The underlying mechanism of increased transcriptional activity likely involves hepatocyte nuclear binding to the \*17 variant as evidenced by electrophoretic mobility shift assays [88].

Results of genetic association studies evaluating the effect of the CYP2C19\*17 variant on clopidogrel response traits have been inconsistent. While some studies investigating patients during clopidogrel treatment have observed a decrease in cardiovascular event rates in individuals carrying the CYP2C19\*17 variant [71, 89-92], others have not [53, 60, 63, 71, 93-97]. Similarly, bleeding was increased in subjects with CYP2C19\*17 in some reports [91-95, 98, 99] and not associated in others [53, 71]. Although meta-analyses [91, 92] with  $CYP2C19*17$  provide support for both a decrease in cardiovascular events and an increased risk of bleeding post treatment, CYP2C19\*2 and CYP2C19\*17 genotypes are in linkage disequilibrium and not independent of one another. Individuals with one or two CYP2C19\*17 variant alleles are less likely to possess a copy of the CYP2C19\*2 allele, and

those with no copies of the CYP2C19\*17 variant are more likely to have CYP2C19\*2 variant alleles. Due to the linked nature of these variants, it has been suggested that enhanced response to clopidogrel in persons with one or more copies of the CYP2C19\*17 variant may be due, at least in part, to the lack of CYP2C19\*2 alleles in those individuals [100••]. Therefore, results reported for CYP2C19\*17 should be considered cautiously unless it is clear the authors have statistically adjusted for the CYP2C19\*2 variant in their association model.

#### **ABCB1**

As clopidogrel is absorbed from the intestinal lumen into the bloodstream, it must pass through intestinal enterocytes where a portion of the drug is immediately transported back into the lumen by the P-glycoprotein ATP-dependent efflux pump (ABCB1), also known as multidrug resistant 1 (MDR1). A common genetic variation in ABCB1, C3435T (rs1045642), affects gene transcription. The T allele of this polymorphism causes overexpression, which would be expected to result in greater extrusion of the drug into the intestinal lumen, less net absorption, decreased drug level in the bloodstream, and decreased response [94]. The frequency of the T allele is 57% in Caucasian, 41% in Asians (Chinese), and 11% in African descent.

Several studies have shown a modest association between the ABCB1 3435T allele and decreased clopidogrel active metabolite [101], increased on-treatment platelet reactivity [102] and cardiovascular events [103]. In addition, while determining which genes to include in a novel clopidogrel resistance risk score, which incorporates genotype and phenotype data, one group found a significant association between ABCB1 genotype and platelet reactivity as well as cardiovascular event risk [95].

Other studies have not found such an association between this ABCB1 variant and clopidogrel response, which may be due to inadequate power to discern a modest effect on clopidogrel response, specific characteristics of the patient populations, or false positive results of other studies. A recent meta-analysis examined 12 previously published studies of ABCB1 C3435T genotype. In the combined dataset, they found no association between ABCB1 genotype and on-treatment platelet reactivity, MI, ischemic stroke, all-cause mortality, stent thrombosis, or long-term major cardiovascular events. However, when stratified by loading dose, they found evidence for association between ABCB1 genotype and long-term cardiovascular events in the 300 mg loading dose group, early major adverse cardiovascular events, and bleeding; no such associations were observed in patients given the 600 mg loading dose [103]. These findings suggest that increased clopidogrel dose may be able to overcome higher efflux rates in T allele carriers.

#### **PON1**

Paraoxonase 1 (*PON1*) was named for its ability to metabolize paraoxon, a product of the detoxification of the insecticide parathion. PON1 is expressed in liver and is associated with HDL-cholesterol in the bloodstream. Two common variants in PON1 are A575G (rs662; Gln192Arg) and T163A (rs854560; Leu55Met), with the Gln and Met variants being associated with lower paraoxonase activity [104, 105]. Bouman and coworkers reported a significant association between PON1 Gln192Arg genotype and active clopidogrel metabolite concentration, level of platelet inhibition, and stent thrombosis [106]. These findings were remarkable since PON1 was not previously recognized to be involved in clopidogrel bioactivation. Curiously, this same study showed no effect of CYP2C19 genotype on on-treatment platelet reactivity or stent thrombosis. Subsequently, several studies failed to replicate association of Gln192Arg PON1 with a variety of endpoints including clopidogrel active metabolite levels [107], platelet function [62, 104, 107, 108],

cardiovascular outcomes [104, 107, 109, 110], and stent thrombosis [107]. The reason underlying these discrepant findings are unclear. One study involving 300 patients undergoing PCI for ischemic heart disease showed a significant association between PON1 Gln192Arg genotype and on-treatment platelet reactivity at 1 and 6 months post-PCI, though with much smaller effect size than CYP2C19\*2, \*17, and ABCB1 genotypes [111]. These findings suggest that Bouman's original study may have benefited from "the winner's curse" and that *PON1* genotype might have a smaller effect on clopidogrel response than initially reported, and that subsequent negative studies were not adequately powered, at least not for the stent thrombosis endpoint. Another study showed that PON1 may form a different thiol metabolite that is scarcer than clopi-H4 called Endo, which is not associated with antiplatelet response [112]. A recent analysis of PON1 Gln192Arg genotype in 424 Chinese with acute coronary syndrome found significant association with on-treatment platelet reactivity in CYP2C19<sup>\*</sup>1 homozygotes but not in CYP2C19<sup>\*</sup>2 carriers, suggesting interaction between clopidogrel metabolic pathways [113].

Also clouding the picture are several studies that have demonstrated that *PON1* genotype may be related more to underlying cardiovascular disease risk than to clopidogrel response. A substudy of the CURE trial showed an association between PON1 genotype and cardiovascular event rates in the placebo group when the results were stratified by treatment arm [114]. These findings suggest a non-pharmacogenomic effect of PON1 genotype on cardiovascular outcome, which fits well with prior data showing PON1 to be associated with HDL particles, and that *PON1* genotype is associated with enzymatic activity and the ability of HDL to prevent oxidation of LDL particles [115]. Planned large scale GWAS using an ultra-dense selection of SNPs will help resolve questions regarding associations of PON1 genetic variants with coronary events and HDL. Overall, the burden of evidence does not support a role for *PON1* genotype in clopidogrel response, meaning further study will be required [116, 117].

#### **P2RY12**

The gene  $P2RY12$  encodes the P2Y<sub>12</sub> ADP receptor, the target for inactivation by clopidogrel on the surface of platelets. Two common linked genetic variants in this gene, G52T (rs2046934) and T744C (rs2046934), distinguish two major haplotypes, denoted H1 and H2, respectively. The H2 allele is believed to be associated with increased expression of P2RY12 [118]. A study in 225 healthy Caucasian volunteers exposed to clopidogrel showed that the H2/H2 genotype is associated with a significant decrease in inhibition of platelet aggregation in comparison to H1/H1 and H1/H2 individuals [119]. Similarly, another study in 557 clopidogrel-treated PCI patients showed H2/H2 homozygote individuals had significantly higher platelet aggregation and lower clopidogrel response [120]. In contrast, other studies, including several that examined clinical outcomes, have failed to show such associations [60, 121, 122] leading to the conclusion that if common variants in  $P2RY12$ have an effect on clopidogrel response, this effect is small and not likely to be clinically important.

#### **CES1**

CES1 converts clopidogrel into an inactive carboxylic acid metabolite from its prodrug and thiolactone intermediate states [31]. An uncommon G/A variant (rs71647871) encodes a nonsynonymous substitution Gly143Gln resulting in marked decrease in catalytic function [123]. The frequency of the decreased function 143Gln allele is ~1%. A decreased function allele would be expected to be associated with decreased metabolism of clopidogrel into its inactive metabolite and conversely increased active metabolite levels and clopidogrel response. Indeed, in 566 healthy participants of the Pharmacogenomics of Anti-Platelet Intervention (PAPI) study, the seven 143Gln carriers had significantly higher active

metabolite levels and more effective inhibition of ADP-simulated platelet aggregation. Although the variant is uncommon in the population, the effect size was found to be approximately two-fold greater than CYP2C19\*2. In 330 PCI patients treated with clopidogrel, the six 143Gln carriers similarly showed more effective inhibition of platelet reactivity. In this same sample, there was a trend toward lower cardiovascular event rates in 143Gln carriers, not statistically significant perhaps due to the small sample size. Although these observations will require replication in larger studies, these data suggest that this relatively uncommon variant, present in its heterozygous form in approximately 2% of the population, may be a clinically important determinant of clopidogrel efficacy [124].

**Other CYPs—**As described above, other cytochrome P450 enzymes likely play roles in *in* vivo metabolism of clopidogrel [125-127]. Although functional variants in several of these enzymes exist and would be predicted to affect clopidogrel efficacy, to date the literature is mixed. It is likely that there are redundant mechanisms for clopidogrel metabolism rendering the effect of any single functional variant in these other CYPs small or non-existent. For example, some studies suggest a role for LOF variants in CYP2C9 in clopidogrel response [128, 129], while others do not [53, 122, 130].

Perhaps variants in other CYP genes play a role in clopidogrel response in subjects with LOF variants in *CYP2C19*, for whom alternate pathways may be more important. A study by Kassimis et al. showed that the \*5 variant of CYP2B6 is associated with significantly higher platelet reactivity during clopidogrel treatment, but only in non-CYP2C19\*2 carriers, thus showing both CYP2B6's importance in and the profound impact of CYP2C19\*2 on ontreatment platelet reactivity [130]. It is also possible that factors that affect activity of these CYPs, such as smoking or concurrent use of drugs that induce expression or inhibit action, may influence clopidogrel response in a genotype-dependent manner. A study suggests that  $CYPIA2$  may explain in part the apparent increased clopidogrel response in smokers – the so-called smokers' paradox – because  $CYPIA2$  is induced by polycyclic aromatic hydrocarbons found in cigarette smoke [131]. A study by Zhou and coworkers demonstrated in Koreans that smokers carrying the CYP1A2\*1F variant (rs762551) had reduced ontreatment platelet reactivity, an effect that was not apparent in non-smokers [132]. In some patients, variants in CYP3A5, a "back-up" pathway for CYP3A4, may explain interaction between clopidogrel and amlodipine, a potent CYP3A4 inhibitor. In subjects homozygous for the loss of function CYP3A5\*3 variant, amlodipine causes a significant increase in onclopidogrel platelet reactivity while no such effect was observed in carriers of at least one functional allele [133]. Another study showed that the  $CYP3A5*3$  variant is only associated with clopidogrel response when clopidogrel is co-administered with itraconazole, a known CYP3A inhibitor [134].

#### **Translation of Clopidogrel Pharmacogenomics into Patient Care—**While

approximately 12% of variation in clopidogrel response may be explained by CYP2C19 LOF variants, data suggest that a large amount of the heritability of response remains unknown. Future studies in search of genetic determinants of clopidogrel response will require much larger sample sizes of clopidogrel-treated patients and the application of genome-wide and NextGen sequencing approaches. The International Clopidogrel Pharmacogenomics Consortium (ICPC) seeks to perform a large GWAS in order to identify novel common variants for clopidogrel response [135]. The PGRN has developed a sequencing panel of 84 "pharmacogenes" (PGRN-Seq) [136]. Early data suggest the existence of much more rare variation in these genes than was previously thought [137]. As additional genetic determinants of clopidogrel response are uncovered, it is anticipated that their addition to already available *CYP2C19* genetic testing will increase the clinical utility of genetic testing toward more effective individualized anti-platelet therapy.

## **Conclusions**

In recent years, there has been much progress in our understanding of the genetic basis of variation in clopidogrel and warfarin response. Solid data now supports findings that common variants in CYP2C9 and *VKORC1* alter warfarin maintenance dose requirements and prospective trials are now underway to learn whether genotype-guided therapy can increase the percent of time in the therapeutic INR range and lower adverse bleeding and thrombotic events. A large body of data now also supports a role of common LOF variants in CYP2C19 on clopidogrel response, including studies that have examined active drug levels, platelet reactivity, and clinical outcomes. There is a likely a real but smaller effect of variants in ABCB1 as determinants of clopidogrel response. At the current time, the aggregate of literature does not support a major effect by PON1, P2RY12, or other CYP genes on clopidogrel response, although variation in these genes may contribute in other ways to the complex architecture of clopidogrel response.

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#### **Fig. 1.**

A suggested algorithm for genotype-guided anti-platelet therapy [86••]. (Adapted with permission from: Scott SA, Sangkuhl K, Gardner EE, Stein CM, Hulot JS, Johnson JA et al. Clinical Pharmacogenetics Implementation Consortium guidelines for cytochrome P450-2C19 (CYP2C19) genotype and clopidogrel therapy. Clin Pharmacol Ther. 2011;90(2):328-32. doi:10.1038/clpt.2011.132) [86••]