

candidate modifier truly plays a role in disease penetrance.

Finally, what should we do with the information gained from studies that have unequivocally identified a modifier gene? Recently, a polymorphism in the RAD51 gene has been associated with a protective effect in women harbouring BRCA1 mutations.<sup>13</sup> It is to be expected that in the near future similar data will appear that has a significant effect on the risk of developing malignancy in persons harbouring germline MMR gene mutations. At this stage clinical decision making is relatively comfortable about providing information concerning monogenetic disease risk; however, this may be tempered by the use of additional information which is less precise in its ability to predict disease likelihood. It is to be expected that there will be more than one modifier gene and that some may well cancel each other out. For this information to be incorporated into clinical practise all modifier genes will need to be identified and appropriate decision algorithms developed for the correct implementation and interpretation of this information ■

RJ Scott is at the School of Biomedical Sciences, University of Newcastle, Newcastle, New South Wales 2305, Australia.  
Tel: +61 2 4921 4974;

Fax: +61 2 4921 4253;

E-mail: [Rodney.Scott@newcastle.edu.au](mailto:Rodney.Scott@newcastle.edu.au)

## References

- 1 Zecevic M, Amos CI, Gu X *et al*: IGF1 gene polymorphism and risk for hereditary non polyposis colorectal cancer. *J Natl Cancer Int* 2006; **98**: 139–143.
- 2 Jakubowska A, Gronwald J, Menkiszak J *et al*: The RAD51 135G>C polymorphism modifies breast cancer and ovarian cancer risk in Polish BRCA1 mutation carriers. *Cancer Epidemiol Biomarkers Prev* 2007; **16**: 270–275.
- 3 Antoniou AC, Sinilnikova OM, Simard J *et al*: RAD51 135G→C modifies breast cancer risk among BRCA2 mutation carriers: results from a combined analysis of 19 studies. *Am J Hum Genet* 2007; **81**: 1186–1200.
- 4 Talseth BA, Meldrum C, Suchy J, Kurzawski G, Lubinski J, Scott RJ: Genetic polymorphisms in xenobiotic clearance genes and their influence on disease expression in hereditary non polyposis colorectal cancer patients. *Cancer Epidemiol Biomarkers Prev* 2006; **15**: 2307–2310.
- 5 Chen J, Sen S, Amos CI *et al*: Association between Aurora-A kinase polymorphisms and age of onset of hereditary nonpolyposis colorectal cancer in a Caucasian population. *Mol Carcinogen* 2007; **46**: 249–256.
- 6 Niessen RC, Sijmons RH, Ou J *et al*: MUTYH and the mismatch repair system: partners in crime? *Hum Genet* 2006; **119**: 206–211.
- 7 Steinke V, Rahner N, Morak M *et al*: No association between MUTYH and MSH6 germline mutations in 64 HNPCC patients. *Eur J Hum Genet* 2008; **16**: 587–592 (this issue).
- 8 Scott RJ, McPhillips M, Meldrum CJ *et al*: Hereditary nonpolyposis colorectal cancer in 95 families: differences and similarities between mutation-positive and mutation-negative kindreds. *Am J Hum Genet* 2001; **68**: 118–127.
- 9 Peltomaki P, Vasen HF: Mutations predisposing to hereditary nonpolyposis colorectal cancer: database and results of a collaborative study. The International Collaborative Group on Hereditary Nonpolyposis Colorectal Cancer. *Gastroenterology* 1997; **113**: 1146–1158.
- 10 Reeves S, Meldrum C, Scott RJ: IGF-1 gene polymorphism and risk for hereditary nonpolyposis colorectal cancer. *J Natl Cancer Inst* 2006; **98**: 1664–1665.
- 11 Pande M, Chen J, Amos CI, Lynch PM, Broaddus R, Frazier ML: Influence of Methylenetetrahydrofolate Reductase gene polymorphisms C677T and A1289C on age-associated risk for colorectal cancer in a Caucasian Lynch syndrome population. *Cancer Epidemiol Biomarkers Prev* 2007; **16**: 1753–1759.
- 12 Al-Tassan N, Chmiel NH, Maynard J *et al*: Inherited variants of MYH associated with somatic G:C→T:A mutations in colorectal tumors. *Nat Genet* 2002; **30**: 227–232.
- 13 Gu Y, Parker A, Wilson TM, Bai H, Chang DY, Lu AL: Human MutY homolog, a DNA glycosylase involved in base excision repair, physically and functionally interacts with mismatch repair proteins human MutS homolog 2/human MutS homolog 6. *J Biol Chem* 2002; **277**: 11135–11142.

## Warfarin Pharmacogenomics

# A big step forward for individualized medicine: enlightened dosing of warfarin

Darlene J Elias and Eric J Topol

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Using genetic testing, a potential new face has been put on one of medicine's oldest, most commonly used and dreaded medications.

Warfarin is an anticoagulant medication prescribed worldwide to prevent stroke and venous thromboembolism. Its use is complex due to a narrow therapeutic

window, variability in dose–response, interactions with drugs and diet and risk of serious bleeding.<sup>1</sup> The optimal dose of warfarin is titrated to prolongation of the patient's blood test, the protime and international normalized ratio (PT/INR). Achieving and maintaining the target PT/INR and dose of warfarin is labor intensive and challenging. The importance of INR within the target range is critically important due to the risk of clinical bleeding with excessive prolongation and risk of thrombosis with inadequate prolongation. Many factors affect the metabolism of warfarin making adjustment of the drug dosage common. The traditionally understood clinical factors such as drug–drug interactions, dietary interactions, age and body surface area account for a significant portion of the variability in warfarin dosing.<sup>1</sup>

Genetic variants can affect warfarin metabolism and two genes in particular have been intensively studied: vitamin K epoxide reductase complex 1 (VKORC1) and a cytochrome P450 gene CYP2C9.<sup>2-5</sup> In addition to an effect on warfarin dose, observational clinical studies have looked at anticoagulation-related outcomes and have found increased risk of over-anticoagulation and bleeding events associated with certain CYP2C9 polymorphisms.<sup>6</sup> It is currently accepted that these two genes, VKORC1 and CYP2C9 explain a significant portion, albeit incomplete, of the unpredictability of warfarin management.

These two genes are the focus in a meticulously designed prospective genetic-based cohort study by Millican *et al* recently published in *Blood*. These investigators studied warfarin induction treatment in orthopedic patients undergoing joint replacement. CYP2C9 and VKORC1 genotyping was determined pre-operatively and used in a complex nomogram-dosing regimen. The warfarin-dosing nomograms were tailored to include clinical factors and genetic factors for two cohort groups; the first group was dosed based upon the CYP2C9 genotype and the second group was dosed based upon both VKORC1 and CYP2C9 genotype. The study end point was therapeutic warfarin dose. The investigators found strong correlation between the warfarin dose predicted by their nomogram and the therapeutic warfarin dose that was required to achieve the therapeutic target INR. Some clinical factors such as smoking, liver disease and blood loss were found to affect the warfarin dose. The investigators are careful to note that their study was in a carefully selected cohort of orthopedic patients but it is reasonable to think these findings could potentially extend to other patient populations.

The scientific and clinical evidence that supports lower warfarin doses for patients with certain genetic variations in CYP2C9 and in the VKORC1 has recently moved the US Food and Drug Administration (FDA) to change the labeling of warfarin (marketed as Coumadin<sup>®</sup>) recommending genetic testing to guide warfarin dosing. Dosing must still be individualized and based upon a patient's PT/INR value.<sup>8</sup> The new warfarin label is not a mandatory or a 'black box' warning and does not require

the genetic testing prior to or during warfarin treatment. But to educate the medical community, FDA has taken a big step forward to assert that certain variations in the two genes may increase the need for more frequent INR monitoring and require lower warfarin doses.

Some will argue that there has not yet been a randomized trial to definitively prove that genotyping for warfarin dosing improves efficacy or safety. But such a trial is soon to be underway, supported by the National Institutes of Health. A randomized trial of genotype-guided dosing of warfarin therapy is planned for 2000 patients randomized to three groups: standard of care (trial and error dosing), a clinical-dosing algorithm, and a clinical-dosing algorithm plus genetic-dosing algorithm. Cost-effectiveness will also be assessed. If safety and efficacy can be taken to a higher level, an end to the trial and error warfarin-dosing era will be a true paradigm shift into the realm of individualized medicine and pharmacogenomics.

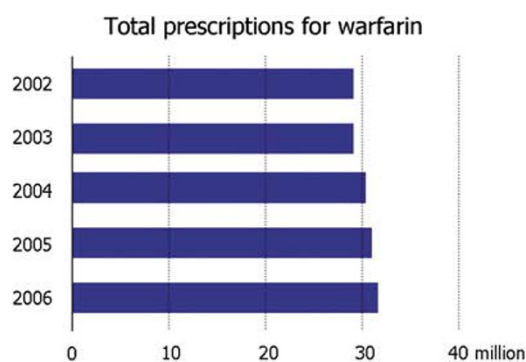
Upwards of 30 genes have been reported to possibly relate to warfarin metabolism but the CYP2C9 and VKORC1 have been shown to be most important and have been studied most intensively.<sup>5</sup> Whether other, yet undiscovered genetic and non-genetic influences on warfarin metabolism will be uncovered remains to be seen. Certainly not all of the genomically related dose variability of warfarin is yet explained.

In the meantime, however, a real dilemma exists for treating physicians and patients taking warfarin. Who to test and how to manage? What dosing nomogram to use? The clinical availability of the genetic testing is limited but presumed

soon to be expanding. How or will the genotyping be reimbursed, given these commercially available tests are quite expensive for both CYP2C9 and VKORC1. And should all this be coordinated centrally, since studies have shown that warfarin monitoring can be improved and INR is more frequently in range with the adverse event rates lower when a centralized anticoagulation service is used compared to usual individual physician care.<sup>9</sup>

All of this potential to improve warfarin dosing by recognizing individual genetic variability is coming at a time when new oral anticoagulants are undergoing intensive study to try and displace or supplant warfarin. Although there are many unanswered questions, there is likely the persistence of warfarin for many years going forward with over 30 million Americans currently on chronic administration (Figure 1). It seems that research efforts that would further determine the genomic and non-genomic basis of warfarin-individualized response would be well worth it. The ability to take a medicine that has been disliked and feared so intensely by both physicians and patients to a level of heightened safety, by virtue of utilizing individual markers, is exciting. The paper by Millican *et al*,<sup>7</sup> along with the FDA new guidance,<sup>8</sup> represents substantive progress to transform therapeutics from the 'one size fits all' to a more enlightened approach. Hopefully, this will serve as an example for the future direction of medicine ■

*DJ Elias and EJ Topol are at the Scripps Research Institute, Scripps Clinic, La Jolla, CA 92037, USA*



**Figure 1** US prescriptions for Warfarin.

## References

- 1 Ansell J, Hirsh J, Poller L *et al*: The pharmacology and management of the vitamin K antagonists: the seventh ACCP conference on antithrombotic and thrombolytic therapy. *Chest* 2004; **126**: 204–233.
- 2 Rieder MJ, Reiner AP, Gage BF *et al*: Effect of VKORC1 Haplotypes on transcriptional regulation and warfarin dose. *N Engl J Med* 2005; **352**: 2285–2293.
- 3 Kamali F, Khan TI, King BP *et al*: Contribution of age, body size, and CYP2C9 genotype to anticoagulant response to warfarin. *Clin Pharmacol Ther* 2004; **75**: 204–212.
- 4 Carlquist JF, Horne BD, Muhlestein JB: Genotypes of the cytochrome p450 isoform, CYP2C9, and the vitamin K epoxide reductase complex subunit 1 conjointly determine stable warfarin dose: a prospective study. *J Thromb Thrombolysis* 2006; **22**: 191–197.
- 5 Wadelius M, Chen LY, Eriksson N *et al*: Association of warfarin dose with genes involved in its action and metabolism. *Hum Genet* 2007; **121**: 23–34.
- 6 Higashi MK, Veenstra DL, Kondo LM *et al*: Association between CYP2C9 genetic variants and anticoagulation-related outcomes during warfarin therapy. *JAMA* 2002; **287**: 1690–1698.
- 7 Millican EA, Lenzini PA, Miligan PE *et al*: Genetic-based dosing in orthopedic patients beginning warfarin therapy. *Blood* 2007; **110**: 1511–1515.
- 8 Matthews A: In Milestone, FDA pushes genetic tests tied to drug. *Wall St J*, August 16, 2007.
- 9 Witt DM, Sadler MA, Shanahan RL, *et al*: Effect of a centralized clinical pharmacy anticoagulation service on the outcomes of anticoagulation therapy. *Chest* 2005; **127**: 1515–1522.