Identification of a Variant in KDR Associated with Serum VEGFR2 and Pharmacodynamics of Pazopanib

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Abstract

Purpose: VEGF receptor (VEGFR) kinases are important drug targets in oncology that affect function of systemic endothelial cells. To discover genetic markers that affect VEGFR inhibitor pharmacodynamics, we performed a genome-wide association study of serum soluble vascular VEGFR2 concentrations [sVEGFR2], a pharmacodynamic biomarker for VEGFR2 inhibitors.

Experimental Design: We conducted a genome-wide association study (GWAS) of [sVEGFR2] in 7,366 healthy Old Order Amish volunteers. Gene variants identified from the GWAS were genotyped serially in a cohort of 128 patients with advanced solid tumor with baseline [sVEGFR2] measurements, and in 121 patients with renal carcinoma with [sVEGFR2] measured before and during pazopanib therapy.

Results: rs34231037 (C482R) in KDR, the gene encoding VEGFR2, was found to be highly associated with [sVEGFR2], explaining 23% of the variance (P = 2.7 × 10−37). Association of rs34231037 with [sVEGFR2] was replicated in 128 patients with cancer with comparable effect size (P = 0.025). Furthermore, rs34231037 was a significant predictor of changes in [sVEGFR2] in response to pazopanib (P = 0.01).

Conclusion: Our findings suggest that genome-wide analysis of phenotypes in healthy populations can expedite identification of candidate pharmacogenetic markers. Genotyping for germline variants in KDR may have clinical utility in identifying patients with cancer with unusual sensitivity to effects of VEGFR2 kinase inhibitors. Clin Cancer Res; 21(2): 365–72. © 2014 AACR.

Introduction

Advances in our understanding of the molecular basis of cancer have led to the identification of a number of novel targets and classes of anticancer agents. However, interindividual variability in efficacy and toxicity creates difficulties in optimizing therapy for individual patients. The discovery of germline and/or somatic genetic markers that predict interindividual differences in therapeutic response promises to improve the efficacy and safety of cancer therapeutics (1–3). These markers also might accelerate the pace and increase the success rate of drug development by identifying subsets of patients who are more likely to respond to a given drug, whereas other markers may define which patients are more likely to experience life-threatening adverse reactions, and in whom that drug should be avoided (or dose attenuated). Unfortunately, the identification of pharmacogenetic markers for a new compound in early clinical trials is a logistical challenge, and thus the discovery of these markers has typically been deferred to late in the development of new drugs or after the drugs have become commercially available when the numbers of persons having received the drugs is sufficiently large (4). To date, most pharmacogenetic studies of anticancer agents have focused on common variants in drug-metabolizing enzymes (7–10).

Angiogenesis inhibitors are an important new class of anticancer agents, but their optimal use requires more detailed understanding of their pharmacology and the biologic basis for...
Translational Relevance

Germline genetic variation can play an important role in the course of cancer and treatment responses. Conventional strategies for discovering germline factors in disease and therapeutic responses in other health conditions can be challenging to apply to cancer pharmacogenomics research. We employed a step-wise approach of studying a reproducibly measurable serum protein, sVEGFR2, in a population of volunteers who did not have cancer, to identify a genetic variant (rs34231037/C482R) as a marker for response to VEGFR2 kinase inhibitors. The association of rs34231037 with serum concentrations of sVEGFR2 [sVEGFR2] was replicated first in unrelated cancer patients. In a separate cohort of patients with renal cancer, the uncommon gene variant was associated with lower baseline [sVEGFR2] measures and carriers experienced greater decline in [sVEGFR2] over 4 weeks of pazopanib exposure compared with noncarriers. We expect this genetic marker might have a clinically significant effect on treatment outcomes with VEGFR2 kinase inhibitors.

Materials and Methods

Human subjects

This study was approved by institutional review boards (IRB) at the University of Chicago (Chicago, IL) and the University of Maryland (Baltimore, MD). All participants from the six different studies in the three study cohorts provided informed consent for use of their specimens in pharmacogenetic studies (see Supplementary Materials and Methods for additional detail).

Study cohort 1. The Amish Heredity and Phenotype Intervention (HAPI) Heart study. The HAPI Heart Study began in 2003 to identify genes that interact with environmental exposures to influence risk for cardiovascular disease. Study design and phenotyping procedures have been previously described in detail (24, 25). Briefly, healthy Amish subjects, ages 20 to 80 years, underwent a detailed medical examination including blood pressure, anthropometry, total fat mass by dual energy X-ray absorptiometry, fasting blood draw for lipids and other cardiovascular markers and for extraction of DNA for genetic studies, and four short-term interventions designed to challenge cardiovascular function. For this study, fresh-frozen sera, collected at 2 independent time points either 6 hours or 1 week apart, were available for measurement of [sVEGFR2] in 736 participants.

Study cohort 2. Biomarker validation and cancer patient replication cohorts. A pharmacokinetic, pharmacodynamic, and pharmacogenetic study of sorafenib and blood pressure elevation in patients with advanced malignancies. Study design and patient population have been previously described (26). Sera and DNA samples before administration of sorafenib were available for 41 participants with advanced cancer.

A randomized phase II trial comparing cetuximab with concurrent pemetrexed/cetuximab therapy for non–small cell lung cancer refractory to primary treatment. This study enrolled 43 patients with advanced non–small cell lung cancer whose disease progressed after initial platinum-based therapy (27). Sera and DNA samples before administration of the first dose of cetuximab were available for 27 participants.

A dose-escalation study of sorafenib in normotensive patients with advanced malignancies (NCT00436579). This study enrolled patients with advanced solid tumors and normal blood pressure to receive sorafenib at standard and higher doses. Sera and DNA samples before administration of sorafenib were available for 60 participants (28).

Study cohort 3. A phase II study of GW786034 (pazopanib) using a randomized discontinuation design in subjects with locally recurrent or metastatic clear-cell renal cell carcinoma (NCT00244764). This study was used to assess the effect of genotype on pharmacodynamics of pazopanib. Details of the study design were previously reported (29). Of the 225 patients enrolled, 121 had DNA and sVEGFR2 serum measurements available from baseline and after 4 weeks of pazopanib treatment.

Serum sample processing

For the HAPI Heart Study, venous blood was drawn from an arm vein into serum separator tubes, maintained at 4°C for 30 to...
60 minutes before centrifugation, and serum separated and stored at –80 °C storage until assay. For study cohorts 2–3, samples were collected from the upper extremity or a central venous port, incubated at room temperature for 30 minutes and then serum was separated by centrifugation. Samples were aliquotted into cryovials and stored at –70 °C until assay.

Measurement of serum [sVEGFR2]

Serum samples were thawed on ice and processed in triplicate according to manufacturer’s specifications (R&D Systems). Samples in which the results deviated from the manufacturer’s performance specifications (CV > 7% among 3 wells) were reanalyzed. No sample required reanalysis more than once. To control for interplate and interbatch variation, aliquots from a single time-point blood draw from two volunteer subjects were run on each plate in triplicate (internal controls). For details of the normalization procedure based on internal control sample measurements, see Supplementary Materials and Methods.

Genotyping

Genome-wide typing and quality control procedures for the Amish HAPI Heart study have been described previously (also see Supplementary Materials and Methods; ref. 24). Of the 736 individuals with both genome-wide SNP data (Affymetrix 500K SNP platform) and serum [sVEGFR2], 730 also had genotyped data on the human cardiovascular disease risk focused BeadChip (also known as the IITMAT-Broad-CARe (IBC) array; Illumina; ref. 30). This array contains 48,742 markers across 1,458 sibling pairs, 213 parent-offspring pairs, 334 avuncular pairs, 458 KDR SNP Associated with Serum VEGF2 and Pazopanib Pharmacodynamics

American) as covariates. The P value reflects a Wald test statistic. For this replication testing, P values < 0.05 were considered significant. For the 121 renal cell cancer subjects (study cohort 3), linear regression was conducted with an additive genetic model using SAS v9.2, including age as a covariate for baseline and week 4 [sVEGFR2], and baseline [sVEGFR2] as a covariate for changes in [sVEGFR2] after pazopanib exposure.

Results

Intra- and interindividual variation in sVEGFR2 levels in normal human serum

In serial serum samples from healthy volunteers, 87% of the total measurement variance of [sVEGFR2] was interindividual, with the remaining small fraction due to within individual measurement differences over time (33). The high ratio of interindividual to intraindvidual variance suggested that the basis for the interindividual variance could be studied further in larger populations without the need for serial measures. To further characterize the sources of interindividual variance, serum [sVEGFR2] was measured in 736 Old Order Amish subjects who had participated in the HAPI Heart Study (refs. 24, 25, 34; 402 men, 334 women; mean age ± SD = 42.8 ± 13.7 years; mean body mass index (BMI) ± SD = 26.5 ± 4.4 kg/m²). Median serum [sVEGFR2] was 9.05 ng/mL (interquartile range: 8.03–10.11) with an approximate normal distribution (Fig. 1). Men had higher concentrations (mean ± SD = 9.33 ± 1.49 ng/mL) than women (mean ± SD = 8.74 ± 1.67 ng/mL; P < 0.0001). Variance component analysis revealed [sVEGFR2] to be associated with age, BMI, and diastolic blood pressure (Table 1). Sex and age accounted for 4.4% of the variation, with age having the greater impact on [sVEGFR2]. Systolic blood pressure, fat mass, and pulse wave velocity (PWV), a measure of large vessel arterial stiffness, were also associated with variation in [sVEGFR2] but explained a trivial proportion of the variance.

Heritability of [sVEGFR2]

The 736 Amish subjects of the HAPI Heart Study constituted 458 sibling pairs, 213 parent-offspring pairs, 334 avuncular pairs,
Table 1. Correlation of serum [sVEGFR2] with selected variables

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<tr>
<td>DBP (mmHg)</td>
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<td>0.0002</td>
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<tr>
<td>Carotid/femoral PWV (m/s)</td>
<td>-6 ± 60</td>
<td>0.63</td>
<td>99 ± 58</td>
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NOTE: Total fat mass was measured by dual energy X-ray absorptiometry.
Abbreviations: BM, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure; PWV, pulse-wave velocity; β, effect size (pg/mL); SE, standard error.

and 153 first cousin pairs. A polygenic model of [sVEGFR2], adjusting for sex and age, demonstrated [sVEGFR2] to be a strongly heritable trait (h² = 0.69). This estimate was virtually unchanged with inclusion of a random household and dominance effect into the model.

Genome-wide association analysis of [sVEGFR2]

The initial agnostic genome-wide association analysis of 736 HAPI Heart Study subjects with the Affymetrix 500K SNP genotype data identified a cluster of SNPs on chromosome 4 significantly associated with [sVEGFR2]. The top 687 serum [sVEGFR2]-associated SNPs were all on chromosome 4 and spanned a 3.5 Mb region that included several candidate genes, including FIP1L1, PDGFRα, KIT, and KDR (Fig. 2 and Table 2). For the most significant SNP, rs725344, the effect size of each copy of the minor T allele (allele frequency = 0.12) was a decrease of 1.52 ng/mL [sVEGFR2] (P = 8 × 10⁻⁶⁰). The strong association of [sVEGFR2] with multiple SNPs on chromosome 4q11-q12 and inferences from the known founder population structure of the Lancaster County Amish guided further analysis. The causative SNP was expected to be in strong linkage disequilibrium with rs725344 and might have been introduced into the Lancaster County Amish population through a single or small number of founders. The rs725344 mutation therefore marks a broader founder haplotype such that all SNPs on this haplotype show association with [sVEGFR2]. Because this haplotype would have been passed down from the founder(s) to the present day Lancaster County Amish for only 12 to 14 generations, opportunity for recombination would be limited and the causative variants could be up to several Mb away. Consistent with this assumption, we performed multivariate regression association analysis with single timepoint serum [sVEGFR2] in 128 unrelated advanced solid tumor patients enrolled in clinical trials at the University of Chicago (Chicago, IL). We detected no association between rs725344 (allele frequency = 0.20) and serum [sVEGFR2] (β = 0.23 ng/mL; P = 0.51) in this heterogeneous cancer patient population.

On the basis of the assumption that rs725344 was in linkage disequilibrium (LD) with a functional variant within a broad linkage peak in the Amish, but not in LD in the heterogeneous cancer patient population, we pursued two approaches to identify variants with detectable effects on [sVEGFR2]. First, we identified candidate variants in the larger population within the 3.5 Mb linkage peak and tested their association with [sVEGFR2] directly in the 128 patients with cancer. Subsequently, we evaluated candidate loci in the KDR gene in the Amish using the Illumina cardiovascular disease (IBC) chip, which had more extensive coverage of KDR, including rare coding region alleles (30).

Evaluation of candidate gene variants for association with [sVEGFR2]

We used the bioinformatics tool SCAN (35) to identify all genes within the locus and then accessed the 1000 Genomes Project (36) to identify all missense polymorphisms within those genes. This approach identified four coding variants (Supplementary Table S1) within FIP1L1, PDGFRα, and KDR with minor allele frequencies > 0.02 in populations of European ancestry. In addition, the common polymorphism in the 5’-untranslated region of KDR, rs7667298, had been demonstrated to affect VEGFR2 expression in vitro (37). None of these candidate variants demonstrated association with [sVEGFR2] in the heterogeneous cancer patient population (study 2 cohort, see Materials and Methods; Supplementary Table S1).

![Figure 2. Genome-wide association of SNPs with serum [sVEGFR2]. Manhattan plot of each SNP on the genotyping platform by chromosome (horizontal axis) versus the –log P value for association with serum [sVEGFR2] (vertical axis). Chr, chromosome.](image-url)
Rs34231037 is associated with sVEGFR2 response to pazopanib. VEGFR2 kinase inhibitors routinely cause circulating [sVEGFR2] measures to decline within the first 4 weeks of exposure (18–23) and the magnitude of change in [sVEGFR2] has been associated with increased response to therapy in thyroid and lung cancer (18, 23). With the biologic relevance of rs34231037 established as a significant predictor of [sVEGFR2] in the Amish and unrelated cancer patients, we hypothesized it might also play a role in differential responses to inhibitors of the VEGF signaling pathway. In an independent group of 121 patients with renal cell cancer treated on clinical trials with pazopanib (study 3 cohort, see Materials and Methods), serial [sVEGFR2] measures were available before, and 4 weeks after the initiation of continuous oral pazopanib therapy 800 mg daily. Patients with the G allele not only had lower baseline [sVEGFR2] measures (Fig. 4A), but also experienced greater decline over 4 weeks in [sVEGFR2] with similar effect size as in the Amish (1.85 ng/mL lower in G allele carriers; $P = 0.025$; Fig. 3B).

As KDR was within 1.3 Mb of the top signal, we considered this gene the prime candidate for more in depth analysis. During the course of our investigation, data from the IBC chip became available from 730 of the 736 original Amish subjects. During the course of our investigation, data from the IBC chip became available from 730 of the 736 original Amish subjects. In the Amish there were 27 nonmonomorphic SNPs in or near KDR. Single SNP association analysis with [sVEGFR2] revealed a missense mutation in exon 11, C482R caused by an A to G change (rs34231037) to have the lowest $P$ value, $2.7 \times 10^{-37}$ (Supplementary Table S2). Among the Amish, in an additive genetic model, the minor G allele lowered [sVEGFR2] approximately 1.80 ng/mL per allele (Fig. 3A). This finding was consistent with our original hypothesis, that (i) rs725344 would be, in the Amish, a proxy on our initial genotyping array in LD with rs34231037 and [sVEGFR2]; and (ii) the SNP would not be in LD with rs725344 among a more heterogeneous population of European ancestry (such as the 128 University of Chicago cancer patient cohort; see Supplementary Results for a description of the LD assessment).

Rs34231037 is a determinant of [sVEGFR2] in cancer patients. The candidate SNP rs34231037 met our expectations for a SNP that would be associated with serum [sVEGFR2] in the heterogeneous population of patients with cancer of European ancestry in the University of Chicago cohort. Mechanistically, we considered that rs34231037 encodes a nonsynonymous variant, C482R, located in the fifth of 7 immunoglobulin-like (Ig-like) domains of the extracellular region, formed by amino acids 421–548. This cysteine is one of four in the fifth Ig-like domain conserved throughout homologues of KDR in the chordates (from T. nigroviridis) (pufferfish), to G. gallus (domestic chicken), to M. musculus (mouse), through H. sapiens; see Supplementary Fig. S2). We genotyped rs34231037 in 128 advanced cancer patients enrolled in University of Chicago trials (study 2 cohort, see Materials and Methods). Using a regression model for additive effects of the allele and incorporating sex, age, body mass index, and self-reported race categories, the rs34231037 minor allele was associated with serum [sVEGFR2] with the same direction and a similar effect size as in the Amish (1.85 ng/mL lower in G allele carriers; $P = 0.025$; Fig. 3B).
either of the cancer cohorts (ever, rs10050046 was not associated with serum [sVEGFR2] in [sVEGFR2]-lowering alleles act independently in the Amish. How- cohort, and 0.09 ng/mL, with [sVEGFR2]. Third, we replicated these in KDR GWAS in a healthy population and identi-

VEGFR2 kinase inhibitors. Second, we performed an agnostic itability of [sVEGFR2] as an endophenotype for response to pharmacogenetic biomarker. In a step-wise approach, we approach of endophenotyping to the discovery of a novel cancer human schizophreniform behavior (39), we employed the in genetic studies, for example of grasshopper body size (38) and this SNP affects the pharmacodynamic response to pazopanib. As 

nized as a pharmacodynamic marker of VEGFR2 inhibition and discover a SNP with reproducible effects on that peptide in other variants associated with [sVEGFR2]

In the Amish, conditional analyses of both the GWAS and IBC chips were run, including rs34231037 as a covariate in the model to determine the impact on other variants in the chromosome 4 region. Several SNPs on chromosome 4 in the 56–57 Mb region remained highly significant from the imputed data, but had lower effect size than rs34231037. The most significant of these other SNPs was rs10050046 located 56 Kb from rs34231037. The minor allele C has frequency 0.37 and was associated with decreased levels of [sVEGFR2] (0.53 ng/mL per allele; \( P = 3.0 \times 10^{-11} \)), less than one-third the magnitude of effect of rs34231037. In the primary GWAS, there was marginal association between rs10050046 and [sVEGFR2] (\( P = 10^{-3} \)). The LD between rs10050046 and rs34231037 is \( r^2 = 0.04 \) and \( D' = 0.8 \) suggesting that the two [sVEGFR2]-lowering alleles act independently in the Amish. However, rs10050046 was not associated with serum [sVEGFR2] in either of the cancer cohorts (−0.04 ng/mL, \( P = 0.86 \) in the study 2 cohort, and 0.09 ng/mL, \( P = 0.67 \) in the study 3 cohort).

Discussion

We performed a GWAS of a serum peptide in the Amish to discover a SNP with reproducible effects on that peptide in patients with cancer. This phenotype [sVEGFR2] is now recognized as a pharmacodynamic marker of VEGFR2 inhibition and this SNP affects the pharmacodynamic response to pazopanib. As in genetic studies, for example of grasshopper body size (38) and human schizophreniform behavior (39), we employed the approach of endophenotyping to the discovery of a novel cancer pharmacogenetic biomarker. In a step-wise approach, we first characterized the repeatability, interindividual variance, and heritability of [sVEGFR2] as an endophenotype for response to VEGFR2 kinase inhibitors. Second, we performed an agnostic GWAS in a healthy population and identified rs34231037/C482R in KDR, the gene encoding the VEGFR2 protein, to be associated with [sVEGFR2]. Third, we replicated these findings in two cancer populations. Fourth, we extended these findings by demonstrat-

that this variant is a marker for pharmacodynamic response to the kinase inhibitor, pazopanib.

The [sVEGFR2] protein is an alternative spliced product of KDR and functions as a physiologic inhibitor of developmental and reparative lymphangiogenesis (17). In situ hybridization demonstrated mammalian expression of the alternative splice product in epithelium such as in the cornea and skin. The product of this transcript appears to be monomeric and to have higher relative avidity for VEGF-C than VEGF-A. In the mouse cornea, [sVEGFR2] preferentially regulates lymphangiogenesis. The extent to which this alternative splice product contributes to the [sVEGFR2] protein detected in human serum and whether the circulating protein plays additional roles in regulating human angiogenesis and lymphangiogenesis is not known.

The function of the rs34231037/C482R variant has been previously characterized in studies of hemangioma (40). The amino acid is located in the extracellular Ig-like domain V, distant from the VEGF ligand–binding site (41). Recombinant cell transfection studies revealed no differences in VEGF-induced phosphorylation or expression of VEGFR2. However, the substitution of arginine for cysteine diminished formation of complexes by VEGFR2 with β1 integrin and the integrin receptor-like protein TEM8. This complex was associated with VEGFR2-mediated activation of VEGFR1 transcription and protein expression. With less VEGFR1 expression, endothelial cells demonstrate greater sensitivity to activation of VEGFR2 signaling by VEGF binding. This amplified sensitivity to VEGF/VEGFR2 ligation might explain the potential for greater sensitivity of G allele carriers to pazopanib treatment and potentially greater anticancer activity of VEGFR2 inhibitors in patients with this variant.

The rs34231037 polymorphism is a common variant in the Amish (minor allele frequency = 0.1) but an uncommon variant in the larger outbred Caucasian population (minor allele frequency = 0.02). We expect this SNP might have a clinically significant effect on outcomes of therapy, as the magnitude of change in [sVEGFR2] has been associated with increased response to therapy in thyroid and lung cancer (18, 23). As allele carriers comprise only a small subset (i.e., approximately 3%) of all patients, almost all individual trials will be underpowered to demonstrate clinically significant effects. We have not excluded additional genetic

![Figure 4. Association of rs34231037 with changes in serum [sVEGFR2] after pazopanib therapy. Dot and boxplots demonstrate: A, replication of the association between the SNP and baseline serum [sVEGFR2] among an independent cohort of 121 renal cancer patients, (B) the serum [sVEGFR2] measurements by genotype in the same 121 subjects after 4 weeks pazopanib therapy, and (C) the absolute change in serum [sVEGFR2] among these subjects by genotype.](image-url)
variants contributing to interindividual differences in baseline [sVEGFR2] and important interactive covariates for explaining differences in response to VEGFR2 kinase inhibitors is the subject of ongoing investigation.

Despite the commercial availability of 9 drugs in the class since 2006, a clinically useful biomarker to guide therapy with VEGFR2 inhibitors remains elusive. Our finding of a germline variant within KDR with reproducible effects on the response of the pharmacodynamic marker [sVEGFR2] warrants further investigation. This might provide important insights into mechanisms underlying interindividual variation in response to kinase inhibitors, and approaches to deliver anticancer therapy more effectively.

Disclosure of Potential Conflicts of Interest

C. F. Xu and L. Pandite are employees of and hold ownership interest (including patents) in GlaxoSmithKline. M. I. Ratian reports receiving a commercial research grant from Oncometrix Science and is a consultant/advisory board member for Genentech. A. Shuldiner is an employee of Regeneron Genetics Center and is a consultant/advisory board member for USDS, Inc. No potential conflicts of interest were disclosed by the other authors.

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Development of methodology: M. I. Maitland, S. Das, N. Bing

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): M. J. Maitland, C. F. Xu, S. Das, N. Bing, Y. Liu, L. Pandite, B. Mitchell


Writing, review, and/or revision of the manuscript: M. I. Maitland, C. F. Xu, E. R. Gamaizone, Y. Thomean, M. R. Levine, N. Bing, Y. Liu, L. Pandite, J. R. O’Connell, B. Mitchell, M. J. Ratian, A. Shuldiner

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): M. I. Maitland, K. A. Ryan, M. R. Levine

Study supervision: M. I. Maitland, L. Pandite, A. Shuldiner

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### Clinical Cancer Research

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