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Human Cancer Biology

Clinical Cancer Research

Novel Functional Germline Variants in the VEGF Receptor 2 Gene and Their Effect on Gene Expression and Microvessel Density in Lung Cancer

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Abstract

Purpose: VEGF receptor 2 (VEGFR-2) plays a crucial role in mediating angiogenic endothelial cell responses via the VEGF pathway, and angiogenesis inhibitors targeting VEGFR-2 are in clinical use. As angiogenesis is a host-driven process, functional heritable variation in *KDR*, the gene encoding VEGFR-2, may affect VEGFR-2 function and, ultimately, the extent of tumor angiogenesis.

Experimental Design: We resequenced *KDR* using 24 DNAs each from healthy Caucasian, African American, and Asian groups. Nonsynonymous genetic variants were assessed for function by phosphorylation assays. Luciferase reporter gene assays were used to examine effects of variants on gene expression. *KDR* mRNA and protein expression and microvessel density (MVD) were measured in non–small cell lung cancer (NSCLC) tumor samples, and matching patient DNA samples were genotyped to test for associations with variants of interest.

Results: *KDR* resequencing led to the discovery of 120 genetic variants, of which 25 had not been previously reported. Q472H had increased VEGFR-2 protein phosphorylation and associated with increased MVD in NSCLC tumor samples. −2854C and −2455A increased luciferase expression and associated with higher *KDR* mRNA levels in NSCLC samples. −271A reduced luciferase expression and associated with lower VEGFR-2 levels in NSCLC samples. −906C and 23408G associated with higher *KDR* mRNA levels in NSCLC samples.

Conclusions: This study has defined *KDR* genetic variation in 3 populations and identified common variants that impact on tumoral *KDR* expression and vascularization. These findings may have important implications for understanding the molecular basis of genetic associations between *KDR* variation and clinical phenotypes related to VEGFR-2 function. *Clin Cancer Res; 17(16); 5257–67. ©2011 AACR.*

Introduction

VEGF receptor 2 (VEGFR-2; encoded by kinase insert domain receptor, *KDR*) is an important factor in tumor development and progression due to its proangiogenic effects (reviewed in ref. 1). VEGFR-2 levels correlate with tumor growth rate, microvessel density (MVD), proliferation, and tumor metastatic potential in several cancers (2, 3). Experimental blockage of the interaction between VEGF-A and VEGFR-2 inhibits tumor growth and metastasis (4). Indeed, angiogenesis inhibitors targeting the tyrosine kinase activity of VEGFR-2 are an effective class of anticancer drugs (5, 6). Although small-molecule angiogenesis inhibitors interact with several targets, they are all characterized by a strong inhibitory activity of VEGFR-2 (7–9). In addition, the *in vivo* activity of one of them, sorafenib, is primarily mediated through VEGFR-2–mediated inhibition of angiogenesis (10).

Because gene expression in humans is in part determined by genetic factors (11) and angiogenesis is a host-mediated process (12), functional germline variation in *KDR* may contribute to variability in tumor endothelial function and, consequently, may affect cancer prognosis and the efficacy of VEGFR-2 inhibitors. Indeed, baseline soluble VEGFR-2 levels have been associated with a reduction in tumor size

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Note: Supplementary data for this article are available at Clinical Cancer Research Online (http://clincancerres.aacrjournals.org/).

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Translational Relevance

Angiogenesis is a host-driven process that represents a crucial step in tumor development. The VEGF receptor 2 (VEGFR-2) mediates angiogenic endothelial cell responses via a downstream signaling pathway, and its activity is targeted by several small molecule angiogenesis inhibitors. However, no biomarkers have yet been identified to guide the use of these drugs. We have characterized germline genetic variation of *KDR*, the gene encoding VEGFR-2, in 3 ethnic groups and identified functional variants that associate with *KDR* mRNA and protein levels and microvessel density in non-small cell lung cancer tumor patient samples. These genetic variants provide strong candidates for the prospective testing of associations with patient outcome, the clinical effect of angiogenesis inhibitors, and other clinical cancer phenotypes related to angiogenesis.

and clinical benefit in response to sunitinib treatment (13). Although no molecular marker is currently used to guide antiangiogenesis therapy (14), the efforts toward identifying genetic prognostic biomarkers and predictive markers of response to VEGFR-2 inhibitors could be highly informed by studies characterizing *KDR* genetic variants. Furthermore, limited data are available on *KDR* germline genetic variation in the population, its ethnic differences, and its effect on gene function or tumoral expression. Hence, in this study, we defined common germline *KDR* variation in different ethnic groups and assessed the phenotypic impact of putative functional variants. These aims were achieved by resequencing healthy Caucasian, African American, and Asian individuals; carrying out bioinformatic and *in vitro* functional analyses; and finally, rationally selecting variants to test their association with *KDR* expression and MVD in non–small cell lung cancer (NSCLC) tumor specimens.

Materials and Methods

KDR resequencing

Twenty-four germline DNA samples each from healthy Caucasians, Asian Chinese, and African Americans obtained from the Coriell Institute Human Variation Collection (available from: http://www.coriell.org) were chosen for resequencing. All 30 exons were sequenced (Fig. 1). In addition, sequenced noncoding regions comprised flanking intronic sequences, promoter, and the 5′-upstream region containing evolutionarily conserved noncoding genomic regions (determined by comparative genomics using the University of California, Santa Cruz genome browser; Supplementary Table S1) and regions determined to contain transcription factor binding sites according to computational prediction using Cluster–Buster (available from: http://zlab.bu.edu/cluster-buster/ Supplementary Table S2; ref. 15). Primers used for PCR amplification are listed in Supplementary Table S3. PCRs were set up using forward and reverse primers, HotStar DNA polymerase (Qiagen), and 10 ng of DNA. After initial 15 minutes of activation at 95°C, touchdown cycles were carried out: 95°C for 30 seconds, touchdown annealing from 65°C to 54.5°C (−1.5°C per cycle) for 30 seconds and 72°C for 1.5 minutes for 7 cycles, following the standard cycle of 95°C for 30 seconds, 55°C annealing for 30 seconds, and 72°C for 1.5 minutes for 30 cycles. PCR products were purified using the MultiScreen PCR Purification Kit (Millipore) and eluted in 30 μL elution buffer. DNA sequencing was carried out at the University of Chicago DNA Sequencing Core Facility by Sanger dye-terminator sequencing. Sequence analysis was carried out using Sequencher (Version 4.7; Gene Codes).

Linkage disequilibrium analysis and selection of tagging single-nucleotide polymorphisms

Summary statistics of DNA sequence variation were calculated using SLIDER (available from: http://genapps.uchicago.edu/slider). Linkage disequilibrium (LD) analysis of single-nucleotide polymorphisms (SNP) among the 3 ethnic groups was carried out using the VG2 program (available from: http://pga.gs.washington.edu/VG2.html). For selection of haplotype tagging SNPs (tSNP), SNPs were clustered using LD Select (16) integrated in the VG2 program. The parameters for the selection of tSNPs were $r^2 \geq 0.8$ and a minor allele frequency (MAF) of 5% or more. Pairwise LD analysis was done by the LD Plotter, and r^2 values were calculated using an iterative expectation-maximization algorithm (17).

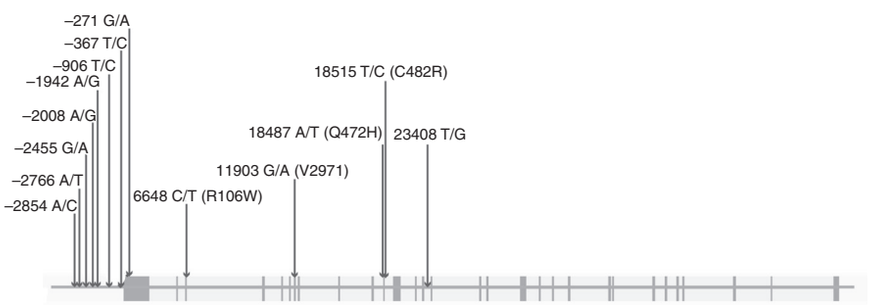

Figure 1. Genomic structure of *KDR* and SNPs investigated in this study. SNPs that were examined in our studies are shown with boxes indicating exons. SNPs are numbered with reference to the first base of the ATG start codon. Nonsynonymous SNPs are shown with the appropriate amino acid variation. The figure does not match the exact scale.

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Bioinformatic analyses

The putative functional effects of SNPs were examined using FastSNP (18). The transcription factor binding site analysis of FastSNP was complemented using PROMO (19). WWW Promoter Scan (available from: http://www.bimas.cit.nih.gov/molbio/proscan/index.html) was used to predict functional *KDR* promoters. National Center for Biotechnology Information (NCBI) open reading frame (ORF) finder (available from: http://www.ncbi.nlm.nih.gov/gorf/gorf.html) was used to determine ORFs.

VEGFR-2 phosphorylation assays

The coding region of *KDR* was PCR amplified from cDNA using the following primers: 5′-TTAAACTTAAGCTTGGTACCATGGAGAGCAAGGTGC-3′ and 5′-TAGACTCGAGCGGCCGCTCACAGATCCTCTTC-3′. The pcDNA5 FRT vector (Invitrogen) was PCR amplified using primers 5′-GCGGCCGCTCGAGTC-3′ and 5′-GGTACCAAGCTTAAG-3′. Vector and insert were joined by In-Fusion Cloning (Clontech) according to the manufacturer's instructions. The *KDR* variants R106W, V297I, Q472H, and C482R were generated using the QuikChange Site-Directed Mutagenesis Kit (Agilent Technologies) as per the manufacturer's instructions.

HEK293 (ATCC) cells were grown for 24 hours in Dulbecco's modified Eagle's medium (DMEM) with 10% FBS and transfected with $Ca_3(PO_4)_2$ precipitation. At 30 hours after transfection, cells were starved overnight in DMEM supplemented with 1% bovine serum albumin (BSA). Transfected cells were stimulated with 1.5 nmol/L VEGF-A_{165}. Cell lysates were resolved on SDS gels, blotted to polyvinylidene difluoride membranes, and immunodecorated with phospho-specific pY1175 or VEGFR-2 55B11 antibodies (Cell Signaling). All experiments were conducted in triplicates, and immunoblots were quantified by densitometric scanning using ImageQuant RT ECL (Affymetrix-GE Healthcare).

Dual-luciferase assays

A pGL2 plasmid (Promega) with *KDR* 5′ upstream promoter region and firefly luciferase gene was a gift from Dr. Patterson (20). Site-directed mutagenesis was carried out by PCR according to the method of the QuikChange Site-Directed Mutagenesis Kit. Two allelic variations were introduced (−367C/T, −271G/A). Plasmids containing all major alleles (−367C, −271G), the −367T allele, the −271A allele, and −367T/−271A alleles were generated.

To generate constructs containing variants at the *KDR* loci −2,854, −2,455, −2,008, and −1,942, 2 PCRs of overlapping sequence were designed. Primers for the PCR amplifying the upstream region were the forward primer 5′-ACCCCAGTTCCTGGTTCAATGCCT-3′ and the reverse primer 5′-GGGAAGCTTGTCTTTTACCTCCCAGA-3′. These primers were used to amplify human genomic DNA with Phusion High-Fidelity polymerase (NEB). This fragment was cloned into pGL4.20 (Promega) using *Bgl*II and *Hin*dIII sites. The second PCR was amplified using the forward primer 5′-GCAATTGTGGGAAGAGAAGGGTGAC-3′ and the reverse primer 5′-GTAAGCTTCCGCAGCGCAGGACAGTT-3′. This PCR fragment was cloned into the construct containing the *Bgl*II-*Hin*dIII fragment in pGL4.20 using the *Hin*dIII site in the reverse primer and an *Ase*I site in the initial construct, which was also present in the overlapping PCR fragment. The final construct contained a fragment between −2,659 and +235 of *KDR*. Site-directed mutagenesis was carried out as before and allelic variations were introduced: −2854A/C (rs1551645), −2455G/A (rs1551641), −2008A/G (rs28517654), and −1942A/G (rs28481683).

SVEC4-10 endothelial cells (a gift from Dr. Mark Lingen) were cultured in DMEM with 10% FBS. SVEC4-10 endothelial cells in 24-well plates were transfected by lipofectamine method (Invitrogen), using the reporter gene plasmid construct of interest and a *Renilla* TK plasmid (Promega). Cells were lysed 40 hours after transfection, and the luciferase assays were then conducted as per the manufacturer's instructions. Each construct was transfected 3 times for each experiment, using triplicate wells. The ratio of firefly to *Renilla* luciferase served as a measure of the luciferase activity. The luciferase activity in each experiment was normalized to the luciferase activity of the wild-type construct.

NSCLC patients and tissue microarray preparation

The cohort consisted of 170 sequential Polish Caucasian patients who were systematically diagnosed with resectable NSCLC and from whom tumors were collected in the tissue bank at the Medical University of Gdansk, Poland. The majority of patients were males, with squamous cell histology, smokers, and older than 60 years. Further details of the cohort are described in Dziadziuszko and colleagues (21). Primary tumors were fresh frozen at the time of surgery and stored at −80°C.

Representative regions of the blocks of consecutive NSCLC patients were selected from an archive of the Medical University of Gdansk (Poland) and microscopic diagnosis was verified by a board-certified pathologist. Hematoxylin-eosin–stained tissue sections with greater than 70% tumor cellularity were selected by the study investigator (R. Dziadziuszko) and verified by 2 pathologists at the University of Colorado Cancer Center. Three cylindrical tissue cores (1.5 mm in diameter) were punched from neoplastic areas with a puncher provided by customized tissue microarray service (MaxArray; Invitrogen). Total RNA and genomic DNA were prepared from corresponding fresh-frozen tumor samples, using AllPrep DNA/RNA kit (Qiagen).

VEGFR-2 and MVD staining by immunohistochemistry

Immunohistochemical staining was carried out using horseradish peroxidase (HRP)-labeled dextrose-base polymer complex bound to secondary antibody (DAKO Cytomation). In brief, 4-μm tissue microarray sections paraffin sections were deparaffinized in xylenes, rehydrated through graded ethanol solutions to distilled water, and then washed in Tris-buffered saline. Antigen retrieval was carried out by heating sections in Citra Plus Buffer

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(Biogenex), pH 6, for 15 minutes in a microwave oven. Endogenous peroxidase activity was quenched by incubation in 3% H_2O_2 in methanol for 5 minutes. Nonspecific binding sites were blocked using Protein Block (DAKO) for 20 minutes. Then tissue sections were incubated for 1 hour at room temperature with the rabbit polyclonal antibody against a 1:100 dilution of VEGFR-2 (catalogue no. 676488; Calbiochem, Merck) for VEGFR-2 staining and with mouse monoclonal antibodies against CD31 (clone JC70A, 1:40; DAKO) for MVD. This step was followed by 30-minute incubation with goat anti-rabbit immunoglobulin (IgG) conjugated to an HRP-labeled polymer (Envision System; DakoCytomation) for VEGFR-2 staining and with goat anti-mouse IgG conjugated to an HRP-labeled polymer (Envision+ System; DAKO) for MVD. Slides were then developed for 5 minutes with 3-3′ -diaminobenzidine chromogen, counterstained with hematoxylin, and coverslipped. Negative controls were obtained by substituting primary antibody with nonimmune rabbit IgGs. The staining quantification was carried out using the automated cellular imaging system at the Human Tissue Research Center at the University of Chicago.

For the automated VEGFR-2 scoring, microarrays were scanned at 40× magnification. Each core was analyzed separately by identifying the most representative tumoral area and scoring it. The average score among the 3 areas chosen was then calculated. Positive staining was calculated by applying 2 thresholds, with one recognizing blue background (hematoxylin stained) cells and another recognizing brown positive cells. The percentage of positivity was the area detected by the brown threshold divided by the sum of the area detected by the brown and blue thresholds. The intensity was calculated by masking out all areas not selected by the brown threshold and calculating the integrated optical density of brown within the remaining area. This value was divided by the area in pixels of the brown mask to calculate an average intensity of a selected area.

For the automated MVD determination, CD31 was analyzed by an ACIS (ChromaVision Medical Systems). The image analysis system's MVD application was configured for vessel detection using CD31-stained slides. This was based on applying chromogen masks for high chromogenic staining (brown threshold) and counterstaining (blue threshold), and the minimal and maximal sizes of the vessels. After selection of appropriate regions for MVD counting, the following measurements were captured digitally for each selected region of tissue: total vessel count, mean vessel area (μm^2 occupied by positively stained vessels), and vessel to tissue area ratio (vessel density percentage calculated by the area of blood vessels occupying the area of counterstained tissue). The vessel count was then averaged for each case. MVD was calculated as positively staining vessel areas (in μm^2) divided by total counterstained tissue area (in μm^2).

Genotyping of *KDR* SNPs

Patients from the NSCLC cohort ($n = 170$) were genotyped for −2766A/T, −906T/C, 18487A/T (Q472H), and 23408T/G, using TaqMan SNP genotyping assays (Applied Biosystems), as per the manufacturer's instructions, using a CFX96 Real-Time System (Bio-Rad, Hercules). Genotyping of −271G/A was carried out using a single base extension (SBE) genotyping assay using the following primers: 5′ -CCACCCTGCACTGAGTCCC-3′ (forward PCR primer) 5′-GCAGCGGAGGACAGTTGAG-3′ (reverse PCR primer with one base edited from C to G) 5′-GAAACGCAGCGAC-CACACA-3′ (downstream extension primer). Denaturing high-performance liquid chromatography was used for separation of SBE products.

cDNA synthesis and quantitative PCR

RNA extracted from lung tumor samples was reverse transcribed into cDNA by using a high-capacity RT kit as per the manufacturer's instructions (Applied Biosystems). *KDR* primers originally designed by An and colleagues (22) were used. *18S* served as a control gene, as it exhibits stable expression in NSCLC tumor tissue (23) and was amplified with sense 5′-CGATGCTCTTAGCTGAGTGT-3′ and antisense 5′-GGTCCAAGAATTTCACCTCT-3′ primers. Quantitative PCR of cDNA samples was completed in 3 independent experiments by using a Bio-Rad CFX96 Real-Time System, iQ SYBR Green Supermix (Bio-Rad), and 6 μL cDNA. Thermal cycling parameters were followed by a disassociation step. Absolute quantification of mRNA levels was achieved using commercial human lung total RNA (Ambion, Applied Biosytems) converted to cDNA as above and serially diluted as an internal reference standard curve. mRNA levels were expressed as the ratio of *KDR* to *18S*.

Statistical analyses

For the luciferase reporter gene and phosphorylation assays, comparisons were made between the variant and the reference alleles by paired *t* tests. The association between each SNP and $\log_2$-transformed *KDR* mRNA, VEGFR-2, or MVD levels was tested using univariate linear regression by assuming additive (AA = 0, AB = 1, BB = 2), dominant (AA = 0, AB/BB = 1), and recessive (AA/AB = 0, BB = 1) models. As these are exploratory studies, a nominal *P* value of 0.05 was regarded as significant. For the significant SNP–phenotype associations, we investigated whether age, sex, histology, and pathologic stage were potential confounding variables by multivariate regression in a model including significant SNPs and patient/tumor characteristics. For mRNA expression, the best combination of 2 associated SNPs was determined by multiple regression analysis. Because we had available only a smaller subset of samples ($n = 66$) for mRNA analysis, and hence greater chance of detecting false discoveries than in the wider cohort of patients, for these analyses with SNP genotypes, false discovery rate estimates (*q*-values) were determined using the adaptive 2-stage procedure defined by Benjamini and colleagues (24) and the Excel-based calculator described by Pike (25). All other analyses were carried out using the lm library in the R Statistical Package (26) and Prism (GraphPad).

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Results

KDR resequencing

KDR resequencing led to the identification of 113 SNPs and 7 insertion/deletions in the 3 ethnic groups (data summarized in Supplementary Table S4). Twenty-five variants were not found in the dbSNP Database (available from: http://www.ncbi.nlm.nih.gov/projects/SNP/build 132). In general, the available HapMap data showed that SNP MAFs in HapMap (matched by ethnic group) were similar to the MAFs generated by our resequencing (Supplementary Table S4). Fifteen SNPs were detected in the *KDR* coding region, and 8 of these variants were nonsynonymous. R106W and P839L had not been previously reported in dbSNP.

Comparison of the variants across the different ethnic groups showed interethnic differences, with African Americans carrying 94 variants compared with 58 for Asians and 51 for Caucasians. A stronger pattern of LD was found in Caucasians and Asians than African Americans (Supplementary Fig. S1). Thirty-eight variants were found in all 3 groups. Of the variants with MAF of greater than 5%, 45 were found in Caucasians, 49 in Asians, and 53 in African Americans. Overall, *KDR* genetic variation was characterized by a low level of LD and this study indicates that 20, 21, and 28 tSNPs should be used to interrogate *KDR* common variation in Caucasians, Asians, and African Americans, respectively (Supplementary Fig. S2).

Effect of nonsynonymous SNPs on VEGFR-2 phosphorylation

Bioinformatic analysis of *KDR* variants (Supplementary Table S5) guided the prioritization of SNPs for *in vitro* functional testing. Of the nonsynonymous variants, R106W, Q472H, and C482R were predicted to affect protein function or be potentially damaging and so we examined their effects on VEGFR-2 phosphorylation. In addition, we also tested V297I because of its high frequency in the 3 populations. In HEK293 cells, Q472H showed a 46% increase in VEGFR-2 phosphorylation after VEGF-A_{165} stimulation ($P = 0.035$; Fig. 2). The other nonsynonymous variants did not show any effect on VEGFR-2 phosphorylation.

Effect of potential regulatory SNPs on *KDR* mRNA and protein expression

Bioinformatic analysis of the *KDR* variants identified 58 potential regulatory variants in noncoding gene regions (Supplementary Table S5). We were particularly interested in common SNPs in the 5′ flanking and promoter regions of the gene, which could be assayed using reporter gene assays. We searched bioinformatically for the *KDR* promoter and identified a region from −599 to −349 bp upstream of the start codon. The only 2 common SNPs identified in the promoter and the adjacent 5′ untranslated region (UTR) were −367T/C and −271G/A. Both SNPs were found to alter transcription factor binding sites after further bioinformatic analysis using PROMO (Supplementary Table S5). In reporter gene assays, we found that constructs containing −271A reduced expression to 49% to 55% ($P < 0.0001$) of that from the construct with the reference, −271G, allele (Fig. 3A). Presence of −367C did not alter expression ($P > 0.05$).

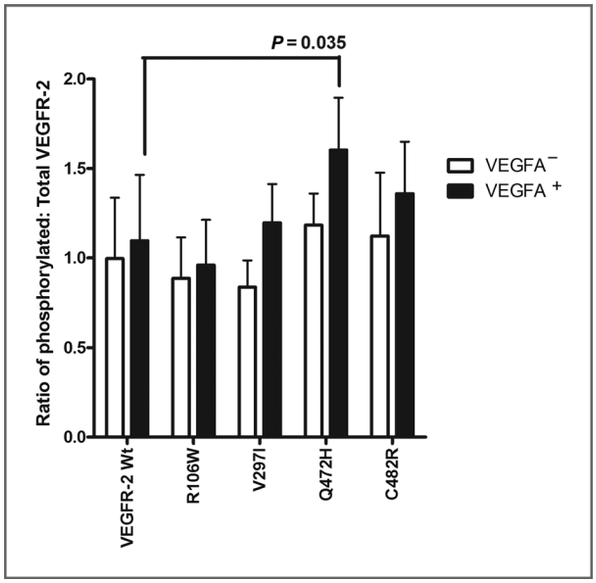

Figure 2. VEGFR-2 phosphorylation in HEK293 cells and effect of nonsynonymous variants. The *y*-axis corresponds to the ratio of phosphorylated VEGFR-2 to total VEGFR-2. Values are normalized to basal phosphorylation levels of reference sequence *KDR*. −, basal phosphorylation levels; +, VEGF-A_{165} stimulation. Wt, reference sequence cDNA. The mean ± SEM of 3 experiments in triplicate is shown. WT, wild type.

We also examined the 5′ flanking region of the gene and identified 4 SNPs that are predicted to alter transcription factor binding sites: −2854A/C, −2455T/A, −2008A/G, and −1942A/G. The effect of these SNPs was tested singly but as 2 pairs of SNPs (−2854A/C and −2455T/A; −2008A/G, and −1942A/G) were in perfect LD in all 3 ethnic groups (Supplementary Figs. S1 and S2), reporter gene constructs were also created that contained the variants linked by LD. In SVEC4-10 cells, constructs containing −2455A or −2854C, or both variants, had 20% ($P < 0.001$), 10% ($P < 0.05$), and 10% ($P < 0.01$) greater expression, respectively, than the reference construct (Fig. 3B).

Association studies of *KDR* variants with *KDR* mRNA and protein expression, and MVD in an NSCLC cohort

Because the −271A, −2455A, −2854C, and Q472H (18487T) variants had functional effects *in vitro*, we prospectively tested their effect on *KDR* gene expression and MVD in tumors. We genotyped −271G/A, −2766A/T (a tSNP for both −2854A/C and −2455T/A; Supplementary Fig. S2) and Q472H in a Caucasian NSCLC cohort. In addition, we also genotyped 2 further variants: −906T/C and 23408T/G. The −906C variant has been associated with serum VEGFR-2 levels and shown to affect expression

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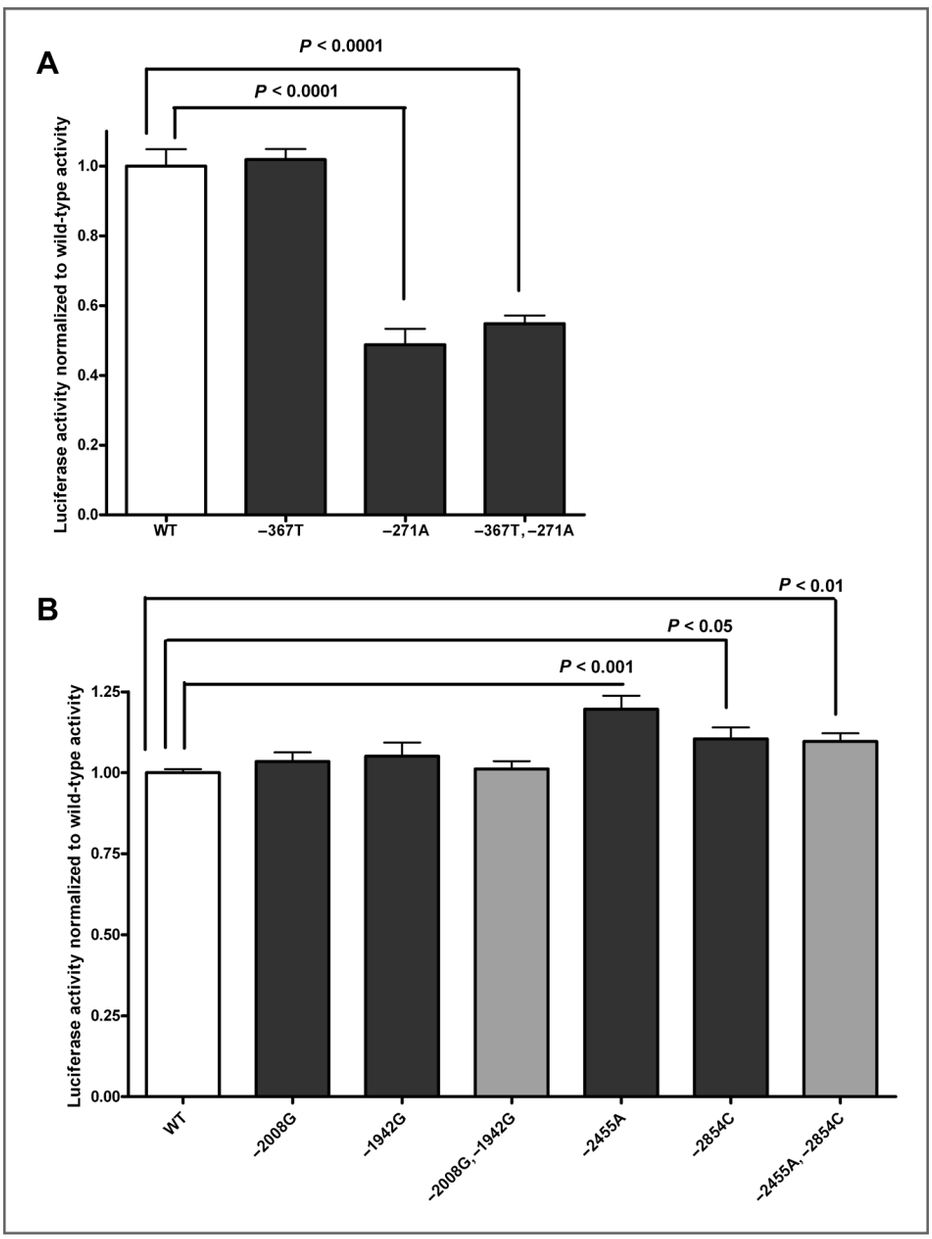

Figure 3. Function of −367T/C and −271G/A (A) and 2854A/C, −2455T/A, −2008A/G, and −1942A/G (B) according to luciferase assays in SVEC4-10 endothelial cells. The mean ± SEM of experiments in triplicate is shown. A, assays examining the −367T/C and −271G/A variants. B, assays examining the −2854A/C, −2455G/A, −2008A/G, and −1942A/G variants. The significant results of paired *t* tests between the wild-type (WT) reference and variant alleles are shown.

in reporter gene assays (27). Bioinformatic analysis predicted that the −906C allele introduces an IKZF2 binding site (Supplementary Table S5); so, as this transcription factor may be involved in mediating *KDR* expression, another *KDR* variant that introduces an IKZF2 binding site, the 23408T allele, was also genotyped to determine the impact of this binding site motif on expression. After genotyping in the NSCLC patients, the MAFs were determined to be 0.33 ($n = 169$ patients), 0.46 ($n = 170$), 0.44 ($n = 166$), 0.29 ($n = 168$), and 0.34 ($n = 169$) for −2766A/T, −906T/C, −271G/A, Q472H, and 23408T/G, respectively, which were comparable with the MAFs of Caucasians from our resequencing and HapMap (Supplementary Table S4). No significant deviation from Hardy–Weinberg equilibrium was observed for any of the SNPs.

We assayed tumoral VEGFR-2 protein and MVD levels in the same individuals by immunohistochemistry ($n = 170$) and quantified *KDR* mRNA levels in a subset of these patients ($n = 66$). Analysis of protein and mRNA levels determined that there was a very modest inverse correlation ($P = 0.03$, $r^2 = 0.07$; Supplementary Fig. S4); hence, we used both mRNA and protein levels to infer the molecular effects of *KDR* SNPs on gene expression. VEGFR-2 protein levels were positively correlated with MVD ($P = 8e\text{-}09$; $r^2 = 0.18$; Supplementary Fig. S5).

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In univariate analyses of mRNA expression, the minor alleles of −2766A/T −906T/C, −271G/A, and 23408T/G correlated with significantly greater expression (Fig. 4A–G). The association of −2766A/T and mRNA expression was consistent with results of the luciferase assay of the −2854A/C and −2455T/A SNPs, which are tagged by −2766A/T. The minor allele of Q472H associated with significantly lower mRNA levels (Fig. 4H–J), probably by altering the splicing machinery due to its vicinity (3 bp) to the intron–exon boundary. After false discovery rate analysis to control for the multiple comparisons, the only association not to maintain significance was −271G/A in the dominant genetic model ($q = 0.05$; Fig. 4F). However, the association of this SNP in the additive model remained significant, as did all the other nominally significant associations with mRNA levels. Multivariate analyses that incorporated combinations of SNP genotypes were carried out. However, possibly due to sample size limitations, the most significant model included only 2 SNPs: 0.98*genotype (−906 TC/CC; $P = 0.037$) + 1.74*genotype (Q472H AA/AT, $P = 0.007$), overall $r^2 = 0.219$ and $P = 0.0004$. The effect of these SNPs seems to be independent, as shown by the lack of LD between them (Supplementary Fig. S3).

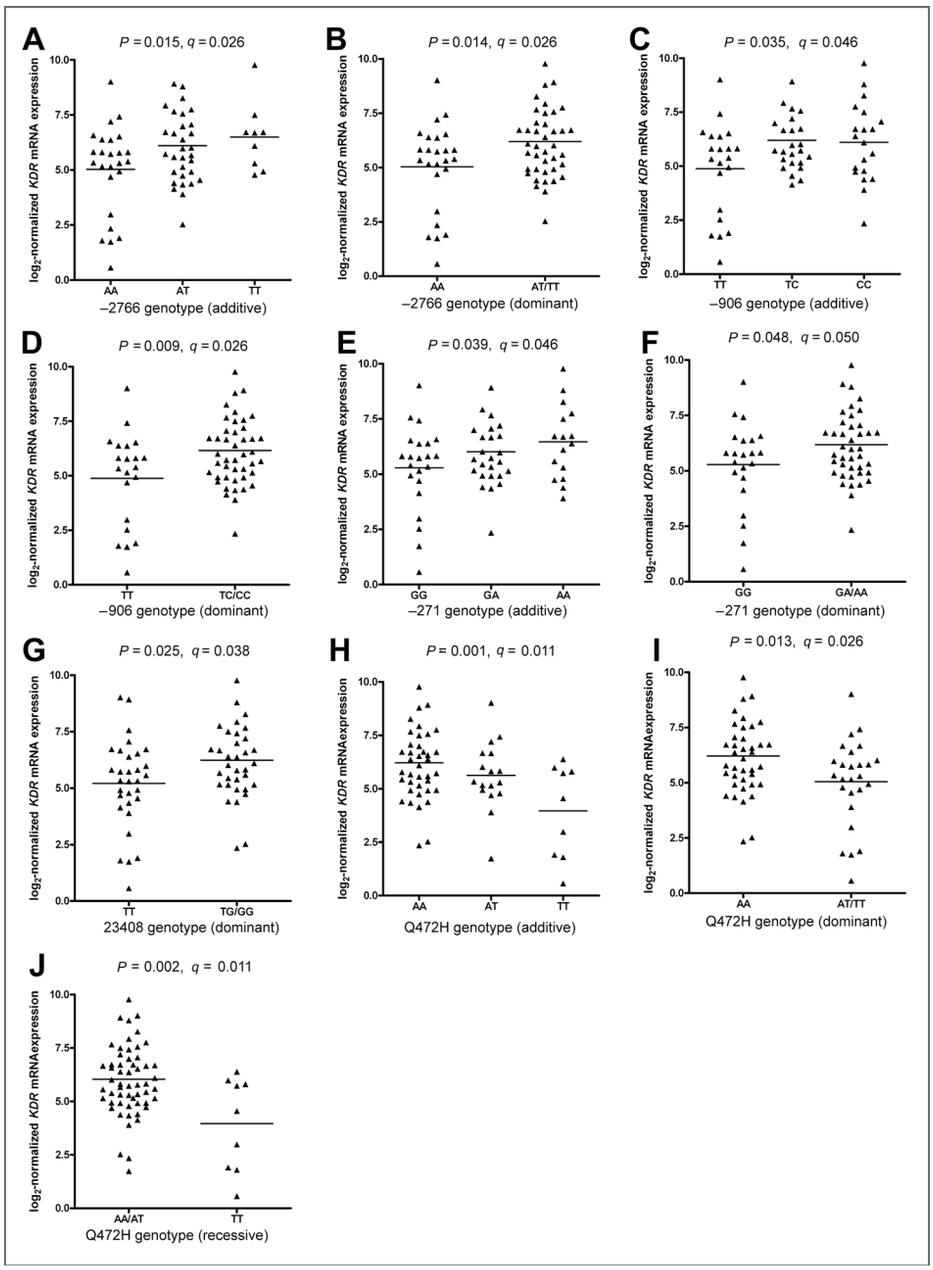

Figure 4. Association between *KDR* genotypes and *KDR* mRNA expression in NSCLC tumor specimens. *KDR* mRNA expression was measured in 66 tumor specimens. The relationship of −2766A/T and mRNA expression in additive (A) and dominant (B) models, respectively; −906T/C genotype and mRNA expression in additive (C) and dominant (D) models, respectively; −271G/A genotype and mRNA expression in additive (E) and dominant (F) models, respectively; 23408T/G genotype and mRNA expression in a dominant model (G); and Q472H genotype and mRNA expression in additive (H), dominant (I), and recessive (J) models, respectively. Nominal statistical significance is denoted by *P* values and the results of false discovery rate testing by *q*-values.

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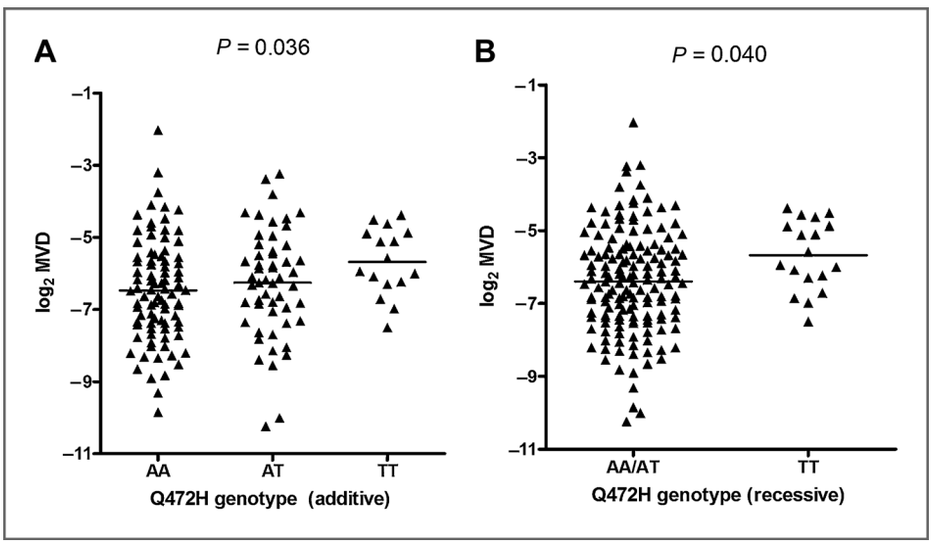

Figure 5. Association between Q472H genotypes and MVD in NSCLC tumor specimens. MVD was measured in 170 tumor specimens. A and B, the relationship between Q472H genotype and MVD in additive and recessive models, respectively.

In univariate analyses of protein expression, no significant associations were found between the genotyped variants and VEGFR-2 protein levels. However, when testing the effect of patient/tumor characteristics, protein expression was lower in later stages of disease (Supplementary Fig. S6). Controlling for early (I–II) versus late (III–IV) stage of disease, we found that the tumors of patients with −271GG/GA genotypes had greater VEGFR-2 levels than tumors from patients with −271AA genotype: −0.32*stage (III and IV; $P = 0.02$) + 0.36*genotype (−271GG/GA; $P = 0.03$); overall $P = 0.01$, $r^2 = 0.054$.

In univariate analysis of MVD, the major allele A of Q472H, coding for wild-type VEGFR-2, associated with lower MVD (additive and dominant: $P = 0.036$ and $P = 0.040$; Fig. 5). After controlling for differences in tumor histology (Supplementary Fig. S7), patients with the Q472H AA genotype (i.e., expressing only wild-type VEGFR-2) were shown to have tumors with lower MVD than patients with AT/TT genotypes: 0.57*histology (adenocarcinoma and large cell carcinoma; $P = 0.01$) −0.67*genotype (Q472H AA; $P = 0.05$); overall $P = 0.005$, $r^2 = 0.050$.

Discussion

This report represents the most extensive molecular genetic study of *KDR*. Our resequencing study identified 120 *KDR* variants, which included 25 previously unreported ones. Furthermore, there were considerable differences between the presence of specific variants and their corresponding frequencies among the 3 ethnic populations. This comprehensive assessment allowed the generation of haplotype tSNPs for genotyping in subjects from Caucasian, African, or Asian backgrounds.

Statistical associations in genetic cancer risk or outcome studies should be supported with molecular mechanistic evidence of SNP function, and the lack of mechanistically based effects of clinical phenotypes is regarded as a major limitation for identifying biomarkers. Very few studies have focused on the identification of common functional *KDR* germline variants (27, 28). We have tested associations of 12 *KDR* SNPs and function in 2 different assays and with molecular phenotypes from tumor samples, and found 5 SNPs that have a significant association with at least one of these measures (Fig. 6). We analyzed 6 SNPs in reporter gene assays and found 3 of these with significant effects. The −2455A and −2854C variants modestly increased reporter gene expression, and these alleles were shown to be associated with increased *KDR* mRNA expression in NSCLC tumors, without an effect on VEGFR-2 protein levels. The −271A variant had a strong negative effect on expression in the reporter assay, and, supportive of this result, patients with the −271AA genotype had less tumor protein expression than subjects with −271GA/GG genotypes, after controlling for disease stage. Furthermore, the observation that VEGFR-2 levels in stages III to IV were significantly lower than in earlier stages seems to be a novel finding in NSCLC.

The decreased protein expression associated with −271A seems to be due to a posttranscriptional mechanism. The −271A allele creates a start codon that introduces an upstream ORF of 207 bp, in conjunction with an in-frame stop codon in the 5′ UTR, and thereby inhibits translation of *KDR* mRNA into protein (29). At the mRNA level in our study, the presence of an A allele was associated with greater tumor *KDR* expression, consistent with the previous association of the −271AA genotype with higher levels of *KDR* mRNA in NSCLC (30). We have also observed a modest negative correlation between mRNA and protein levels. Indeed, discordance between mRNA and protein levels of *KDR* has been found under low glucose conditions (31), which are common in the tumor microenvironment (32). The mechanistic explanation of this finding is that glucose depletion may upregulate *KDR* mRNA expression through the unfolded protein response but downregulate VEGFR-2 levels via a protein degradation mechanism (31).

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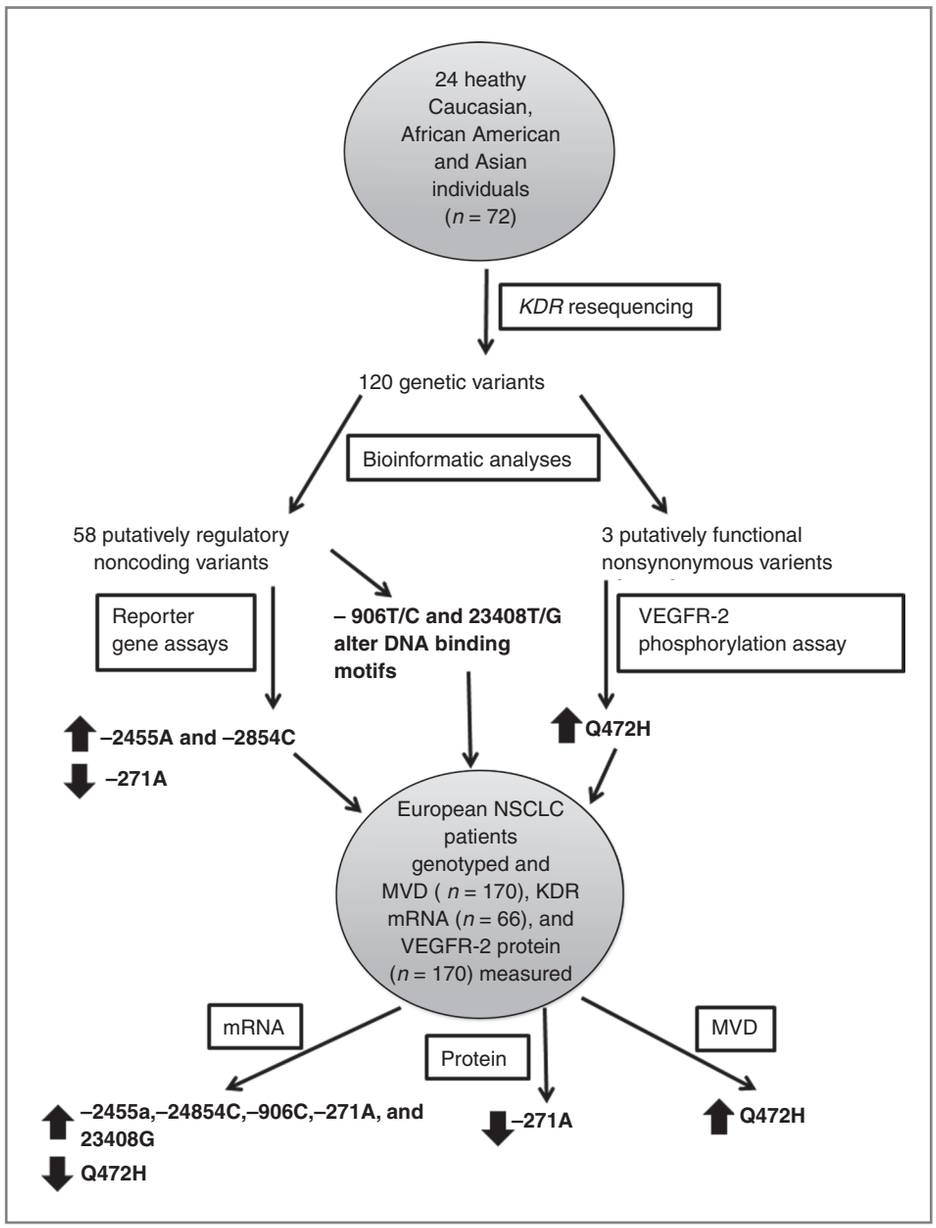

Figure 6. Summary of experimental and analytical approaches used and significant findings. *KDR* was resequenced in 3 ethnic groups, each containing 24 healthy individuals. The genetic variants identified from the resequencing were analyzed for function by using bioinformatic tools. Putatively functional SNPs were examined using reporter gene or VEGFR-2 phosphorylation assays. Functional SNPs, including 2 further putatively functional SNPs, were genotyped in a cohort of European NSCLC patients. These genotypes were tested for associations with *KDR* mRNA, VEGFR-2 protein, and MVD levels from matching tumor samples. SNPs significantly ($P < 0.05$) associated with a phenotype of interest are designated by a block arrow. An up arrow indicates that the variant is associated with increased levels of the phenotype; conversely, a down arrow indicates that the variant is associated with decreased levels of the phenotype.

We examined 2 other putatively regulatory SNPs, −906T/C and 23408T/G, for associations with *KDR* expression. The −906C variant introduces an IKZF2 binding site and increases reporter gene expression in human umbilical vein endothelial cells (27); in agreement with this observation, we found this variant associated with higher expression of mRNA in NSCLC tumors. Bioinformatic analyses predicted that 23408G disrupts an IKZF2 binding site, but this allele was associated with higher mRNA levels. Therefore, it seems that the presence/absence of an IKZF2 binding site motif is not the cause of the differential expression. Instead, this effect may be due to the interaction of another transcription factor, such as GATA2, which putatively binds at this locus (Supplementary Table S4). Alternatively, there may be a functional SNP in LD with 23408T/G that mediates this effect.

Q472H was predicted to have effects on protein function, and this variant had increased phosphorylation after VEGF-A_{165} stimulation. Wang and colleagues examined VEGF-A_{165} binding of VEGFR-2 and found that Q472H increased the binding efficiency (27). In univariate analysis, we observed greater MVD in patients with the Q472H TT genotype. Adenocarcinomas have been shown to have greater MVD (33), and we observed higher MVD in adenocarcinomas and large cell carcinomas (Supplementary Fig. S7). We controlled for tumor histology and again found a correlation between patients expressing the Q472H variant and greater MVD. Although we observed

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an inverse relationship between Q472H and mRNA levels, Q472H did not associate with protein levels, measured by immunohistochemistry of total VEGFR-2 (both phosphorylated and unphosphorylated). Therefore, the effect of Q472H on MVD is likely due to increased activation of the VEGFR-2 receptor through increased phosphorylation, as shown by our finding from the phosphorylation assay. Moreover, this study has identified a germline variant as a potential determinant of increased tumor vasculature in NSCLC.

A potential drawback of this study is the lack of laser-capture microdissection and the possibility that the molecular phenotypes of *KDR* in this study are not entirely representative of tumor vasculature. To minimize this effect, we used tumor blocks displaying greater than 70% tumor cellularity. Although it has been clearly shown that VEGFR-2–positive vessels are mainly absent or rare in normal lung vessels and that VEGFR-2 expression is not detected in malignant lung cells (34), we cannot rule out that VEGFR-2 expression in the stromal cells may be a confounder. However, nonmicrodissected lung cancer specimens are well accepted in the field as the material for molecular studies (35).

Our findings highlight the difficulty of identifying common germline variants with large effect sizes in genotype–phenotype association studies. Nevertheless, even small changes in gene expression may increase cancer susceptibility. In mice, a 20% reduction in expression of *Pten*, a gene involved in the regulation of angiogenesis (36), led to a dramatic increase in tumor incidence (37). Furthermore, we found that a combination of 2 SNPs can account for 22% of the variation in tumoral levels of *KDR* mRNA. The contribution of untested functional germline SNPs may partly explain the relatively small effect sizes. Also, we did not examine somatic DNA alterations such as gene amplification, which could have significant effects on gene expression. Indeed, increased *KDR* copy number has been reported in some cancers (38, 39). However, the goal of this study was to characterize regions informative of function by focusing mainly on known regulatory regions.

We acknowledge that the results of this exploratory study are preliminary. The significant associations of SNP genotypes and *ex vivo* molecular phenotypes observed should be validated in an independent cohort with well-defined microdissected tissue. However, we believe that this lack of validation may be somewhat mitigated by supportive findings from −2854A/C, −2455T/A, −271G/A, and Q472H in our *in vitro* reporter gene and phosphorylation assays, and from the corroborative reports, discussed previously, of the functionality of −906T/C, −271G/A, and Q472H.

We have generated the knowledge basis to guide the prospective evaluation of *KDR* variants for identification of clinical biomarkers and for validating their clinical utility. Our study will inform the selection of SNPs in accordance with their functional effects and expected frequencies in the corresponding ethnic group. For example, Q472H, which increases VEGFR-2 phosphorylation, associates with MVD levels and shows a large variation in allele frequencies, ranging from 0.10 in African Americans to 0.52 in Asians (Supplementary Table S4). Our findings may have implications for the molecular genetics of angiogenesis not only in lung cancer but also in other tumors. Their effect on the outcome of treatment with VEGF pathway inhibitors should be evaluated prospectively.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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