Predictive Biomarkers and Personalized Medicine

A Genome-Wide Association Study of Overall Survival in Pancreatic Cancer Patients Treated with Gemcitabine in CALGB 80303

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Abstract

Background and Aims: Cancer and Leukemia Group B 80303 was a randomized, phase III study in patients with advanced pancreatic cancer treated with gemcitabine plus either bevacizumab or placebo. We prospectively collected germline DNA and conducted a genome-wide association study (GWAS) using overall survival (OS) as the endpoint.

Experimental Design: DNA from 351 patients was genotyped for more than 550,000 single-nucleotide polymorphisms (SNP). Associations between OS and SNPs were investigated using the log-linear 2-way multiplicative Cox proportional hazards model. The subset of 294 genetically European patients was used for the primary analysis.

Results: A nonsynonymous SNP in interleukin (IL)17F (rs763780, H161R) and an intronic SNP in strong linkage disequilibrium (rs7771466) were associated with OS using genome-wide criteria (P ≤ 10−7). Median OS was significantly shorter (P = 2.61 × 10−8) for the rs763780 heterozygotes [3.1 months; 95% confidence interval (CI), 2.3–4.3] than for the patients without this variant (6.8 months; 95% CI, 5.8–7.3). After adjustment by stratification factors, the P value for the association was 9.51 × 10−7.

Conclusions: The variant 161R form of IL-17F is a natural antagonist of the antiangiogenic effects of wild-type 161H IL-17F, and angiogenesis may play an important role in the metastatic spread of pancreatic cancer. In this preliminary study, we hypothesize that the angiogenetic potential of pancreatic cancers in patients with variant IL-17F is higher than that of tumors in patients with wild-type IL-17F, conferring worse prognosis. This exploratory GWAS may provide the foundation for testing the biology and clinical effects of novel genes and their heritable variants through mechanistic and confirmatory studies in pancreatic cancer. Clin Cancer Res; 18(2); 577–84. ©2011 AACR.

Introduction

Pancreatic cancer has a very poor prognosis and the lowest survival by stage of any solid tumor (1). Gemcitabine is the cornerstone of chemotherapy in this disease but has a very modest impact (2), and although numerous clinical trials have been conducted, only the combination of gemcitabine and erlotinib achieved a modest increase in median overall survival (OS) over gemcitabine alone (3). Novel agents and/or novel molecular biomarkers are urgently needed. One approach is to identify novel candidate genes putatively involved in the biology of pancreatic cancer.

It is likely that germline variants will be able to predict the outcome of patients with cancer, and there is epidemiologic evidence that prognosis has an inherited component (4). To test this, we conducted a genome-wide association study (GWAS) in Cancer and Leukemia Group B (CALGB) study 80303, a randomized, double-blind, phase III study in 602
patients with advanced pancreatic cancer treated with gemcitabine plus either bevacizumab or placebo. There was no superiority in OS of the gemcitabine–bevacizumab arm compared with the gemcitabine placebo arm (5).

As a part of the study, we prospectively collected germline DNA for pharmacogenetic studies, originally focusing on the association of candidate genes with treatment outcome. We subsequently amended the study to conduct a GWAS to identify novel associations. In GWAS, germline DNA of patients can be scanned using high-density single-nucleotide polymorphism (SNP) chips that assess hundreds of thousands of SNP markers (6). This approach is unbiased and does not rely on a priori knowledge about the role of candidate markers for the outcome of interest. The goal of this study was to identify novel genes associated with OS in pancreatic cancer.

Patients and Methods

Clinical trial and patients

CALGB 80303 was a double-blind, placebo-controlled randomized (1:1) phase III multi-institution study of bevacizumab, in combination with gemcitabine. Eligible patients had histologically or cytologically confirmed adenocarcinoma of the pancreas not amenable to potentially curative surgery, as previously described (5). Patients were required to have an Eastern Cooperative Oncology Group (ECOG) performance status of 0 to 2 and adequate bone marrow, renal, and hepatic function. Gemcitabine (1,000 mg/m²) was given i.v. over 30 minutes on days 1, 8, and 15 of a 28-day cycle. Bevacizumab, 10 mg/kg, or placebo was administered i.v. after gemcitabine on days 1 and 15 of each 28-day cycle. Treatment was discontinued for progressive disease, unacceptable adverse events, or patient withdrawal of consent.

Patients were stratified according to extent of disease (locally advanced vs. metastatic), ECOG performance status (0–1 vs. 2), and prior radiotherapy (yes vs. no). Patients received a minimum of 2 cycles of treatment unless unacceptable toxicity or early progression of disease occurred. Patients were evaluated for response according to the Response Evaluation Criteria in Solid Tumors (7) every 2 cycles. Confirmatory scans were obtained at least 4 weeks following initial documentation of objective complete or partial response. OS, with date of randomization as its reference point, was the primary study endpoint.

The companion pharmacogenetic protocol (CALGB 60401) was approved by the Institutional Review Boards of the University of Chicago (Chicago, IL), and the Riken Institute (Yokohama, Japan). Only patients who consented to CALGB 60401 were included in this study. The patient and tumor characteristics of the subgroup of patients genotyped in this study are comparable with those of patients in the main clinical trial (Table 1).

DNA samples and genotyping platforms

Of the 602 randomized patients on the main clinical study (5), blood samples were collected from 365 patients who consented to the pharmacogenetic analysis. The samples were shipped to the CALGB Pathology Coordinating Office (PCO) at Ohio State University (Columbus, OH). DNA was extracted from a single 5- to 10-mL peripheral whole blood sample collected using EDTA vacutainer tubes (purple tops) before beginning the study treatment using a commercially available kit from Qiagen. The concentration and quality of DNA were measured by ultraviolet spectro-photometry (Nanodrop). DNA of sufficient yield and quality (i.e., at least 2.5 μg and a minimum concentration of 50 ng/mL) was obtained on 352 of the blood specimens (96%). DNA samples were randomly placed on a 96-deep well plate, each well containing 1 sample at a concentration of 50 ng/μl and volume of 50 μl (by dilution with dH2O if needed).

The Illumina HumanHap550v3 Genotyping BeadChip was used to genotype more than 550,000 SNPs in these samples. In addition, more than 7,000 SNPs in 267 candidate (i.e., hypothesized a priori to be drug-related) genes were also genotyped in the same chip (8). Genotyping was conducted at the Center for Genomic Medicine, Riken Institute.

Quality control of the genotyping results and the phenotypic data

Cases excluded from analysis were closely related patients. We assessed the relatedness among patients by identity by state, and the only individual removed from the identity by state was one set of duplicates (n = 1; as shown in Fig. 1). Patients who were not treated or went off-study before completing 2 cycles of therapy were also excluded (n = 13). The remaining 338 patients formed the basis for...
the association analyses. Among the 561,466 SNPs typed on the platform, 44,108 SNPs were excluded because of call rates less than 95%. Among the remaining 517,358 SNPs, 21,894 SNPs with minor relative allelic frequencies (MAF) less than 0.01 were removed. Finally, among the 495,464 remaining SNPs, 88 SNPs with strong evidence for departure from Hardy–Weinberg equilibrium (HWE, \( P < 10^{-8} \)) were removed. Among the 495,376 SNPs passing the filter, 484,523 were autosomal. Among these, 330,690 SNPs had a minor genotypic count (MGC) of more than 9 and were used in the association analyses.

Patient registration, data collection, and data analysis were conducted by the CALGB Statistical Center. Data quality was ensured by careful review of data by CALGB Statistical Center staff and the study chairperson.

### Population structure analysis

Self-reported ethnicity information was available for each patient. However, this was confirmed by estimating the genetic ancestral origin of patients using the principal components analysis software implemented in Eigenstrat (9). This was done by combining our case data with the European, Asian, and African population SNP data from HapMap. Genetically European patients enrolled in CALGB 80303 were then selected by choosing only those individuals who closely clustered with the European HapMap samples when using all SNPs in the HumanHap550K BeadChip. This resulted in 294 patients of genetically estimated European ancestry and in 26 patients of genetically estimated African ancestry. The CALGB 80303 samples lined up as expected against the reference HapMap samples (Supplementary Fig. S1). A strong concordance between genetically estimated ancestry and self-reported race was observed.

### Functional studies

The putative functional effects of the 20 most significant SNPs associated with OS were examined using FastSNP (http://fastsnp.ibms.sinica.edu.tw/), a Web-based bioinformatic application (10). FastSNP can identify genetic
regulatory regions and nonsynonymous and nonsense amino acid changes and determine the effects of SNPs on exon splicing enhancer and silencer motifs and transcription factor–binding sites. For the same purpose, we also have used our genome-wide data of gemcitabine cytotoxicity in lymphoblastoid cell lines (11).

Statistical analysis of the associations

Our primary analysis determined the association between SNPs and OS in both arms combined, in patients of European ancestry only. For the SNP by OS association analyses, the Cox score (log-rank) test was used, and the analyses were powered against the additive genetic model. The robustness of the genetic associations in the unadjusted analysis (i.e., our primary analysis described above) was tested by including covariates in the model, testing within the framework of a multivariable additive log-linear Cox proportional hazards model (12). These covariates were randomization stratification factors (performance status, prior radiotherapy, and extent of disease), treatment arm, and genetic ancestry (based on the 3 principal components). In the genome-wide feature selection process for the genetically European population, only SNPs with MGC > 9 were considered. The most significant SNP, *IL17F* rs763780, for OS in patients of European ancestry was also tested in the patients of African ancestry in an unadjusted analysis. The Cox proportional hazards function from the R (12) extension package survival (13) was used. The *P* values were not adjusted for multiple comparisons. For a Q-Q plot, see Supplementary Fig. S2. We have used $1/10^7$ (0.05 of 500,000) as the *P* value cutoff point for genome-wide significance.

Results

The OS [median, 95% confidence interval (CI)] in the genotyped patients of European ancestry was 6.3 months (5.1–8.0) in the placebo arm and 5.9 months (4.9–7.1) in the bevacizumab arm, comparable with the median OS observed in the overall clinical study (5). The number of available SNPs for association with OS was 484,523. Here, we present the results of the primary analysis of the SNP versus OS association in patients of European ancestry (*N* = 294) in both arms combined (Fig. 2).

Of the 20 SNPs that showed the most significant association with OS, 9 were in annotated genes, 1 was near a gene, and 10 were in intergenic regions (Table 2). All SNPs in genes were intronic, with the exception of the coding SNP rs763780 in *IL17F*.

The SNP with the highest statistical significance was rs763780 in *IL17F* ($P = 2.61 \times 10^{-8}$), with an MAF of 0.04 (Fig. 2). Patients who were rs763780 heterozygous had reduced median OS of 3.1 months (2.3–4.3) compared...
Table 2. Twenty most significant SNPs associated with OS in patients of European ancestry in both arms combined

<table>
<thead>
<tr>
<th>SNP</th>
<th>Chromosome</th>
<th>Gene</th>
<th>Feature</th>
<th>MAF</th>
<th>5' Flanking gene</th>
<th>3' Flanking gene</th>
<th>Risk allele/control allele</th>
<th>P (unadjusted)</th>
<th>HR (95% CI)</th>
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<td>A/G</td>
<td>6.16E-05</td>
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NOTE: SNP annotation information is according to the SCAN database (31) using dbSNP version 129. The base change is according to the Illumina TOP stranding method for determining strand and allele (32). The rs10883617 SNP is located <1 Kb 5' of BTRC. The SNP call rate and HWE are shown in Supplementary Table S3. Abbreviation: NA, intergenic SNP.
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with patients without the variant (no patients were homozygous for the variant), who had a median OS of 6.8 months (5.8–7.3; Fig. 3A). This SNP was also in strong linkage disequilibrium ($r^2 = 0.955$) with another IL17F SNP (rs7771466) having the second highest statistical significance ($P = 1.66 \times 10^{-7}$) and a similar effect on OS [3.1 months (2.4–4.3) vs. 6.6 months (5.8–7.2)]. A similar trend was observed in the subset of patients of African ancestry (Supplementary Fig. S3). The associations between the SNPs in IL17F and OS, after adjusting for the stratification factors, treatment arm, and genetic ancestry within Europeans, do not meet the criterion for genome-wide statistical significance ($1 \times 10^{-7}$; Supplementary Table S1).

In silico analysis of the putative function of the intronic IL17F rs7771466 variant (in very strong linkage disequilibrium with the nonsynonymous rs763780) indicates that (i) rs7771466 introduces an additional CDX1 transcription factor–binding site to one present in the wild-type sequence and (ii) rs763780 abolishes an exonic splicing silencer and introduces 2 exonic splicing enhancers (Supplementary Table S2).

Discussion

We interrogated more than 550,000 heritable variants in patients with advanced pancreatic cancer treated with chemotherapy in CALGB 80303. To our knowledge, this is the first GWAS in a population of patients with cancer in the context of a randomized, placebo-controlled clinical trial. This preliminary study generates hypotheses on the role of the IL17F gene in the biology of advanced pancreatic cancer. If replicated, the IL17F SNPs might have prognostic significance.

IL17F encodes interleukin (IL)-17F, a cytokine with the ability to induce stromal cells to secrete proinflammatory cytokines. The most significant SNP in this study is rs763780 in IL17F, a base substitution that alters the histidine to arginine at amino acid 161 (H161R). In vitro functional experiments showed that in contrast to the wild-type 161H IL-17F the 161R variant form lacks the ability to activate the mitogen-activated protein kinase pathway, thereby restricting cytokine and chemokine production (14). Wild-type 161H IL-17F has also shown a strong antiangiogenic effect by markedly inhibiting the angiogenesis of human endothelial cells and inducing them to produce IL-2, TGF-β, and monocyte chemoattractant protein-1 (15). A recent study has also shown the antiangiogenic and antitumor properties of wild-type IL-17F in vivo (16). With respect to these activities, the variant 161R form of IL-17F is a natural antagonist of the antiangiogenic and proinflammatory effects of wild-type 161H IL-17F. For example, the 161R variant has been associated with protective effects in Asian patients with inflammatory and autoimmune conditions (17, 18). The resulting proangiogenic effects of the variant 161R of IL-17F could be further magnified by the concomitant increased expression driven by the noncoding rs7771466 IL17F variant. This variant is almost in complete linkage disequilibrium with the nonsynonymous rs763780, and its minor allele seems to increase IL-17F expression through splicing enhancement and introduction of an additional CDX1 transcription factor–binding site. The putative synergistic effect of these IL17F variants should be verified in experimental models of SNP functionality and angiogenesis.

As angiogenesis has been thought to play an important role in the growth and metastatic spread of pancreatic cancer (19), we hypothesize that the angiogenesis potential of tumors of patients with the variant 161R IL-17F is higher than that of tumors with wild-type 161H IL-17F, conferring worse prognosis. However, other mechanisms related to the proinflammatory effects of IL-17F cannot be excluded.

The IL17F rs763780 is the most important candidate SNP discovered by this study, due to (i) the genome-wide significance, (ii) its already established molecular function, (iii) the mechanistic hypothesis explaining the association with reduced OS, and (iv) the suggestion that a trend could be detected in patients of African ancestry, despite the very
small sample size. This study proposes that rs763780 in IL17F might have a prognostic effect in patients with advanced pancreatic cancer, also because stratification by treatment arm does not seem to negatively affect the association (Supplementary Table S1). Because gemcitabine is given in both arms, a true interaction between gemcitabine and IL17F SNPs cannot be tested. In addition, a review of the clinical characteristics of the patients heterozygous for IL17F rs763780 did not show any obvious difference with respect to the characteristics of the overall population accrued into this study (data not shown).

In addition to IL17F, this study proposes additional genes as putatively involved in determining differences in survival among patients with advanced pancreatic cancer. Among the SNPs listed in Table 2, rs11644322 in WWOX showed a gene–dosage effect, with median OS in the heterozygous patients (5.3 months, 4.3–6.9) that was intermediate between the other 2 genotype groups (3.3 months, 2.9–5.7, for the variant homozygotes; 7.1 months, 6.0–8.4, for the wild-type homozygotes; \( P = 1.31 \times 10^{-5} \); Fig. 3B). WWOX codes for the WW domain–containing oxidoreductase, a tumor suppressor in several tumors, including pancreatic cancer (20). WWOX SNPs showed the strongest linkage for prostate cancer susceptibility in a recent genome-wide scan (21). In multiple myeloma, LOH of 16q23, the location of WWOX, was associated with adverse survival and reduced WWOX expression (22). Germline variants from a recent study mapped WWOX as one of the genes associated with clinical staging in lung cancer (23). Contrary to the amino acid changing SNP in IL17F, the molecular functions of the SNPs in WWOX are not known at this time. Because of their association with reduced OS, the established tumor suppressor role of WWOX, and their intrinsic location, we hypothesize that these SNPs might reduce the expression of WWOX, diminishing its tumor suppressor properties and leading to worse prognosis.

An SNP (rs10883617) near BTRC was associated with reduced OS, as homozygote patients had a reduced median OS (3.6 months, 2.7–6.8) as compared with heterozygous patients (6.1 months, 4.9–7.3) and patients who were not carriers of this variant (6.9 months, 5.9–8.2; \( P = 3.94 \times 10^{-5} \); Fig. 3C). BTRC (B-transducin repeat containing) encodes a protein involved in the ubiquitination processes that showed an oncogenic activity in several cancers including pancreatic cancer (24–26). In most tumors, overexpression of BTRC results in the degradation of IκB, an inhibitor of the NF-κB transcription factor, and thus the activation of NF-κB and the uncontrolled cell proliferation in these tumors. The use of our functional results in lymphoblastoid cell lines treated with gemcitabine indicated that BTRC rs10883617 is associated with increased IC50 and, hence, resistance to gemcitabine \( (r = 0.21, P = 0.008) \). As inhibiting and silencing NF-κB have been shown to increase the sensitivity of pancreatic cancer cells to gemcitabine (27, 28), we hypothesize that BTRC rs10883617 might have a predictive value in patients with pancreatic cancer treated with gemcitabine, via a NF-κB–mediated effect.

This study is limited by the large number of multiple comparisons typical of GWAS, increasing the chance of false-positive associations. This limitation could be overcome by independent replication of the findings. Replication studies in cancer treatment outcome have intrinsic difficulties, as there may not be an existing trial (to be used for replication) with the same eligibility criteria and drug treatment of the trial used for discovery. In a relatively uncommon disease such as pancreatic cancer, the access to a sufficiently powered replication set is particularly challenging. Ideally, validation of our top hits should be conducted in patients treated with gemcitabine and randomized to an experimental treatment, to ensure that the populations are comparable. A few published trials (29, 30) in which patient DNA has already been collected may be considered for replication, due to similarity of treatment and/or disease, and randomized treatment. In addition, the MAF of the variants in IL17F is low in Caucasians (0.05 from HapMap), potentially limiting the ability to replicate this association in this population. However, the MAF of the variants in IL17F is higher in Asians (0.13).

The results of this study are preliminary because of the limited sample size and the low MAF of the IL17F SNP. Because of the refractoriness to treatment of advanced pancreatic cancer and the lack of established markers of survival, the dissemination of these findings to the scientific community could facilitate their replication by others, even as we continue to conduct replication and validation studies. The association of IL17F variants with efficacy could also be tested in tumors other than pancreatic cancer. To support these future investigations, our data are now available in the Database of Genotypes and Phenotypes (dbGaP) in accordance with NIH policy.

Disclosure of Potential Conflicts of Interest

H. Hurwitz has commercial research grant from Roch/Genentech and honoraria from Speakers Bureau of Roch/Genentech. M.I. Ratain is a consultant or an advisory board for Genentech and has meeting support from Genentech and Eli Lilly. No potential conflicts of interest were disclosed by other authors.

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