A Single Nucleotide Polymorphism in Inflammatory Gene RNASEL Predicts Outcome after Radiation Therapy for Localized Prostate Cancer


Abstract

Purpose: To study associations between single nucleotide polymorphisms (SNP) in Ribonuclease L (RNASEL), a gene implicated in inflammation and prostate cancer risk, and outcomes after radiation therapy.

Experimental Design: We followed participants in the prospective US Health Professionals Follow-Up Study treated with radiation therapy for early-stage prostate cancer. Three SNPs were genotyped based on previously determined functional and biological significance. We used multivariable Cox proportional hazards models to assess per-allele associations with the primary outcome defined as time to a composite endpoint including development of lethal prostate cancer or biochemical recurrence.

Results: We followed 434 patients treated with radiation therapy for a median of 9 years. On multivariate analysis, the rs12757998 variant allele was associated with significantly decreased risk of the composite endpoint [HR: 0.65; 95% confidence interval (CI), 0.45–0.94%; P = 0.02] driven by decreased biochemical recurrence (HR: 0.60; 95% CI, 0.40–0.89%; P = 0.01) and men treated with external beam (HR: 0.58; 95% CI, 0.36–0.93%; P = 0.02). In contrast, in 516 men from the same cohort treated with radical prostatectomy, we found no significant impact of this variant on outcome. Furthermore, the rs12757998 variant allele significantly modified the association between androgen deprivation therapy and outcomes after radiation therapy (p-interaction = 0.02).

Conclusion: We show an association between RNASEL SNP rs12757998 and outcome after radiation therapy for prostate cancer. This SNP is associated with increased circulating C-reactive protein and interleukin-6, suggesting a potential role for inflammation in the response to radiation. If validated, genetic predictors of outcome may help inform prostate cancer management.

Introduction

Radiation therapy in prostate cancer, either external beam or brachytherapy, is an effective therapy for men with early-stage, organ confined prostate cancer (1, 2). However, not all patients are cured, some because of occult metastases at the time of treatment and others because of failure of local control of cancer. In either scenario, cure or failure to cure may be driven by both host and somatic factors. More specifically, the role of inherited genetic variation to predict outcome after radiation therapy is biologically plausible and has been investigated somewhat in radiation therapy (3–5). Most studies have focused on polymorphisms in DNA damage response genes and examined toxicity outcomes (6–9). In contrast, data regarding the effects of genetic variation on treatment-specific cancer outcomes are more limited.

Ribonuclease L (RNASEL) is compelling as a potential modulator of response to radiation therapy in prostate cancer given its role in inflammation and response to infection. RNASEL is a putative tumor-suppressing enzyme that may inhibit growth and proliferation and induce apoptosis (10–12), and is implicated in the cleavage of viral RNA and the interferon-mediated immune response (13). Polymorphisms in RNASEL, located on chromosome 1q25, have been inconsistently linked to hereditary and general prostate cancer risk (14–26). In particular, the minor variant of single nucleotide polymorphism (SNP)
Translational Relevance
Radiation therapy is an accepted treatment for localized prostate cancer; however, there are no commonly used factors that predict outcome specifically after this treatment. In this article, we observed an association between variation in a biologically relevant single nucleotide polymorphism in the Ribonuclease L (RNASEL) gene and outcome after prostate radiotherapy in a large cohort of men enrolled in the prospective US Health Professionals Follow-Up Study that were extensively followed for cancer-specific outcomes. This finding remained significant after adjusting for other known prognostic factors, and was limited to patients who received external beam radiation as opposed to brachytherapy. Moreover, this association was not found in patients derived from the same cohort treated with radical prostatectomy instead of radiotherapy. These data are of translational relevance because they generate the hypothesis that inherited variation in RNASEL may predict outcome after radiotherapy in a treatment-specific manner that could eventually be used to help guide treatment.

rs12757998, located immediately downstream of the RNASEL coding region, was recently associated with an increased risk of prostate cancer and specifically higher-grade tumors (19), and was associated with elevated serum levels of the inflammatory markers C-reactive protein (CRP) and interleukin (IL)-6 (19).

The role of inflammation and the immune system in radiation-induced cancer cell death is complex and incompletely defined (27, 28). Preclinical data suggest that, at least under certain circumstances, the immune system may augment cytotoxic effects of radiation therapy and may even be required for tumor eradication (29, 30). Conformal radiation therapy given to prostate cancer patients induces a local inflammatory response and has been showed to increase circulating IL-6 levels (31–34). Therefore, we hypothesized that by modulating this response, inherited variation in RNASEL could affect prostate cancer outcomes after definitive radiation therapy for early-stage prostate cancer and sought to explore this association among men with prostate cancer in the US Health Professionals Follow-Up Study (HPFS).

Materials and Methods
Study population
The prospective HPFS enrolled 51,529 male medical professionals in 1986 to investigate the causes of cancer and heart disease. These cohort participants are subsequently followed with biennial questionnaires designed to collect information about medical diagnoses and lifestyle factors. Response rates to these surveys are high (approximately 96%). Between 1993 and 1995, 18,018 participants provided a blood sample for analysis. The study base for this project was men in the blood cohort who were diagnosed with prostate cancer between 1993 and 2010.

The Institutional Review Board at the Harvard School of Public Health approved the HPFS study. Participants provided written informed consent for review of their medical records.

Genotype assessment
We characterized genetic variation for 3 SNPs within the RNASEL gene: rs486907, rs627928, and rs12757998. These SNPs were selected based on previously established functional significance (16, 19, 35–37). Genotyping was done in a blinded fashion after extraction of DNA from whole blood using a standard QIAmp kit (QIAGEN Inc.) protocol using Biotrove Open Array SNP Genotyping Platform at the Harvard Medical School—Partners Healthcare Center for Genetics and Genomics. All SNPs had greater than 90% completion and the concordance was greater than 99% for blinded quality control samples. Pairwise r2 values for these SNPs in the study population were: rs486907-rs627928 0.61, rs486907-rs12757998 0.27, and rs627928-rs12757998 0.15.

Assessments of prostate cancer outcomes
Participants initially report a new prostate cancer diagnosis on biennial questionnaires, and cases are confirmed through detailed review of medical records and pathology reports whenever possible (>90%). In addition, detailed information on clinical features at diagnosis and initial treatments are abstracted from the review. In HPFS, men with prostate cancer are specifically followed with biennial questionnaires to assess factors related to follow-up treatments, prostate-specific antigen (PSA) outcomes, clinical progression, and development of metastases.

Our primary outcome was a composite progression endpoint consisting of the development of lethal prostate cancer or biochemical recurrence. Lethal prostate cancer was defined as participants who developed bone metastases or experienced a prostate cancer-specific death. We ascertained prostate-specific causes of death using reports from families, as well as postal service and National Death index records. Study physicians then confirmed these deaths by reviewing the available medical records in more than 98% of cases. Similarly, we determined biochemical recurrence from available medical records and from physician questionnaires based on accepted treatment-specific definitions as described previously (for radical prostatectomy, PSA higher than 0.2 ng/ml after surgery and for at least 2 consecutive measures; for radiation, an increase of 2 or more ng/ml higher than the nadir PSA; for brachytherapy, an increase of 1 or more ng/ml higher than the nadir PSA for at least 2 consecutive measures; ref. 38). If records were not available, we also identified recurrence through patient self-reports of PSA increase from participant questionnaires; these accounted for 44% of biochemical recurrence events. Date of composite failure was defined as the date of the earliest event. Men for whom we could not ascertain the
date of biochemical recurrence but who also developed lethal prostate cancer were considered to have failed at the date at which they developed lethal cancer and all men were included in time to biochemical failure analyses, including those who eventually developed lethal prostate cancer.

**Population for analysis**

We included participants who previously provided a blood sample for genotyping and were then diagnosed with early-stage (T1-3N0/M0/x) prostate cancer after enrollment in HPFS. To reduce the possibility of population stratification we limited our study to Caucasians, who account for the majority (95%) of HPFS participants. We limited our study to men with disease most likely to be curable with local therapy at the time of diagnosis by further excluding participants with an initial PSA greater than 50 ng/mL or men in whom lethal prostate cancer was identified less than 1 year after their diagnosis. Our primary analyses involved men initially treated with any form of definitive radiation therapy, but who did not receive a radical prostatectomy. To determine whether the association could be generalized to another outcome group, we then evaluated men who were initially treated with radical prostatectomy and not radiation therapy, but who otherwise satisfied all of the same inclusion and exclusion criteria.

**Statistical analyses**

We examined variation in RNASEL and participant characteristics at diagnosis using Pearson correlations (age at diagnosis) and chi-squared trend tests (PSA, Gleason score, clinical stage). We undertook time to event analyses, calculating follow-up time from date of treatment initiation to date of the composite outcome and the individual components of lethal prostate cancer and biochemical recurrence. Men were censored if they died of other causes or at the end of the study (December 2011). We used Cox proportional hazard regression models to calculate maximum likelihood HR and 95% confidence intervals (CI) of the association between variation and RNASEL and cancer outcomes. We analyzed genetic effects using the additive model, considering the presence of 0, 1, or 2 copies of the minor allele as an ordinal variable. In multivariable models, we adjusted for PSA at diagnosis (continuous; ng/mL), clinical stage (T1/T2 vs. T3), Gleason score (<7 vs. 7 vs. >7) as well as age at treatment to examine independent associations of SNPs on cancer outcomes. We also conducted exploratory analyses including multiplicative interaction terms in our adjusted models to evaluate whether the associations of RNASEL SNPs differed by participant characteristics at diagnosis (age, Gleason score, PSA, stage) and whether variation in SNP rs12757998 modified the associations between neoadjuvant and/or adjuvant androgen deprivation therapy use and outcome.

All reported P-values are 2-sided, with P<0.05 considered statistically significant. SAS version 9.1 (SAS institute Inc.) was used for all analyses.

**Results**

**Participant and treatment characteristics**

We included 434 men who received radiation therapy and were diagnosed with prostate cancer and treated between 1992 and 2011 in our main analysis (Supplementary Fig. S1). Patient characteristics are shown in Table 1. The median age at diagnosis and treatment was 72 years. Most participants were diagnosed with early-stage (T1/T2) disease (98%) with Gleason scores less than 7 (69%) and PSA levels less than 10 ng/mL (73%). One hundred seventy-three patients (40%) received androgen deprivation as a component of their initial treatment and 191 patients (44%) received brachytherapy, forty-eight of who also received external beam radiation.

The distribution of allelic variation in the 3 genotyped RNASEL SNPs is shown in Table 1. There were no significant associations between the presence of allelic variants and age at treatment, PSA at diagnosis, Gleason score or clinical stage (data not shown).

**Outcomes**

With a median follow-up of 9 years through 2011, 100 (23%) men had a recurrence or developed lethal disease (Table 1). Among these 100 men, 9 developed lethal prostate cancer without recorded biochemical recurrence, 77 had a biochemical recurrence only, and 14 had a biochemical recurrence and developed lethal prostate cancer. Among men who experienced outcomes, median time to the composite endpoint, lethal prostate cancer, and biochemical recurrence was 4.3, 7.3, and 4.3 years, respectively. Time to biochemical recurrence was similar in the 14 men who eventually developed lethal cancer and the 77 men who did not (4.1 years compared with 4.3 years). Time to lethal prostate cancer was 7.8 years in the 14 men with previously detected biochemical recurrence as compared with 6.4 years in the 9 men without detected biochemical recurrence. For the 334 men who remain progression free, the follow-up was 9.8 years. Among these men, 80 were censored because of deaths unrelated to prostate cancer.

Univariate associations are shown in Supplementary Table S1. SNP rs12757998, but not rs486907 or rs627928, was associated with a significantly prolonged time to the composite outcome (HR: 0.70; 95% CI, 0.50–0.99%; P = 0.04). Examination of median time-to-event stratified by genotype for men who reached the composite outcome did not suggest that this result was driven by a small number of outliers with an exceptionally long time to failure (Supplementary Fig. S2). This association of rs12757998 remained significant after adjusting for patient age at treatment, Gleason score, PSA at diagnosis, and clinical stage (Table 2; HR: 0.65; 95% CI, 0.45–0.94%; P = 0.02). None of the SNPs had a significant effect on time to the development of lethal prostate cancer. Only rs12757998 had a significant effect on time to biochemical recurrence (HR: 0.60; 95% CI, 0.40–0.89%; P = 0.01). In contrast, as a control to assess the specificity of the effect to radiation therapy, we examined the effect of SNP rs12757998 in 516 participants from the
patients treated with radical prostatectomy, 94 (18%) reached the composite outcome. In these men, rs12757998 was not associated with time to the composite outcome (multivariate HR: 0.87; 95% CI, 0.61–1.25%; P = 0.45; p-interaction = 0.26) or biochemical recurrence (multivariate HR: 0.86; 95% CI, 0.60–1.25%; P = 0.43; p-interaction = 0.19).

Interaction and subgroup analyses

Further exploratory analyses showed no evidence of interaction between allelic variation in rs12757998 and age, PSA at diagnosis, Gleason score, and clinical stage on time to the composite outcome (P > 0.05, data not shown). However, variation in rs12757998 did modify the effect of androgen deprivation therapy (Table 3, p-interaction = 0.02). In men homozygous for the major allele variant, the use of androgen deprivation therapy was associated with a significantly reduced hazard for the composite endpoint and biochemical recurrence (HR: 0.38; 95% CI, 0.20–0.72%; P = 0.003 and HR: 0.42; 95% CI, 0.22–0.79%, P = 0.007, respectively). In contrast, associations between androgen deprivation and outcomes were not statistically significant in men with at least 1 variant rs12757998 allele. Including this interaction in our multivariate analyses further strengthened associations between variation in rs12757998 and outcomes (P = 0.002 for the composite endpoint and P = 0.0007 for biochemical recurrence).

We also evaluated the impact of brachytherapy on the effect of allelic variation in rs12757998 (Table 2). The effect of allelic variation in rs12757998 on time to the composite outcome and biochemical recurrence was less pronounced in men who received brachytherapy (HR: 0.85; 95% CI, 0.46–1.59%; P = 0.61) as compared with men treated with external beam radiation only (HR: 0.58; 95% CI, 0.36–0.93%; P = 0.02). Finally, as rs12757998 has previously been associated with the development of high-grade disease, we evaluated the effects of variation in rs12757998 on the subset of men with Gleason ≥ 7 (Table 2). In these participants, the effect of allelic variation on the composite endpoint was particularly apparent in men treated with radiation therapy (HR: 0.55; 95% CI, 0.31–0.96%; P = 0.03) as compared with men who received a radical prostatectomy (HR: 1.11; 95% CI, 0.88–1.82%; P = 0.69).

Discussion

Our prospective study among men with early-stage prostate cancer evaluated whether variation in 3 SNPs in RNASEL, a gene with previously established biological and functional significance influenced prostate cancer outcomes after radiation therapy. Presence of the minor allele in SNP rs12757998 conferred a significant reduction in risk of the composite outcome that was driven by a decreased risk of time to biochemical recurrence. This association remained significant after adjusting for known predictors of recurrence including Gleason score, tumor stage, and PSA. We found no associations between polymorphisms in the 2 other SNPs and biochemical recurrence.
We found that the presence of the minor allele variant in rs12757998 was associated with a decreased risk of progression in our analysis. We previously found this variant was associated with an increased risk of prostate cancer overall and specifically of high-grade disease (19). The effects may illustrate the complex role inflammation and immunity may have in prostate cancer carcinogenesis and its subsequent response to radiation treatment. Although an increased propensity for inflammation may contribute to tumor development, a treatment-induced inflammatory response could also mediate tumor cell death. Indeed, decreased RNASEL protein levels were recently associated with resistance of prostate cancer cell lines to apoptosis induced by topoisomerase inhibitors and the tumor necrosis pathway (39) and interferon-related genes have been implicated in radiation responsiveness in both cell lines and human patients (40, 41). More specifically, we previously showed that rs12757998 was associated with elevated levels of circulating IL-6 (19), thus potentially influencing the typical

<table>
<thead>
<tr>
<th>SNP</th>
<th>Hazard ratio (95% CI)</th>
<th>P-value</th>
<th>Hazard ratio (95% CI)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs486907 (C-T)</td>
<td>1.02 (0.75–1.38)</td>
<td>0.91</td>
<td>1.03 (0.75–1.41)</td>
<td>0.88</td>
</tr>
<tr>
<td>rs627928 (A-C)</td>
<td>0.99 (0.73–1.32)</td>
<td>0.91</td>
<td>0.96 (0.71–1.32)</td>
<td>0.82</td>
</tr>
<tr>
<td>rs12757998 (G-A)</td>
<td>0.65 (0.45–0.94)</td>
<td>0.02</td>
<td>0.60 (0.40–0.89)</td>
<td>0.01</td>
</tr>
</tbody>
</table>

Table 2. Multivariate hazard ratios of associations between SNPs in RNASEL and outcomes after radiation therapy, Health Professionals Follow-up Study

<table>
<thead>
<tr>
<th>Subgroup analyses examining associations with rs12757998</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brachytherapy use (radiotherapy patients only)</td>
</tr>
<tr>
<td>Yes (n = 191)</td>
</tr>
<tr>
<td>0.85 (0.46–1.59)</td>
</tr>
<tr>
<td>No (n = 243)</td>
</tr>
<tr>
<td>0.58 (0.36–0.93)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Patients with Gleason 7 or 8 disease</th>
</tr>
</thead>
<tbody>
<tr>
<td>Radiation (n = 131)</td>
</tr>
<tr>
<td>0.55 (0.31–0.96)</td>
</tr>
<tr>
<td>Radical prostatectomy (n = 148)</td>
</tr>
<tr>
<td>1.11 (0.68–1.82)</td>
</tr>
</tbody>
</table>

Abbreviations: CI, confidence interval; PSA, prostate-specific antigen; SNP, single nucleotide polymorphism.

aAdjusted for patient age, Gleason score, PSA at diagnosis and clinical stage.
bHazard ratio per minor allele.
cLethal prostate cancer or biochemical recurrence.
dNo significant effects on time to lethal prostate cancer among any SNPs or subgroups tested.
ep-interaction = 0.22 for the composite endpoint; p-interaction = 0.34 for biochemical recurrence.

Among men with rs12757998 variant allele (A) in men treated with brachytherapy, 29 men (15%) reached the composite outcome, and 26 (14%) had a biochemical recurrence. Among men with Gleason 7 or 8 disease, 89 (32%) reached the composite outcome (44 of whom were treated with radiation) and 81 (29%) had a biochemical recurrence (38 of whom were treated with radiation).

We found that the presence of the minor allele variant in rs12757998 was associated with a decreased risk of progression in our analysis. We previously found this variant was associated with an increased risk of prostate cancer overall and specifically of high-grade disease (19). These 2 effects may illustrate the complex role inflammation and immunity may have in prostate cancer carcinogenesis and its subsequent response to radiation treatment. Although an increased propensity for inflammation may contribute to tumor development, a treatment-induced inflammatory response could also mediate tumor cell death. Indeed, decreased RNASEL protein levels were recently associated with resistance of prostate cancer cell lines to apoptosis induced by topoisomerase inhibitors and the tumor necrosis pathway (39) and interferon-related genes have been implicated in radiation responsiveness in both cell lines and human patients (40, 41). More specifically, we previously showed that rs12757998 was associated with elevated levels of circulating IL-6 (19), thus potentially influencing the typical

<table>
<thead>
<tr>
<th>Effects of ADT</th>
<th>Hazard ratio (95% CI)</th>
<th>P-value</th>
<th>Hazard ratio (95% CI)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>In men with rs12757998 major allele (G)</td>
<td>0.38 (0.20–0.72)</td>
<td>0.003</td>
<td>0.42 (0.22–0.79)</td>
<td>0.007</td>
</tr>
<tr>
<td>In men with rs12757998 variant allele (A)</td>
<td>1.34 (0.69–2.59)</td>
<td>0.39</td>
<td>1.64 (0.80–3.36)</td>
<td>0.18</td>
</tr>
</tbody>
</table>

Abbreviations: ADT, androgen deprivation therapy; CI, confidence interval; PSA, prostate-specific antigen; SNP, single nucleotide polymorphism.

aAdjusted for patient age, Gleason score, PSA at diagnosis and clinical stage.
bp-interaction = 0.02 for the composite endpoint; p-interaction = 0.01 for biochemical recurrence (variant allele considered additively).
cLethal prostate cancer or biochemical recurrence.
dNo significant effects on time to lethal prostate cancer.
eAt least 1 variant allele.

Table 3. Association between variation in rs12757998 and outcomes after androgen deprivation therapy

Abbreviations: ADT, androgen deprivation therapy; CI, confidence interval; PSA, prostate-specific antigen; SNP, single nucleotide polymorphism.

aAdjusted for patient age, Gleason score, PSA at diagnosis and clinical stage.
bp-interaction = 0.02 for the composite endpoint; p-interaction = 0.01 for biochemical recurrence (variant allele considered additively).
cLethal prostate cancer or biochemical recurrence.
dNo significant effects on time to lethal prostate cancer.
eAt least 1 variant allele.
higher biologically effective doses that overcome the lead to prostate cancer cell death, possibly by delivering that may have differential effects on the processes that apy, a localized and dose-escalated form of radiation ther-
effect was reduced in participants treated with brachyther-
there was no benefit from the minor variant of rs12757998,
the composite outcome of lethal and recurrent prostate
association with the composite endpoint would be bor-
significant with a corrected in rs12757998 and biochemical recurrence would remain
even after applying a conservative measure such as a
accurate despite the fact that our cohort consisted of well-
tumor tissue (44), the use of
tive prostate cancer treatment (43). Given the potential
iation can predict treatment-specific outcome after defini-
treatment modality and brachytherapy on associations
variation across the RNASEL gene. Although we chose to
sequence 3 RNASEL SNPs based on previous study find-
ings (16, 19, 35–37), including 2 known missense muta-
tions, the mechanism by which rs12757998 may act to
increase circulating inflammatory mediators or impact radi-
ation-response remains unknown, and this variant could
potentially be a marker for the true causal variant. Also,
although there were relatively few men who developed lethal prostate cancer, we cannot exclude the possibility that our
inability to detect a statistically significant association
between rs12757998 and lethal cancer was not the result
of a differential biologic effect rather than a lack of power.
Similarly, our secondary, exploratory analyses were likely
underpowered to detect significant interaction effects of
treatment modality and brachytherapy on associations
with rs12757998. However, we also cannot exclude the
possibility that more events, particularly among men treated
with brachytherapy, would have revealed a significant asso-
ciation between variation in rs12757998 and outcome in
this group.

In summary, we have identified a polymorphism in the
RNASEL gene that is statistically significantly associated
with radiation treatment-specific outcome in HPFS partici-
pants diagnosed with early-stage prostate cancer. Although
additional studies are needed to confirm this association
and elucidate the functional significance of this polymor-
phism, our results suggest the immune system and inflam-
matory mediators could impact prostate cancer’s response
to radiation therapy. Future studies could potentially exam-
ine relationships between immune and inflammatory
response and radiation responsiveness in other malign-
nancies. If confirmed, our results also suggest that genetic
polymorphisms could eventually help better individualize
treatment for early-stage prostate cancer.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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P. L. Nguyen, E. Giovannucci, L. A. Mucci
Writing, review, and/or revision of the manuscript: J. D. Schoenfeld, D.
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Mucci

RNASEL Predicts Prostate Cancer Outcome


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Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): J. L. Kasperzyk, S. A. Kenfeld

Study supervision: I. M. Shui was additionally supported by US Army Prostate Cancer Post-doctoral Fellowship; M. M. Epstein is supported by National Institutes of Health research training grant R25 CA095866; P. L. Nguyen was supported by a grant from an anonymous family foundation; and L. A. Mucci, P. L. Nguyen, and N. I. Martin are supported by the Prostate Cancer Foundation. The project was supported by grants from the National Institutes of Health/National Cancer Institute (grant numbers R01 CA133891, R01CA141296-02, and P01 CA055075).

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