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Gene expression profiles among murine strains segregate with distinct differences in the progression of radiation-induced lung disease

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ABSTRACT
Molecular mechanisms underlying development of acute pneumonitis and/or late fibrosis following thoracic irradiation remain poorly understood. Here, we hypothesize that heterogeneity in disease progression and phenotypic expression of radiation-induced lung disease (RILD) across murine strains presents an opportunity to better elucidate mechanisms driving tissue response toward pneumonitis and/or fibrosis. Distinct differences in disease progression were observed in age- and sex-matched CBA/J, C57L/J and C57BL/6J mice over 1 year after graded doses of whole-thorax lung irradiation (WTLI). Separately, comparison of gene expression profiles in lung tissue 24 h post-exposure demonstrated >5000 genes to be differentially expressed (P<0.01; >twofold change) between strains with early versus late onset of disease. An immediate divergence in early tissue response between radiation-sensitive and -resistant strains was observed. In pneumonitis-prone C57L/J mice, differentially expressed genes were enriched in proinflammatory pathways, whereas in fibrosis-prone C57BL/6J mice, genes were enriched in pathways involved in purine and pyrimidine synthesis, DNA replication and cell division. At 24 h post-WTLI, different patterns of cellular damage were observed at the ultrastructural level among strains but microscopic damage was not yet evident under light microscopy. These data point toward a fundamental difference in patterns of early pulmonary tissue response to WTLI, consistent with the macroscopic expression of injury manifesting weeks to months after exposure. Understanding the mechanisms underlying development of RILD might lead to more rational selection of therapeutic interventions to mitigate healthy tissue damage.

KEY WORDS: Radiation pneumonitis, Lung fibrosis, Gene expression profiling, Murine strain differences

INTRODUCTION
Radiation-induced lung disease (RILD) remains the most common healthy tissue complication associated with radiation treatment of thoracic tumors. The disease is defined by two distinct phases, pneumonitis and fibrosis, that are separated in both time and histopathological sequelae (Travis, 1987). Radiation pneumonitis affects 5-15% of patients undergoing thoracic radiotherapy. It is defined as an early, transient phase that occurs between 1 and 7 months after exposure, with a peak incidence at 3-4 months. Development of pneumonitis during the course of treatment or shortly thereafter can potentially compromise cancer cure and, in rare instances, be life-threatening (Williams et al., 2010). In contrast, pulmonary fibrosis is more common and affects ≥50% patients treated with radiation for thoracic tumors, including lung cancers, breast cancers and mediastinal lymphomas (Appelt et al., 2014). Fibrosis is progressive, and clinical manifestations occur months to years after completion of therapy, with symptoms ranging from nonproductive cough to dyspnea on exertion.

Despite decades of research, no U.S. Food and Drug Administration-approved therapies are available to prevent, mitigate, and/or treat radiation pneumonitis and/or fibrosis; nor do well-defined biological markers predict individual risk for development of disease. This is, in part, a result of the biological complexity of RILD, in which injurious mechanisms begin at the time of exposure and progress through a clinically latent period before overt onset of pneumonitis and/or fibrosis (Bentzen, 2006). Progressive fibrosis has been observed to occur in the absence of clinically symptomatic radiation pneumonitis. In experimental models, the ability to dissociate radiation pneumonitis from fibrosis by dose fractionation and pharmaceutical interventions suggests that these two pathologies might be distinct and result from independent (although perhaps overlapping) underlying mechanisms of injury (Travis and Tucker, 1986).

It is well known that murine models of RILD display broad heterogeneity in temporal onset, radiation dose response, and phenotypic expression of disease, reflecting variations observed in humans. Over the past decade, the majority of preclinical studies have used a survival endpoint of 120-180 days for evaluation of therapeutic interventions against RILD. However, because of the protracted latency period between time of exposure and development of RILD in some strains, the use of survival endpoints ≤180 days might not permit full progression of disease, leading to bias in data interpretation. Further, few studies take into consideration animal age at time of irradiation or sex-based differences in pulmonary radiation response, each of which can confer strong variation in severity and incidence of pneumonitis and fibrosis following thoracic radiation exposure.

We previously reported on the dose-response relationship and pathophysiological comparability of RILD in three murine strains (CBA/J, C57BL/6J and C57L/J), nonhuman primates (NHPs), and humans over the first 180 days after exposure (Jackson et al., 2014).
Our study design and strain selection were informed by three decades of preclinical research in RILD (Sharplin and Franko, 1989a,b; Terry et al., 1988; Travis et al., 1981, 1980). Consistent with earlier reports, the predominant histological feature in moribund C57L/J and CBA/J mice was an acute pneumonia over dose ranges of 9.0-13.0 and 13-16 Gy, respectively. In the C57BL/6J strain, the lungs displayed scarred, retracted fibrosis over a dose range of 12.5-15 Gy (Jackson et al., 2010, 2011, 2012, 2014).

In this study we expand on our previous findings to report on the natural history of disease progression up to 1 year after thoracic irradiation and define the genes and/or pathways that segregate to ‘pneumonitis-prone’ versus ‘fibrosis-prone’ using differential gene expression analysis. The data demonstrate significant differences in dose response, time to disease onset, and phenotype of injury. Moreover, ultrastructural damage and gene expression profiles suggest that tissue response to radiation within the first 24 h determines tissue fate. Taken together, we report the importance of appropriate strain selection, control over biological variables, and sufficient follow-up time to accurately identifying new therapeutic targets and testing of new medical interventions.

RESULTS
Natural history of disease progression for RILD in CBA/J, C57L/J, and C57BL/6J mice
Longitudinal studies were performed to assess the progression of RILD over a 1-year (360-day) period post-exposure using signs of major morbidity and/or mortality as the primary endpoint. Secondary endpoints to assess signs and severity of lung damage included qualitative and quantitative indices of pulmonary function, edema and/or congestion, and histopathological damage.

Data demonstrate that in pneumonitis-prone CBA/J mice, animal sex had no significant effect on mortality (P=0.80) or time to death (P=0.37; Fig. 1A). For every 75 cGy increase in radiation dose, the odds of death by day 360 increased by 2.9 times (95% CI: 1.86-4.61; P=0.0001).

No significant association between sex and time to death (P=0.52) or mortality (P=0.095) was noted among C57L/J mice (Fig. 1B). In this strain, the odds of death increased by 1.46 times (95% CI: 1.31-1.61) for every 75 cGy increase in radiation dose (P<0.0001).

In contrast, a significant sex by radiation dose interaction effect (P<0.0001) was seen in C57BL/6J (BL6) mice; therefore, the effect of radiation dose on time to death was evaluated separately by sex (Fig. 1C,D). For every 1 Gy increase in radiation dose, the odds of dying by day 360 also increased, but female B6 mice had a higher rate of death than males with increasing radiation dose. In this study, female C57BL/6J mice irradiated at a dose of 17-18 Gy were excluded from final analysis because of loss of animals from excessive barbering and ulcerative dermatitis (common in this strain and exacerbated by radiation).

Dose and quantification of exposure: influence of murine strain, sex and radiation dose on risk of dying following thoracic irradiation
Probit analysis was performed to determine the probability of major morbidity and/or mortality within the first 360 days post-exposure in each strain. There was a shift in the position of the dose-response curve across strains. The lethal dose for 50% of animals over the first 360 days (LD50/360) was 12.65 Gy (95% CI: 12.28-13.02) in sex-matched CBA/J mice (Fig. 2A) and 9.15 Gy (95% CI: 8.74-9.57) in sex-matched C57L/J mice, indicating greater pulmonary sensitivity in the latter strain (Fig. 2B). The LD50/360 for male C57BL/6J mice was 11.24 Gy (95% CI: 10.78-11.72) and for female C57BL/6J mice was 10.58 Gy (95% CI: 10.28-10.89; Fig. 2C). Overlay of the dose-response curves for sex-matched mice is shown in Fig. 2D. In all strains, the rate of disease progression measured by median survival time was inversely related to radiation dose (Fig. 2E). At supralethal doses median survival time reached a plateau, after which an increase in radiation dose did not result in a shorter latency period.

Clinical and pathological manifestations of radiation-induced lung injury (RILD) across strains
There was a dose-dependent increase in wet lung weight, consistent with edema and congestion, in all three strains. In CBA/J mice, histological features included increased alveolar wall thickness (Fig. 3Ai,ia), edema/congestion and macrophage accumulation (Fig. 3Ai,iiib), and alveolar consolidation without contracted fibrosis (Fig. 3Aiii,iiic). Histological examination of lung tissue from C57L/J mice demonstrated greater cellular (Fig. 3iv,3icii), edema/congestion (Fig. 3Bi,ia-c), areas of involvement (Fig. 3Biii, iv), epithelial hyperplasia in bronchioles, and fibrosis (Fig. 3v) than either CBA/J or C57BL/6J mice. Furthermore, several animals displayed marked to severe accumulation of alveolar macrophages, consistent with acute pneumonitis and fibrosis.

Typical pathological findings in C57BL/6J mice were mild to moderate diffuse accumulation of alveolar macrophages with mild to moderate septal thickening and fibrosis (Fig. 3Ci). Less area of involvement was seen in the C57BL/6J strain than in the C57L/J strain (Fig. 3Ciii,iii). In the C57BL/6J strain, there was little evidence of bronchiolar epithelial hyperplasia. In both C57L/J and C57BL/6J mice, a positive correlation was noted between alveolar macrophage accumulation and fibrosis (P<0.001). Pleural effusions (>0.5 g pleural fluid accumulation) in CBA/J mice were primarily observed over a narrow radiation dose range of 12.75-13.5 Gy. In male C57BL/6J mice, effusions were seen across all doses but were primarily confined to a dose range of 10-13 Gy. In female C57BL/6J mice, the majority of effusions occurred at doses of 11-12 Gy, where ~70% of mice in each of those dose groups displayed effusions that likely contributed to mortality. Consistent with our previous studies, pleural effusions were not observed in C57L/J mice.

Progression and pathobiology of RILD following whole-thorax lung irradiation (WTLI)
In a separate experiment, we examined ultrastructural damage in lung tissue at 24 h post-exposure to a single dose of 15 Gy WTLI to compare early tissue response to radiation across strains. At this time point, ultrastructural abnormalities were observed in all three strains, although histopathological changes were not yet evident under a light microscope (Fig. 4A). In C57L/J mice, findings were consistent with acute lung injury, including interstitial cell necrosis, lethal cell injury and apoptosis, epithelial denudation, and disruption of the basement membrane, all of which are indicative of injury that is unresolvable without therapeutic intervention. The major ultrastructural pathology in evaluated lungs of CBA/J mice was severe bronchial epithelial cell damage. In contrast, injury in C57BL/6J mice was less severe and primarily characterized by mild endothelial and epithelial cell swelling and interstitial edema. Bronchial epithelial damage was not observed in evaluated sections from C57BL/6J mice.

Pathophysiological mechanisms of RILD elucidated through differential gene expression analysis across murine strains
To better understand the unique gene expression patterns among murine strains before and after radiation, unsupervised hierarchical
Cluster analysis was performed. Cluster analysis was performed in a blinded fashion without *a priori* knowledge of the data. Principal component analysis (PCA) of the gene expression data demonstrated distinct clusters dependent on strain, pathology, time to disease onset and radiation dose response (Fig. 4B). For response time, CBA/J and C57L/J were categorized as ‘acute responders’ based on their shorter median survival time, consistent with acute onset of pneumonitis, and C57BL/6J mice were categorized as ‘delayed responders’ because of the prolonged latency period prior to onset of clinical symptoms following WTI and fibrotic phenotype at the dose range evaluated. We identified 5088 genes differentially expressed between acute and delayed responders (*P*<0.01; >twofold change in expression). Of these, 1445 genes were upregulated and 3642 were downregulated in acute responders in contrast to delayed responders.

A total of 3781 genes were differentially expressed after 15 Gy single-dose irradiation to the thorax between C57BL/6J versus CBA and C57L/J mice (*P*<0.01; >twofold change). PCA showed co-clustering of gene expression in acute responders versus delayed responders.

Next, we compared differences in gene expression profiles between 0 and 12.5 Gy, 0 and 15 Gy, and 12.5 and 15 Gy in each of the three strains (Fig. 4C). To derive biological meaning from the given data sets, differentially expressed genes were analyzed for...
enrichment of functional annotation using Ingenuity Pathways Knowledge Base (QIAGEN, Redwood City, CA). The significance of association between genes from the dataset and the functional pathway was calculated by Ingenuity pathway analysis (IPA) using a right-tailed Fisher exact test. Fig. 4D shows the top five highly enriched canonical pathways in each strain.
Fig. 3. See next page for legend.
Top toxicology pathways enriched in pneumonitis- and fibrosis-prone mice

Gene expression profiles altered in pneumonitis- and non-pneumonitis-prone mice 24 h after radiation

Discussion
Fig. 4. Lung injury profile among strains at 24 h post-exposure to 0, 12.5, or 15 Gy whole-lung thorax irradiation. (A) Transmission electron micrographs demonstrate prominent ultrastructural differences among C57L/J, CBA/J and C57BL/6J mice 24 h after thoracic irradiation with a single dose of 15 Gy (n=3/strain). In C57L/J mice, prominent endothelial (EC) and epithelial cell (P1/PII) swelling with capillary occlusion is noted. Interstitial cell (IC) necrosis and inflammatory cell infiltrates are also seen. Abundant lethal cell injury and apoptosis, characterized by cytoplasmic blebbing, nuclear membrane invagination, mitochondrial (M), and endoplasmic reticulum (ER) swelling, are noted. Bronchial epithelial cells are severely swollen and apoptotic in the lungs of both C57L/J and CBA/J mice. The primary ultrastructural features in C57BL/6J lungs are significant interstitial edema and mild endothelial and endothelial cell swelling. Inflammation is not as prominently observed in C57BL/6J mice as in C57L/J. E, erythrocyte; L, lymphocyte. (B) Unsupervised principal component analysis (PCA) of lung tissue samples demonstrates clustering of genes according to (1) strain; (2) expected pathology at 12.5-15 Gy (i.e. pneumonitis only, mixed pneumonitis and fibrosis, or fibrosis only); (3) median time of survival at 12.5-15 Gy (<140 or >140 days); and (4) radiation dose and strain. For PCA, C57L/J and CBA/J mice are defined as acute responders (average mortality <140 days) and C57BL/6J as delayed responders (average mortality >140 days). Grouping of individual tissue samples between the two groups suggests distinct differences in gene expression between acute and delayed responders. Close clustering of individual samples denotes the biological reproducibility of results. (C) Total number of upregulated and downregulated genes (P<0.01, >twofold change) between 0, 12.5 and 15 Gy in each strain suggests that a highly complex biological response is induced by radiation in lung tissue. (D) Top five IPA canonical pathways with the highest gene enrichment in each strain.
4 months after exposure. This is comparable with the time course of the pneumonitis phase observed in C57L/J mice in this study, where few deaths occurred 200-360 days post-exposure. Also similar is the observed lack of sex-dependent difference in dose response in this strain, as sex (male versus female; \( P = 0.62 \)) has not been observed as a risk factor for development of RILD in humans (Vogelius and Bentzen, 2012).

In this study, pleural effusions were observed in CBA/J and C57BL/6J but not C57L/J mice, primarily after 26 weeks post-WTLI. The relevance of effusions to lung injury in radiation cancer treatment is unclear, as pleural fluid accumulation is rarely seen in patients. However, Garofalo et al. found that NHPs develop significant pleural effusions following WTLI, which is mitigated by steroid (dexamethasone) treatment regimens (Garofalo et al., 2011).

### Table 1. Selected genes up- or downregulated in acute responders (CBA/J, C57L/J) compared with delayed responders (C57BL/6J)

<table>
<thead>
<tr>
<th>Gene</th>
<th>Name</th>
<th>Biological process</th>
<th>Cellular component</th>
<th>( P ) value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Genes upregulated in acute responders (CBA/J, C57L/J) compared with delayed responders (C57BL/6J)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Serpina1</td>
<td>Serine (or cysteine proteinase inhibitor, clade A, member 1; or alpha-1 antitrypsin)</td>
<td>Response to cytokine stimulus</td>
<td>Extracellular</td>
<td>1.4×10⁻¹⁰</td>
</tr>
<tr>
<td>Orm1/2</td>
<td>Orosomucoid 1.2 (or alpha-1 acid glycoprotein)</td>
<td>Acute phase response</td>
<td>Extracellular</td>
<td>1.2×10⁻⁰⁴</td>
</tr>
<tr>
<td>Mtap2</td>
<td>Microtubule associated protein 2</td>
<td>Negative regulation of microtubule polymerization</td>
<td>Cytoplasm</td>
<td>9.46×10⁻¹¹</td>
</tr>
<tr>
<td>Alad</td>
<td>Aminolevulinate, delta dehydrogenase</td>
<td>Heme biosynthetic process</td>
<td>Extracellular</td>
<td>3.17×10⁻¹⁶</td>
</tr>
<tr>
<td>Afp</td>
<td>Alpha fetoprotein</td>
<td>SMAD protein signal transduction</td>
<td>Extracellular/extracelluar</td>
<td>3.12×10⁻⁰⁶</td>
</tr>
<tr>
<td>Vegfc</td>
<td>Vascular endothelial growth factor-C</td>
<td>Angiogenesis</td>
<td>Extracellular</td>
<td>6.82×10⁻⁰⁶</td>
</tr>
<tr>
<td>Ppaip1</td>
<td>Polyadenylate binding protein-interacting protein 1</td>
<td>Positive regulation of translation</td>
<td>Cytoplasm</td>
<td>9.05×10⁻³</td>
</tr>
<tr>
<td>Fze1</td>
<td>Fascication and elongation protein zeta 1</td>
<td>Mitochondrial localization</td>
<td>Cytoplasm</td>
<td>5.61×10⁻⁰³</td>
</tr>
<tr>
<td>Tshb</td>
<td>Thyroid-stimulating hormone, beta subunit</td>
<td>Hormone activity</td>
<td>Extracellular</td>
<td>2.15×10⁻⁰⁸</td>
</tr>
<tr>
<td>Fam20b</td>
<td>Family with sequence similarity 20, member B</td>
<td>Phosphorylation; metabolic process</td>
<td>Integral to membrane</td>
<td>7.71×10⁻²¹</td>
</tr>
</tbody>
</table>

| **Selected genes downregulated in acute responders (CBA/J, C57L/J) compared with delayed responders (C57BL/6J)** |                                                   |                                            |                 |
| Rps9       | Ribosomal protein S9                             | Positive regulation of cell proliferation              | Cytoplasm          | 6.63×10⁻²⁶   |
| Galc       | Galactosylceramide                               | Galactosylceramide catalytic process                  | Mitochondrion/lysosome| 1.83×10⁻²⁶   |
| Trip11     | Thyroid hormone receptor interacting 11         | Transcription from Pol II promoter                    | Nucleus            | 2.19×10⁻²²   |
| Ptgl1      | Pituitary tumor transforming gene 1              | DNA repair                                             | Nucleus            | 3.60×10⁻²⁰   |
| Ang        | Angiogenin                                        | Activation of phospholipase C                         | Extracellular      | 6.18×10⁻⁰³   |
| Mid1       | Midline 1                                         | Positive regulation of stress-activated MAPK cascade   | Cytoplasm           | 1.15×10⁻²⁰   |
| Sox11      | SRY-box containing gene 11                       | Positive regulation of transcription from RNA polymerase II promoter | Cytoplasm/nucleus | 1.33×10⁻⁰⁷   |
| Hfe        | Hemachromatosis                                  | Antigen processing and presentation; iron homeostasis | MHC class I protein complex | 7.84×10⁻⁰⁹   |
| Erdr1      | Erythroid differentiation receptor-1             | Somatic stem cell maintenance                         | Unknown             | 2.91×10⁻⁰⁵   |
It is tempting to hypothesize that the use of dexamethasone as a standard of care for radiation pneumonitis in the clinic might explain why the pathology is not routinely observed.

Lung tissue collected at the time of scheduled or unscheduled euthanasia was examined microscopically for comparison of tissue damage among strains during early and late phases of injury. Acute radiation pneumonitis is characterized histologically by alveolar wall thickening, interstitial edema and congestion of the airways, inflammatory cell infiltration, epithelial denudation of the airways, and presence of hyaline membranes (Travis, 1987; Travis and Tucker, 1986). In this study, the lungs of CBA/J mice displayed inflammation characterized by macrophage accumulation and interstitial edema, along with moderate collagen deposition within the alveolar space at doses >13 Gy (Fig. 3A). Severe pneumonitis was observed in the lungs of moribund C57L/J mice, often with abundant fibrotic lesions (Fig. 3B). In the C57BL/6J strain, mild-to-moderate pneumonitis was
TGF-β gene enrichment to pathways such as Nrf2-mediated oxidative response and divergence in mechanisms underlying disease development and expression of disease were observed (Fig. 4). Variation in gene differences in pulmonary response to thoracic irradiation. Distinct alterations in the lungs of C57BL/6J mice were mild with neither suggestive of acute lung injury. In contrast, ultrastructural necrosis, along with lymphocyte infiltration, were also observed, likely resulting in capillary occlusion that can affect blood flow to the tissue. Epithelial cell apoptosis and interstitial cell observed, probably in the lung sections was relatively radiosensitive C57L/J strain, prominent swelling of endothelial and alveolar epithelial cells in the lung sections was observed, likely resulting in capillary occlusion that can affect blood flow to the tissue. Epithelial cell apoptosis and interstitial cell necrosis, along with lymphocyte infiltration, were also observed, suggestive of acute lung injury. In contrast, ultrastructural alterations in the lungs of C57BL/6J mice were mild with neither inflammation nor significant bronchiole epithelial damage observed in the examined tissue sections.

Gene expression profiling was performed to compare strain differences in pulmonary response to thoracic irradiation. Distinct strain-dependent differences consistent with heterogeneity in phenotypic expression of disease were observed (Fig. 4). Variation in gene enrichment to pathways such as Nrf2-mediated oxidative response and TGF-β1 signaling between and among strains suggests an immediate divergence in mechanisms underlying disease development and progression toward a pneumonitis and/or fibrosis phenotype (Fig. 5). Taken together, these data indicate the importance of selecting the appropriate murine model of WTLI for probing the mechanisms underlying RILD and testing new therapeutic interventions.

Here, gene expression profiling with microarrays identified the genes Serpin1 (P<1.4×10^{-10}) and Orm1 (P<1.12×10^{-4}), which encode serine protease inhibitor A1AT and serine protease carrier AAG, respectively, as the top differentially expressed genes between acute (C57L/J, CBA/J) and late (C57BL/6) responders (Fig. 6). Although differences in Serpin1 expression were not statistically significant at P<0.05 using qRT-PCR, Orm1 showed a statistically significant increase after radiation in both CBA/J (P<0.05) and C57L/J (P<0.001) mice. Protein expression was evaluated in lung tissue 24 h after sham irradiation or thoracic irradiation in C57BL/6J, CBA/J and C57L/J mice (n=5 strain and dose). The lack of correlation between mRNA and protein expression might result from the lag time between transcription and translation.

A literature search to compare pathophysiological findings and pathways of interest between our experimental model and human pulmonary response to radiation demonstrated that acute phase proteins have been previously implicated in radiation-induced normal tissue toxicity across species, including rodents, NHPs and humans. Zherbin et al. identified an increase in A1AT at the peak of radiation illness following total body irradiation in an NHP model (Zherbin et al., 1987). More recently, Jakobsson et al. observed an increase in both A1AT and AAG in the sera of patients with gastrointestinal toxicity following pelvic irradiation for anal or uterine cancer (Jakobsson et al., 2010). Using a bioinformatics approach, Oh et al. (2011) found a correlation between alpha-2 macroglobulin, also an acute-phase protein, and radiation pneumonitis in non-small cell lung cancer patients following fractionated radiation.

Our model of RILD differs from the clinical regimen in that wide-field, single doses of WTLI were delivered rather than localized, fractionated irradiation. However, prior studies have shown that phenotypic variation observed among murine strains extends to clinically relevant fractionation schemes and dose volumes. Nonetheless, WTLI is a useful model for establishing qualitative and quantitative endpoints to correlate pathophysiological mechanisms that orchestrate the divergence of tissue response with disease outcomes (e.g. pneumonitis and/or fibrosis).

In conclusion, data in this study point toward an immediate divergence in normal pulmonary tissue response to radiation among three murine strains with well-characterized differences in natural history of disease progression following thoracic irradiation.

**MATERIALS AND METHODS**

**Animals**

Experiments were conducted at Duke University (Durham, NC) and the University of Maryland School of Medicine (UMSOM, Baltimore, MD). All experiments were performed in compliance with the Animal Use Protocols approved by the Institutional Animal Care and Use Committee at each institution. To establish the natural history of disease progression across murine strains, age- and sex-matched C57L/J, CBA/J and C57BL/6J mice were purchased from Jackson Labs, Bar Harbor, ME, and allowed to acclimate for 2 weeks prior to radiation exposure. Age- and sex-matched sham-irradiated controls were included for comparison of normal lung tissue among mice. Animals were identified by ear tags with a unique ID number and cage card throughout the study. Animal holding rooms were maintained at 21±3°C with 30-70% relative humidity. A 12-h light/dark cycle was maintained with lights turned on at ∼07:00 h and off at ∼19:00 h. Animals were provided hyperchlorinated (10 ppm) water and fed 2018SX Teklad Global 18% Protein Extruded rodent diet ad libitum throughout the study.
Whole-thorax lung irradiation (WTLI)
The X-RAD 320 irradiator (Precision X-ray Inc., North Branford, CT) was commissioned by a board-certified medical physicist following the guidance of Task Group 61 of the American Association of Physicists in Medicine (Ma et al., 2001). Quality assurance and quality control procedures were followed during each radiation run to ensure reproducibility of radiation output and accurate dose measurements.

Animals, 10-12 weeks of age, were allocated to groups of 20 (50% male, 50% female) to receive a single dose of uniform whole-lung exposure across the dose range to induce 0 to 100% lethality over the first 180 days post-exposure consistent with earlier studies (Jackson et al., 2014). Anesthetized animals (70-100 mg/kg ketamine, 10-20 mg/kg xylazine) were irradiated in the prone position with 320 kVP X-rays (HVL = 1 mm Cu, filter=2.00 mm Al, dose rate=1.25±0.03 Gy/m) at UMSOM. Radiation was delivered to the thorax through adjustable apertures with 8 mm lead shielding of the head and abdomen. For sham irradiation, animals (20 per strain) were treated in the same way except that the radiation source was not activated.

Respiratory function analysis
Respiratory function was assessed using the Buxco whole-body plethysmograph (Wilmington, NC) as previously described (Jackson et al., 2012). Lung function measurements were recorded on alternating weeks, beginning before the time of irradiation and continuing for up to 180 days post-exposure, and at the time of euthanasia (data not shown).

Euthanasia criteria
Moribund mice were euthanized by sodium pentobarbital (>100 mg/kg) followed by bilateral thoracotomy after cessation of respiration for >1 min. Imminent moribund was determined by ≥20% body mass loss (single criterion) or if the animal met at least three of the following criteria: (1) <20% body mass loss with no recovery within 2 days; (2) inactivity, defined as no movement unless actively stimulated, on two consecutive days; (3) lack of grooming that worsened after 24 h; (4) enhanced Pause (Penh), a unitless index of lung function, of >2.5 times the animal’s baseline; and/or (5) persistent hunched posture on two consecutive days.

Observation frequency and schedule
Animals were followed for survival for up to 360 days after radiation exposure. Routine cage-side observations to assess gait, coat, behavior and activity were documented daily for the duration of the study. Animal body mass was assessed every 2 weeks throughout the study. Supportive care measures in the form of fluids, antibiotics and steroids were not provided in this study.

Necropsy and tissue harvest
At the time of euthanasia, a bilateral thoracotomy was performed. The lungs and heart were removed, and pleural effusions measured as previously described. Lungs were separated (left versus right), and masses were individually collected and recorded. The left lung was rinsed in PBS, inflated with 10% neutral buffered formalin, and placed in 10% neutral buffered formalin for fixation. The three right lung lobes were separated and snap frozen in liquid nitrogen. Heart mass was collected and recorded. The heart was fixed in 10% neutral buffered formalin.

Histopathology
Tissue sections (5 μm thick) were stained with Hematoxylin and Eosin (H&E) or Masson’s trichrome at Charles River Pathology Associates (Frederick, MD). Scoring of fibrosis, alveolar and perivascular inflammation was performed by an independent observer blinded to animal strain, radiation dose and time of death. A board-certified pathologist at Charles River Pathology Associates, blinded to sample group, evaluated a subset of tissue sections to confirm findings.

Animals and radiation exposure for differential gene expression analysis
Gene expression analysis with microarrays was performed as previously described (Jackson et al., 2016). Briefly, female C57BL/6J, CBA/J and C57L/J mice (Jackson Labs, Bar Harbor, ME) were irradiated at 10-12 weeks of age with 12.5 or 15 Gy of 320 kVp X-rays (Precision X-ray Inc.; HVL = 2.00 mm Al, dose rate=67 Gy/m) at Duke University. Age-matched sham-irradiated mice were included as controls. Mice were euthanized 24 h post-exposure by pentobarbital overdose (>250 mg/kg). Lung tissue was excised, embedded in optimal cutting temperature (OCT) compound, and frozen over dry ice. Tissue was stored at −80°C until analysis.

RNA isolation and affymetrix mouse gene chip hybridization
At the time of analysis, the right upper lobe from three to four mice per group was excised from OCT, placed in RNAlater (Fisher Scientific) for 5 min, and homogenized in 2 ml lysis buffer (QIAGEN, Valencia, CA) with zirconia-silica beads using a BeadBeater (BioSpec Products, Bartlesville, OK). RNA isolation was performed using the QIAGEN RNeasy kit according to the manufacturer’s protocol with slight modifications (Barry et al., 2010). For gene expression analysis, samples were not pooled. Total RNA was assessed for quality with Agilent 2100 Bioanalyzer G2939A (Agilent Technologies, Santa Clara, CA) and Nanodrop 8000 spectrophotometer (Thermo Scientific–Nanodrop, Wilmington, DE). Hybridization targets were prepared with MessageAmp Premier RNA Amplification Kit (Applied Biosystems–Ambion, Austin, TX) from total RNA, hybridized to GeneChip Mouse Genome 430 2.0 arrays in Affymetrix GeneChip hybridization oven 645, washed in Affymetrix GeneChip Fluidics Station 450, and scanned with Affymetrix GeneChip Scanner 7G according to standard Affymetrix GeneChip Hybridization, Wash, and Stain protocols (Affymetrix, Santa Clara, CA).

Data normalization and quality control for microarray analysis
To guard against batch effects or other technical factors impacting array data, we followed the following procedures. Animals were maintained under identical housing conditions and euthanized on the same day. Mice were irradiated in groups of 10 and alternated by strain along the radiation platform to minimize effects resulting from non-uniform radiation distribution or internal errors in the radiation procedure. Previous radiation field uniformity tests indicate <6% difference across the field. Samples were processed and hybridized in a single batch to protect against batch effects. RNA extraction and preprocessing methods used in this study are well characterized. To ensure reproducibility and minimize error, samples were not pooled but run independently. Gene expression values were normalized using robust multichip average (RMA) (Oliver et al., 2008). Unsupervised analysis, including principal component analysis (PCA) and hierarchical clustering, was performed to understand natural variations among the samples.

Quantitative real-time PCR
Gene expression was validated using quantitative real-time reverse transcriptase PCR (ABI 7900HT, Applied Biosystems, Foster City, CA) as previously described (Xu et al., 2007). Briefly, the High Capacity cDNA Archive Kit (Applied Biosystems) was used according to the manufacturer’s protocol to convert RNA to cDNA. Assays-on-Demand Gene Expression primer sets were purchased from Applied Biosystems. Real-time PCR was performed using TaqMan Universal PCR Master Mix according to the TaqMan Gene Expression Assay protocol (Applied Biosystems). Relative gene expression was determined using the comparative CT method (ACT method). Data were analyzed using two-way analysis of variance (ANOVA) and multiple comparisons test.

Western blot analysis of protein expression
The snap-frozen right lung lobe (n=5/group) was placed in a 2 ml tube filled with 1 ml zirconia-silica beads (BioSpec Products) and 2 ml ice-cold homogenization buffer (1% sodium deoxycholate, 5 mM Tris-HCl pH 7.4, 2 mM EDTA, 10 mg/ml aprotinin, 0.5 mM phenylmethylsulfonyl fluoride, 1 mM pepstatin A, 0.1 mg/ml benzamidine with or without phosphatase inhibitors). Tissue was then homogenized using the Mini-Beadbeater (BioSpec Products). Protein concentration was determined using the Nanodrop Spectrophotometer (Thermo Scientific). Western blot was
performed as previously described (Zhang et al., 2012). The anti-alpha-1 antitypsin antibody was purchased from Abcam, Cambridge, MA (AB43105; 1:1000) (Chambers and Johnston, 2003), and for alpha-1 acid glycoprotein was purchased from R&D Systems, Minneapolis, MN (MAB5934; 1:2 mg/ml). To control for loading efficiency, blots were stripped and reprobed with GAPDH or α-tubulin antibody (Sigma-Aldrich, Billerica, MA). Differences between groups were analyzed by Student’s t-test.

Transmission electron microscopy

C57L/J and C57BL/6J mice were irradiated to the whole thorax with a single dose of either 0 Gy or 15 Gy using the dosimetric parameters described above. Twenty-four hours later, animals were euthanized by sodium pentobarbital overdose (>250 mg/kg), and a bilateral thoracotomy was performed. Lung tissue was extracted, the lobes separated, and the left lobe fixed with 10% neutral buffered formalin. The left lung was then cut into longitudinal sections for electron microscopy or paraffin embedding. Paraffin embedded tissue was cut into 5 μm-thick sections and stained with H&E for evaluation of histopathological damage as described above. For transmission electron microscopy, the Duke Electron Microscopy facility, a shared resource, prepared the tissue as previously described (Miller et al., 1976). Briefly, thick sections were cut (0.5 μm) and stained with Toluidine Blue. Sections were visualized under a light microscope to determine the location for ultrathin sections. Mild inflammation was seen in C57L/J thick sections but not in C57BL/6J sections. Ultrathin sections were stained with uranyl acetate and lead citrate and visualized using a Philips CM12 transmission electron microscope.

Statistical analysis for natural history of disease progression

Statistical analysis was performed at the Indiana University School of Medicine (Indianapolis, IN) using SAS version 9.3. Proportions of mice that survived to day 360 were presented by radiation dose groups and by radiation dose and sex. A logistic regression model for 360-day mortality was fit to examine the association of radiation dose and mortality by day 360 adjusted for sex. The model included radiation dose, sex, and the radiation dose by sex interaction effect in the model. Radiation dose was included in the model as a continuous variable. Lethal doses (i.e. LD10/360-LD99/360) and their 95% confidence intervals were estimated using logistic regression models for 360 day mortality with the natural log of radiation dose included in the model as a continuous variable. Lethal doses (i.e. LD10/360-LD99/360) and their 95% confidence intervals were estimated using logistic regression models for 360 day mortality with the natural log of radiation dose. A dose-response curve was plotted. A Cox proportional hazard regression model was fitted to compare time to death between radiation dose groups adjusted for sex. The radiation dose by sex interaction effect was also tested. Kaplan–Meier survival curves were presented by radiation dose groups. Median survival times were estimated by radiation dose group. All statistical analyses were conducted as two-sided tests at 0.05 significance levels. One-way ANOVA was utilized to compare differences in gene expression among strains, radiation doses, and response (acute pneumonia versus delayed injury) types, separately. Two-way ANOVA was used to compare the strain and radiation dose effect simultaneously.

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Competing interests

The authors declare no competing or financial interests.

Author contributions

I.L.J. conceptualized, designed and oversaw conduct of the studies, interpreted data, and drafted the manuscript. F.B., C.P.G., and B.P.K. performed statistical and bioinformatics analysis of animal survival and gene expression data. A.Z., R.P., G.G., and D.W. performed natural history experiments in animals. Z.V. contributed to the overall conceptualization and study design, methodology and provided funding for the manuscript. All authors reviewed the manuscript draft. I.L.J. and Z.V. finalized the manuscript.

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Data availability


References


