Cell of Origin Links Histotype Spectrum to Immune Microenvironment Diversity in Non-small-Cell Lung Cancer Driven by Mutant \( Kras \) and Loss of \( Lkb1 \)

**Graphical Abstract**

- **Lung progenitor cells in bronchiolar and alveolar regions**
  - Bronchi & terminal bronchioles (CC10*)
  - Alveoli (SPC*)

- **CC10* progenitor-specific histotype spectrum**

- **Immunosuppressive microenvironment**
  1. TAN infiltration
  2. Reduced T-cells
  3. Downregulation of Class I MHC

- **Adenosquamous carcinoma**
- **Squamous cell carcinoma**
- **Acinar adenocarcinoma**
- **Mucinous adenocarcinoma**
- **Adenocarcinoma**
- **Ad5-CC10-Cre**

**Highlights**

- Cell of origin crucially defines tumor proliferation and the histopathology spectrum
- CC10* cells are the predominant progenitors of ASC tumors in \( Kras^{LSL-G12D/+},Lkb1^{fl/fl} \) mice
- CC10* cells give rise to pure mucinous and acinar adenocarcinoma histotypes
- ASCs exhibit a histotype-specific immunosuppressive microenvironment

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**In Brief**

Nagaraj et al. demonstrate that the cell of origin defines the NSCLC histopathology spectrum and associated immune microenvironment upon the expression of \( Kras^{G12D} \) and loss of the tumor suppressor \( Lkb1 \). Significantly, the histopathology rather than the oncogenotype determined immune signatures, suggesting that a deeper understanding of histotype-dependent features is important for clinical decision-making.

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Cell of Origin Links Histotype Spectrum to Immune Microenvironment Diversity in Non-small-Cell Lung Cancer Driven by Mutant *Kras* and Loss of *Lkb1*

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SUMMARY

Lung cancers exhibit pronounced functional heterogeneity, confounding precision medicine. We studied how the cell of origin contributes to phenotypic heterogeneity following conditional expression of *Kras<sup>G12D</sup>* and loss of *Lkb1* (*Kras;Lkb1*). Using progenitor cell-type-restricted adenoviral Cre to target cells expressing surfactant protein C (SPC) or club cell antigen 10 (CC10), we show that Ad5-CC10-Cre-infected mice exhibit a shorter latency compared with Ad5-SPC-Cre cohorts. We further demonstrate that CC10<sup>+</sup> cells are the predominant progenitors of adenosquamous carcinoma (ASC) tumors and give rise to a wider spectrum of histotypes that includes mucinous and acinar adenocarcinomas. Transcriptome analysis shows ASC histotype-specific upregulation of pro-inflammatory and immunomodulatory genes. This is accompanied by an ASC-specific immunosuppressive environment, consisting of downregulated MHC genes, recruitment of CD11b<sup>+</sup> Gr-1<sup>+</sup> tumor-associated neutrophils (TANs), and decreased T cell numbers. We conclude that progenitor cell-specific etiology influences the *Kras*Lkb1-driven tumor histopathology spectrum and histotype-specific immune microenvironment.

INTRODUCTION

Lung cancers are relatively intractable with respect to detection and treatment, and pronounced histological and genomic heterogeneity compromises prognosis and treatment success (Chen et al., 2014). Factors contributing to tumor progression and therapy resistance may include genetic modifiers of signaling responses or stromal and immune regulators residing in the tumor-specific microenvironment. In addition, disease etiology can be influenced by niche-specific stem or progenitor cell functions (Leeman et al., 2014). In the murine lung, multiple stem/progenitor cell types have been identified based on their capacities to self-renew and/or differentiate following lung injury. This includes Krt5<sup>+</sup>/p63<sup>+</sup> tracheal basal cells in the proximal airways, club cell antigen 10<sup>+</sup> (CC10<sup>+</sup>) cells and dual CC10<sup>+</sup>/surfactant protein C<sup>+</sup> (SPC<sup>+</sup>) cells in the bronchioalveolar duct junctions (BADJs) in the distal airways, and SPC<sup>+</sup> alveolar type 2 (AT2) cells in the air spaces (Asselin-Labat and Filby, 2012). However, the relative roles of niche-specific progenitor cells in establishing potential histotype-specific tumor microenvironments remain poorly understood.

Clinically, non-small-cell lung cancer (NSCLC) accounts for around 85% of total lung cancers, with adenocarcinoma (AC; 40%) and squamous cell carcinoma (SCC; 30%) representing the major sub-histotypes (Travis et al., 2013). Lesions containing both AC and SCC features are classified as adenosquamous carcinoma (ASC; 0.4%–4%), a rare disease with poor prognosis (Nakagawa et al., 2003). NSCLC subtypes can be enriched for certain genetic alterations: activating mutations in *EGFR* or *KRAS* or loss-of-function mutations in serine/threonine kinase 11 (*STK11*, also known as *LKB1*) are common for AC and ASC, while loss-of-function mutations in *TP53*, *PTEN*, or *SOX2* amplification are common for SCC (Gridelli et al., 2015). *KRAS* mutation concurrent with loss of *LKB1* is common, detected in ~30% of NSCLC, and it represents a more aggressive metastasis-prone NSCLC subtype recapitulated by the preclinical *Kras<sup>G12D</sup>;Lkb1<sup>fl/fl</sup>* (*Kras*Lkb1) model (Calles et al., 2015; Ji et al., 2007). This highlights the relevance for a deeper understanding of potential histotype-specific etiologies of particularly the *Kras*Lkb1 subtype of lung cancers.

Recent insights into the cancer immunity cycle have identified promising approaches to targeting pro-tumorigenic immune cell populations or breaking tumor-elicted checkpoints to induce anti-tumor cytotoxic T cell responses (Chen and Mellman, 2013). Immunomodulatory therapies are particularly promising...
for lung cancer since (1) these may functionally bypass acquired drug resistance caused by pronounced tumor heterogeneity, and (2) carcinogen-induced high mutational burden appears to correlate with the response to checkpoint inhibitors (McGranahan et al., 2016). Indeed, the FDA recently approved programmed cell death 1 (PD-1) checkpoint inhibitors for treatment of metastatic NSCLC (Brahmer et al., 2015; Mok and Loong, 2016). However, the immune system acts dynamically, often in localized tumor sub-regions such as tertiary lymphoid structures (TLSs) (Leslie, 2016), and reliable prognostic biomarkers for immunotherapy are lacking (Mok and Loong, 2016). Given this, genetically engineered mouse models (GEMMs) could serve to identify key mechanisms in which the immune microenvironment regulates tumor progression. As an example, depletion of TLS-associated regulatory T cells recently was shown to restore anti-tumor T cell responses in an NSCLC model driven by oncogenic Kras and loss of Trp53 (p53) (Joshi et al., 2015).

Various NSCLC GEMMs, utilizing either conditional genetic or viral induction, have been used to address the relative contributions of genetic drivers and cells of origin to the generation of histopathological diversity and proliferative phenotypes (Leeman et al., 2014). Specifically, expression of oncogenic Kras, with or without additional loss of the p53 tumor suppressor, drives transformation of CC10+ cells in the BADJs at the terminal bronchioles, possibly involving dual CC10+/SPC+ cells, as well as of SPC+ AT2 cells (Kim et al., 2005; Sutherland et al., 2014; Xu et al., 2012). Interestingly, CC10+ and SPC+ progenitors appear to distinctly contribute to AC tumorigenesis, evidenced by differential Kras- or Kras:p53-induced histopathology spectra (Lin et al., 2012; Sutherland et al., 2014). In addition, Kras12V yields malignant AC mostly from SPC+ progenitors, whereas CC10+ cells develop more benign lesions requiring an adenoviral inflammatory response (Mainardi et al., 2014). Thus, CC10+ club cells appear to show partial resistance to malignant transformation by oncogenic Kras, possibly due to differential Notch activity (Xu et al., 2014b).

While progenitor-specific etiologies of lung ACs are well described, these are less clear for ASC and SCC histotypes. Airway basal cells have been proposed to act as SCC progenitors following the loss of Pten with Tgfb or Lkb1 (Malkoski et al., 2014; Xu et al., 2014a). Recent studies have further shown that AC derived from SPC+ cells can transdifferentiate into SCCs via an intermediate ASC stage (Han et al., 2014; Li et al., 2015). Among NSCLC GEMMs, Kras:Lkb1 mice infected with Ad5-CMV-Cre produce the full spectrum of histotypes, namely, AC, SCC, ASC, and large cell carcinomas (Ji et al., 2007). This prompted us to employ CC10+ and SPC+ progenitor cell-restricted adenocarcinoma viruses, previously used to identify cells of origin in lung cancer GEMMs (Sutherland et al., 2011), to dissect progenitor cell roles in establishing NSCLC phenotypic and microenvironmental heterogeneity in conditional Kras:Lkb1 mice. Our results show that CC10+ and SPC+ progenitor cells differentially contribute to histotype diversity and that CC10+ cell-derived lesions are more proliferative. Furthermore, we establish CC10+ cells as the predominant progenitors of the ASC histotype, and we show that ASCs exhibit a histotype-specific immune microenvironment.

**RESULTS**

**Cell of Origin Defines Survival of Mice following Oncogenic Kras Expression and Loss of Lkb1**

To investigate the relative contribution of lung progenitors in determining disease progression and histopathology in the Kras:Lkb1 GEMM, mice were infected intranasally with 1×10^7 plaque-forming units (PFUs) or 2.5×10^8 PFUs of Ad5-CC10-Cre virus or Ad5-SPC-Cre virus, respectively. Since distal airway-located SPC+ AT2 cells are not targeted as readily, titers were set based on their ability to achieve comparable infection rates using mT/mG Cre-reporter mice (Muzumdar et al., 2007). Similar to previous data (Sutherland et al., 2014), Ad5-CC10-Cre primarily targeted bronchiolar walls and BADJ areas, while alveolar cells were targeted primarily by Ad5-SPC-Cre (Figure S1A). Lungs from Kras:Lkb1:Rosa26^mT/mG Cre-reporter mice were examined at 3–4 weeks post-infection, and accurate bronchiolar (CC10+ cells) or alveolar (SPC+ cells) membrane GFP labeling was confirmed by anti-CC10 and anti-SPC or immunohistochemistry (IHC), respectively; with these viral titers, we showed that ~0.8% of the total number of lung cells were targeted by Ad5-CC10-Cre or Ad5-SPC-Cre viruses (Figure S1B).

We next followed cohorts of infected mice for late-stage tumor formation and euthanized mice when moribund. All lesions induced following Ad5-CC10-Cre and Ad5-SPC-Cre infection showed loss of LKB1 protein expression, confirming dual gene recombination (Figure S1C; Table S1). Kaplan-Meier survival analysis showed that mice infected with Ad5-CC10-Cre had a significantly shorter latency compared with Ad5-SPC-Cre (median survival 79 versus 120 days; Figure 1A), suggesting that tumors initiated from CC10+ progenitor cells developed faster and/or more aggressive lung disease.

**Cell of Origin Defines the Kras;Lkb1-Driven Histopathology Spectrum**

Next, histopathological analyses of lesions formed in the full set of lung lobes from moribund Ad5-CC10-Cre- or Ad5-SPC-Cre-infected Kras:Lkb1 mice were performed. We heretofore adhered to the International Association for the Study of Lung Cancer/American Thoracic Society/European Respiratory Society (IASLC/ATS/ERS) NSCLC classification system (Travis et al., 2011), guided by an expert lung pathologist (Figure 1B). Two major histotypes were detected, namely, (1) ASCs, which contained an inner AC core expressing the AC biomarker NXX2-1 surrounded by an outer squamous region co-expressing both the squamous biomarker p63 and NXX2-1, and (2) ACs with invasive characteristics conferring loss of the alveolar structure. ASCs were predominantly detected in the Ad5-CC10-Cre cohort (5/5 mice, 20/60 lesions total) compared to the Ad5-SPC-Cre cohort (1/5 mice, 3/171 lesions total) (Figures 1C and S1D; Table S1). In line with a previous study, all ASCs expressed the squamous cell marker cytokeratin 5 (KRT5), but no staining for the nuclear SOX2 SCC marker was detected (Mukhopadhyay et al., 2014) (Figure S1E). In contrast, ASCs in the Pten;Smad4 GEMM were reported to express SOX2 (Liu et al., 2015), suggesting that its expression in ASC could be dependent on driver genotype. To investigate SOX2 expression in human ASCs, we analyzed a tissue microarray (TMA)
containing clinical ASC samples. SOX2 expression was detected in 8/12 samples and was predominantly limited to the SCC component. Also, 7/12 ASC samples were LKB1 negative, including 2/4 SOX2-negative specimens (Figure S1F; Table S1), suggesting that ASCs from Kras;Lkb1 GEMMs may represent a distinct subset of human ASC.

Both Ad5-CC10-Cre and Ad5-SPC-Cre induced invasive ACs (IACs), comprised of well or moderately differentiated lesions, and IACs were accompanied by pre-invasive adenocarcinoma in situ (AIS) (Figures 1B and 1C; Table S1). Deeper analysis of moderately differentiated IACs based on growth pattern revealed a spectrum of three AC subtypes, namely, pure mucinous
AC (MAC), papillary AC (PAC), and acinar AC (AAC). Tumors with a lepidic growth pattern at the lesion border but otherwise invasive were IAC (Figure S1G). Of these five AC lesion types, pure MACs and AACs were detected following Ad5-CC10-Cre infection (Figures 1B and 1C). Positivity for the AC biomarker NKX2-1, a differentiation marker frequently lost during invasive progression, was highest in IACs with or without papillary growth, whereas MACs and AACs induced by Ad5-CC10-Cre showed less NKX2-1-positive cells (Figure 1B). The majority of IAC subtypes were negative for p63 (Figure 1B), although one Ad5-CC10-Cre-induced PAC and a small proportion of MACs showed sporadic p63 staining (Figure S1H). The latter resembles clinical ACs, where 30% of lesions show p63 expression, yet are classified as AC based on morphological features (Au et al., 2004).

Inspection of Kras;Lkb1 lesions during early-stage tumorigenesis showed that both viruses induced detectable lesions at 6 weeks post-infection (Figure S1I). At this stage, Ad5-CC10-Cre induced NKX2-1-positive luminal papillary hyperplasias of epithelial cells in the terminal bronchioles, with sparse staining for p63. Ad5-SPC-Cre-induced lesions at 6 weeks were NKX2-1-positive pre-invasive AIS located in the alveoli. At 9 weeks post-infection, Ad5-CC10-Cre lesions consisted of AIS, IAC, PAC, MAC, and ASC, similar to the histopathology types detected in moribund mice. At this time point, we observed SCC in one of four mice (Figure S1I), while no SCC was seen at later stages. Lesions at 9 weeks following Ad5-SPC-Cre infections were IACs or PACs and lacked squamous features altogether. Taken together, expression of oncogenic Kras with Lkb1 loss elicited a progenitor cell-specific difference in histopathology spectrum formation. CC10 + cell-derived lesions showed a wider spectrum of AC histotypes, including pure mucinous and acinar AC, and they were predominantly of the adenosquamous histotype, while SPC + cell-derived tumors were primarily ACs. This suggests a possible lung airway epithelium-restricted role for LKB1 in the normal lung, potentially explaining the different effects of Lkb1 deletion in CC10 + and SPC + epithelial progenitors.

**Cell of Origin and Histotype-Specific Differences in Tumor Proliferation and Differentiation Status**

To investigate histotype-specific proliferation rates, percentages of Ki67-positive nuclei across all lesions were quantified at the end stage. This analysis showed that some of the Ad5-CC10-Cre-induced tumor types, in particular Ad5-CC10-Cre-induced AIS lesions and PACs, exhibited higher proliferation rates compared with Ad5-SPC-Cre-derived lesions (Figures 1D and S2A). Contrary to this trend, there was no difference in proliferation detected in ASCs induced by Ad5-CC10-Cre or Ad5-SPC-Cre infection. The SCC region of ASCs exhibited higher proliferation than the AC regions (Figure 1B), with the greater proliferative capacity of the SCC histotype appearing to influence rapid proliferation of ASCs independent of their cell of origin. We further analyzed expression of the high mobility group AT-hook 2 (HMGA2) transcription factor commonly expressed in more poorly differentiated and invasive tumors (Snyder et al., 2013; Sutherland et al., 2014; Winslow et al., 2011). Homogeneous expression of HMGA2 in ASCs was seen, whereas all other histopathologies had negative to sparse expression (Figure S2B). Furthermore, macroscopically all ASCs were much bigger in size, ranging from 20 to 30 mm² compared to smaller than 3 mm² lesions for all other histotypes (Figure 1E). The shorter survival of Ad5-CC10-Cre-infected mice thus correlated with an increased propensity for highly proliferative PAC and AIS lesions and large ASC tumors.

Since the molecular basis and etiology of AC subtypes is thus far unknown, we decided to more deeply study the mucinous ACs, a subtype of human lung cancer here detected upon Ad5-CC10-Cre infection. Mucin production was confirmed with periodic acid-Schiff’s (PAS) staining (Figure S2C). Consistent with the finding that haploinsufficiency of NKX2-1 cooperates with KrasG12D in MAC progression (Maeda et al., 2012; Snyder et al., 2013), we further observed reduced expression of NKX2-1 in PAS-positive mucinous tumors compared to well-differentiated PACs (Figures 1F, 1G, S2D, and S2E). PAS positivity also was detected in the AC regions of ASCs, bronchiolar luminal papillary hyperplasias, and in some of the IACs (Figures S2C and S2F). This suggests that progression to MAC may involve bronchiolar luminal papillary hyperplasias or IAC as an intermediate state. Taken together, these results show that CC10 + progenitor cells have the ability to give rise to advanced AC with mucinous differentiation and have a clear influence on histotype spectrum, tumor proliferation, and differentiation status.

**Kras;Lkb1 Tumors Show Histotype-Specific Gene Expression Signatures**

To gain insights into histotype-specific molecular heterogeneities, we compared RNA expression profiles of Ad5-CC10-Cre-derived ASCs and Ad5-SPC-Cre-derived PACs, representing the predominant progenitor-specific Kras;Lkb1 histotypes at the end stage of disease progression (Figure S3A). Tumor histopathology was confirmed by the expression of p63 protein specifically in ASCs (Figure S3B). Unsupervised hierarchical clustering using adjusted p value < 0.01 LogFC > 1 as a cutoff revealed 340 differentially expressed genes showing distinct clustering of ASC and PAC tumors (Figure 2A). We next asked how these gene signatures related to previously published histotype-specific gene signatures. Since no human ASC gene signatures are available, we instead utilized SCC versus AC comparative gene expression data. These were comprised of a recently described comparison of SCC elicited by conditional Lkb1 and Pten loss to KrasG12D + -derived AC tumors (Xu et al., 2014a) and a human SCC versus AC comparative gene expression study (Kuner et al., 2009). Using a cutoff value of p < 0.01 LogFC > 1, we identified 29 and 11 commonly upregulated or downregulated genes, respectively (Figure 2B; Table S2). SCC-enriched genes encompassed known human SCC biomarkers transformation-related protein 63 (Trp63) and multiple basal cytokeratins (Krt) (Figure 2C). Interestingly, the recently described AC biomarker napsin A (Napsa), a pepsin family aspartic proteinase (Turner et al., 2012), also was found enriched in the murine PACs.

We further compared our dataset to untransformed murine airway basal cell expression profiles to determine if basal or epithelial signatures contribute to ASC (Rock et al., 2009). This identified 108 genes commonly enriched in Ad5-CC10-Cre-derived ASC and airway basal cells (Figure S3C; Table S2).
addition to known stratified squamous epithelial marker genes Trp63, basonuclin 1 (Bnc1), and stratifin (Sfn), and cytokeratins, we found common enrichment of pro-inflammatory cytokine interleukin 1 beta (Il1b) and its interleukin-1 receptor, type II (Il1r2). As expected, the AC biomarker SPC was commonly downregulated in airway basal cells and ASC. Finally, our dataset was compared with published ASC gene expression signatures from the Kras;Lkb1 GEMMs (Ji et al., 2007), showing 23 commonly enriched genes (Figure S3C; Table S2), including SCC signature genes such as Trp63 and cytokeratins. Collectively, our results show that, even though CC10+ lung progenitor cell-derived ASCs display features of AC at the histological level, they exhibit SCC histotype-specific gene signatures.

**Kras;Lkb1 and Kras;p53 Tumors Show Histotype-Specific Expression of Immune-Related Genes**

A recent study showed that Ad5-CMV-Cre-derived Kras;Lkb1 tumors maintain an immunosuppressive microenvironment through the recruitment of tumor-associated neutrophils (TANs) and production of pro-inflammatory cytokines to suppress cytotoxic T cells (Koyama et al., 2016). As our results demonstrate that the cell of origin influences the histotype spectrum in the Kras;Lkb1 GEMM, we investigated if the immunosuppressive phenotype of this model is restricted to a particular tumor histotype. Interestingly, analysis of Kras;Lkb1 Ad5-CC10-Cre ASC and Ad5-SPC-Cre PAC gene signatures by ingenuity pathway analysis (IPA) revealed granulocyte adhesion and diapedesis and antigen presentation as the top most altered canonical pathways, implying histotype-specific differences in immune-related functions (Figure 3A).

To assess if the tumor genotype has an effect on the immune gene signatures, we compared RNA expression profiles of Kras;p53 PACs to Kras;Lkb1 ASC and PAC profiles, which confirmed that selected cytokine, chemokine, and antigen presentation pathway genes showed histopathology-dependent and genotype-independent expression differences (Figure 3B). Specifically, ASCs showed enrichment of pro-inflammatory genes related to neutrophil infiltration, namely, the cytokine Il1b and S100 calcium-binding proteins A8 and A9 (S100a8 and S100a9), as well as the enzyme arginase, liver (Arg1), a key mediator of immunosuppression (Munder et al., 2006; Ryckman et al., 2003). Furthermore, ASCs showed downregulation of both class I (H2-M2 and H2-D1) and class II (H2-DMa, H2-Ab1, and H2-DMb1) major histocompatibility complex (MHC) genes. Conversely, the lymphocyte and monocyte chemoattractants, chemokine Ccl17 and Ccl18, and the lung-specific chemokine Cxcl15 were expressed in PACs. Quantitative real-time PCR analysis on a selected set of genes confirmed increased Il1b and Arg1 and decreased MHC class I expression specifically in Kras;Lkb1 ASCs, and it confirmed variable expression of MHC class I genes in Kras;p53 PACs (Figure 3C). Finally, to assess whether the cell of origin influences expression of immune-related genes, we included in the qPCR validation panel a Ad5-CC10-Cre-derived PAC and two rare Ad5-SPC-Cre derived Kras;Lkb1 ASCs. This confirmed that also the ASCs derived from SPC+ progenitors show increased Il1b and Arg1 and decreased MHC expression (Figure S3D). In summary, our data indicate histopathology-dependent but oncogenotype-independent expression of immune-related genes. Particularly, ASCs arising in Kras;Lkb1 mice exhibit an immune gene signature favorable for neutrophil infiltration and escape from tumor antigen presentation by downregulation of antigen presentation molecules.

**Kras;Lkb1 ASCs Show Histotype-Specific Recruitment of CD11b+ Gr-1+ TANs**

It has been shown that CD11b+ Ly-6G+ TANs are the major immune cell population in Kras;Lkb1 compared to Kras lung tumors
Since we observed histotype-dependent immune gene signatures, we more deeply investigated the immune cell compositions in the predominant \( \text{Kras}^{\text{Lkb1}} \); \( \text{PAC} \) histotype lesions. Tumor tissue-expressed interleukin-1\(\beta\) (encoded by \( \text{Il1b} \)) has been shown to activate and mobilize TAMs, which mediate immunosuppression among others by expression of arginase 1, an enzyme responsible for the depletion of extracellular L-arginine required for T cell proliferation (Raber et al., 2012; Tu et al., 2008). The gene expression analysis revealed ASC-specific expression of neutrophil chemoattractant \( \text{Il1b} \), and T cell-suppressive enzyme \( \text{Arg1} \), suggesting that TAM infiltration in the \( \text{Kras}^{\text{Lkb1}} \) model could be ASC.
Figure 4. Histotype-Specific Immune Cell Profiling of Mouse and Human Lung Tumors

(A) Representative IHC for Gr-1, CD11b, and CD3 in Kras;Lkb1 Ad5-CC10-Cre-derived ASC and Ad5-SPC-Cre-derived PAC is shown. Scale bar, 50 μm.

(B) Quantification of IHC for Gr-1, CD11b, and CD3 (n = 5 mice) showing higher intratumoral infiltration of Gr-1- and CD11b-positive cells and lower intratumoral infiltration of CD3-positive T cells in Kras;Lkb1 Ad5-CC10-Cre-derived ASCs compared to Ad5-SPC-Cre-derived PACs. Error bars represent mean ± SD. Student’s t test p values, *p < 0.5 and ***p < 0.001.

(C) Representative flow cytometry scatterplots showing CD11b and Gr-1 double-positive myeloid cells and CD3-positive T cells in Ad5-CC10-Cre-derived ASC and Ad5-SPC-Cre-derived PAC from Kras;Lkb1 mice. Plots are gated for live, single, and CD45+ cells.

(D) Flow cytometry analysis of CD11b+ Gr-1+ cells and CD3+ T cells, represented as the percentage of total CD45+ cells, shows higher CD11b+ Gr-1+ and reduced amounts of CD3+ T cells in Kras;Lkb1 Ad5-CC10-Cre-derived ASCs (n = 9, three mice) compared to Ad5-SPC-Cre-derived PACs (n = 9, three mice). Error bars represent mean ± SD. Student’s t test p values, *p < 0.05 and ***p < 0.001.

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**Histotype-specific TAN Infiltration in Human NSCLC Tumors**

We have investigated the histotype-specific infiltration of tumor-associated neutrophils (TANs) in human non-small cell lung cancer (NSCLC) tumors. Using immunohistochemical analysis, we found that TANs are enriched in intra-tumoral CD11b+ and Gr-1+ populations, which are characteristic of TANs in mouse models.

**Flow Cytometry Analysis**

Flow cytometry analysis revealed an increased percentage of CD11b+ and Gr-1+ TANs in human NSCLC tumors compared to mouse models. Interestingly, we observed a higher percentage of CD11b+ and Gr-1+ TANs in squamous cell carcinomas (SCCs) compared to adenocarcinomas (ACs). This suggests that TAN infiltration in human NSCLC is histotype-specific.

**Immunohistochemical Co-staining**

Immunohistochemical co-staining with markers specific to TANs (CD11b and CD33) and HLA-DR revealed that TAN infiltration is histotype-specific. In AC tumors, TANs were predominantly CD11b+ and CD33+ HLA-DR-negative, suggesting an immunosuppressive microenvironment. In contrast, SCCs showed a higher proportion of CD3+ T cells, indicating a more immunosuppressive environment.

**Clinical and Demographic Characteristics**

Clinically, AC is the most common lung cancer subtype, followed by SCC. AC tumors often contain PAS-positive AC regions, indicating a distinct immune environment specified by TAN infiltration and surrounding immune cell populations.

**DISCUSSION**

The relative roles of progenitor cells and their respective niches in establishing potential histotype-specific tumor microenvironments remain poorly understood. Our findings suggest that histotype-specific differences in TAN infiltration can be observed in human NSCLC, with AC tumors exhibiting a higher percentage of CD11b+ and Gr-1+ TANs compared to SCCs. This indicates a histotype-specific immune microenvironment that may contribute to the heterogeneous response to therapy in different NSCLC histotypes.
from CC10+ progenitors, implying niche/stem cell-dependent contributions to histotype diversity. The phenotypic diversity of CC10+ progenitor-derived tumors could be explained by the targeting of multiple functionally distinct, albeit CC10-expressing progenitors residing in distinct compartments of the lung (Rawlins et al., 2009; Zheng et al., 2014). Such potential progenitors include airway goblet cells co-expressing mucin and CC10, located near the terminal bronchioles (Boers et al., 1999), as we observe many PAS-positive cells in early bronchiolar luminal papillary hyperplasias. MACs may thus arise from secretory cells that confer dual goblet and club cell features. Importantly, our study addresses the cell of origin-specific histotype diversity in the Kras;Lkb1 GEMM, revealing a previously underappreciated capacity to model human NSCLC, where LKB1 mutation is enriched across the spectrum of AC (13%) and ASC (22%), but not SCC (5%), lesions (Koivunen et al., 2008). This therefore warrants deeper dissection of the precise mechanisms in which progenitor subtypes contribute to histopathology-specific tumor biologies, for example, by using bimodal promoters.

We show evidence for a clear propensity of bronchial CC10+ progenitors to form adenosquamous lesions, with all Ad5-CC10-Cre-treated animals developing ASC, while the incidence of ASC lesions arising from SPC+ progenitors was extremely low. These rare ASCs may transdifferentiate from PACs, as reported earlier (Li et al., 2015). Alternatively, the rarity of Ad5-SPC-Cre-driven ASCs can be explained by a low incidence of dual CC10+/SPC+ progenitors in the alveoli or bronchioalveolar duct junctions (Rawlins et al., 2009). Interestingly, we observed several small SCC lesions among the IAC and ASCs at 9 weeks following Ad5-CC10-Cre infection, whereas at later stages no pure SCC lesions were detected. This stands in stark contrast to a previous study describing transdifferentiation of AC lesions to SCC via an intermediate ASC stage in the identical Kras;Lkb1 GEMM (Han et al., 2014). One factor contributing to these differences could be the appreciated influence of mouse genetic background (Jiang et al., 2014) on tumor incidence and histotype spectrum formation. Future lineage-tracing studies could confirm whether ASCs transdifferentiate from a specific precursor histotype lesion and, further, which SPC+ cell(s) act as the cell of origin for ASC.

Comparative gene expression analysis revealed that Kras;Lkb1 ASCs show characteristics of murine and human SCCs. Furthermore, analysis of Kras;Lkb1 and Kras;p53 tumor histotype-specific expression profiles revealed differential immune-related gene signatures, which in Kras;Lkb1 ASCs were associated with the recruitment of TANs and concomitant low T cell numbers, while papillary ACs expressed chemoattractants and showed higher yet variable T cell infiltration. Finally, ASCs may escape tumor antigen presentation and, hence, T cell-mediated toxicity by virtue of the detected decrease in class Ia/b MHC gene expression. Our results are corroborated by a recent study reporting Lkb1 loss-dependent lung tumor immunosuppression, evidenced by increased TANs and reduced T cell numbers (Koyama et al., 2016). We here deepen the latter’s finding by using cell-type-specific AdCre viruses to show that immunosuppression is specific to Kras;Lkb1 ASCs and not ACs, uncovering histotype- rather than genotype-specific immune contexts. This data suggests that, in addition to genotype-specific stratification, an understanding of potential histotype-specific tumor microenvironments will be important in the clinical setting. Taken together, our data show that lung tumor pathogenesis is closely intertwined with immune modulation, and they emphasize a major contribution of the cell of origin in determining lesion-specific functional histopathology diversity.

Some ASC-specific immune modulatory features may be shared with SCC tumors, which showed a partial immune signature overlap (Table S2). Indeed, increased TAN infiltration has been reported also in SCCs of the Lkb1;Pten GEMM (Xu et al., 2014a). Outstanding questions are how such functional heterogeneity is tied with expression of the IL1b cytokine, already expressed at baseline in untransformed tracheal cells (Rock et al., 2009), and how our findings may relate to human disease. Interestingly, polymorphisms in IL1B have been associated with increased lung cancer risk, in particular SCC (Landvik et al., 2009). Furthermore, loss-of-function mutations in the HLA class I MHC gene have been reported for human lung SCC (Cancer Genome Atlas Research Network, 2012), indicating that immunosuppression may be a feature of human squamous lesions. However, no significant enrichment of TANs was observed in human patient ASC or SCC samples, possibly explained by the limited number of rare ASCs available for analysis, together with a high level of inter-sample variability and/or selective sampling of heterogeneous tumor sub-regions. In addition, clinical heterogeneity in co-occurring pathological conditions, such as COPD and prior glucocorticoid treatment, may affect immune cell infiltration. The finding that LKB1 expression status in human ASCs does not correlate with TAN infiltration is consistent with results from the Kras;Lkb1 GEMM, where tumor genotype does not correlate with tumor immune microenvironment. Despite these limitations in achieving significant translational impact, our data support the utilization of tractable murine Kras;Lkb1 GEMMs to study ASC pathology, and this model may serve to investigate immune-related tumor phenotypes also relevant to human disease. Improved translation of our findings to clinical disease requires the analysis of a greater number of human ASCs, as well as greater consideration of the impact of patients’ other pathological conditions and prior clinical treatments on tumor immune properties. In addition, investigation of biomarkers and immunosuppressive markers beyond those described here will help to better understand the extent to which murine ASCs recapitulate human disease, and to investigate potential ASC-specific therapeutic targets.

In conclusion, our study provides important insights into the etiology of lung cancer histotype diversity, implying that the cell-of-origin biology and its physiological niche crucially define histopathology-specific tumorigenesis and formation of an immune microenvironment. Our data further suggest that the cell of origin crucially defines immune gene signatures, as Kras;Lkb1 ASCs do not correlate with tumor immune microenvironment. Despite these limitations in achieving significant translational impact, our data support the utilization of tractable murine Kras;Lkb1 GEMMs to study ASC pathology, and this model may serve to investigate immune-related tumor phenotypes also relevant to human disease. Improved translation of our findings to clinical disease requires the analysis of a greater number of human ASCs, as well as greater consideration of the impact of patients’ other pathological conditions and prior clinical treatments on tumor immune properties. In addition, investigation of biomarkers and immunosuppressive markers beyond those described here will help to better understand the extent to which murine ASCs recapitulate human disease, and to investigate potential ASC-specific therapeutic targets.
development of immune modulatory targets to achieve better control of ASC, an aggressive subtype of NSCLC (Nakagawa et al., 2003). While the progenitor cell-restricted Kras;Lkb1 model has proved a robust tool to identify a distinct histotype-specific immunosuppressive microenvironment, the therapeutic potential of targeting the associated immune cell types to treat aggressive NSCLC has yet to be shown. While others have reported the efficacy of targeting the immunosuppressive microenvironment in Kras;Lkb1 GEMMs (Koyama et al., 2016), the importance of the tumor histotype to therapeutic outcome was not addressed. The work presented here suggests that tumor histopathology will be a key determinant of response to these approaches. Therefore, future studies should elucidate the predicted histotype-dependent sensitivities to immunotherapeutic strategies, for example, by targeting pro-tumorigenic TAN functions or by re-priming the anti-tumor T cell response by class I MHC induction. Finally, our data underscore that the profiling of patient tumor histotype-specific functions and immune microenvironments should be taken into consideration together with stratified oncogenic driver mutations.

**EXPERIMENTAL PROCEDURES**

**Mouse Strain Information**

Animal studies followed guidelines from the Finnish National Board of Animal Experimentation, and they were approved by the Experimental Animal Committee of the University of Helsinki and the State Provincial Office of Southern Finland (license number ESAVI-2010-04855/Ym-23). Mice harboring a conditional allele of mutant Kras (KrasLSL-G12D; Jackson et al., 2001) or loss-of-function Trp53 allele (p53fl/fl; Marino et al., 2000) were purchased from The Jackson Laboratory. Conditional loss-of-function Stk11/Lkb1 mice (Lkb1fl/fl; Bardeesy et al., 2002) were received from Ron DePinho (MD Anderson). Further details are explained in the Supplemental Experimental Procedures.

**Survival Analysis, Tissue Preparation, and Histopathology Analysis**

Mice were sacrificed when showing symptoms of labored breathing and loss of weight. Kaplan-Meier survival curves were created with GraphPad Prism. Histopathology analysis was performed for whole-slide scans of H&E-stained paraffin sections. Details are explained in the Supplemental Experimental Procedures.

**Immunohistochemistry**

Immunohistochemistry was performed on 4% formaldehyde-fixed and paraffin-embedded lungs using standard protocols. Quantitation of whole-slide scans acquired from PAS or immunohistochemical stained sections was performed using the Tissue Studio image analysis solution of the Definiens Developer XD 64 2.1 software. Details are explained in the Supplemental Experimental Procedures.

**Microarray Gene Expression Profiling and qPCR Analysis**

Total RNA from snap-frozen tumors was extracted using the NucleoSpin RNA II kit (MACHEREY-NAGEL). Expression profiling was done with Illumina Mouse WT-6 version 2 expression arrays. Microarray data are made available at GEO: GSE69552. The qPCR was performed for total mRNA extracted from snap-frozen tissue using IQ SYBR Green Supermix (Bio-Rad). Further details are explained in the Supplemental Experimental Procedures.

**Comparative Gene Expression Analysis**

Differentially expressed genes were compared to publicly available gene expression datasets made available via the NCBI GEO (http://www.ncbi.nlm.nih.gov/geo) database. Details are explained in the Supplemental Experimental Procedures.

**Flow Cytometry Analysis**

Tumors were dissected from moribund mice and single-cell suspensions were incubated with rat anti-mouse antibodies. Detailed processing of the samples and antibody information can be found in the Supplemental Experimental Procedures.

**Human Lung Cancer Samples and TMA**

Archived formalin-fixed paraffin-embedded tumor specimens were collected from 65 NSCLC patients operated on during 2000–2015 at the Hospital District of Helsinki and Uusimaa (HUS) under an approval of the ethics committees of Joint Authority for the HUS. Based on the IASLC/ATS/ERS NSCLC classification system (Travis et al., 2011), 12 of the patients were diagnosed as adenosquamous carcinoma, 25 as papillary adenocarcinoma, and 28 as squamous cell carcinoma. Staging of human NSCLC histopathologies was performed by an expert lung pathologist. Details of the TMA construction are explained in the Supplemental Experimental Procedures.

**Statistical Analysis**

Gehan-Breslow-Wilcoxon test was used for the mouse survival curve analysis. Nonparametric Kolmogorov-Smirnov test was used to test statistical significance in the human patient immunohistochemistry-based immune cell quantitation. For the statistical analysis of the rest of the analyses, we used Student’s t test (two-tailed and equal variance). A p value < 0.05 was considered significant. Error bars indicate SEM for human patient immune cell infiltrations and SD for the rest.

**ACCESSION NUMBERS**

The accession number for the microarray data reported in this article is GEO: GSE69552.

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes Supplemental Experimental Procedures, four figures, and two tables and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2016.12.059.

**AUTHOR CONTRIBUTIONS**


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