**Tumor and Stem Cell Biology**

**KrasG12D and p53 Mutation Cause Primary Intrahepatic Cholangiocarcinoma**

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**Abstract**

Intrahepatic cholangiocarcinoma (IHCC) is a primary cancer of the liver with an increasing incidence and poor prognosis. Preclinical studies of the etiology and treatment of this disease are hampered by the relatively small number of available IHCC cell lines or genetically faithful animal models. Here we report the development of a genetically engineered mouse model of IHCC that incorporates two of the most common mutations in human IHCC, activating mutations of Kras (KrasG12D) and deletion of p53. Tissue-specific activation of KrasG12D alone resulted in the development of invasive IHCC with low penetrance and long latency. Latency was shortened by combining KrasG12D activation with heterozygous or homozygous deletion of p53 (mean survival of 56 weeks vs. 19 weeks, respectively), which also resulted in widespread local and distant metastasis. Serial analysis showed that the murine models closely recapitulated the multistage histopathologic progression of the human disease, including the development of stroma-rich tumors and the premalignant biliary lesions, intraductal papillary biliary neoplasms (IPBN), and Von Meyenburg complexes (VMC; also known as biliary hamartomas). These findings establish a new genetically and histopathologically faithful model of IHCC and lend experimental support to the hypothesis that IPBN and VMC are precursors to invasive cancers. Cancer Res; 72(6); 1557–67. ©2012 AACR.

**Introduction**

Intrahepatic cholangiocarcinoma (IHCC) is thought to arise from the intrapathologic biliary system based on common histologic and molecular properties (1). These tumors are characterized by an aggressive course and early metastasis. The incidence of IHCC is on the rise and although effective palliative chemotherapy has recently been defined, treatment options for the majority of patients remain limited (2, 3). Many aspects of its biology and genetics remain incompletely defined including key questions relating to (i) the cell(s)-of-origin, (ii) the precursor lesions in the liver, their molecular profiles, and their relationship to fully established IHCC, and (iii) the functional impact of oncogenes and tumor suppressor genes on malignant progression.

Although the genetic basis for IHCC has not been fully elucidated, mutations in a number of established oncogenes and tumor suppressors are well described. Recurrent mutations have been observed in the KRAS oncogene, which is activated in 20% to 50% of tumors (4–6). Mutations in BRAF were described in 2 European cohorts but have not been reported in the U.S. studies (1). p53 inactivation is the most common tumor suppressor lesion, observed in 37% of IHCC (7). In addition, subsets of IHCC show mutations or deletions of SMAD4 and p16INK4A (4, 8).

Pathologic studies of the biliary system in diseased livers and of biliary lesions adjacent to IHCC have led to a proposed multistage progression model for the development of invasive cancers from the normal hepatic epithelium (9). In particular, lesions known as biliary intraepithelial neoplasia (BilIN) and intraductal papillary biliary neoplasms (IPBN) are thought to be precursors of IHCC and have been graded according to the degrees of architectural distortion and cellular atypia (10, 11). Additional lesions of the biliary tract include malformations of the ductal systems referred to as biliary hamartomas or Von Meyenburg complexes (VMC), although the relationship of these lesions to IHCC is less clear (12, 13). Importantly, despite these detailed pathologic descriptions, the genetic features of the different biliary ductal lesions and the capacity of these lesions to give rise to IHCC remain undefined.

Experimental model systems have been central to providing basic and preclinical insights into many cancer types. Although a number of advances have been made in this regard in IHCC,
there is currently an incomplete array of systems for the study of this malignancy. For example, only a small number of IHCC cell lines are reported in the literature, with most published experimental studies employing no more than 2 or 3 lines. Alternatively, studies often employ a combination of IHCC, EHCC, and gallbladder cell lines, although these different types of biliary cancer carry distinct mutational profiles. A number of carcinogen-induced models of primary liver tumors in mammalian systems have been described (14–17) and the transcription of viral oncoproteins has also enabled transformation of carcinogen-treated hepatic epithelium both in vitro and in vivo (18, 19). Genetically engineered mouse (GEM) models have also been developed to model tumors with similarities to IHCC. p53 mutant mice develop cholangiocarcinomas upon repeated carcinogen exposure, although there is long latency in this model (20). Liver-targeted delivery of mouse polyoma virus middle T antigen (PyMT) using a transgenic avian retroviral system induces focal regions of IHCC as well as more prominent hepatocellular carcinoma (HCC) lesions in Trp53 and Ink4a/Arf knockout mice (21). Mixed HCC/IHCC histology is also seen in mice with liver-specific inactivation of the NF2, Savi, and Mst1/Mst2 tumor suppressor genes, although HCC is the predominant component in each case (reviewed in ref. 22). Combined homozygous deletion of conditional Smad4 and Pten alleles in the liver via crosses to the Albumin-Cre strain causes tumors histologically similar to IHCC (23). Although providing important systems to study malignant transformation of liver cells, these models have not been reported to exhibit progressive precursor lesions of the biliary tract nor do they accurately incorporate the most common genetic lesions seen in the human disease.

GEM models designed to mimic both genetic and pathologic aspects of cancer have proven critical to drug development efforts, biomarker identification, and the study of early disease (24, 25). To create a model of IHCC based on oncogenic mutations commonly observed in the human disease, we generated compound mutant mice with Albumin-Cre–mediated somatic activation of Kras\(^{G12D}\) and deletion of p53 in the hepatic parenchyma. We report that cooperation between these 2 relevant genetic alterations in the hepatic epithelium leads to a model of IHCC that recapitulates the histologic and molecular features of multistage progression of human IHCC. We employ this model to study the role of preinvasive lesions as precursors to IHCC and use a panel of IHCC-derived cell lines to show that autophagy may be an important targetable pathway in this malignancy as in some other Kras-driven carcinomas. Thus, our work establishes a relevant and faithful preclinical model system with which to study this challenging disease.

Materials and Methods

Mice: mutant mouse strains

All animal studies were conducted in accordance with the AAALAC accredited University Committee on Animal Resources (UCAR). All mouse strains used in these studies have been previously described and characterized (26–28). Specifically Kras\(^{G12D}\), p53\(^{−/−}\), and Alb-Cre mutants were intercrossed to achieve the desired cohorts as outlined above. The genetic background was mixed. Individual mice within experimental cohorts were followed until signs of illness including poor grooming, abdominal bloating, diminished activity, or weight loss, at which point a full necropsy was done followed by histologic analysis.

Histology

Two board-certified pathologists with a specialization in hepatic histopathology independently reviewed and classified tumors. In all cases there was agreement about the histologic diagnosis. Lymph nodes, lungs, and spleen were included in a survey for metastasis in all individuals with tumors.

Tumor cell lines

After sampling of tumors for histology and molecular profiling, 3- to 5-mm samples of tumor derived from mutant mouse strains described above were cut adjacent to sample evaluated histologically and subjected to collagenase/trypsin digestion. After washing, cells were placed in Dulbecco’s modified Eagle’s medium (DMEM) with 10% fetal calf serum and fed until a confluent monolayer was formed. Cells were passaged 3 to 4 times before molecular characterization that included IF staining with CK-19 to establish ductal origin and repeated genotyping for Kras and p53 to establish hepatic origin.

Immunohistochemistry

Formalin-fixed paraffin sections were hydrated and heat-mediated antigen retrieval was carried out when necessary. Sections were then incubated with primary antibody overnight at 4°C. Species- and isotype-matched IgG were used in place of the primary antibodies as a negative control.

Western blotting

Whole tissues (liver and whole tumor) were snap frozen in liquid nitrogen and crushed immediately using an electronic pestle into ice-cold lysis buffer. Cells used were grown to 60% to 80% confluence in the presence of fresh complete media rinsed 2× with PBS and scraped off the plate in the presence of ice-cold lysis buffer. Cell Signaling lysis buffer (catalog no. 9803) including Sigma Protease Inhibitor Cocktail (catalog no. P8340), Sigma Phosphatase Inhibitor Cocktail 2 (catalog no. P5726), and Sigma Phosphatase Inhibitor Cocktail 3 (catalog no. P0044) were used for all experiments. Protein concentration was determined using the Bradford assay.

Antibodies

Cell Signaling: glyceraldehyde-3-phosphate dehydrogenase (GAPDH; H4C10) #2118, P-Akt Ser473 #9271, Akt #9272, p44/42 mitogen-activated protein kinase (MAPK; Erk1/2, 137F5) #4695, P-p44/42 MAPK (Erk1/2; Thr202/Tyr204; D13.14.4E) #4695, p53 (IC12) #2524, LC3A (D506) #4599, Santa Cruz: alpha-Tubulin (TU-02) sc-8035, p21 (H-164) sc-756, p16 (M-156) sc-1207, Smad4 (B-8) sc-7966, cytokeratin 19 (M-17) sc-3311, Abcam: p19ARF ab80, Progen: p62. Dako: pan-CY #Z0622 1:1000, AFP (A0008) 1:400.
Autophagy assays
Culture conditions: cells were grown in DMEM with 10% FBS, l-glutamine, and no antibiotics, and media was changed every 1 to 2 days or the morning before analysis. pBabe-LC3-GFP (Addgene, 11546) was used to produce virus using NIH3T3 cells. Standard infection protocol with polybrene was followed to establish low-passage cell explants with the GFP-LC3 autophagy reporter. To determine GFP-LC3 foci was followed to establish low-passage cell explants with the NIH3T3 cells. Standard infection protocol with polybrene was used to produce virus using LC3-GFP (Addgene, 11546) was used to produce virus using LC3-GFP (Addgene, 11546). At least 50 cells were counted for each cell line under different treatment conditions. Cells containing more than 5 puncta were considered positive for autophagy. For the cell proliferation assays, cells were seeded in 24-well plates at 10,000 cells per well. Treatment with CQ at the indicated dose was done the day after plating. At the indicated time points, cells were fixed with 10% formalin and stained with 0.1% crystal violet. Dye was extracted with 10% acetic acid and optical density at 595 nm was determined as a measure of relative cell density.

Statistical analysis
All statistical analysis was done using Prism statistical software version 4.0a May 11, 2003. Survival was determined by the absence of liver pathology on autopsy were censored.

Results
Mutations in Kras and p53 are among the most commonly described genetic changes in IHCC. To model these genetic features in the mouse, we used a conditionally activated allele for Kras\(^{G12D}\) (LSL-Kras\(^{G12D}\)) and a conditional knockout allele for p53 (p53\(^{fl/fl}\), refs. 26, 27). The LSL-Kras\(^{G12D}\) allele is expressed at endogenous levels after Cre-mediated excision of a transcriptional stopper element and the p53\(^{fl/fl}\) allele is engineered to sustain Cre-mediated excision of exons 2 to 10 rendering the gene functionally inactive. Although the cell of origin of IHCC is not established, both the differentiated biliary epithelial cells as well as resident progenitor cells within the liver, commonly referred to as "oval cells," have been implicated (29). Further complicating the understanding of the ontogeny of IHCC is the finding that human IHCC harbors regions of abnormal intermediate hepatocytes and that HCC expresses markers typically seen in IHCC (30). Given the undefined cellular origins of these tumors, we sought an approach that would target mutations throughout the adult liver. To accomplish this, we used the Albumin-Cre (Alb-Cre) transgene that is initially active in liver progenitors during late embryogenesis and has been shown to produce effective recombination of floxed alleles in both the adult hepatocytes and cholangiocytes (Fig. IA; ref. 28). Cohorts of compound mutant mice were created with the experimental genotypes Alb-Cre;Kras\(^{G12D}\) (\(n = 8\)), Alb-Cre;Kras\(^{G12D}\);p53\(^{L/+}\) (\(n = 20\)), and Alb-Cre;Kras\(^{G12D}\);p53\(^{L/+}\) (\(n = 22\))—from here on designated Kras, Kras-p53\(^{L/+}\), and Kras-p53\(^{L/+}\) mice, respectively.

Kras\(^{G12D}\) cooperates with p53 inactivation to cause hepatic transformation
Kras, Kras-p53\(^{L/+}\), and Kras-p53\(^{L/+}\) cohorts were produced at the expected ratios and showed no evidence of early developmental abnormalities. These animals were monitored until they developed signs of illness (abdominal bloating, vomiting...
diminished activity, and cachexia). Most of the Kras mice were healthy up to an age of 75 weeks, although 1 of 8 developed a lethal liver mass at 36 weeks of age. p53 deficiency greatly increased the penetrance and accelerated disease onset as the Kras-p53L/þ and Kras-p53L/L mice developed tumors as early as 32 and 9 weeks, respectively (mean survival 52 weeks and 19 weeks; Fig. 1B). Upon necropsy these animals were found to have solid liver tumors ranging in size from 2 to 20 mm and presented as isolated nodules (n = 14 mice) or as multiple independent lesions (n = 6 mice; Table 1). In many animals, cystic fluid-filled lesions were found adjacent to the solid masses (Fig. 1C). Hepatic lesions frequently showed hemorrhage into the peritoneal cavity and had evidence of tumor necrosis. Tumors were highly metastatic, with 75% of tumor-bearing animals displaying gross evidence of invasion into adjacent organs (diaphragm, bowel, pancreas, and stomach) or distant metastasis (with dissemination to the lymph nodes, spleen, lungs, and peritoneal cavity; Fig 2B and Table 1). Mice harboring Alb-Cre;p53L/L (n = 10) were followed to 1 year of age without evidence of illness, and subsequent necropsy and histologic survey did not reveal abnormal hepatic pathology (data not shown). Thus, KrasG12D promotes metastatic liver tumorigenesis that is significantly accelerated by the heterozygous and homozygous inactivation of p53.

**Table 1. Tumor histology, number of nodules, precursor lesions found, sites of metastasis, and age**

<table>
<thead>
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<th>ID</th>
<th>Age (wk)</th>
<th>Tumor type</th>
<th>Size (cm)</th>
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<th>Gross metastasis/invasion</th>
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**Albumin-Cre; Kras GEM models recapitulate the histopathologic features of human IHCC**

Microscopic analysis of the liver tumors revealed that 83% showed IHCC histology, with 66% (n = 19) containing exclusively IHCC and 17% (n = 5) showing a mixed phenotype of IHCC and HCC elements. A smaller number had exclusively HCC histology (17% n = 5; Table 1, and Fig. 2A). The IHCC showed a range of cellular differentiation, including well-differentiated tumors with clear glandular architecture and areas of mucin production, as well as poorly differentiated tumors with minimal gland formation and large pleomorphic cells showing nuclear atypia and frequent mitosis (Fig. 2A). Often different grades of differentiation were seen in the same tumor. The histologic spectrum of IHCC was similar among the different mouse cohorts.
To further characterize the tumors, we stained tissue sections for cytokeratins (pan-CK) that mark the biliary epithelium and have been used clinically to distinguish IHCC from HCC. Correspondingly, immunohistochemistry for pan-CK revealed robust staining of the regions with the biliary ductal morphology, consistent with IHCC histopathology (Fig. 2C). In mixed tumors, the areas of glandular epithelium stained positive for pan-CK (Fig. 2Aiii arrowhead and Fig. 2C arrowhead), whereas the regions morphologically consistent with HCC were pan-CK negative (Fig. 2Aiii arrow). We also stained tissue sections for alpha-fetoprotein (AFP) a marker of HCC. Immunochemistry for AFP showed staining of all HCC and HCC components of mixed tumors, whereas IHCC and IHCC components of mixed tumors did not stain (Fig. 2Ciii). Early metastasis is a hallmark of human IHCC and similarly microscopic IHCC metastases were found in nearly all animals examined, including those without evident gross metastasis. These lesions were found in the lung, lymphatic system and the spleen, peritoneal cavity, and veins (Fig. 2B). Trichrome staining revealed collagen deposition throughout the IHCC but not in most HCC, a pattern reminiscent of the corresponding human tumors, in which IHCCs, but not HCC, are characterized by a dense stroma (desmoplasia; Fig 2D). Overall, the histopathologic appearance of the murine IHCC displayed a striking similarity to the human disease, exhibiting varying degrees of differentiation and early metastasis.

**IHCC is associated with IPBN and Von Meyenburg complexes, or biliary hamartomas**

Histologic survey of hepatic parenchyma adjacent to IHCC, as well as isolated regions of grossly normal liver, revealed the presence of premalignant lesions within the bile ducts. These lesions resembled intraductal papillary neoplasms of the bile ducts (IPBN) and biliary hamartomas (also known as VMC) that have been described in humans (11, 12). In several cases, there was evidence that the IHCC arose directly from IPBN (Fig. 1C and Fig. 3B). The presence of additional lesions in regions distal to the primary tumors suggests that there was multifocal initiation of these precursor lesions. IPBN were grossly evident (Fig. 1Cii lower cystic lesion with arrowhead), characterized by dilated bile ducts (Fig. 3Ai and iii) and were found connected to the biliary tree. These structures were lined by pancreaticobiliary and intestinal epithelium and exhibited varying degrees of dysplasia, with a notable frequent association of the largest lesions with contiguous areas of invasive carcinoma (Fig. 3B). Although a papillary architecture was not universally appreciated, the presence of low-grade dysplasia in some areas and high-grade dysplasia/carcinoma in situ in others mimicked

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Figure 2. Kras-p53 IHCC recapitulates the histology of the human disease. A, histology of primary liver tumors; from left to right (i) well-differentiated IHCC 200× with inset showing mucin producing cells (arrow), (ii) poorly differentiated IHCC 200× with inset showing mitotic figure (arrow), and (iii) mixed IHCC/HCC with arrow pointing toward area of HCC versus glandular appearance of IHCC (arrowhead). B, extensive metastasis (indicated by letter T) were observed grossly and histologically in the (i) lung (L), (ii) spleen (S), and (iii) within the diaphragmatic lymphatic system. C, pan-CK IHC of IHCC (i) and mixed IHCC/HCC (ii), upper region is nonstaining HCC component and lower region showing glandular structures (arrowhead) which are pan-CK positive. AFP IHC of mixed IHCC/HCC (iii), upper region is AFP staining HCC component and lower region showing nonstaining IHCC component. D, trichrome IHC showing collagen deposition within IHCC (left) but not in HCC (right).
the typical presentation seen in the human disease (Fig 3Ai–iv). These observations support the IPBN-to-IHCC progression model for this cancer type.

In addition to the IPBN, another type of structural abnormality was seen in focal regions of the biliary ducts, consisting of dilated, haphazardly arranged ductal structures embedded in a fibrous stroma adjacent to portal areas. Such structures, found in 36% of animals harboring IHCC \( (n = 5/14; \text{Fig. 4i–v}) \), showed resemblance to biliary hamartomas or VMCs described in humans. Whereas these lesions were typically small and focused, in 2 animals we also observed more extensive lesions that extended through an entire lobe of the liver (Fig. 4Aii). Whereas VMCs are generally regarded as benign, recent case reports of cholangiocarcinoma arising from a VMC have raised the question of its potential role as an IHCC precursor lesion (12, 31). Consistent with this notion, we found IHCC

Figure 3. IPBN is identified separately and in association with IHCC, showing areas of low- and high-grade cellular atypia. A, fluid filled cystic structure (i; low power) showed progressive cellular atypia (ii and iii) arrowheads point to epithelium showing an atypical low-grade columnar biliary epithelium (ii) and high-grade region with large nuclei, prominent nucleoli, and marked cellular atypia (iii). IPBN were found within the context of normal liver (iv). B, IPBN adjacent and contiguous with invasive IHCC. C, smaller IPBN (i) displayed an intestinal type epithelium (ii; arrowhead indicates mucin producing cell).

Figure 4. VMCs, or biliary hamartomas, are prevalent and found in association with IHCC in the Kras-p53 model. A, i, low-power view of VMC (circled in dashed black line between portal tracts), ii, IHC with pan-CK Ab of VMC within the hepatic parenchyma. B, i, VMC at high power showed small caliber biliary epithelium surrounded by stroma. ii, VMC shows strong staining with pan-CK Ab, iii, VMC associated with a well-differentiated cholangiocarcinoma.
functions of p53 and p19Arf in constraining tumor progression. These p53-deleted tumors showed strong staining for pan-Ck consistent with their ductal morphology. The findings of both IPBN and VMC, both independent of and in association with IHCC, among mutant Kras-p53 animals provided experimental evidence for a progression model of IHCC that includes both IPBN as well as VMC.

**Molecular features of IHCC**

To characterize the molecular features of IHCC arising in the Kras-p53 mice, we used both early-passage cell lines derived from the primary tumors and whole tumor lysates. Tumor cells were used to evaluate other established tumor suppressor genes and provide a pure tumor-derived material without stromal contamination. CK-19, a common marker of IHCC, confirmed the origins of early-passage tumor explants with all derivative cells showing positive immunostaining (data not shown). As expected p53 and its downstream target, p21, were not expressed in the IHCC (Fig. 5A) consistent with somatic deletion (data not shown). Among tumors arising in Kras-p53D124S mice, we found loss of the wild-type allele in 4 of 6 animals consistent with spontaneous deletion during the course of tumorigenesis (Fig. 5B). Next, we examined Smad4 and p16Ink4a, which are additional tumor suppressors known to be inactivated in human IHCC (43, 32, 33). Western blot analysis showed that Smad4 expression was maintained in all 6 IHCC examined, whereas p16Ink4a expression was absent in 2 lines (#335 and 460). The p19Arf tumor suppressor, expressed from a common locus with p16Ink4a was also absent in line #335, suggesting somatic deletion of the Ink4a/Arf (CDKN2A) locus. All other lines retained various levels of p19Arf expression in these p53-deficient tumors, consistent with the overlapping functions of p53 and p19Arf in constraining tumor progression (34). The spontaneous loss of wild-type p53 in tumors arising in the Kras-p53D124S cohort and the sporadic loss of p16Ink4a mirrors the molecular profile of the human disease and is in keeping with key functions of the p53/p19Arf and Rb/p16INK4A pathways in suppressing KRAS-driven tumorigenesis.

Next we carried out a molecular analysis of IHCC to determine the status of pathways that are commonly altered in human IHCC. Whole IHCC lysates were compared with both normal liver as well as with normal appearing liver from Kras-p53 animals. Both MAPK/mitogen-activated protein kinase extracellular signal–regulated kinase (MEK) and phosphoinositide 3-kinase 3-kinase (PI3K)/AKT/mTOR signaling pathways have been shown to be active and important for growth and survival in tumors characterized by KRAS mutation, and strategies to target these downstream effectors of KRAS are in development in IHCC (35, 36). Consistent with KRAS activation and signaling through MAPK/MEK signaling pathways, we found total ERK1/2 levels to be elevated in tumors compared with both normal liver as well as liver harboring concurrent Kras/p53 mutations (Fig. 5C) that latter of which exhibited no increased activity of the pathway despite the presence of a Kras mutation in the majority of cells. Phosphorylation of residues Thr 202 and Tyr 204 indicative of Erk1/2 activity was present in IHCC, but not found in the untransformed hepatic epithelium (Fig. 5C). Similarly PI3K/AKT pathway activity was seen as apparently arising directly from adjacent VMC in 4 animals (Fig. 4ii). VMC showed strong staining for pan-Ck consistent with their ductal morphology (Fig. 4ii and 4bii). The spontaneous loss of wild-type p53 in tumors arising in Kras-p53L/þ animals compared with IHCC tumor lysates evaluating expression of tumor suppressor genes. Twenty-five micrograms of protein were loaded in each lane and murine pancreatic cell lines with previously defined genetic profiles (p53 or Ink4a/Arf mutant vs. wild type) were used as controls (49). p53 expression is absent in all IHCC, as is p21 expression. Whereas the majority of tumors retained expression of p19Arf, line #335 lost expression. Lines #460 and #335 both showed absent p16Ink4a expression. SMAD4 expression was maintained across all lines. B, PCR reactions to detect the p53-WT allele (bottom) and p53-null allele. C, Western blot analysis of whole liver lysates from 10 weeks old wild-type and Kras-p53D124S animals compared with IHCC tumor lysates evaluating the relative activity of RAS effectors ERK and AKT showing activity of ERK and AKT. Total LC3 levels were increased in IHCC as compared with normal and mutant liver (LC3 is lower band, upper band is nonspecific).
evidenced by phosphorylation of AKT Ser 473 in IHCC. Enhanced expression and activation of components of both MAPK/MEK and PI3K pathways is consistent with the observations made among human tumors as well as with other tumors driven by KRAS and points toward the potential utility of inhibitors under development targeting these pathways.

**IHCC are characterized by elevated levels of autophagy required for growth**

The panel of cell lines from our GEM model provides a genetically defined experimental system to begin to test the role of key pathways in the pathogenesis of the KRAS-p53 mutant subset of IHCC. Notably, tumors driven by mutated RAS have been difficult to target as compared with cancers which harbor more "druggable" mutated or amplified oncogenes (37). Combinational approaches focused on key downstream pathways, such as combined PI3K and MEK inhibition as discussed above, may offer strategies toward effective treatments. At the same time insights into the unique metabolic requirements of RAS-driven tumors and, in particular, a dependence on autophagy have also led to new therapeutic inroads (38–40). Autophagy (or macroautophagy) is the process of autodigestion (or "self-eating") that both maintains cellular homeostasis and enables cells to meet basic energy requirements in times of stress. 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expression to subpopulations of cells within the liver (biliary, hepatocyte, or other intermediaries) could clarify this issue.

Both IPBN and VMCs were found as isolated lesions as well as in association with IHCC in our GEM model. IPBN are an established precursor to human IHCC, whereas the relationship of VMC to malignant tumors in humans has not been defined. VMCs are found in approximately 5% of adults in tumor types including pancreatic cancer. For example, Kras-p53 mediated transformation of early liver progenitors (hepatoblasts), adult progenitors (e.g., oval cells), and more mature forms of the biliary epithelium or hepatocytes may be associated with a different cellular differentiation program during early tumorigenesis. Alternatively, such differences in precursor lesions may reflect the differential impact of additional acquired molecular alterations driving IHCC progression, as has been reported in pancreatic cancer GEM models (46).

Autophagy is active in derivative cell lines and blockade of autophagy with CQ inhibits growth of derivative cell lines consistent with findings in other Kras-driven tumors (38, 39). Although most RAS-driven cancer cell lines have evidence of active autophagy, the effect of blocking this process has variable effects on cell proliferation, with certain tumor types—including pancreatic cancer—exhibiting

Figure 6. Kras-p53 IHCC exhibits high basal levels of autophagy and is growth inhibited by CQ. A, IHCC cells were infected with a retrovirus expressing GFP-LC3 and grown in complete media with serum and fixed for confocal fluorescence microscopy. These were analyzed for the presence of LC3 dots, representing autophagic vesicles, and quantified. The % of autophagic cells (of total number of 100 counted) with more than 5 foci are shown in the top right corners of each picture. Below is shown a Western blot showing high levels of LC3-II as compared with LC3-I, also consistent with a high level of basal autophagy. B, IHCC cells were cultured under normal growth conditions in which the total number of LC3 foci was markedly increased in the presence of CQ (error bars are shown, Student t test is used for comparison, P < 0.001 for all cell lines treated). C and D, growth of IHCC cell lines is inhibited in the presence of CQ P < 0.001 for samples 335, 518, and 339 and P < 0.01 for samples 449 (two-way ANOVA, error bars are shown for all data points, those not evident on the graphs fall within the area encompassed by the triangle or circle data point). Consistent with a block in autophagic flux induced by CQ treatment we observed that treated lines had an accumulation of LC3-II and induction of p62 as compared with day 0 control, with the exception of #518 in which p62 expression was absent.

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marked sensitivity to CQ, whereas growth of lung cancer cell lines was effected to a lesser extent. We find that cell lines from our model are significantly growth inhibited with a corresponding block in autophagy by CQ. This fits well with evidence from human tumors and cell lines suggesting the importance of autophagy in the human disease and provides impetus to further evaluate CQ and other drugs that may impact this process in IHCC (47, 48).

In summary, we have created a tractable IHCC GEM model on the basis of the genetics of the human disease. The multistage evolution of the tumors provides a context to explore questions about the role of different cells of origin and the molecular and histologic progression of precancerous stages of IHCC. In addition, the highly reproducible development of IHCC in this model provides a foundation for testing the influence of additional genetic lesions on tumor biology and a platform for the preclinical testing of promising new therapies.

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

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