Autophagy sustains pancreatic cancer growth through both cell autonomous and non-autonomous mechanisms

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Abstract

Autophagy has been shown to be elevated in pancreatic adenocarcinoma (PDAC) and its role in promoting established tumor growth has made it a promising therapeutic target. However, due to limitations of prior mouse models as well as the lack of potent and selective autophagy inhibitors, the ability to fully assess the mechanistic basis of how autophagy supports pancreatic cancer has been limited. To test the feasibility of treating PDAC using autophagy inhibition and further our understanding of the mechanisms of pro-tumor effects of autophagy, we developed a novel mouse model that allowed the acute and reversible inhibition of autophagy. We observed that autophagy inhibition causes significant tumor regression in an autochthonous mouse model of PDAC. A detailed analysis of these effects indicated that the tumor regression was likely multifactorial, involving both tumor cell intrinsic as well as host effects. Thus, our study supports autophagy inhibition in PDAC may have future utility in the treatment of pancreatic cancer and illustrates the importance of assessing complex biological processes in relevant autochthonous models.

Statement of Significance

This work demonstrates that autophagy is critical pancreatic tumor maintenance through tumor cell intrinsic and extrinsic mechanisms. These results have direct clinical relevance to ongoing clinical trials as well as drug development initiatives.

Introduction

Pancreatic ductal adenocarcinoma (PDAC) has a high mortality rate, with a ~7% five-year survival rate for all stages of the disease. Currently available treatments, are not effective for the majority patients, only modestly extending survival (1). Given its profound lethality and resistance to available therapies, there is a dire need for new treatment approaches for PDAC.

One of the characteristic features of PDAC is the upregulation of autophagy and it has been shown that inhibition of autophagy suppresses tumor cell growth \textit{in vitro} and in xenograft models (2). In \textit{Kras}-driven genetically engineered mouse models (GEMMs) of PDAC, cells lacking autophagy were less efficient in progressing into PDAC (3,4). Several mechanisms have been proposed of how autophagy may support tumor growth in PDAC and other tumor types, including providing metabolic fuel sources as well as to allow cancer cells to deal with a variety of stressors (5,6). In PDAC, it has been shown that autophagy inhibition decreased proliferation,
increased DNA damage and apoptosis (7). In a non-small-cell lung cancer (NSCLC) mouse model, lack of autophagy caused accumulation of dysfunctional mitochondria and dysregulation of lipid catabolism (8). Besides its impact on tumor cells directly, autophagy inhibition may have anti-tumor effects by modulating the tumor microenvironment (9). Indeed a recent study from our group demonstrated a cross-talk between stromal and tumor cells in PDAC, where autophagy was required in stromal cells to secrete alanine that was taken up by tumor cells to support growth (10).

The pro-tumorigenic role of autophagy in tumorigenesis had been studied and validated using genetically engineered mouse models (GEMMs) of multiple other tumors such as melanoma (11), breast (12), lung (13), brain (14), and prostate (15) using conditional knockouts of various autophagy genes. However, with the exception of one study in lung cancer, these have all relied on loss of autophagy during the tumorigenesis process and not acutely in the fully formed tumor (16). Moreover, the nature of these models allows only for the irreversible loss of autophagy and therefore limits questions that can be asked such as duration of inhibition needed and reversibility of potential toxicities.

Because of autophagy’s supporting role in tumor growth, it became a target of interest in cancer treatment. The drug hydroxychloroquine (HCQ) has been tested in multiple clinical trials to assess the efficacy of autophagy inhibition in PDAC and other cancers (17-20). While HCQ does inhibit autophagy, it acts at the level of the lysosome, so it will impact additional lysosomal processes (which could actually have additional anti-tumor effects) (21). Moreover, there are potency issues with the drug, requiring high micromolar levels to inhibit autophagy and observe anti-tumor effects (22,23). Interestingly, early data supports that the addition of HCQ to chemotherapy in localized PDAC increases the tumor response (24,25).

To overcome some of these obstacles, we sought to create a model where autophagy could be acutely inhibited in a reversible fashion in a fully formed tumor. This would be akin to the therapeutic scenario, much in the way a pharmacological inhibitor works. As selective and potent inhibitors targeted to the early phases of autophagy are still in various phases of development, we took a genetic approach to model such inhibition paradigms using a previously identified dominant negative mutant of Atg4B that was reported to effectively inhibit autophagy (26). In this study, we took advantage of this dominant negative mutant to generate an inducible mouse model of autophagy inhibition and evaluated the effectiveness of autophagy inhibition in treating PDAC, as well as further explored the mechanisms of autophagy in supporting tumor growth.
growth. Indeed, we demonstrated striking tumor responses in a treatment refractory PDAC GEMM, including some complete responses. Importantly, the innovative design of the model allowed us to demonstrate that autophagy inhibition suppresses tumor growth via tumor cell intrinsic as well as extrinsic factors.

Results

Generating an inducible mouse model of autophagy inhibition

Autophagy is a multistage process and the formation of the autophagosome is an essential step to package different cargo for autophagic degradation. To form the autophagosome membrane, a cysteine protease -- Atg4B, is required to conjugate LC3 with phosphatidylethanolamine (PE) and delipidate LC3-II after lysosome degradation. An enzymatically inactive mutant, Atg4B<sup>C74A</sup>, was previously found to be able to sequester free LC3 in vitro and therefore act as a dominant negative inhibitor of autophagy degradation (26). We developed a transgenic mouse line that carries the mSt-Atg4B<sup>C74A</sup> gene under the control of TetOn cassette (hereafter referred to as Atg4B<sup>CA</sup>) (Figure S1). The dominant negative Atg4B<sup>C74A</sup> mutant was fused with an mStrawberry fluorescent marker, allowing its expression to be easily tracked. The reverse tetracycline-controlled transactivator (rtTA) at the Rosa26 locus was preceded by a stopper cassette allowing the expression to be controlled via cre-recombinase. Therefore, the combination of TetOn and LoxP expression systems allowed the expression of Atg4B<sup>CA</sup> to be temporally controlled and spatially restricted (Figure 1A).

We crossed the Atg4B<sup>CA</sup> (either one or two copies +; ++); Rosa-rtTA<sup>LSL</sup> transgenic mouse to a well-established pancreatic cancer genetically engineered mouse model (GEMM): LSL-Kras<sup>G12D</sup>, p53<sup>lox/+</sup>, p48Cre<sup>+</sup>. To determine the efficiency of autophagy inhibition, we first generated cell lines derived from tumors to assess the ability of the Atg4B<sup>CA</sup> to inhibit autophagic flux in vitro. As shown in Figure 1B, treatment of cells with doxycycline (Dox) resulted in expression of the Atg4B<sup>CA</sup> as indicated by the mStrawberry fluorescence. Expression of the Atg4B<sup>CA</sup> inhibited autophagy as shown by decreased LC3 puncta, with two copies (++) showing even more potent inhibition with greater loss of puncta (Figure 1C and D). These results were confirmed by western blotting showing an accumulation of the non-lipidated LC3-I bands upon expression of the Atg4B<sup>CA</sup> and decrease of LC3II band, as well as an accumulation of the cargo receptor P62 (Figure S2A and C). As expected, longer Dox treatment induced
greater levels of the Atg4B$^{CA}$ expression and showed more autophagy inhibition (Figure 1E and S2A).

We next tested the tight regulation of Atg4B$^{CA}$ expression by showing dependence on the required alleles and the presence of Dox (Figure 1F). In contrast to the control groups, the two test groups treated with Dox: Atg4B$^{CA+}$ and Atg4B$^{CA++}$ that were expected to express Atg4B$^{CA}$ allele stained positive for mStrawberry (Figure 1F). Consistent with the in vitro data, potent autophagy inhibition by expression of Atg4B$^{CA}$ was confirmed in vivo. LC3 puncta were present in the two control groups (not expressing Atg4B$^{CA}$), but were absent in the two Atg4B$^{CA}$ expressing groups; where the staining pattern was diffuse in nature (Figure 1G). Autophagy cargo receptors Nbr1 and P62 accumulated, forming aggregates in Atg4B$^{CA++}$ expressing tumors as well as normal pancreas indicating an inhibition of autophagic flux (Figure S2B-D).

We also examined autophagosome formation at ultrastructural level by electron microscopy. As shown in Figure 1H, most double membrane vesicular structures were closed in Atg4B- tumor samples, while a significantly increased number of open double membrane vesicular structures were present in Atg4B$^{CA++}$ tumors indicating a failure of completion of autophagosome formation. This observation of increased ratio of open to total autophagic structures was consistent with in vitro characterization of this dominant negative as previously reported(26).

Lastly, the Atg4B$^{CA}$ mediated inhibition of autophagy could be reversed by removal of Dox as shown in Atg4B$^{CA++}$ cells (Figure S2E). Consistent with the ability to reversibly regulate autophagy inhibition in vitro, expression of mStrawberry was reduced after removal of Dox in Atg4B$^{CA++}$ tumors in vivo (Figure S2F).

**Inhibition of autophagy decreases growth of fully formed PDAC**

To evaluate the effect of autophagy inhibition on tumor growth, we used high-resolution ultrasound imaging to identify PDAC and follow their growth (Figure S3A). We generated four groups of mice that did not express Atg4B$^{CA}$ due to lack of the genetic alleles or Dox exposure. The four negative control cohorts of mice did not express Atg4B$^{CA}$ and showed no significant differences in tumor growth or tumor specific survival (Figure S3B - C). Thus, for comparison we combined all mice not expressing Atg4B$^{CA}$ in one group denoted as Atg4B- from here forward.

To study how autophagy inhibition affected established PDAC growth, we first allowed tumors to form and measured volume by serial high resolution ultrasound. During the study, we didn’t observe significant effect of Doxycycline food or autophagy inhibition on weight of tumor-bearing mice (Figure S3D and E). Compared to controls, the Atg4B$^{CA+}$ (Atg4B$^{CA+}$, p53$^{ox/+}$, LSL-Kras$^{G12D}$,
Rosa-rtTA<sup>LSL</sup>, p48Cre<sup>+</sup>) group showed slower tumor growth kinetics and extended tumor-specific survival (Figure 2A and B). However, after an initial delay in tumor progression all tumors resumed growth and mice finally succumbed to tumor burden. An assessment of these tumors at endpoint revealed that all mice (n=10) at the end of the study had lost expression of the Atg4B<sup>CA</sup> to various degrees, with 5 of 10 tumors showing nearly complete loss of Atg4B<sup>CA</sup> expression (Figure S4A). Once tumor cells lost Atg4B<sup>CA</sup> expression, autophagosome formation resumed consistent with silencing of the Atg4B<sup>CA</sup> allele or outgrowth of cells that did not express Atg4B<sup>CA</sup> (Figure S4B). To test this hypothesis we assessed a cohort of tumor bearing mice at serial time-points for Atg4B<sup>CA</sup> expression after starting Dox and observed a gradual loss of Atg4B<sup>CA</sup> expression over time (Figure S4C). Furthermore, primary cell lines harvested from tumors showed loss of the Atg4B<sup>CA</sup> allele in four of five tumors (Figure S4D and E).

To examine if there was a dose response effect of autophagy inhibition, we next analyzed tumor growth and survival in mice with two copies of the Atg4B<sup>CA</sup> (Atg4B<sup>CA+</sup>). Strikingly, this cohort showed a more significant anti-tumor response, with 6 out of 10 tumors showing frank regression after 4 days of Dox treatment and 3 out of these 6 mice maintained inhibited growth with less than doubling of the initial tumor volume after 2 weeks of treatment (Figure 2C). However, despite these dramatic responses there was no significant increase of survival in the Atg4B<sup>CA+</sup> group compared to control group (Fig 2D). After examining the Atg4B<sup>CA+</sup> tumors at endpoint, we found that all four mice that had died within 3 weeks showed histological disruption of the normal pancreas architecture with significant areas of metaplasia, which were composed of abnormal ductal-like, mucin-rich cells stained positive for CK19 (Figure S5A). Additionally, the pancreata showed loss of β-islets in both the Atg4B<sup>CA+</sup> and control mice likely due to tumor replacement of normal pancreata (Figure S5B). Serum insulin levels were not significantly changed in Atg4B<sup>CA+</sup> mice compared to Atg4B- mice, indicating there was not likely frank diabetes. Consistent with this, there was only minimal expression of Atg4B<sup>CA+</sup> in the β-islets (Figure S5B) due to differences in expression of the allele between the tissues. We further stained for amylase and found a dramatic loss of normal acinar cells, indicating a profound disruption of the exocrine pancreas in the Atg4B<sup>CA+</sup> expressing tumor-bearing mice (Figure S5C). To further understand the correlation of autophagy inhibition, loss of acinar cells, and metaplasia, we examined the histology of pancreata of non-tumor bearing Atg4B<sup>CA+</sup>, p53<sup>oxi</sup>, Rosa-rtTA<sup>LSL</sup>, p48Cre<sup>+</sup> mice. After over 40 weeks on Dox diet to induce Atg4B<sup>CA</sup> expression, there was no loss of acinar cells, metaplasia, or ductal transformation (Figure S5D). Thus we concluded that this metaplastic phenotype was likely due to the nature of the transgenic model,
where all cells of the pancreas express oncogenic \textit{Kras}^{G12D} and was consistent with our previous studies showing that inhibition of autophagy predisposes mutant Kras-expressing mice to acinar-ductal metaplasia (benign tumor initiation) (4).

Because our model allows the reversible inhibition of autophagy, we sought to understand whether intermittent inhibition would also be effective in inhibiting PDAC growth, similar to the way chemotherapy is often given on a periodic basis. In this regard, we fed mice with Dox for a week and then placed them back on normal chow for a week. This was repeated for multiple cycles and tumor response was monitored by ultrasound. With this intermittent treatment, only 2 of the 11 mice succumbed to the metaplasia related death as those observed in Atg4B^{CA++} continuous treatment group. Impressively, 36\% of the mice (4 out of 11) had significant sustained responses (less than doubling initial tumor volume) that was maintained for up to 15.5 weeks. 7 out of 11 mice had significant responses at the first week, then tumor resumed growth in the off-dox cycle and eventually mice met protocol endpoint. There was no difference of tumor size at detection between the subgroup of mice with the sustained responses to the autophagy inhibition (n=4) and the rest of the mice (n=7) (Figure S5D). Overall, this intermittently treated cohort showed significant tumor growth delay which resulted in an increased survival compared to the control group (Figure 2C and D). Consistent with the improved response, most of the tumor cells retained expression of Atg4B^{CA} when harvested at the end of Dox cycle (Figure S2F) and PCR of all Atg4B^{CA++} tumor cell lines confirmed their maintenance of the Atg4B^{CA} allele (Figure S4D).

Despite the varied individual long-term response to autophagy inhibition, all tumors in Atg4B^{CA++} groups responded within a week after Dox treatment initiation either by regression or stable disease (Figure 2E). We defined tumor as regressing if the relative growth compared to detection volume is less than 1, indicating that the volume had decreased compared to the initial size. After 1 week, 0 out of 28 mice in control group while 7 out of 21 Atg4B^{CA++} mice showed regression (p=0.0014 by Fisher’s exact test). To measure if Atg4B^{CA} expression alone could induce apoptosis, we used Atg4B^{CA++} primary cell lines and found no cl-Casp3 expression under normal culture condition with 10\% FBS. However, if we starved cells with HBSS, we observed increased cl-Cap3 expression in Atg4B^{CA} expressing cells (Figure 2F). This suggested that blocking autophagy under nutrient restricted circumstances sensitized cells to death and was consistent with the fact that more apoptosis was seen in vivo next to areas of necrosis (suggesting they were poorly perfused and nutrient deprived). Both single-copy (Atg4B^{CA+}) and two-copy (Atg4B^{CA++}) tumors showed increased apoptosis compared to controls (Figure 2G).
We then analyzed proliferation in tumors by measuring Ki67 expression. Consistent with the decreased growth, we found there was a significant reduction of proliferating cells in Atg4B\textsuperscript{CA+} and Atg4B\textsuperscript{CA++} groups (Figure 2H).

Using a Kras-driven lung GEMM, we were able to extend these findings to lung cancer by monitoring tumor growth with magnetic resonance imaging (MRI) (Figure S6A). Once tumor was identified, mice were randomly assigned to Dox diet as in the PDAC studies. Similar to the PDAC model, we noticed a significant growth deficit in Atg4B\textsuperscript{CA+} mice (Figure S6B). Atg4B\textsuperscript{CA+} tumors showed less Ki67+ cells compared to Atg4B- tumors, indicating less proliferation (Figure S6C). However, unlike PDAC, lung tumors did not show significant increases in apoptosis. This may reflect the unique PDAC microenvironment which is known to be poorly perfused, hypoxic, and nutrient poor (27).

**Cell intrinsic and extrinsic factors impact tumor growth in response to autophagy inhibition**

Previous work from our group has shown that in various systems that autophagy supports PDAC tumor cell growth through effects on the tumor cell itself (2). More recently, we identified that autophagy in the stromal compartment was critical for a metabolic cross-talk to fuel tumor cells (10). Therefore, we set out to explore the contributions of autophagy to various aspects of tumor growth taking advantage of the unique features of the Atg4B\textsuperscript{CA} model. Consistent with previous findings of autophagy inhibition in PDAC, tumor derived cell lines from the Atg4B\textsuperscript{CA++} model showed reduced clonogenic growth as well as significantly decreased growth in soft agar (Figure 3A and B). To confirm the cell autonomous effects of autophagy inhibition, we performed xenograft studies where we implanted Atg4B- cells in the left flank and Atg4B\textsuperscript{CA++} cells in the right flank of the same nude mice. After allowing tumors to form, we then randomized mice to a normal or a Dox diet and compared the growth rates of Atg4B\textsuperscript{CA++} to Atg4B-. Consistent with the in vitro data, autophagy inhibition decreased the tumor growth kinetics (Figure 3C, S7). However, in contrast to the autochthonous model, there were no tumor regressions. Similarly, orthoptopic injections of Atg4B\textsuperscript{CA++} cells into the pancreata of nude mice showed significantly decreased growth kinetics, but again no regressions (Figure 3D). The more profound responses seen in the autochthonous model, suggested that certain aspects of this model were influencing the response of the tumor, such as the more accurate modeling of the tumor microenvironment. Consistent with this idea, it appeared that the inflammatory infiltrate was more robust in autochthonous tumors expressing the Atg4B\textsuperscript{CA} (Figure S8A). As an initial
characterization, we performed IHC to assess for various immune cell populations. While we did not observe any differences in the presence of intratumoral T-cells (Figure S8A), the Atg4B<sup>CA++</sup> tumors had significantly more CD68+ macrophages present (Figure 3E). To confirm these findings, we assessed for the presence of macrophages in the tumors of Atg4B- and Atg4B<sup>CA++</sup> mice using flow cytometry as well as immunofluorescence staining with another marker, F4/80 (Figure S8B). This again demonstrated a significant increase in macrophages in the Atg4B<sup>CA++</sup> tumors. In contrast to the autochthonous model, we found there was no increase of macrophages in Atg4B<sup>CA++</sup> tumors grown in nude mice (Figure 3F). We performed some initial characterization of the macrophage subtype of the tumor infiltrating macrophages. We used iNOS (which often represents anti-tumor, pro-inflammatory macrophages) and Arg1 (often enriched in pro-tumor macrophages). Interestingly, we found both iNOS+ and Arg1+ macrophage populations were increased in Atg4B<sup>CA++</sup> tumors indicating multiple macrophage populations infiltrate the tumor (Figure S8C and D).

The increase of intratumoral macrophages could either be a cause of the increased tumor response to autophagy inhibition seen in the autochthonous model or merely a consequence of attempting to clear increased numbers of dying tumor cells. To determine if the macrophages were influencing tumor response to autophagy inhibition, we depleted macrophages using liposomal clodronate (28) and assessed the efficacy of Atg4B<sup>CA++</sup> expression as compared to mice treated with a control PBS liposomal solution. We first demonstrated that the clodronate significantly impaired the increased macrophage infiltration seen in the Atg4B<sup>CA++</sup> tumors (28) (Figure S8E). Strikingly, depletion of macrophages markedly impaired the response of tumors to autophagy inhibition (Figure 3G), while having no significant effect on Atg4B- tumor growth (Figure S8F). Taken together, this data demonstrated that autophagy inhibition in PDAC cells has direct effects on tumor cell growth, but macrophage-mediated mechanisms are also involved in the anti-tumor response.

**Stromal Autophagy and PDAC growth**

We had previously demonstrated through co-culture and co-injection studies that autophagy inhibition in the stroma can influence growth of the PDAC tumor cells through the secretion of amino acids (10). The design of the Atg4B<sup>CA</sup> system would allow us to test this in a more sophisticated fashion. We first bred Atg4B<sup>CA</sup>, Rosa-rtTA<sup>LSL</sup> mice to Ubc-ERT/Cre<sup>+</sup> mice that express Cre-recombinase in all tissues after exposure to tamoxifen. After 5 days of tamoxifen injections followed by a week on Dox diet, most major tissues from Atg4B<sup>CA+</sup>, Rosa-rtTA<sup>LSL</sup>,...
Ubc-ERT/Cre* mice had expression of Atg4B<sup>CA</sup> and this expression lasted until harvest at 52 weeks. Due to the limitation of Col1A knock-in locus where mSt-Atg4B<sup>CA</sup> cDNA was integrated, there was no expression of Atg4B<sup>CA</sup> in brain or muscle, and expression in most other tissues was mosaic in nature consistent with previous report (29) (Figure S9A). Thus we did not observe any behavior abnormalities or premature death as had been reported in the Atg7 adult knockout mice (Figure S9B). There was only one mouse from the Atg4B<sup>CA++</sup> group that died earlier than 30 weeks due to a hernia. Based on the H&E histology examination of all mice older than 52 weeks, no significant difference was found among all groups. Overall, in this model, the whole-body inhibition of autophagy in a mosaic fashion did not appear to have any grossly detrimental effect on normal organs.

Next, we wanted to distinguish the cell autonomous effect vs. non-cell autonomous effects of autophagy inhibition on tumor seeding efficiency and growth. We used mouse tumor cell lines harvested from primary tumors and performed orthotopic injection into MHC H2 matched hosts (50% B6 and 50% FVB/N). First, we injected Atg4B<sup>CA++</sup> tumors into Atg4B<sup>CA++</sup> mice or Atg4B- mice on normal or Dox diets as shown in Figure 4A. Three groups of mice were generated to allow a pairwise comparison on the effect of autophagy inhibition in tumor cells or whole body: Atg4B- tumors in Atg4B- mice (BD- TU-, n=13), Atg4B<sup>CA++</sup> tumors in Atg4B- mice (BD- TU++, n=11) and Atg4B<sup>CA++</sup> tumors in Atg4B++ mice (BD++ TU++, n=16). After 3 weeks, both groups that had Atg4B<sup>CA++</sup> expressed in the tumor (either BD- or BD++) showed significant difference in the development of tumors compared to group where there was no autophagy inhibition in either the tumor or whole body (BD- TU-) (Figure 4B). These results indicate that cell autonomous autophagy inhibition plays a major role in controlling tumor seeding efficiency. Furthermore, tumor growth rate was unaffected by the whole-body expression and was determined predominantly by cell intrinsic expression of Atg4B<sup>CA++</sup> (Figure 4C). However, we noticed that although the ultimate ability to form tumors was determined by the expression of Atg4B<sup>CA</sup> in the tumor itself, there was an early trend of delayed tumor formation in mice with whole body expression of Atg4B<sup>CA++</sup> (Figure 4B). Indeed, at the earliest time-points the seeding efficiency was lowest in BD++ TU++ group where both body and tumor cells had autophagy inhibition (Figure 4B). To further explore the whole-body effect of autophagy inhibition on tumor take, we injected Atg4B- cell lines into Atg4B<sup>CA++</sup>, Rosa-rtTA<sup>LSL</sup>, Ubc-ERT/Cre* mice on either normal or Dox diet (Figure 4D). Two groups were generated to understand the non-tumor cell autonomous effects of autophagy inhibition: Atg4B- tumors in Atg4B- mice (BD- TU-, n=15) and Atg4B-tumors in Atg4B<sup>CA++</sup> mice (BD++ TU-, n=16). We found there was indeed a significantly delayed
tumor take in the BD++ group (Figure 4E). Once a tumor successfully established, there was no significant difference in tumor growth between Atg4B- and Atg4B<sup>CA++</sup> mice (Figure 4F). Importantly, Dox alone did not impact tumor seeding (Figure S10A).

In line with our previous work demonstrating the importance of stellate cell autophagy in supporting tumor growth, we found a negative selection against the expression of the Atg4B<sup>CA</sup> in stellate cells at the endpoint of the experiment when tumors have formed (Fig S10B). In contrast, the Atg4B<sup>CA</sup> was expressed in stellate cells in normal pancreas (Fig S10C). This negative selection in the tumor supports the concept that stellate cell autophagy is important for tumor growth in the pancreas and consistent with our prior work demonstrating an autophagy-dependent metabolic cross-talk (10).

**Discussion**

In this study, we addressed several questions regarding the inhibition of autophagy as a therapeutic target in pancreatic cancer. While hydroxychloroquine (HCQ) is being tested in PDAC as well as multiple other cancers and has shown some preliminary successes (30), the drug not only inhibits autophagy but also inhibits other aspects of lysosomal scavenging. Therefore, it is not possible to specifically assess the contributions of its anti-autophagy effects. In addition, there are potency issues with HCQ that may limit its utility (31). Together, these limitations require the development of more potent and specific autophagy inhibitors to rigorously test this approach in the clinic. Such inhibitors are in various phases of development.

In the interim, the inducible Atg4B<sup>CA</sup> model allowed us to address several fundamental questions that are critical to optimally bring autophagy inhibition forward to the clinic. Firstly, it allowed us to model the impact of potent inhibition at the early part of the autophagic process in fully formed tumors. Secondly, the inducible nature of the model allowed us to test the impact of intermittent autophagy inhibition. In essence, we have been able to utilize this new model to create a “genetic drug”. Combining this model with a pancreatic cancer GEMM, we have shown that these tumors show robust responses to autophagy inhibition. Indeed, our data also suggests that intermittent dosing of future autophagy inhibitors could be a viable strategy to create a therapeutic index. Although the mosaic nature of the model limited our ability to assess toxicity of whole body inhibition of autophagy, the lack of observed toxicity and histological damage of tissues suggests that autophagy inhibitors may be tolerated by patients when dosed appropriately. It is important to note that the Atg4B<sup>CA</sup> transgene did not express in the CNS, which may also explain the lack of toxicity in our model, as CNS toxicity is a major cause of
morbidity in previous studies (16). Given the relative ease of designing small molecules that cannot cross the blood-brain-barrier (BBB), future autophagy inhibitors may be designed with favorable toxicity profiles. Such an approach was taken with newly designed glutaminase inhibitors (32), where the known CNS toxicity was mitigated by limiting BBB penetration.

Using this new model, we have also been able to address some debated biological questions regarding the role of autophagy in pancreatic cancer. In particular, it has allowed us to deconvolute the cell autonomous (impacts the tumor cell directly) and non-cell autonomous (impacts tumor growth through its role on other cell-types) and show that both are relevant to its role in tumor promotion (Figure 4G). Similar to what we have previously shown, autophagy inhibition in the context of tumor initiating mutations (Kras mutation and p53 loss) can predispose to metaplasia and pre-malignant lesions (PanIN). This is highlighted in the genetic model where the entire pancreas has these oncogenic and tumor suppressor mutations, a situation that would not occur in the context of the human disease. Indeed, we do not see these marked histological changes in the context of autophagy inhibition in pancreata where oncogenic Kras is not expressed. Therefore, we believe that this will not likely be a significant issue in the therapeutic situation in patients where these genetic lesions are restricted to neoplastic tissue. While this “model effect” is not likely a concern for therapy (treating patients with established cancer), it might suggest that using autophagy inhibitors chronically as a chemopreventative strategy could be an issue.

One of the novel findings in this study was that the impact on tumor regression, when autophagy was inhibited in the tumor itself, was partially mediated by macrophages. Indeed, we could significantly inhibit the responses to the Atg4B^{CA} by depleting macrophages in the mouse. As macrophage modulation is being tested in PDAC as a therapeutic approach (28,33), whether combining such agents with autophagy inhibitors would be beneficial remains to be determined. We speculate that autophagy could regulate macrophage infiltration by degradation of inflammation-regulators, as well as directly affecting cytokine secretion as has been shown previously (34). The fact that autophagy inhibition systemically impacts tumor engraftment, supports the additional contribution of non-cell autonomous effects in the efficacy of autophagy inhibition. One likely explanation for this effect is the autophagy-dependent metabolic cross-talk between the tumor cells and the stroma previously described by our group. Although, we cannot rule out the contribution of other systemic effects of autophagy inhibition such as potentially heightened immune surveillance as an example. However, the fact that there appears to be stromal and immunological mediators that contribute to the anti-tumor effects of...
autophagy inhibition further supports both a cell autonomous and non-autonomous protumorigenic role for autophagy in PDAC and provides the strongest evidence to date that acute and potent inhibition of autophagy is effective in treating this disease in mouse models. One limitation of the study is that we haven’t yet assessed the impact of autophagy inhibition in different host cell types in the PDAC microenvironment other than stellate cells (10). Future studies will define the broader role of autophagy in distinct cell populations and how these influence tumor growth. Lastly, future studies will develop rationally designed therapeutic combinations with autophagy inhibition to guide trials with newer autophagy inhibitors.

**Materials and Methods**

Construction of targeting vector and screening of ES cells

The mStrawberry-Atg4B\textsuperscript{C74A} cDNA fragment was cloned from the mStrawberry-Atg4B\textsuperscript{C74A} plasmid generously gifted by Dr. Tamotsu Yoshimori (Addgene plasmid # 21076, Osaka University, Suita, Osaka) (26), and into pCol-TGM that was a gift from Scott Lowe (Addgene plasmid # 32715) (35). The pBS31- mStrawberry-Atg4B\textsuperscript{C74A} targeting vectors were co-electroporated into C2 mouse embryonic stem cells (Thermo Scientific Open Biosystems, #MES4305) with a plasmid expressing FLPE recombinase (pCAGGS-FlpE, Thermo Scientific Open Biosystems, Waltham MA, #MES4488) as previously described (29). ES cells were screened for integration of the transgene by PCR and correctly targeted ES cells were injected into C57Bl/6 blastocysts. Chimeras were crossed to the FVB/NJ inbred mice (The Jackson Laboratory, Bar Harbor, ME #001800).

Mice

All mice used in this study were housed in the pathogen-free animal facilities in Dana Farber Cancer Institute (Boston, MA). All procedures were approved by the Dana Farber Animal Care and Use Committee (Protocol number: 10-055) and carried out in strict accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. In \textit{Rosa-rtTA}\textsuperscript{LSL} mice the doxycycline-responsive reverse tetracycline transactivator (rtTA) is knocked into the transcriptional start site at the ubiquitously expressed \textit{Rosa26} locus and is preceded by a lox-stop-loom (LSL) cassette (36). PDAC mice contained \textit{Kras}\textsuperscript{G12D} allele knocked into the endogenous \textit{Kras} locus, preceded by an LSL cassette (37); \textit{p53}\textsuperscript{lox/+} allele where lox-P sites are inserted in the intron 1 and intron 10 respectively (38); and the \textit{p48Cre} allele that harbors a cre-recombinase gene in the endogenous \textit{Ptf1a} locus (39). \textit{Ubc-ERT/Cre}\textsuperscript{*} mice (Jackson Laboratory, Bar Harbor, ME) (40) were backcrossed to B6.
background and then bred with \textit{Atg4B}^{CA++}, \textit{Rosa-rtTA}^{LSL} mice. All mice included in the survival analysis were euthanized when criteria for disease burden were reached or when targeted analysis end points were reached.

Measurement of tumor volume by ultrasound

All mice were kept on a normal diet and screened weekly for tumor presence upon reaching 6 weeks of age. Once a tumor was detected, the mouse was randomly assigned to either the control group by being kept on the normal diet or treatment group by being switched to doxycycline diet (625 mg/kg Dox). Tumors were at least 2mm in diameter prior to enrollment (volumes ranged from 4 to 80mm$^3$). Tumor volumes (in mm$^3$) were measured twice a week by 3D ultrasound imaging (VisualSonics Vevo 770). The tumor relative growth rate was measured by normalizing each tumor volume to its first measurement at detection.

Lung cancer model and Magnetic resonance imaging

Single nodule murine lung cancer was induced by intrathoracic injection of Adeno-Cre virus (Gene Transfer Vector Core Facility at the University of Iowa) into \textit{Kras}^{G12D} mice at the age of 6-8 weeks as described previously (41). Animals were randomly assigned to various treatment groups as indicated once tumors had formed. Tumor growth was evaluated every two weeks using MR imaging until the tumor burden met euthanasia criteria. Mice were imaged on a 4.7 Tesla BioSpec 47/40 MRI scanner (Bruker BioSpin). Animals were anesthetized with 1-3% isoflurane via a nose cone. A gradient echo flow compensated (GEFC) sequence using a repetition time of 372.5 ms, echo time of 7.0 ms, and flip angle of 30° were used throughout the study. The slice thickness was 1 mm, and the number of slices was 17-20, which was sufficient to cover the entire lung. The acquisition matrix size was 256 x 128, the reconstructed matrix size was 256 x 256, and the field of view was 2.56 x 2.56 cm$^2$. Motion artifacts were minimized by application of cardiac and respiratory gating to all MRI studies. All animals were scanned by using the described settings and parameters. Tumor volume (mm$^3$) per animal was quantified by manual segmentation of the visible lung opacities present in each axial image sequence (a maximum of 10 consecutive scans were evaluated per mouse) to calculate tumor volumes using 3D Slicer (version 3.6.3) as described previously (41).

Immunohistochemistry

All samples were harvested for histology analysis at end-point unless otherwise specified. Samples resected from mice were fixed overnight in formalin, and then stored in 70% EtOH
before processing and embedding. Immunohistochemistry were conducted on 5 µM sections. Tissue sections were deparaffinized, rehydrated and boiled for 15 minutes with a pressure cooker in 10mM pH 6.0 Citrate buffer. Slides were incubated in 3% hydrogen peroxide for 30 minutes and then blocked in serum for 1 hour. Primary antibody was added to the section and incubated overnight at 4°C. Sections were further incubated with biotin-conjugated secondary antibody for 1 hour, Avidin-Biotin Complexes for 30 minutes (Vector Laboratories, MI) and developed by 3,3-diaminobenzidine following by hematoxylin staining. After staining, the sections were dehydrated and mounted in permount mounting medium (SP15-100, Fisher Scientific, MA). Primary antibody and dilution used: RFP rabbit polyclonal (1:500, 600-401-379, Rockland, PA); Cleaved-Caspase 3 rabbit polyclonal (1:200, D175, Cell signaling, MA); Ki67 rabbit polyclonal (1:100, clone K2, Ventana Medical Systems); CK19 (1:50, DSHB, University of Iowa, IA); Insulin (1:500, 3014S, Cell signaling, MA); Amylase (1:1000, Sigma, MO); CD68 mouse monoclonal (1:200, Kp-1, Cell Marque, CA); CD3 (1:500, Cell Marque, CA); Desmin (1:200, cloneD33, Dako); LC3 (1:500, NBP-19167, Novus Biologicals, CO). Images were taken by using light Microscope Leica DM2000 with camera. LC3 staining was modified with additional steps using TSA biotin system following manufacturer's instruction (NEL700A001KT, PerkinElmer, MA). Arginase 1 (1:100, NBP1-32731, Novus Biological, CO) stained IHC slides were scanned with 20x objective using Leica SCN400F whole-slide scanner, the DAB and hematoxylin stained area were calculated using ImageJ and analyzed using GraphPad Prism 7.03.

Immunofluorescence (IF)

Cells were grown on round coverslips in 12-well plate and fixed with 4% formaldehyde for 15 minutes. Fixed cells were blocked with 5% BSA / 0.3% Triton X-100 in PBS for 1 hour, and then incubated with primary antibody diluted in 1% BSA / 0.3% Triton X-100 in PBS overnight at 4°C. After being incubated with fluorochrome-conjugated secondary antibody for 1 hour at room temperature in dark, cells were mounted in ProLong Gold anti-fade mounting medium DAPI (P36931, ThermoFisher, MA). Images were taken with 6 channel fluorescent microscope Nikon Eclipse 80i with camera.

F4/80 and iNOS IF were performed on tumor sections: F4/80 (1:400, MCA497GA, Cl:A3-1, BioRad, CA), iNOS (1:600, LS-C88790/110398, LSBio, WA) and DAPI (D1306, ThermoFisher, MA) IF was performed using Opal™ 4-color manual IHC kit (NEL810001KT, PerkinElmer, MA) following manufacturer's protocol. Images with F4/80+ signals were taken with 40x objective.
using Leica DM6B. The ratio of total area of fluorescence was calculated and normalized with the total area of DAPI using ImageJ.

Western

Proteins were extracted with RIPA buffer and separated on 4–12% stacking SDS–PAGE gel, and then transferred to PVDF membrane (Biorad). Membranes were blocked with 5% non-fat milk and then incubated with the primary antibody overnight at 4°C. Following TBST washing, membranes were incubated with peroxidase-conjugated secondary antibody for 1 hour and exposed on film using the enhanced chemiluminescence (ECL) detection system (Thermo Scientific). Antibodies used were: RFP rabbit polyclonal (1:1000, 600-401-379, Rockland, PA); Cleaved-Caspase 3 rabbit polyclonal (1:500, D175, Cell signaling); LC3B (1:500, NB600-1384, Novus Biological), and β-Actin (1:3000, A2066, Sigma, MO).

Serum insulin measurement

Serum was collected at harvest, where whole blood was allowed to clot then after centrifugation the supernatant was carefully collected, aliquot and stored in -80°C. Insulin level was measured using mouse insulin Elisa kit (10-1247-01, Mercodia, Sweden) following manufacturer’s instruction.

Colony assay

Cells were pretreated with or without doxycycline for 7 days before plating into 6-well plates. 500 cells per well were plated in growth medium with 10% FBS with or without 2 µg/ml doxycycline. After 6 days, cells were fixed in 80% methanol and stained with 0.2% crystal violet and colonies were counted. The surviving fraction was calculated using the plating efficiency.

Soft agar assay

Each cell line was plated in triplicate in 6-well plate. 3 ml medium with 1% agar (Difco 214200, BD, NJ) was used as bottom gel. After the bottom layer solidified, 10^4 cells suspended in 2 ml medium with 0.4% agar were poured on bottom gel. After 2 weeks, colonies were stained with p-iodonitrotetrazonium violet (I-8377, Sigma, MO). Number of colonies was counted from pictures taken at low power lens of microscopy. Size of colonies was analyzed by Image-J software.

Cell culture
All cell lines used in the study were primary PDAC lines derived from mouse primary tumors and grown in RPMI 1640 (11875, Thermo Fisher, MA) with 10% FBS and 1% Penstrep and were derived during the last two years. Mice were genotyped to confirm the correct alleles for cell line derivation. Cell cultures were maintained in a humidified incubator at 37 °C with 5% CO₂. All primary tumor cell lines were harvested from ~5mm³ chunk of tumor, minced and digested in 4% collagenase/dispase for 1hr, then filtered through a 70 µM restrainer. Cell lines were routinely tested and all negative for mycoplasma infection. Inducibility and presence of the Atg4b dominant negative were tested by adding Dox to culture media.

Orthotopic injection

Primary tumor cell lines were harvest from tumor bearing naive mice at a B6/FVB mix background. Haplotype of each cell lines were identified according to their MHC II loci by PCR analysis as described in (42,43). Since host mice were all F1 from B6 (Ubc-ERT/Cre⁺) and FVB/N (Atg4BCA⁺⁺, Rosa-rtTA⁻LSL) crosses, we used cell lines carrying both B6 haplotype MHC2b and FVB/N haplotype MHC2a to minimize allograft rejection. Mice were anesthetized by intraperitoneal injection of Ketamine (10mg/ml)/Xylazine (1mg/ml) cocktail at the ratio of 10µl cocktail per 1g body weight. After local shaving and disinfection, the upper left abdominal cavity was opened by a 1 cm long incision. The spleen was pulled to expose the tail of the pancreas. 10 µl of ice-cold tumor cells (3×10⁵) mixed with Matrigel (1:1) was then slowly injected into the pancreas using an ice-cold 22-gauge Hamilton syringe (20736, Sigma, MO). To prevent leakage, a bubble need to be visible at the injection site and the needle was not removed for 15 seconds. After injection, the abdominal cavity was closed with absorptive suture and stainless-steel staples. Mice were given Buprenorphine to alleviate pain after surgery and monitored following protocol.

Ultrasound screening was used for tumor seeding efficiency assessment starting 1 week after injection. Lesion with diameter over 2mm was denoted as successful seeding. For mice with positive seeding, tumor growth was followed up to 4 weeks.

Xenograft

Primary mouse tumor cells (10⁵) were suspended in PBS, mixed with Matrigel (BD Biosciences) at 1:1 ratio, and subcutaneously injected into nude female mice (Nu/Nu; Charles River Laboratories) in a final volume of 100 µl. Each mouse was inoculated with Atg4B- cells on the left flank and Atg4BCA⁺⁺ cells on the right flank. 10 mice were kept on normal diet and 10 mice
were kept on doxycycline diet 1 weeks after injection when tumors reached volumes of 40mm$^3$. Tumor length and width were measured twice a week using caliper. The volumes of tumor were calculated using the formula \((L \times W^2)/2\).

Electron microscopy

Tumors were fixed with Karnovsky’s fixative (15732-SP, Electron Microscopy Sciences, PA). Embedding, sectioning and staining were done in the Harvard Medical School EM Facility. The EM pictures were captured by a conventional transmission electron microscope (JEOL 1200EX) equipped with an AMT 2k CCD camera.

Immune profiling

Spleen and pancreatic tumors were harvested from tumor bearing mice, minced in 3ml lysis buffer (HBSS+ 50U/ml DnaseI + 0.5mg/ml Collagenase D + 2.5mM MgCl2) and incubated at 37 °C for 30 minutes. Tissue chunks were ground with rubber grinder and passed through a 70 µm cell restrainer. Cells were incubated with 5ml 1x RBC lysis buffer (420301, Biolegend, CA) for 4 minutes, then diluted in 2%FBS in 1xPBS to a final volume of 30ml and spun down. Live cells were determined by LIVE/DEAD® fixable aqua dead cell stain kit (Molecular Probes). The cell pellets were re-suspended in PBS with 2% FBS for Fluorescence-activated cell sorting (FACS) analysis. Cells were stained with cell surface markers as indicated followed by fixation/permeabilization using foxp3 fixation/permeabilization kit (eBioscience). Cells were imaged on BD LSRFortessa (BD Biosciences) and analyzed using FlowJo software (Tree Star). Pancreas infiltrating immune cells were stained with different combinations of fluorochrome-coupled antibodies against mouse CD45 (clone 30-F11, Biolegend), F4/80 (clone BM8, Biolegend).

Depletion of macrophage

Clodronate liposomes /PBS control liposomes were purchased from [www.clodronateliposomes.com](http://www.clodronateliposomes.com). Dose injected were calculated based on the weight of mice to be treated at a ratio of 10µl per 1g body weight (example: 200µl liposome for 20g mouse). Once a tumor bearing mouse was identified, it was assigned to clodronate or PBS liposome groups in an alternating fashion. 1$^{st}$ dose of clodronate or PBS liposome was administrated on the same day tumor was identified and following doses were given twice a week.

Statistics


Overall survival events included death as defined by protocol with censoring for alive at last follow-up. Survival plots were generated using the Kaplan-Meier method. The log-rank test was used to compare survival distributions between groups. The seeding efficiency of mice with orthotopic injection was compared using a Fisher’s exact test. Statistical analyses were performed using with Prism 7 (GraphPad Software).

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**References**


Figure 1. Generation and functional analysis of the inducible Atg4B<sup>CA</sup> mouse model. A, Tissue-specific promoter driven Cre expression will remove STOP cassette to express reverse tetracycline-controlled transactivator (rtTA). Doxycycline binds rtTA to turn on Tet-On cassette and induce Atg4B<sup>C74A</sup> expression. B, Immunofluorescence staining of LC3 (green) and RFP (red) in Atg4B<sup>CA+</sup> tumor cells treated with or without Dox for 6 days. noD indicates no Dox treatment. Blue, DAPI stained nuclei. Scale bars: 5µM. C, Representative immunofluorescence staining of LC3 and RFP in Atg4B<sup>CA++</sup> tumor cells showing level of autophagy. Scale bars: 5µM. D, Quantification of LC3+ puncta per cell in Atg4B<sup>CA+</sup> and Atg4B<sup>CA++</sup> tumor cells. Dox treatment reduced autophagy level in basal (Top panel) or Chloroquine treated (+CQ at Bottom panel) condition indicating inhibited autophagic flux. More than 10 fields per cell line were measured. SD plotted as Error bars. **p<0.001, *p<0.05 by T-test. E, Western blot showing expression of RFP, LC3I/II in Atg4B<sup>CA+</sup> and Atg4B<sup>CA++</sup> cells treated with Dox for 3 days (3d) and 6 days (6d). F, Representative IHC images of PDACs stained for RFP with no expression (top panel), one copy (bottom left) and two copies (bottom right) expression of Atg4B<sup>CA</sup>. Scale bars: 500µM. G, Representative IHC images of PDACs stained for LC3 with no (top panel), one copy (bottom left) and two copies (bottom right) of Atg4B<sup>CA</sup> expression. Inserts were 3 folds enlargement of the white framed areas; autophagosomes (LC3+ puncta) were marked by white arrowhead. Scale bars: 10µM. H, Electronic microscope pictures showing ultrastructure of tumors from Atg4B- and Atg4B<sup>CA++</sup> tumors. Two samples of each genotype were examined and a total of 10 fields were measured in the graph. ***p<0.001 by T-test.

Figure 2. Impact of autophagy inhibition on PDAC growth in Atg4B<sup>CA+</sup> and Atg4B<sup>CA++</sup> mice. A, Comparison of tumor growth between Atg4B- control and Atg4B<sup>CA+</sup> mice. Tumor volumes were measured by ultrasound and relative growth was plotted against time (weeks) since initial tumor identification (0wk), Dox diet (625 mg/kg Dox) was given after tumor identification. Numbers of mice in each group at each time-point are indicated in the graph. B, Survival analysis of mice plotted in A. p-value by Log-rank test. C, Comparison of tumor growth among Atg4B- control, Atg4B<sup>CA++</sup> and Atg4B<sup>CA++</sup> intermittently induced (Int) groups. Tumor volumes were measured by ultrasound and relative growth was plotted against time (weeks) from initial tumor identification (0wk). Numbers of mice in each group at each time-point are indicated in the graph. D, Survival analysis of mice plotted in C. p-value by Log-rank test. E, Relative growth comparison between Atg4B- (n=28) and Atg4B<sup>CA++</sup> (n=21) tumors after Dox treatment for one week. **P<0.001 by T-test. F, Western blot of RFP, cl-Casp3 and LC3I/II in starved (HBSS treated) Atg4B- and Atg4B<sup>CA++</sup> tumor cells treated with or without Dox. G, IHC analysis of cl-Casp-3 staining in Atg4B- and Atg4B<sup>CA+</sup> tumors. Scale bar: 100µM. cl-Casp3+ cells/ field was compared as shown in the right plot. Each dot represents one mouse with more than 5 fields measured per mouse. H, IHC analysis of Ki67 staining in Atg4B- and Atg4B<sup>CA+</sup> tumors. Scale bar: 50 µM. Proliferation index as Ki67+ cell ratio was compared as shown in the right plot. Each dot represents one mouse with more than 5 fields measured per mouse.

Figure 3. The cell intrinsic and extrinsic effect of autophagy inhibition on tumor growth. A, Plot of colony number (mean+SD) formed in Atg4B- and Atg4B<sup>CA++</sup> cells. Each group contained 3 individual cell lines and each cell line was repeated three times. *P<0.05 by T-test. B, Plot of
colony number and size formed in Atg4B- and Atg4B<sup>CA++</sup> cells grown in soft agar. Each group contained 3 individual cell lines and each cell line was repeated three times. *P<0.05 by T-test. C, Relative growth of Atg4B<sup>CA++</sup> and Atg4B- sub-cutaneous xenografts on Dox diet. n=10 in each group, *p<0.05. D, Relative growth of orthotopic pancreatic tumors. ***p<0.0001, *p<0.05. E, Representative images of CD68 IHC in Atg4B- and Atg4B<sup>CA++</sup> autochthonous tumors showing macrophage infiltration. Scale bar: 100 µM. Quantification of CD68+ cells per field showed significantly increased number of macrophages in the Atg4B<sup>CA++</sup> group (n=6) vs. Atg4B- group (n=6), 5-10 randomly selected fields were quantified for each tumor. **p=0.0021 by T-test. F, Representative images of CD68 IHC in Atg4B<sup>CA++</sup> tumors orthotopically injected in nude mice either on or off doxycycline food. Scale bar: 100 µM. There was no significant difference in macrophage infiltration between the Atg4B<sup>CA++</sup> (n=5) group and the Atg4B- group (n=5), 8 fields were randomly selected for each tumor. G, Relative growth of Atg4B<sup>CA++</sup> tumors treated with empty liposome (PBS-Lipo) (n=6) or clodronate liposome (Clod-Lipo, n=5). ***p<0.001, *p<0.05 by T-test.

**Figure 4.** Autophagy inhibition impairs tumor seeding efficiency through cell autonomous and non-cell autonomous mechanisms. A, Schematic experimental design to demonstrate how tumor take was affected by autophagy inhibition. B, Detection of tumor take with ultrasound after orthotopic injection of Atg4B<sup>CA++</sup> cells into Atg4B<sup>CA++</sup>, Rosa-<i>rTa<sub>LSL</sub></i>, Ubc-<i>ERT/Cre<sup>+</sup></i> mice on normal diet (BD- TU-, n=13), Atg4B-,Ubc- mice on Dox diet (BD- TU++, n=11) and Atg4B<sup>CA++</sup>, Rosa-<i>rTa<sub>LSL</sub></i>, Ubc-<i>ERT/Cre<sup>+</sup></i> mice on Dox diet (BD++ TU++, n=16). Numbers of mice with detected tumors are shown in the graph. *p<0.05 by Fisher’s exact test. C, Relative tumor growth of orthotopically-injected tumors plotted in B. *p<0.05. D, Schematic of experimental design to assess the non-cell autonomous effect of autophagy inhibition on tumor take. E, Detection of tumor take with ultrasound after orthotopic injection of Atg4B- cells into Atg4B<sup>CA++</sup>, Rosa-<i>rTa<sub>LSL</sub></i>, Ubc-<i>ERT/Cre<sup>+</sup></i> mice on normal diet (BD- TU-, n=15) and on Dox diet (BD++ TU-, n=16). Numbers of mice with positive seeding were shown in the graph. **p<0.001, *p<0.05 by Fisher’s exact test F, Relative tumor growth of orthotopically-injected tumors plotted in C. No significant differences are seen between groups at any time points. G, Model of cell autonomous and non-cell autonomous mechanisms of autophagy inhibition impacting PDAC growth.
Figure 1.
**Figure 4.**

**A**
Normal diet

**B**

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*P<0.05*

**C**

Tumor volume change (fold)

**D**
Normal diet

**E**

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**F**

Tumor volume change (fold)

**G**

Tumor cells → Autophagy Inhibition → (Tumor cell autonomous) → ↓ proliferation → Recruitment of macrophages → Dead cells → Apoptosis → Proliferation↓

Tumor cells → Autophagy Inhibition → (Systemic) → Metabolites → Recruitment of macrophages → Impaired metabolic crosstalk → Altered microenvironment → Dead cells
Autophagy sustains pancreatic cancer growth through both cell autonomous and non-autonomous mechanisms

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