Targeting Autophagy in BRAF-Mutant Tumors

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Summary: Recent studies have highlighted the opportunity to treat cancer by inhibiting autophagy, but have also raised important caveats with this idea. An article in this issue of Cancer Discovery adds to accumulating evidence suggesting that we should focus our efforts (at least initially) on specific tumors where we are most likely to see beneficial effects. Cancer Discov; 5(4); 353–4. ©2015 AACR.

See related article by Xie et al., p. 410 (3).

Macroautophagy (which we refer to as autophagy) is the process by which cellular material is delivered to lysosomes via vesicles called autophagosomes. Autophagy is widely viewed as being important in cancer and, in the last year, several clinical trials reported deliberate attempts to inhibit autophagy along with various other anticancer drugs in multiple tumor types. The key word in the previous sentence is “deliberate”—we also know that many anticancer agents inadvertently alter autophagy (in some cases stimulating and in others inhibiting the process). This means that even during standard therapy, autophagy is likely being manipulated in patients with cancer whether we want to do so or not. Is such autophagy manipulation a good thing or a bad thing to be doing? The big issue is that autophagy has multiple, often critical functions in cancer cells and xenografts with the BRAF<sup>V600E</sup> mutation can also overcome resistance to RAF inhibitors (8). Similarly, brain tumor cells with the same BRAF mutation are killed by autophagy inhibition even in the absence of extra stresses, and a patient with a BRAF-mutant brain tumor was successfully treated with the autophagy inhibitor chloroquine to overcome acquired resistance to the RAF inhibitor vemurafenib (9). Importantly, this new study (3) shows that deletion of Atg7 improves the effectiveness of the <em>Braf</em><sup>V600E</sup> inhibitor dabrafenib in a melanoma GEMM. Thus, a pattern seems to be emerging whereby RAS pathway–driven and especially BRAF-mutant tumors have increased dependence on autophagy, allowing effective treatment with autophagy inhibition and improving RAF inhibitor therapy effectiveness.

However, although it is clear that disruption of autophagy in these tumor models usually has a profound effect on metabolism and causes accumulation of damaged mitochondria, there are also potentially important differences in the responses of tumors in the various models. Sometimes, autophagy-dependent tumor cells die when autophagy is inhibited even in the absence of added stress (9), but in pancreas tumors the effect of autophagy inhibition is primarily on cell growth, not survival (5). Xie and colleagues (3) add another phenotype because, in this study, autophagy inhibition caused melanoma cell senescence, while also potentiating dabrafenib-induced senescence. There is also some confusion regarding the role of RAS, which is the immediate upstream activator of RAF. In most studies, tumors with mutant RAS respond to autophagy inhibition; however, this can be context dependent, too, with some tumor cells displaying growth inhibition when autophagy is blocked with chloroquine and others showing the opposite effect even when they have the same oncogenic RAS genes (10). Some of the variable effects may be due to when autophagy is inhibited. In most of the GEMMs, autophagy was inhibited simultaneously with activation of the oncogenic signal so that the tumor developed with no ability to activate autophagy. This may be different from those situations where autophagy is inhibited in a fully formed tumor, as would be the case when treating people.

Most importantly, it has been questioned whether any benefits of autophagy inhibition could be outweighed by toxicity...
from blocking this process. Most mouse studies, including the latest one (3), inhibited autophagy only in the tumor cells. In humans, we cannot do that. If we inhibit autophagy in people, we will do so with drugs such as chloroquine, which will affect both tumor cells and the rest of the body. Will that cause problems? The clinical studies with chloroquine and hydroxychloroquine have shown few signs of toxicity. For example, one patient whose brain tumor is being treated by autophagy inhibition with chloroquine (9) has been treated with a combination of chloroquine and vemurafenib for over 2 years with no signs of toxicity from the autophagy inhibitor. However, one area of unusually high agreement in the autophagy field is that chloroquine is a poor autophagy inhibitor, especially in vivo. For instance, it has other effects in addition to blocking autophagy. In addition, chloroquine levels that are achievable in tumors are variable and, even in the best cases, probably are only just enough to inhibit autophagy. Therefore, the trivial explanation for why this drug is well tolerated is that it is doing a poor job of inhibiting autophagy. Karsli-Uzunbas and colleagues (4) modeled a “perfect” autophagy inhibitor by studying the effect of an acute whole-body knockout of an essential autophagy gene (Atg7) in adult mice with cancer. The encouraging result was that the tumors went away; however, a cup-half-empty view of this study is that the mice died anyway because autophagy inhibition caused neurodegeneration after a few weeks. Obviously, a cancer treatment that caused tumors to go away but led to death by neurodegeneration shortly afterward is not much use. Thus, a critical question for the field is whether a useful antitumor response will require that we inhibit autophagy so effectively that the beneficial effects would be outweighed by toxicity on normal tissues, especially the brain. Xie and colleagues (3) addressed this question and found that chloroquine treatment was, like Atg7 knockout, an effective way to suppress the same BrafV600E-driven tumors. This is important because it suggests that if you treat the right sort of tumors (i.e., those that really depend on autophagy), even a drug that we all agree is a pretty lousy autophagy inhibitor can inhibit autophagy enough to get the antitumor responses we want without overt toxicity. In cancer medicine, this sort of thing often comes up: for example, global and irreversible knockout of topoisomerases would likely be very toxic in a mouse, but this does not mean we cannot use topoisomerase inhibitors in the clinic. The key is to inhibit the target (in this case, the process of autophagy) incompletely—usually not a problem with drugs, which, unlike knockout of genes that are essential for a given process, never work with 100% efficiency—but enough to get tumor-specific effects. In this view, autophagy inhibition is simply another case where we have to balance benefits and costs and come up with ways to identify patients who will and will not benefit from the treatment.

There are still many important questions we need to answer. Why does RAF mutation make tumor cells so reliant on autophagy? Why do some tumor cells die and others do not upon autophagy inhibition, and why do some become senescent? Why are there differences among RAS-mutant tumors? Are there similarities among autophagy-dependent tumors that will allow us to identify them all even if they do not have mutant RAF? Is the autophagy that is often induced by other anticancer drugs (as opposed to the basal autophagy that is going on all the time in mammalian cells) especially important for determining whether a tumor cell will live or die? Can we make better GEMMs that will allow us to model reversible and different extents of inhibition of autophagy and thus determine when and how much autophagy inhibition is needed to maximize beneficial effects while minimizing toxicity in cancer treatment?

The information we already have, however, suggests that to effectively treat cancer by autophagy inhibition, we will need at least two things: (i) a drug to inhibit autophagy, preferably with better pharmacologic properties and more specificity than chloroquine, and (ii) a way to identify people whose tumor is autophagy dependent. The accumulating evidence in melanoma, lung, and brain tumors with human cell lines, genetically engineered mice, human tumor xenografts, and even the first patients suggests that BRAF mutation may be a good place to start looking for autophagy-dependent tumors to test these ideas.

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