

Genetic ablation or pharmacological inhibition of autophagy suppresses intrinsic resistance of breast cancer to HER2-targeted therapies

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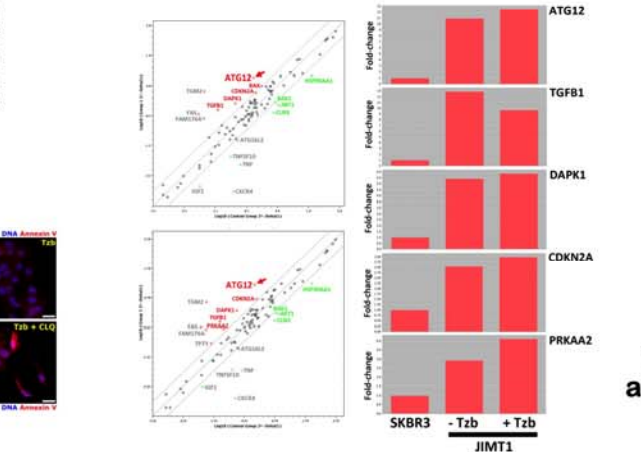


Autophagy, an evolutionary conserved catabolic process whereby cells generate energy and building blocks by promoting large-scale recycling of cytoplasmic macromolecules and organelles, represents a novel drug-targetable molecular mechanism underlying *de novo* (primary) refractoriness of HER2 gene-amplified breast cancer (BC) to HER2 inhibition. JIMT-1 cells, which were obtained from a HER2-positive BC patient that rapidly progressed on trastuzumab (Herceptin™) *ab initio* and that show cross-resistance to multiple HER1/2 inhibiting drugs including lapatinib (Tykerb™), were found to constitutively exhibit an enhanced autophagic vesicle content as assessed by immunoblotting of endogenous ATG8/LC3 lipidation and confocal imaging of the recruitment of ATG8/LC3 to autophagic vesicles. A significant decrease in the expression status of the specific autophagy receptor p62/SQSTM1 -a protein selectively degraded by autophagy- confirmed further a constitutive activation of the autophagic flux in trastuzumab-refractory JIMT-1 cells. When the Human Autophagy RT2 Profiler™ PCR Array was employed to profile the expression of 84 genes involved in autophagy, ATG12 was the most differentially up-regulated gene (>10-fold) as compared with trastuzumab-responsive SKBR3 cells. Upon collection of the transcriptional profile of the ATG12 gene across two sets of > 50 widely used BC cell lines, HER2+ BC cells with well-established *de novo* resistance to trastuzumab were characterized by expressing significantly higher levels of ATG12. When lentiviral-delivered small hairpin RNA was employed to stably & specifically knock-down ATG12 gene, JIMT-1 ATG12-shRNA cells were more significantly growth-inhibited by trastuzumab (up to 5-fold) than parental JIMT-1 cells. Moreover, the half-maximal inhibitory concentration (IC₅₀) values for the small-molecule HER1/2 Tyrosine Kinase Inhibitors gefitinib, erlotinib and lapatinib were drastically reduced by up to 10 times in response to ATG12 gene silencing. Knockdown of autophagy-regulatory genes other than ATG12 (e.g. ATG5, ATG8/LC3B) similarly suppressed refractoriness to trastuzumab as well as co-existing resistance to other HER1/2-targeted agents. Knockdown of autophagy-specific genes, however, did not alter basal sensitivity of JIMT-1 cells to multiple cytotoxics including doxorubicin, cisplatin, paclitaxel and vinorelbine. When lysosomal degradation was pharmacologically inhibited by using the antimalarial lysosomotropic drug chloroquine we found a massive accumulation of abnormal autophagolysosomes that promoted synergistic re-sensitization of JIMT-1 cells to the growth inhibitory and apoptotic activity of trastuzumab. In summary, autophagy-specific genes appear to play a potent protective role against HER2 inhibiting drugs currently in use. Given that genetic and pharmacological targeting of autophagy was found to be detrimental to intrinsic BC refractoriness to HER2-targeted therapies, our current findings may provide rationale for novel, chloroquine-based therapeutic approaches aimed to circumvent primary-resistance and potentiate the efficacy of both trastuzumab and lapatinib in patients treated for HER2-positive BC disease.

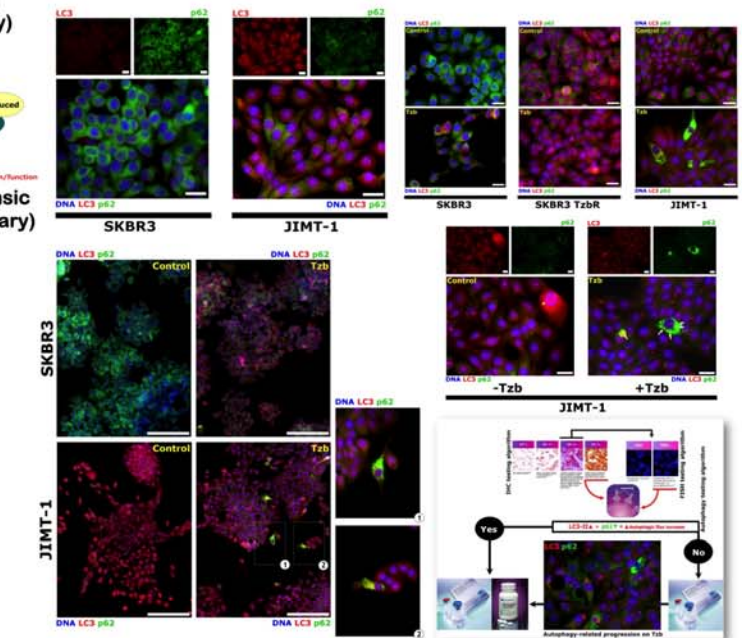
Autophagy and resistance to trastuzumab



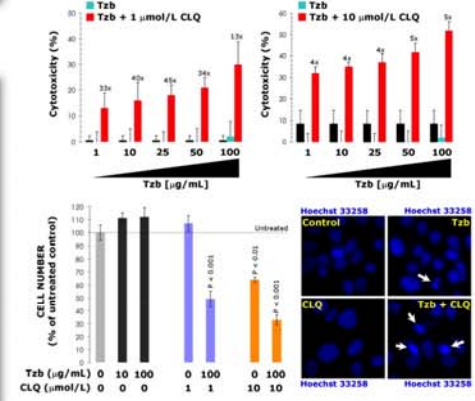
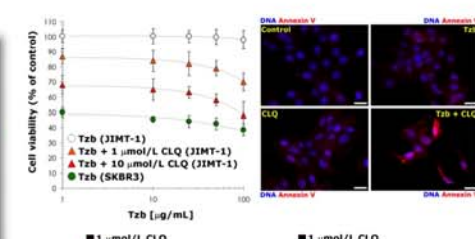
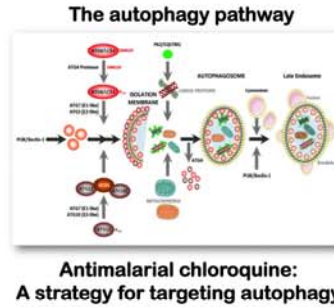
Up-regulation of autophagy-specific genes and De novo resistance to trastuzumab



Autophagy activation in BC models with De novo resistance to trastuzumab



Pharmacological inhibition of autophagy flux and reversal of primary resistance to trastuzumab



Genetic ablation of the autophagy-specific gene ATG12 and reversal of primary resistance to anti-HER2 therapies

