

How does estrogen work on autophagy?

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ABSTRACT

Macroautophagy/autophagy is vital for intracellular quality control and homeostasis. Therefore, careful regulation of autophagy is very important. In the past 10 years, a number of studies have reported that estrogenic effectors affect autophagy. However, some results, especially those regarding the modulatory effect of 17 β -estradiol (E2) on autophagy seem inconsistent. Moreover, several clinical trials are already in place combining both autophagy inducers and autophagy inhibitors with endocrine therapies for breast cancer. Not all patients experience benefit, which further confuses and complicates our understanding of the main effects of autophagy in estrogen-related cancer. In view of the importance of the crosstalk between estrogen signaling and autophagy, this review summarizes the estrogenic effectors reported to affect autophagy, subcellular distribution and translocation of estrogen receptors, autophagy-targeted transcription factors (TFs), miRNAs, and histone modifications regulated by E2. Upon stimulation with estrogen, there will always be opposing functional actions, which might occur between different receptors, receptors on TFs, TFs on autophagy genes, or even histone modifications on transcription. The huge signaling network downstream of estrogen can promote autophagy and reduce overstimulated autophagy at the same time, which allows autophagy to be regulated by estrogen in a restricted range. To help understand how the estrogenic regulation of autophagy affects cell fate, a hypothetical model is presented here. Finally, we discuss some exciting new directions in the field. We hope this might help to better understand the multiple associations between estrogen and autophagy, the pathogenic mechanisms of many estrogen-related diseases, and to design novel and efficacious therapeutics.

Abbreviations: AP-1, activator protein-1; HATs, histone acetyltransferases; HDAC, histone deacetylases; HOTAIR, HOX transcript antisense RNA

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Introduction

Macroautophagy/autophagy is a biochemical process necessary for the maintenance of intracellular homeostasis, and its failure can lead to pathological problems such as metabolic diseases, tumors, and developmental defects. Considering that interfering with autophagy is a potential therapy for several diseases, autophagy has become a promising and attractive target for the pharmaceutical industry [1,2]. However, the regulatory mechanisms and pathophysiological states of autophagy have not been fully elucidated, especially for tumors [2,3]. Estrogen is a sex hormone that plays an important role not only in the development of female secondary sexual characteristics, but also in bone development, cardiovascular system protection, and homeostasis [4]. In addition, the occurrence and development of many tumors have been shown to be estrogen dependent [4]. Increasingly, ESR (estrogen receptor) ligands are being designed, synthesized, and used to treat related diseases, and some have already been used clinically [5]. As early as a few decades ago, it was reported that estrogen affects the autophagy of renal tubules [6,7]. In the past 10 years, a number of studies have reported that ESR ligands affect autophagy-related proteins and morphologies in different tissues [8–40]. However, these reports are quite scattered (Table 1, 2). Some results, especially those regarding the modulatory effect on autophagy of 17 β -

estradiol (E2), the major endogenous estrogen in mammals, seem inconsistent (Table 1) [8–20]. In view of the importance of the crosstalk between estrogen signaling and autophagy, this review summarizes the ESR ligands reported to affect autophagy (characteristic autophagy proteins and key morphologies). In addition, tissue and subcellular distribution of the ESRs, autophagy-targeted TFs, miRNAs, and histone modifications are discussed as well. Finally, we examine the potential crosstalk between estrogen signaling and the autophagy pathway and summarize the molecular mechanisms involved in the regulation of autophagy by estrogen. We hope this will not only enrich our understanding of the known estrogenic regulation, but also promote more insight into the molecular mechanisms of estrogen's action on autophagy.

Regulation of E2 on autophagy

As early as the 1970s, an association between castration and altered ultrastructural patterns of autophagosomes and lysosomes in different tissues was reported [6,7]. In early reports, castration leads to a higher rate of autophagy with an increased number of lysosomes and degrading organelles, which suggested for the first time that the systemic deprivation of steroid sex hormones could be linked to autophagy [6,7]. However,

Table 1. The regulation of E2 on autophagy.

Ligand	Action	Disease	Cell Line or Animal	Tissue	Dose	Effector proteins	Autophagy morphology	Ref
E2	Induce	Breast cancer	MCF-7	breast	10 nM	MAP1LC3-II/MAP1LC3-I, SQSTM1, BCL2, ESR1↓	autophagosome	[8]
		Hypoxia-induced pulmonary hypertension	PAEC	lung	1, 10 nM	MAP1LC3-II, ER-independent	NA	[9]
		Nephrotoxicity	Male Sprague-Dawley rats	proximal renal tubule	75 µg/kg/day	MAP1LC3-II, MAP1LC3-I, IIF27, MAPK1↓	NA	[10]
		Osteoporosis	mProx24	bone	0.2 mg/kg/day	MAP1LC3-II/MAP1LC3-I, SQSTM1, SOCS3, STAT3↓, MAPK1	autophagosome	[11]
		Ovarian cancer	MC3T3-E1	bone	10 nM	MAP1LC3-II/MAP1LC3-I, BCL2, BECN1, AKT1, ULK1	NA	[12]
		Parkinson disease	Skov-3, Ovar-3(HTB-161), A2780 (ESR1 ⁻), A2780CP (ESR1 ⁻)	ovary	10 µM	MAP1LC3B-II, MAP1LC3B-I, AKT1↓BECN1↓, GAPDH↓	acidic vesicular organelles	[13]
		Renal cell carcinoma	/	CNS	1 mg/kg/day	MAP1LC3-II, MAPK1	autolysosomes/ autophagosomes	[14]
	restrict (prevent induced autophagy)	Testicular germ cell tumors	RCC cell lines	kidney	7, 28 µM	MAP1LC3B-II, MAP1LC3B-I, SQSTM1	autophagosome	[15]
		Heart disease	TCAM2	testis	1, 10, 100 nM	BECN1, AMBRA1, PIK3C3, UVRAG, PIK3CA-III, ESR2↓, AKT1↓	autophagic vesicles	[16]
		Myocardial injury	H9c2 cells	heart	10 nM	MAP1LC3-II, MAP1LC3-I, ESR2, AKT1, BNIP3	NA	[17]
		Spinal cord injury	cardiomyocytes	heart	10 nM	MAP1LC3-II/MAP1LC3-I, ATG5↓, BECN1↓	NA	[18]
		Ovariectomy	PC12	adrenal medulla	20 nM	MAP1LC3-II, MAP1LC3-I, SQSTM1, BECN1↓, ATG5↓, ATG7↓	NA	[19]
			/	proximal tibias	10 µg/kg/day	MAP1LC3-II, MAP1LC3-I, SQSTM1, ATG5↓, BECN1↓	acidic vesicular	[20]

Abbreviations: AKT1/PKB, AKT serine/threonine kinase 1; AMBRA1, autophagy and beclin 1 regulator 1; ATG, autophagy related; BECN1, beclin 1; BNIP3, BCL2 interacting protein 3; CNS, central nervous system; E2, 17 β -estradiol; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; IIF27/p27, interferon alpha inducible protein 27; MAP1LC3/LC3, microtubule associated protein 1 light chain 3; MAPK1/ERK, mitogen-activated protein kinase 1; PAEC, pulmonary artery endothelial cells; PIK3C3/VPS34, phosphatidylinositol 3-kinase catalytic subunit type 3; PLIN2/ADRP, perilipin 2; SOCS3, suppressor of cytokine signaling 3; SQSTM1/p62, sequestosome 1; STAT, signal transducer and activator of transcription; ULK1, unc-51 like autophagy activating kinase 1; UVRAG, UV radiation resistance associated. ↓, genes are upregulated by E2 unless so marked, which indicates that E2 downregulates them.

both the molecular mechanisms and signaling mediators of autophagy were poorly known then. In recent years, increasing research has shown that autophagy is involved in the effects of estrogen on various diseases (Table 1).

The process of autophagy requires the coordination of numerous proteins. To determine whether autophagy is inhibited or promoted not only depends on the single index of biomarker proteins such as MAP1LC3, but also on changes of autophagy flux, autophagy substrates, and key autophagy morphology [41]. For example, chloroquine inhibits autophagy by blocking the fusion of lysosomes with autophagosomes, resulting in the accumulation of MAP1LC3-II and autophagosomes. Therefore, some of the actions on autophagy shown in Table 1 need further confirmation. However, it is clear that E2 has multiple effects on autophagy. In many cases, E2 plays a role in promoting autophagy [8–16], but at other times, when cellular autophagy has been stimulated by hypoxia, lipopolysaccharides (LPS), spinal cord injury, or ovariectomy, E2 shows a restrictive effect on gene expression of some autophagy proteins [17–20]. Similar phenomena have also been observed for resveratrol, which can prevent the upregulation of autophagy induced by rapamycin (Table 2).

Both endogenous and exogenous ESR ligands perform biological functions with specific receptors, classical nuclear receptors (ESR1 and ESR2), and a membrane receptor, GPER1 (G protein-coupled estrogen receptor 1) [5]. In the classical pathway, activated ESRs undergo conformational changes after binding with estrogen, release from the heat shock proteins (HSPs), and then transfer to the nucleus and form homologous or heterologous dimers. In the nucleus,

ESRs interact with the estrogen responsive element (ERE) and regulate the expression of target genes, including some autophagy-related genes, directly or indirectly through TFs [42]. Different from ESRs, GPER1 in the cytoplasm mainly takes part in the rapid response of cells to estrogen [42].

Based on the classical pathway, ESR antagonists such as tamoxifen, raloxifene, and fulvestrant have been designed, synthesized, and used in clinical treatment of ESR-positive breast cancer [5]. However, these ESR antagonists are GPER1 agonists and are able to induce rapid activation of protein kinases, cAMP production, and gene transcription via GPER1 [42]. Some specific regulators targeting GPER1 have been developed but have not yet been used in the clinic. Unexpectedly, there is a slight difference between their effects on autophagy (Table 2).

ESR distribution in organs and subcellular locations

As shown in Figure 1, compared to ESRs, GPER1 is more widely expressed in human tissues. GPER1 is predominately expressed in the thyroid gland, skeletal muscle, adrenal gland, and kidney [43]. In some organs, both ESR1 and ESR2 are expressed with GPER1 [44], whereas in others, only one subtype of ESR is mainly expressed. It is worth mentioning that only ESR2 has ever been reported to be expressed in the stomach [45].

The expression of these receptors and their intracellular distribution are different in different cell types, and the effects of estrogen on their distribution are also different [46–49]. The subcellular localization of the receptors is closely related to their functions, and it changes in different

Table 2. The regulation of autophagy by ESR ligands ^a.

Disease	Tissue	Cell line	Ligand	Type	Dose	Effector proteins	Autophagy morphology	Ref
Breast cancer	breast	MCF-7	Fulv	ER antagonist	1 μM	MAP1LC3-II, MAP1LC3-I, BCL2↓, BECN1, MAPK/ERK, AKT1↓	autophagosomes	[21,22]
		T47D, MCF-7, BT-474, tam	4-OH TAM	ER antagonist	0.5, 1, 5 μM	MAP1LC3-II, NO, MAPK1, PLIN2, BCL2↓	autophagosomes, lysosomes/ autolysosomes increased	[23,24]
		MCF-7, MCF-7 tamR, LCC2, MDA-MB-231	TAM	SERM	1, 3, 5 μM	MAP1LC3-II/MAP1LC3-I, SQSTM1, BECN1, MAPK1/3, BAX-BCL2, ATG12-ATG5	autophagic vacuoles, increases autophagosomes /MDC-labeled vesicles	[21,22,25-28]
		MCF-7	raloxifene	SERM	10 μM	MAP1LC3-II, BECN1, ATG12-ATG5 conjugates	autophagic flux, autophagic vacuoles	[29]
		MCF-7/LCC1, MCF-7/LCC9, MCF-7CL	L17, WAY-20,070	ESR2 agonist	10 nM	MAP1LC3-II/MAP1LC3-I, BCL2↓, ESR1↓	NA	[30]
		MCF-7, (CCD1059sK	genistein	GPER1 agonist	100 μM	MAP1LC3/MAP1LC3B, BAX-BCL2	autophagosome	[31]
Diabetic cardiac function I	heart	H9c2	resveratrol	mixed ER agonist/ antagonist	100 μM	estrogen-regulated genes	induces RICTOR and activates AKT1	[33]
Glioblastoma	glioblastoma	U87, X1016, JX6	TAM	SERM	9, 12 μM	MAP1LC3-II, MAP1LC3-I, ATG5↓	induces autophagic vacuole formation	[35]
Oral squamous cell carcinoma	mouth	SCC4, SCC9, HSC-3	G15	GPER1 antagonist	0-20 μM	MAP1LC3B-II, MAP1LC3B-I, BCL2↓, AKT1↓, MAPK1↓, GPER1↓	autophagosome	[36]
Osteosarcoma	bone	MG63	2-ME	GPER1 agonist	10 μM	MAP1LC3-II/MAP1LC3-I	NA	[37]
Ovarian cancer	ovary	PEO1, BG-1, SKOV-3R	Fulv	ER antagonist	1 μM	MAP1LC3-II, MAP1LC3-I, IGF1R, PARP1, ESR1↓	induces autophagy (not alone)	[38,39]
Toxoplasmosis	breast	MCF-7	TAM	SERM	5, 10 μM	MAP1LC3-II, MAP1LC3-I	NA	[40]

^a Abbreviations: 2-ME, 2-methoxyestradiol; 4-OH TAM, 4-hydroxytamoxifen; BAX, BCL2 associated X, apoptosis regulator; BCL2, BCL2, apoptosis regulator; Fulv, fulvestrant; MTOR, mechanistic target of rapamycin kinase; MDC, monodansylcadaverine; RICTOR, RPTOR independent companion of MTOR complex 2; SERM, selective estrogen receptor modulator; TAM, tamoxifen. ↓, genes are upregulated by ESR ligands unless so marked, which indicates that ESR ligands downregulate them.

cell types and physiological states. For example, upon binding with E2, ESRs located in endothelial cytosolic/nuclear and endothelial surface membranes are upregulated and activate NOS3 (nitric oxide synthase 3) via genomic and nongenomic pathways, respectively [50]. The nitric oxide (NO) synthesized in this manner can suppress MTOR expression and induce autophagy [51]. Mitochondrial ESRs (mtESRs) are expressed in many human cells including cardiac muscle, lens epithelium, and osteosarcoma, hepatoma, and breast cancer cells [52-55], and mediate the synthesis of mitochondrial respiratory chain proteins (MRCs) via induction with E2 [55-57]. The expression levels of mtESRs also increase with exposure to E2 [55-57]. However, the fate of mtESRs and their role during selective mitochondrial autophagy (mitophagy) is not yet clear. The subcellular localization of GPER1 might be related to different tumor characteristics. GPER1, being localized in the cytoplasm in breast cancer, is correlated with non-ductal carcinoma with better tissue differentiation and lower tumor grade, which is more common in luminal A and B breast cancers [58]. In contrast, when GPER1 is localized in the nucleus, tumors are poorly differentiated or there is triple-negative breast cancer (TNBC), and the prognosis is even worse [58]. Both ESR1 and GPER1 are distributed in lysosomes in an E2-dependent manner, revealing the existence of a lysosome-dependent degradation pathway

for these receptors [59,60]. Whether ESR1 and GPER1 distributed in lysosomes participate in autophagy upon fusion with autophagosomes, and their corresponding pathophysiological effects, is unclear.

In general, the intracellular translocation of these receptors remains controversial and appears to be frequently determined by estrogen, though they are clearly involved in the association between estrogen and autophagy (Figure 2).

TFs involved

As shown in Figure 3 and Table 3, all of the receptors that might mediate the regulation of estrogen on core autophagy proteins via TFs. These TFs are involved in the regulation of all autophagic processes, including autophagy induction, vesicle nucleation and elongation, and retrieval.

CEBPB

CEBPB links autophagy to the biological clock and maintains nutrient homeostasis by stimulating autophagic gene expression [61]. The increase of nuclear CEBPB protein is dependent on MAPK14. The phosphorylation of MAPK14 is in turn dependent on PLA2G1B (phospholipase A2 group IB), PRKC/ PKC activation, and oxidative stress [62]. Expression levels of ESRs and PRKCA are inversely related [63]. CREBBP/CREB

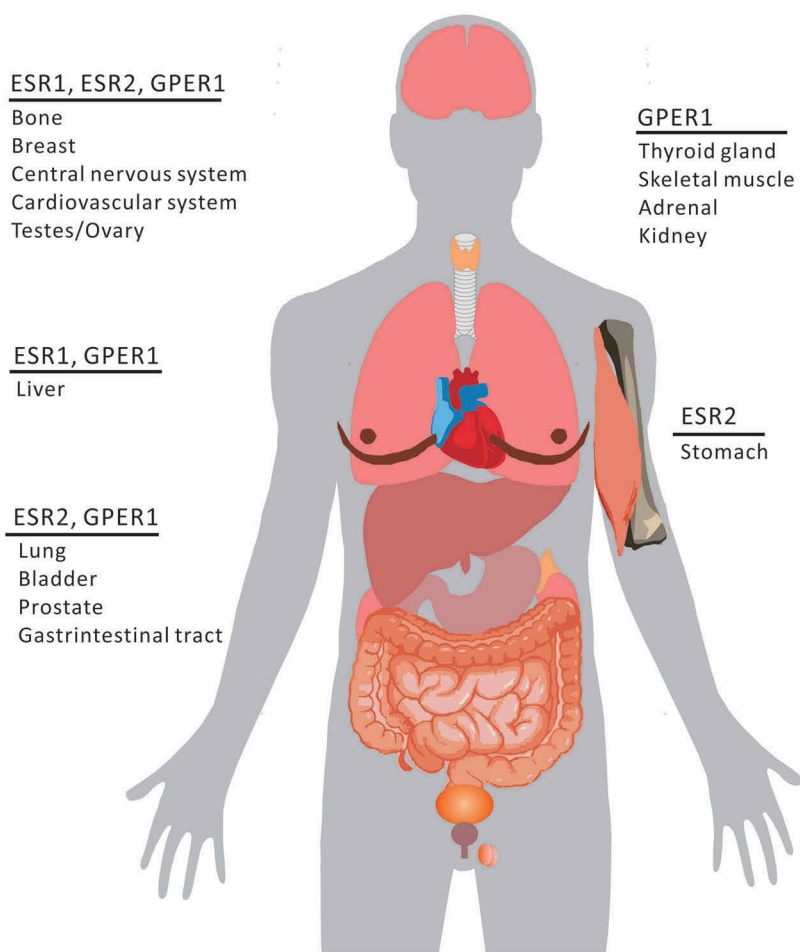


Figure 1. Schematic view of ESR distribution in organs.

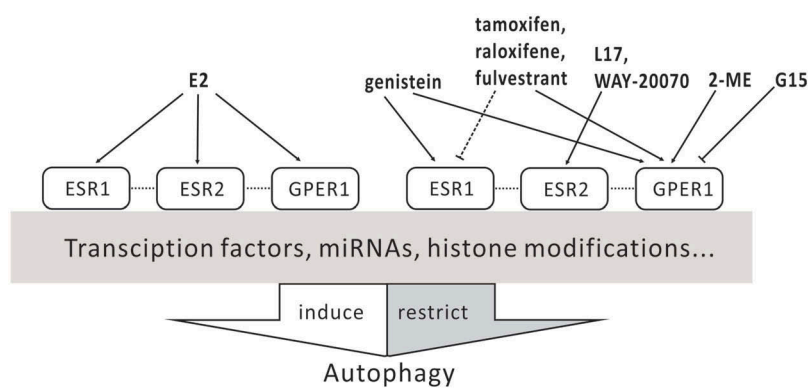


Figure 2. Action of ESR ligands on autophagy. Dashed lines indicate tissue type-dependent activation or inhibition; dotted lines indicate crosstalk between receptors.

(CREB binding protein) controls CEBPB expression by interacting with 2 sites near the TATA box [64]. Recent research has shown that the breast tumor cell-activated phosphoinositide 3-kinase-AKT1 signaling pathway induces cytoplasmic GPER1 translocation of carcinoma-associated fibroblasts in an XPO1 (exportin 1)-dependent pattern, and leads to the activation of the estrogen-GPER1-cAMP-PRKA/PKA-CREB signaling axis that triggers the aerobic glycolysis switch in carcinoma-associated fibroblasts [65].

FOXO3

The *Atg14* gene is a direct target of FOXOs, and FOXOs positively regulate *Atg14* gene expression [66]. In skeletal muscle, both the ubiquitin-proteasomal and autophagic-lysosomal pathways, the 2 major systems of protein breakdown, are under control of FOXO3. BNIP3 appears to mediate the effect of FOXO3 on autophagy [67]. The activation of FOXO3 by PRKAA2 (protein kinase AMP-associated catalytic subunit alpha 2) induces the expression of MAP1LC3-II, ATG8, BECN1, and BNIP3 in

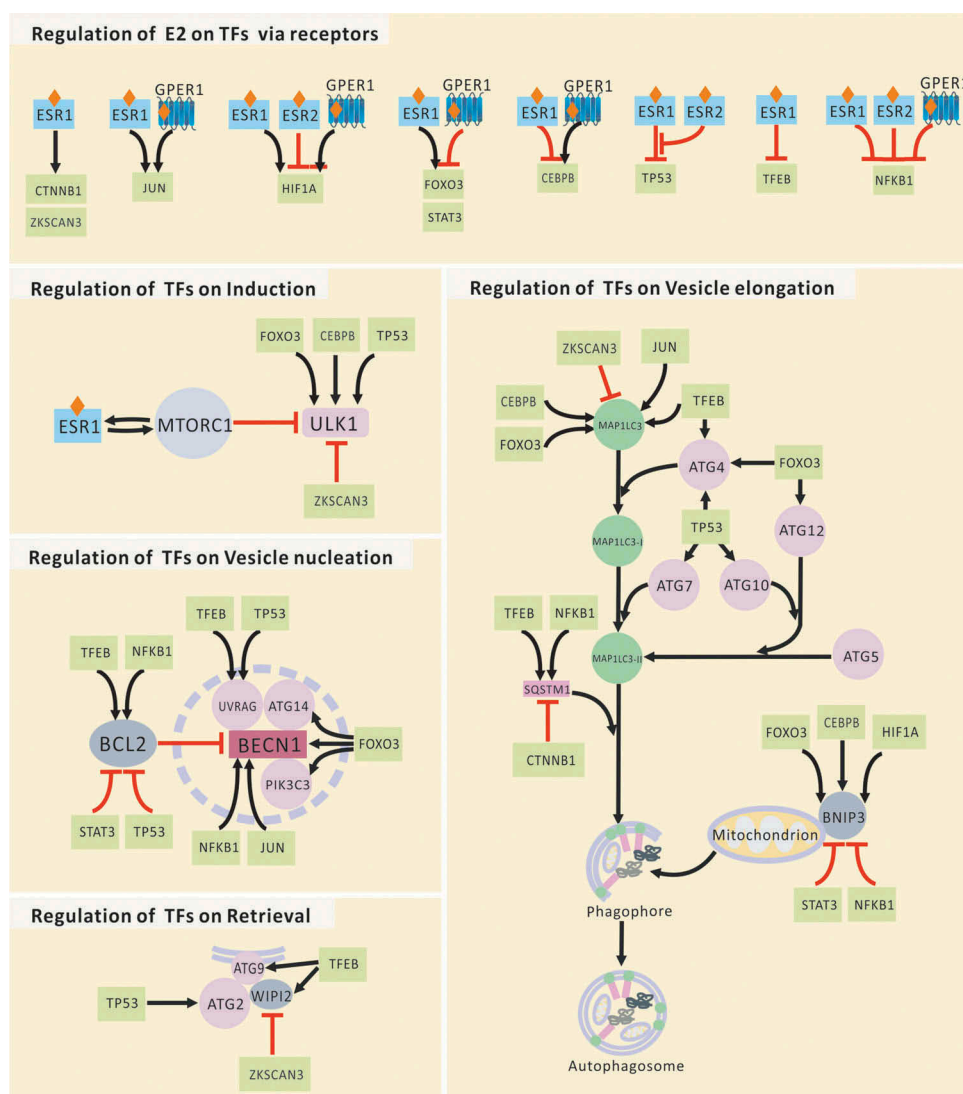


Figure 3. Regulation of E2 on core autophagy proteins via TFs. JUN, subunit of AP-1; TP53, tumor protein p53.

mouse skeletal muscle [67,68]. Constitutive activation of FOXO3 induces MAP1LC3-II and BNIP3 expression and leads to reversible heart atrophy in active *Foxo3* transgene mice by constitutive tetracycline regulation [69]. E2 strongly enhances the effects of FOXO3 via ESR1 [70]. In addition, estrogen mediates the inactivation of FOXO3 by GPER1 [71]. FOXO3 proteins in human and mouse have the same AKT1 phosphorylation sites and similar regulatory properties [71].

TP53

TP53 is present in both the nucleus and cytoplasm, and its regulation in autophagy depends on its subcellular localization. The target autophagy genes of TP53 include *ULK1*, *ULK2*, *ATG2B*, *ATG4A*, *ATG4C*, *ATG7*, *ATG10*, *VMP1* (vacuole membrane protein 1), and *UVRAG* [72]. Initially, ESR1 was reported to be a suppressor of TP53 that can recruit nuclear receptor corepressors (NCOR1 and NCOR2) and HDAC1 (histone deacetylase 1) [73]. However, recent research has shown that ESR2 can attenuate the crosstalk between ESR1 and TP53 by reducing the recruitment of both NCOR1 and NCOR2 by ESR1. ESR2

antagonizes ESR1-TP53-mediated transcriptional regulation by reducing ESR1-TP53 binding via physical interaction [74]. In addition, the *MDM2* proto-oncogene, which is both a TP53 target gene and a negative feedback regulator of TP53, has bidirectional effects on ESR1 by direct interaction [75].

ZKSCAN3

ZKSCAN3 and TFEB regulate lysosomal biogenesis and autophagy in an opposing manner [76]. ZKSCAN3 is a repressor of several autophagy-related genes, including *MAP1LC3* and *WIPI2* (human homologs of yeast Atg18). *WIPI2* has a positive role in the cycling of ATG9. ZKSCAN3 and TFEB are regulated in an opposing manner [76]. For instance, PRKC leads to reduced phosphorylation, nuclear translocation, and activation of TFEB by inactivating GSK3B with a MTORC1-independent mechanism; however, PRKC activates MAPK8/JUN NH₂-terminal kinase (mitogen-activated protein kinase 8) and MAPK14, which phosphorylate ZKSCAN3, leading to its translocation and inactivation. ZKSCAN3 phosphorylation at Thr153 by MAPK9 or MAPK14 is required for ZKSCAN3 cytoplasmic translocation

Table 3. Autophagy proteins regulated by E2 via TFs.

Autophagy proteins	TFs	Effect of TFs on Autophagy	Tissue or Cell Line	Ref	Receptor	Effect of E2 on TFs	Tissue or Cell Line	Ref
Regulation of autophagy induction								
ULK1	CEBPB	Enhance	Mouse liver	[61]	ESR1	PRKCA enhances CEBPB by MAPK14 PRKCA and ESR1 are inversely related E2 activates GPER1-cAMP-PRKA-CREB CREB controls CEBPB by TATA box E2 enhances FOXO3 E2 inactivates FOXO3	HL-60 Breast cancer MCF-7 Rat liver MCF-7 MCF-7 MCF-7 MCF-7	[62] [63] [144] [65] [70] [71] [73] [74]
	FOXO3	Enhance	Mouse skeletal muscle	[68]	GPER1	ESR1 represses TP53-mediated transcription ESR1 antagonizes ESR1-TP53-mediated transcriptional regulation		[63] [77]
	TP53	Enhance	Human HCT116 cells	[72]	ESR1	ESR1 is inversely related to PRKC PRKC inactivates ZKSCAN3 by MAPK14	Breast cancer Mouse	[63] [77]
	ZKSCAN3	Suppress	Human HeLa cells	[145]	ESR1			
Vesicle nucleation								
ATG14	FOXO3	Enhance	Mouse liver	[66]	ESR1	E2 enhances FOXO3	MCF-7	[70]
BCL2	NFKB1	Enhance	Rat hippocampal neurons	[78]	GPER1 ESR1 ESR2	Estrogen inactivates FOXO3 ESR1 inhibits NFKB1 activity ESR2 inhibits NFKB1 activity	MCF-7 MCF-7 MCF-7, HeLa, HEK293, HepG2 HeLa, U937, HCASMC, COV434, MDA-MB-231	[71] [82] [82] [83] [88,89]
	TFEB	Enhance	Mouse liver	[87]	GPER1 ESR1 ESR2	Activation of GPER1 decreases the transcriptional activities of NFKB1 MTORC1 inhibits TFEB (p)-MTORC1 expression is mainly related to ER	HeLa MCF-7 MCF-7	[91] [86] [83]
	STAT3	Suppress	B cell lymphoma	[84]	ESR1	ESR1 increases STAT3 transactivation	MCF-7	[73]
	TP53 (TP63, TP73)	Suppress	Human HCT116 cells	[72,146]	GPER1	GPER1 decreases STAT3	MDA-MB-231	[74]
BECN1	FOXO3	Enhance	Mouse skeletal muscle	[68,147]	ESR1 ESR2	ESR1 represses TP53-mediated transcription ESR2 antagonizes ESR1-TP53-mediated transcriptional regulation	MCF-7 MCF-7	[70] [71]
	JUN	Enhance	Human cancer cells CNE2 and Hep3B	[92]	GPER1 ESR1	E2 inactivates FOXO3 E2 induces the MAPK1/3, JUN, and MAPK14-dependent mitochondrial apoptotic pathway	Mouse spermatocyte-derived cell GC-2 MCF-7	[94] [95]
	NFKB1	Enhance	Human T-cells	[79]	GPER1 ESR1 ESR2	ESR1 inhibits NFKB1 ESR2 inhibits NFKB1	MCF-7, HeLa, HEK293, HepG2 HeLa, U937, HCASMC, COV434, MDA-MB-231	[82] [82] [83]
PIK3C3	FOXO3	Enhance	Mouse skeletal muscle	[67]	GPER1 ESR1	GPER1 decreases NFKB1 E2 enhances FOXO3	MCF-7	[70]
UVRAG	TP53	Enhance	Human HCT116 cells	[72]	GPER1 ESR1 ESR2	E2 inactivates FOXO3 ESR1 represses TP53-mediated transcription ESR2 antagonizes ESR1-TP53-mediated transcriptional regulation	MCF-7 MCF-7 MCF-7	[71] [73] [74]
	TFEB	Enhance	Mouse liver	[87]	ESR1	MTORC1 inhibits TFEB (p)-MTORC1 expression is mainly related to ER	HeLa MCF-7	[88,89] [91]
Vesicle elongation								
ATG4	FOXO3	Enhance	Mouse skeletal muscle	[147]	ESR1 GPER1	E2 enhances FOXO3 E2 inactivates FOXO3	MCF-7 MCF-7	[70] [71]
	TFEB	Enhance	Mouse liver	[87]	ESR1	MTORC1 inhibits TFEB (p)-MTORC1 expression is mainly related to ER	HeLa MCF-7	[88,89] [91]
	TP53	Enhance	Human HCT116 cells	[72]	ESR1 ESR2	ESR1 represses TP53-mediated transcription ESR2 antagonizes ESR1-TP53-mediated transcriptional regulation	MCF-7 MCF-7	[73] [74]
ATG7	TP53	Enhance	Human HCT116 cells	[72]	ESR1 ESR2	ESR1 represses TP53-mediated transcription ESR2 antagonizes ESR1-TP53-mediated transcriptional regulation	MCF-7 MCF-7	[73] [74]
ATG10	TP53	Enhance	Human HCT116 cells	[72]	ESR1 ESR2	ESR1 represses TP53-mediated transcription ESR2 antagonizes ESR1-TP53-mediated transcriptional regulation	MCF-7 MCF-7	[73] [74]
ATG12	FOXO3	Enhance	Mouse skeletal muscle	[147]	ESR1 GPER1	ESR2 enhances FOXO3 E2 inactivates FOXO3	MCF-7 MCF-7	[70] [71]

(Continued)

Table 3. (Continued).

Autophagy proteins	TFs	Effect of TFs on Autophagy	Tissue or Cell Line	Ref	Receptor	Effect of E2 on TFs	Tissue or Cell Line	Ref
BNIP3	CEBPB	Enhance	Mouse liver	[61]	ESR1	PRKCA enhances CEBPB by MAPK14 PRKCA and ESR1 are inversely related E2 activates GPER1-cAMP-PRKA-CREB CREB controls CEBPB by TATA box	HL-60 Breast cancer MCF-7	[62] [63] [144]
	FOXO3	Enhance	Mouse skeletal and heart muscle	[67,69,147]	GPER1	E2 enhances FOXO3 by ESR1 Estrogen mediates inactivation of FOXO3 by GPER1	Rat liver MCF-7 MCF-7	[65] [70] [71]
MAP1LC3	NFKB1	Suppress	Human pancreatic cancer cells	[80]	ESR1 ESR2	ESR1 inhibits NFKB1 ESR2 inhibits NFKB1	MCF-7 MDA-MB-231	[82] [83]
	HIF1A	Enhance	Human HEK293 cells	[96]	GPER1	GPER1 decreases NFKB1 ESR1 directly upregulates HIF1A ESR2 inhibits activity of HIF1A	HEK293 HUVEC	[99] [97]
MAP1LC3	STAT3	Suppress	Human U87 cells	[85]	ESR1	GPER1 upregulates HIF1A GPER1 inhibits HIF1A ESR1 increases STAT3 transactivation GPER1 decreases STAT3	MDA-MB-231	[83] [83]
	CEBPB	Enhance	Mouse liver	[61]	ESR1	PRKCA enhance CEBPB by MAPK14 PRKCA and ESR1 is inversely related E2 activates GPER1-cAMP-PRKA-CREB CREB controls CEBPB by TATA box	MDA-MB-231 HL-60 Breast cancer MCF-7	[86] [62] [63] [144]
SQSTM1	FOXO3	Enhance	Mouse skeletal and heart muscle	[67-69]	ESR1	E2 enhances FOXO3	Rat liver MCF-7	[65] [70]
	TFEB	Enhance	Mouse liver	[87]	GPER1	E2 inactivates FOXO3 MTORC1 inhibits TFEB	MCF-7 HeLa	[71] [88,89]
SQSTM1	JUN	Enhance	Human nasopharyngeal carcinoma cells	[93]	ESR1	(p)-MTORC1 expression is mainly related to ER E2 induces the MAPK1/3, JUN, and MAPK14-dependent mitochondrial apoptotic pathway	MCF-7	[91]
	ZKSCAN3	Suppress	Human HeLa cells	[145]	GPER1	ESR1 is inversely related to PRKC PRKC inactivates ZKSCAN3 by MAPK14	GC-2 MCF-7 Breast cancer	[95] [63] [77]
SQSTM1	CTNMB1/β-catenin	Suppress	Human HT29 cells	[136]	ESR1	There is functional interaction between CTNMB1 and ESR1	Mouse MCF-7, HCT116 cells, SW480,	[148]
	NFKB1	Enhance	Human IMR90 and A549 cells	[81]	ESR1 ESR2	ESR1 inhibits NFKB1 ESR2 inhibits NFKB1	<i>Drosophila</i> eye MCF-7, HeLa, HEK293, HepG2 HeLa, U937, HCASMC, COV434.	[82] [82] [83]
SQSTM1	TFEB	Enhance	Mouse liver	[87]	GPER1 ESR1	GPER1 decreases activity of NFKB1 MTORC1 inhibits TFEB (p)-MTORC1 expression is mainly related to ER	MDA-MB-231 HeLa MCF-7	[88,89] [91]
	ATG2	Enhance	Human HCT116 cells	[72]	ESR1	ESR1 represses TP53-mediated transcription ESR2 antagonizes ESR1-TP53-mediated transcriptional regulation	MCF-7	[73]
ATG9	TFEB	Enhance	Mouse liver	[87]	ESR1	MTORC1 inhibits TFEB (p)-MTORC1 expression is mainly related to ER	MCF-7 HeLa	[74] [88,89]
WIPI2	TFEB	Enhance	Mouse liver	[87]	ESR1	MTORC1 inhibits TFEB (p)-MTORC1 expression is mainly related to ER	MCF-7 HeLa	[91] [88,89]
Retrieval	ZKSCAN3	Suppress	Human HeLa cells	[145]	ESR1	ESR1 is inversely related to PRKC PRKC inactivates ZKSCAN3 by MAPK14	MCF-7 Breast cancer Mouse	[63] [77]

Abbreviations: A549, human lung adenocarcinoma cells; CEBPB, CCAAT enhancer binding protein beta; COV434, Human ovarian granulosa tumor cells; CREBBP, CREB binding protein; FOXO3, forkhead box O3; GC-2, a mouse spermatocyte cell line; GCT, granulosa cell tumors; HCASMC, human colon carcinoma cells; HEK293, human embryonic kidney 293 cells; HepG2, a human liver cancer cell line; HIF-1A, hypoxia inducible factor 1 subunit alpha; HL-60, human promyelocytic cells; HT29, human colorectal carcinoma cells; HUVEC, human umbilical vein endothelial cells; IMR90, normal human lung fibroblasts; MAPK9/JNK2, mitogen-activated protein kinase 9; MAPK14/p38, mitogen-activated protein kinase 14; MTORC1, mechanistic target of rapamycin kinase complex 1; NFKB1/NF-κB, nuclear factor kappa B subunit 1; PRKC/PKC, protein kinase C; SMCs, human coronary artery smooth muscle cells; STAT3, signal transducer and activator of transcription 3; SW480, a p53 double-mutant cell line; TFEB, transcription factor EB; U87, human primary glioblastoma cells; U937, human macrophage cells; WIPI2, WD repeat domain, phosphoinositide interacting 2 (a homolog of yeast Atg18); ZKSCAN3, zinc finger with KRAB and SCAN domains 3.

and promotes lysosome biogenesis [77]. The expression levels of ESRs and PRKC are inversely related [63].

NFKB1

NFKB1 upregulates the expression of both BCL2 and BECN1 [78,79]. However, NFKB1 silences *Bnip3* gene transcription by competing with E2F1 (E2F transcription factor 1) for binding to the *Bnip3* promoter [80]. The ubiquitin-binding protein SQSTM1 is required for RAS-induced NFKB1 activation in human tumors [81]. ESRs mediate the inhibition of NFKB1 activity at several levels [82]. Activation of GPER1 by the specific agonist G-1 leads to significant inhibition of the phosphorylation, nuclear localization, and transcriptional activities of NFKB1 [83]. Both IL6 (interleukin 6) and VEGFA (vascular endothelial growth factor A) are inhibited accordingly [83].

STAT3

Functional crosstalk between BCL2, RAC1, and activated STAT3 exists and promotes a permissive redox milieu for cell survival [84]. STAT3 signaling events occur downstream of MMP14/MT1-MMP (matrix metalloproteinase 14). Gene silencing of *MMP14* and *STAT3* abrogates both STAT3 phosphorylation and BNIP3 expression [85]. Activation of GPER1 inhibits HIF1A and STAT3 signals in TNBC cells [83]. Upon LEP (leptin) treatment, ESR1 increases the transactivation and target gene expression of *STAT3* by direct binding. In addition, the enhancement of LEP-mediated activation of STAT3 is independent of ESR1 ligands [86].

TFEB

As a master regulator of lysosomal biogenesis, TFEB promotes the transcription of several lysosomal genes by directly binding to their promoters. Autophagy-related genes *Map1lc3*, *Sqstm1*, and *Atg9* are also upregulated by TFEB [76,87]. Under well-nourished conditions, MTORC1 inhibits TFEB by its post-translational modification of phosphorylation. In contrast, under starvation conditions, lysosomal disruption and pharmacological inhibition of MTORC1 activates TFEB [88,89]. Upon estrogen stimulation, ESR1 binds to RPTOR (regulatory associated protein of MTOR complex 1) [90]. The MTOR kinase can phosphorylate Ser104/106 of ESR1 and promote the transcription of ER target genes [90,91].

JUN

JUN is involved in the regulation of both *BECN1* and *MAP1LC3* transcription [92,93]. In ESR- or GPER1-positive GC-2 cells, E2 induces the MAPK1/3, JUN, and MAPK14-dependent mitochondrial apoptotic pathway [94]. In ESR-negative GPER1 or CYP19A1/aromatase-positive SKBR3 cells, tamoxifen acts as a GPER1 agonist and recruits the FOS-JUN complex to AP-1-responsive elements that are located within the *CYP19A1/aromatase* promoter [95].

HIF1A

The expression of BNIP3, BECN1, and ATG5 required for selective mitochondrial autophagy depends on HIF1A [96]. ESR2 inhibits HIF1A activity by decreasing the binding of HIF1A to the promoter of the *VEGFA* gene, which attenuates *VEGFA* transcription induced by hypoxia [97]. Activation of GPER1 by both E2 and G-1 increases VEGFA via upregulation of HIF1A via the GPER1-EGFR-MAPK1-FOS signaling pathway [98]. The *HIF1A* gene itself contains an estrogen response element, and its expression is directly regulated by ESR1 [99].

MiRNAs involved

In addition to the transcription factors listed above, E2 can regulate the expression of some autophagy-related proteins by suppressing or stimulating miRNA expression.

MIR214

Estrogen treatment downregulates the *MIR214* family [100]. *MIR214* directly targets mitochondrial uncoupling proteins (UCPs) [101]. UCPs are members of the larger family of mitochondrial anion carrier proteins (MACPs), and UCP2 is involved in uncoupling oxidative phosphorylation and facilitating energy dissipation as heat [102]. UCP2 overexpression not only decreases nonspecific destructive intracellular reactive oxygen species (ROS), but also induces autophagy and endocrine resistance by the phosphorylation of AKT1 and MTOR [21].

MIR21

Regulation of *MIR21* transcription by E2 varies depending on experimental conditions, cell line, and control genes used in the analysis. In HepG2 human hepatoma cells, E2 inhibits *MIR21* expression via ESR1 [103]. In MCF-7 cells, *MIR21* is upregulated by the ESR2 selective ligand diarylpropionitrile (DPN) [104]. In systemic lupus erythematosus, estrogen-regulated STAT1 activates and promotes TLR8 expression via *MIR21* [105]. Both the expression and functional loss of STAT1 are related to the development of mammary adenocarcinomas [106]. STAT1 suppresses ATG12 and BECN1 [107]. *MIR21* also targets *BCL2* mRNA in rat and human beta cells [108].

Long noncoding RNA HOTAIR

E2-GPER1 induces HOTAIR through the suppression of *MIR148A* [109]. In hepatocellular carcinoma, HOTAIR activates autophagy by upregulating ATG3 and ATG7 [110]. In endometrial cancer cells, HOTAIR regulates autophagy and contributes to cisplatin-induced resistance [110]. In addition, BECN1, multidrug resistance (MDR), and ABCB1 (ATP binding cassette subfamily B member 1) are all regulated by HOTAIR [111].

MIRLET7G

In MCF-7 cells, E2 suppresses the expression of *MIRLET7G* in a time- and MAP2K/MEK-MAPK-dependent manner [104]. *Mirlet7g* regulates autophagy in mouse granulosa cells by targeting IGF1R (insulin like growth factor 1 receptor) and downregulates AKT-MTOR [112]. Direct regulation of *MIRLET7G* by E2 via ESR1 has been reported [104,113].

In addition, *MIR30D* increases with hormone deprivation in MCF-7 cells. *MIR30D* regulates autophagy genes including *BECN1*, *ATG5*, *ATG12*, and *ATG2* [76]. However, dextran-coated charcoal stripping to treat serum in the original report could eliminate many hormones from the serum, which leaves the effect of estrogens on *MIR30D* unclear [104].

Histone modifications involved

Histones are the chief protein components of chromatin. Various posttranslational modifications on histones are mainly produced by histone-modifying enzyme complexes in a dynamic manner [76]. These post-translational modifications, including acetylation and methylation, can influence the overall chromatin structure and have clear functional consequences [76]. Acetylation is a modulator of the ligand-dependent gene regulatory activity of ESRs [114]. Estrogen can interfere with the nuclear regulation of autophagy by regulating proteins in histone modifier complexes. Such regulation of histone modification by estrogen is likely to play a role in estrogen-dependent signaling pathways in a variety of estrogen target tissues in both normal and pathological states.

HDACs

In skeletal muscle, HDAC1 and HDAC2 regulate autophagy by inducing autophagic gene expression and autophagosome formation. Loss of these HDACs leads to the accumulation of toxic autophagic intermediates in the myofibers of mice [115]. In cardiomyocytes, HDAC inhibitors suppress autophagy. HDAC1 and HDAC2 are required for the autophagic response, and the overexpression of HDAC2 alone increases autophagy [116]. E2 or dipropyl nitrile and β -LGND2 (ESR2 agonists) comparably suppress HDAC2 production, phosphorylation, and the resulting prohypertrophic mRNA expression induced by angiotensin II [117]. The expression of ESR1 can be reactivated by destabilization or reduction of the corepressor complex, formed by MTA1 (metastasis associated 1), IFI16 (interferon gamma inducible protein 16), and HDACs, on the *ESR1* promoter [118].

HATs

Several HATs have ubiquitination-linked enzymatic activity. As a HAT, KAT2B (lysine acetyltransferase 2B) acetylates both histone and non-histone proteins and promotes autophagy by inhibiting the AKT1-MTOR signaling pathway [119]. DNA binding and transactivation activities of ESR1 are enhanced by acetylation at lysines 266 and 268 by EP300, which can be reversed by native deacetylases such as SIRT1 (sirtuin 1) [114]. KAT7, another HAT, promotes the

degradation of ESR1 through ubiquitination in a proteasome-dependent manner. KAT7 knockdown promotes ESR1 expression [120]. *In vitro*, E2 inhibits the E3 ubiquitin ligase activity of KAT7 on ESR1 [120].

Post-translational status of histone H3

ESR1 silences TP53-activated transcription by directing the assembly of SUV39H1/histone-lysine N-methyltransferase (suppressor of variegation 3–9 homolog 1) and histone H3 lys9 trimethylation (H3K9me3) at estrogen-repressed genes [74]. ESR2 downregulates SUV39H1/H2 and releases the ESR1-induced transcriptional block by abrogating the repressive heterochromatin conformation of H3K9me3 [74]. Furthermore, ESR2 stimulates the accumulation of trimethylated histone H3 lys4 (H3K4me3) and POLR2/RNA polymerase II on ESR1-repressed genes, which then induces the transcription of the repressed genes involved in TP53-based tumor suppression [74].

Balancing acetylation at H4K16

Dynamic histone modifications play a pivotal role in cell-regulatory events [121]. The acetylation of histone H4 at lysine 16 (H4K16) can influence higher-order chromatin structure, which plays an important role in transcription [76]. Acetylated H4K16 is a primary histone substrate of native deacetylase SIRT1 [76]. In addition, SIRT1 has several non-histone targets, including ATG5, ATG7, MAP1LC3, FOXOs, E2F1, TP73, PPARGC1A (PPARG coactivator 1 alpha), NFKB1, and TP53, all of which are involved in the regulation of autophagy [76]. In oxygen-glucose deprived neurons, estrogen promotes PRKAA2 activation through ESR1 [122]. Estrogen increases SIRT1 expression and activation [123]. In *sirt1*-knockout neurons, estrogen-induced PRKAA2 activation disappears, which prevents the neuroprotection of estrogen [122].

Concluding remarks and future perspectives

The modulation of estrogenic effects relating to autophagy could contribute to the development of potential strategies to treat numerous human diseases (Table 1, 2). To clarify the estrogenic function of autophagy between normal physiological and pathological conditions, including tumors, there have been several studies on the estrogenic regulation of autophagy in ESR-positive breast cancers [124–128]. Arguably, much of what is known has come from this area, reflecting the fact that breast cancer is the most common cancer in women, and 70% are treated with drugs that target ESR action. The roles of autophagy in cancer have been confounded by numerous laboratory studies showing that both the enhancement and inhibition of autophagy seem to improve cancer treatment outcomes [129,130]. A similar situation is also seen in other diseases, such as clinically relevant murine models of ischemic stroke [131]. Moreover, several clinical trials are already in place combining both autophagy inducers (rapamycin, everolimus) and autophagy inhibitors (chloroquine, 3-methyladenine) with endocrine therapies [132,133]. Not all patients experience benefit, which further confuses and complicates our understanding of the main effects of autophagy in breast cancer.

Based on previously reported models [134,135], a hypothetical model (Figure 4) is presented here to help understand how the estrogenic regulation of autophagy affects cell fate. Autophagy is vital for intracellular quality control and homeostasis. Therefore, careful regulation of autophagy is very important because either excessive or insufficient autophagy can be destructive to cells [136]. It has been proven that estrogen can delay the apoptosis of breast cancer cells via ESRs [137]. For the treatment of estrogen-related cancer cells, estrogen needs to be antagonized, which might be because of the protective effect of estrogen on cell balance via regulation of autophagy as shown here.

As shown in this review, upon stimulation with estrogen, most autophagy-related genes are under the regulation of

more than one TF, and most TFs are under the regulation of 2 or 3 receptors of estrogen. In addition, estrogen can interfere with autophagy via nuclear regulation by histone modifications. Thus, there will always be opposing functional actions, which might occur between different receptors, receptors on TFs, TFs on autophagy genes, or even histone modifications on transcription. In addition to those mentioned above, such as ESR1 and ESR2 [74], TFEB and ZKSCAN3 [76], and TP53 and MDM2 [75], need to be further explored in the future. The huge signaling network downstream of estrogen can promote autophagy and reduce overstimulated autophagy at the same time, which allows autophagy to be regulated by estrogen in a restricted range. Estrogen's mechanism of balancing autophagy is obviously more

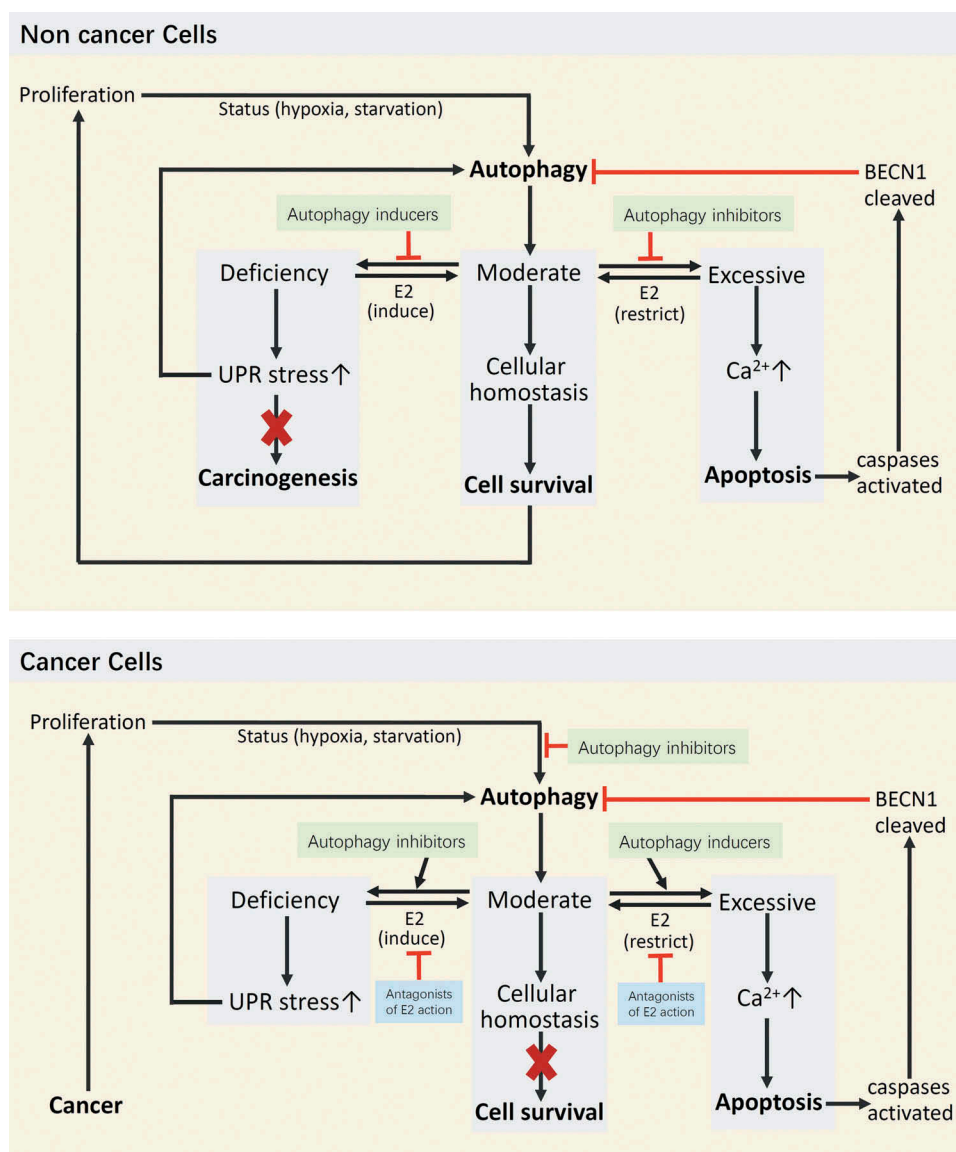


Figure 4. Model of how estrogenic regulation of autophagy affects cell fate. E2 helps maintain moderate autophagy and cellular homeostasis. Both deficient and excessive autophagy are abnormal. Deficient autophagy can lead to unfolded protein response (UPR) stress, which may reestablish homeostasis through the induction of autophagy. However, the UPR can further lead to carcinogenesis. The proliferation of cancer may induce a status of hypoxia and starvation, both of which can induce autophagy. Here, if a new balance is achieved, cells still have a chance to survive, which is bad for the treatment of cancer. Only when excessive autophagy releases enough calcium from the endoplasmic reticulum to the cytoplasm can apoptosis be triggered. Furthermore, activated caspases will cleave BECN1 and turn off autophagy. Autophagy inducers may prevent carcinogenesis when autophagy in non-cancer cells is deficient, or they may promote excessive autophagy in cancer cells and lead to apoptosis. Autophagy inhibitors seem to block the survival of cancer cells during starvation; however, the inhibition of autophagy cannot persist. The persistent stimulation of UPR stress also promotes autophagy.

complicated than this. For instance, estrogen in the blood can cause negative feedback to reduce levels of hormones in the body. In addition to estrogen, other hormones, such as androgens, also play a role in autophagy [138]. Some estrogen-regulated TFs and miRNAs can target ESRs, thereby forming another negative feedback loop to fine-tune estrogen-mediated cellular responses, including autophagy [104,139].

Because autophagy is tightly controlled by estrogen (Figure 5), it would make sense to determine the fluctuation range of autophagy corresponding to estrogenic regulation under various physiological and pathological conditions. This leads to a major problem for autophagy research – autophagy is a dynamic process that is hard to assess in living organisms (especially humans) by existing methods *in vitro* [129]. Considering the correlation between autophagy and cell substance balance, if we indirectly characterize autophagy by assessing the material and energy balance in cells instead of focusing solely on the process of autophagy itself, it will be easier to choose between autophagy inducers and inhibitors in

the future. Of course, the optimal choice of markers remains to be determined. However, it is foreseeable that developing dynamic markers of cellular balance will be conducive to studying autophagy manipulation and clinical therapeutics.

So far, studies of estrogen function on autophagy have mainly focused on breast tissue, however there are still many issues that need to be clarified. Take for example the TFs: although the effects of estrogen on TFs have mostly focused on breast cancer cells, the effects of TFs on autophagy are rarely seen in breast cancer cells (Table 3). In other tissues such as brain and bone, the role of autophagy has also been studied for its importance [140,141]. With regard to estrogenic regulation of autophagy in these tissues, there are also some related studies (Tables 1 and 2). Except for the issues mentioned above for breast cancer, more issues need to be solved for the diseases of these tissues. Take for example gliomas: there have been no clinical studies combining both autophagy inducers and autophagy inhibitors with ESR ligands, though they all have independent clinical trials [142,143]. The specificity of drug distribution in these tissues also need to be addressed [143].

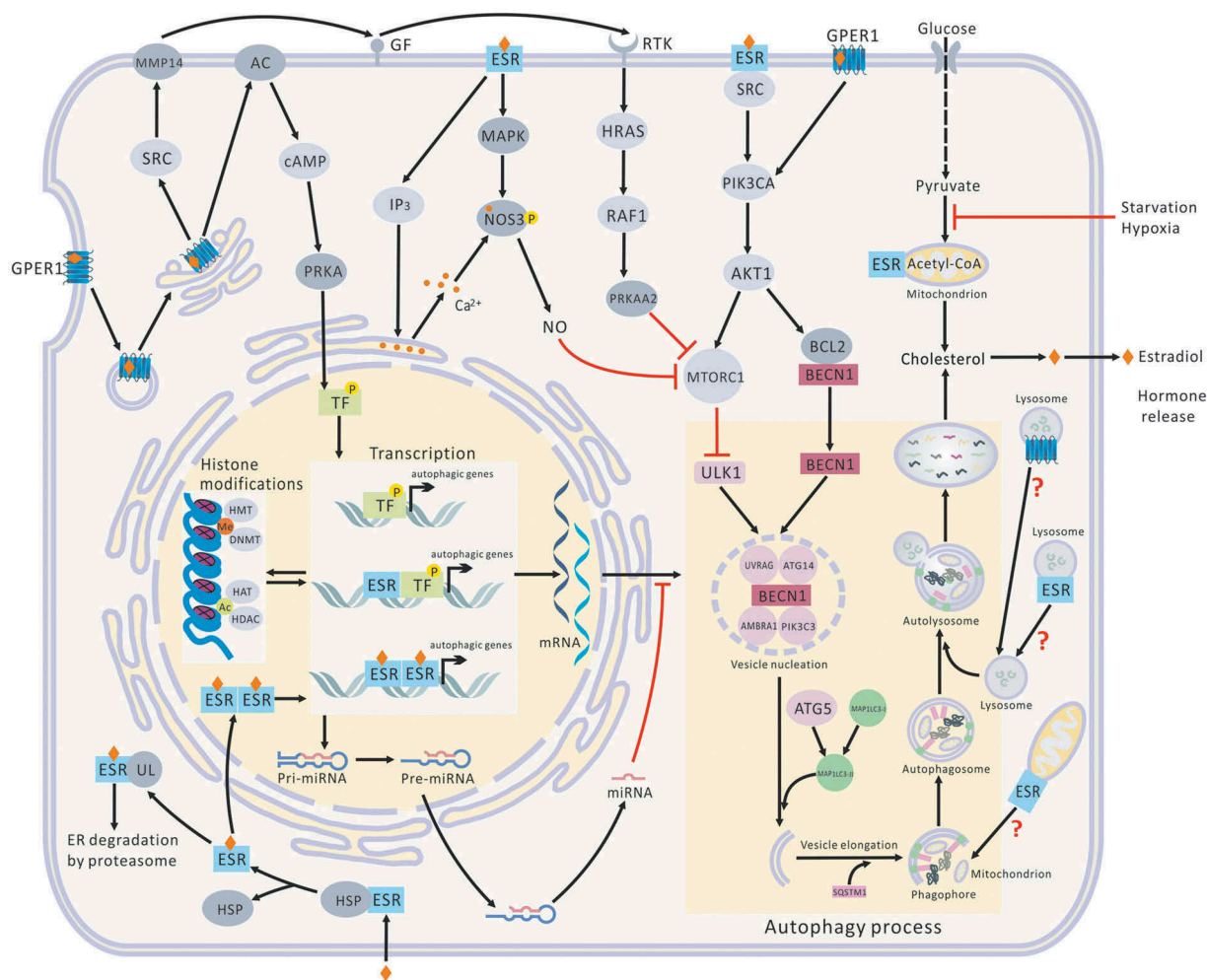


Figure 5. Association between estrogen and autophagy. E2 balances the expression of core autophagy proteins through diverse transcription factors, miRNAs, and histone modifications via signaling pathways downstream of the receptors. The autophagic proteins controlled by E2 are involved in the entire process of autophagy. Lipids released by autophagy are the major source of cholesterol, the precursor of estrogen biosynthesis. E2 in the blood causes a negative feedback to reduce circulating levels of hormones. E2 activates NOS3 and initiates the synthesis of NO via membrane ESRs. NO induces autophagy by suppressing MTOR expression. In addition, some estrogen-regulated TFs and miRNAs can target ESRs. As the major mechanism for ESR degradation in eukaryotic cells, ESRs dissociate from complexes with HSPs upon binding of E2, are ubiquitinated by ubiquitin ligases (ULs), and are targeted for degradation. The fate of mtESRs and lysosomal ESR1 and GPER1 during autophagy is not yet clear. Ac, acetylation; GF, growth factor; HSPs, heat-shock proteins; HRAS, HRas proto-oncogene, GTPase; Me, methylation; MAPK, MAPK proto-oncogene, serine/threonine kinase; RTKs, receptor tyrosine kinases; SRC, SRC proto-oncogene, non-receptor tyrosine kinase; ULs, ubiquitin ligases.

In addition, although GPER1 is more widely distributed in human tissues than ESRs and is expressed in TNBC cells and associated with drug resistance of ESR antagonists in endocrine therapy, GPER1 antagonists are very few and have not been developed to work in humans [5]. Whether ESR1 and GPER1 distributed in lysosomes participate in autophagy upon fusion with autophagosomes, and the corresponding pathophysiological effects, are not clear. High levels of some autophagy biomarkers such as MAP1LC3, or autophagy morphologies such as autophagosomes triggered by the induction or accumulation caused by autophagy inhibition, need stricter distinction in future research. These directions might allow us to better understand the multiple associations between estrogen and autophagy, the pathogenic mechanisms of many estrogen-related diseases, and to design novel and efficacious therapeutics.

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