Degradation of Endocytosed Gap Junctions by Autophagosomal and Endo-/lysosomal Pathways: A Perspective

Matthias M. Falk · John T. Fong · Rachael M. Kells ·
Michael C. O'Laughlin · Tia J. Kowal ·
Anastasia F. Thévenin

Abstract Gap junctions (GJs) are composed of tens to many thousands of double-membrane spanning GJ channels that cluster together to form densely packed channel arrays (termed GJ plaques) in apposing plasma membranes of neighboring cells. In addition to providing direct intercellular communication (GJIC, their hallmark function), GJs, based on their characteristic double-membrane-spanning configuration, likely also significantly contribute to physical cell-to-cell adhesion. Clearly, modulation (up-/down-regulation) of GJIC and of physical cell-to-cell adhesion is as vitally important as the basic ability of GJ formation itself. Others and we have previously described that GJs can be removed from the plasma membrane via the internalization of entire GJ plaques (or portions thereof) in a cellular process that resembles clathrin-mediated endocytosis. GJ endocytosis results in the formation of double-membrane vesicles [termed annular gap junctions (AGJs) or connexosomes] in the cytoplasm of one of the coupled cells. Four recent independent studies, consistent with earlier ultrastructural analyses, demonstrate the degradation of endocytosed AGJ vesicles via autophagy. However, in TPA-treated cells others report degradation of AGJs via the endo-/lysosomal degradation pathway. Here we summarize evidence that supports the concept that autophagy serves as the cellular default pathway for the degradation of internalized GJs. Furthermore, we highlight and discuss structural criteria that seem required for an alternate degradation via the endo-/lysosomal pathway.

Abbreviations

AGJ	Annular gap junction
CME	Clathrin mediated endocytosis
Cx	Connexin
DAG	Diacylglycerol
GFP	Green fluorescent protein
GJ	Gap junction
GJIC	Gap junction mediated intercellular communication
LAMP	Lysosomal associated membrane protein
LC3	Microtubule-associated protein light chain 3
PAEC	Pulmonary artery endothelial cell
PE	Phosphatidyl-ethanolamine
PKC	Protein kinase C
RNAi	RNA interference
SQSTM1	Sequestosome 1
SUMO	Small Ub-like modifier
TPA	12-O-tetradecanoylphorbol 13-acetate
Ub	Ubiquitin
WGA	Wheat germ agglutinin
YFP	Yellow fluorescent protein

Introduction

Direct cell-to-cell communication is a pivotal cellular function of multicellular organisms. It is established by gap junction (GJ) channels, that bridge apposing plasma membranes of neighboring cells. Typically, tens to thousands of GJ channels cluster into densely packed two-dimensional arrays, termed GJ plaques that can reach several micrometers in diameter. GJ channels are assembled from a

M. M. Falk (✉) · J. T. Fong · R. M. Kells ·
M. C. O'Laughlin · T. J. Kowal · A. F. Thévenin
Department of Biological Sciences, Lehigh University,
111 Research Drive, Iacocca Hall, D-218, Bethlehem,
PA 18015, USA
e-mail: mmf4@lehigh.edu

ubiquitously expressed class of four-pass trans-membrane proteins, termed connexins, with connexin 43 (Cx43) being the most abundantly expressed type. Six connexin polypeptides oligomerize into a ring to form a hexameric transmembrane structure with a central hydrophilic pore, called a hemi-channel or connexon. Once trafficked to the plasma membrane, two connexons, one provided by each of two neighboring cells, dock head-on in the extra-cellular space to form the complete double-membrane spanning GJ channel that is completely sealed-off to the extracellular space. Recruitment of additional GJ channels along the outer edge enlarges the GJ plaques, while simultaneous removal of older channels from plaque centers balances GJ channel turnover (Falk et al. 2009; Gaietta et al. 2002; Lauf et al. 2002). In addition to providing intercellular communication (their hallmark function), GJs, based on their characteristic double-membrane-spanning configuration and their tight extracellular head-to-head docking, are also likely to contribute significantly to physical cell-to-cell adhesion that generally is attributed to the adhesive force exerted by adherens- and tight junctions. Down-regulation of cell–cell adhesion contributes to many physiological and pathological conditions in which cells physically uncouple from their neighbors. For example, this uncoupling is seen during cell migration in development and wound healing, mitosis, apoptosis, leukocyte extravasation, ischemia, hemorrhage, edema, and cancer metastasis. Thus, to effectively reduce or abolish cell-to-cell adhesion under such conditions, all major types of cell–cell adhesion structures (including desmosomes, adherens, tight, and gap junctions) will either have to reduce their adhesive force, or will have to be removed from the plasma membrane.

GJ channels are known to gate such that physiological parameters including intracellular pH, Ca^{2+} concentration and Cx phosphorylation can modulate the status of GJ channels (opened, closed) and the extent of GJ-mediated intercellular communication (GJIC) (Delmar et al. 2004; Laird 2005; Lampe and Lau 2004; Moreno 2005; Pahujaa et al. 2007; Solan and Lampe 2009; Warn-Cramer and Lau 2004). Importantly, however, GJ channel gating (channel closure, not channel removal) is unlikely to significantly affect the level of GJ-mediated cell-to-cell adhesion. Alternatively, the extent of GJIC could also be regulated by splitting GJ channels (similar to adherens junctions), or by reducing the number of plasma membrane-located GJs. Both mechanisms also would contribute to a reduction in physical cell-to-cell adhesion. Goodenough and Gilula (1974) and Ghoshroy et al. (1995) reported that connexons, once docked, appear inseparable under physiological conditions, suggesting that GJs, especially under conditions where physical cell–cell adhesion needs to be reduced/abolished, will be removed from the plasma membrane. Here, we summarize recent findings that support the view that GJ removal from the plasma membrane is achieved by the internalization/endocytosis of GJs. Next, we will address two potential cellular degradation pathways, autophagosomal versus endo-/lysosomal, that both have been described recently to degrade endocytosed GJs (Fig. 1). We provide evidence that supports the concept that autophagy appears as the most likely cellular degradation pathway for removing internalized GJs from the cytoplasm. Finally, we discuss important structural criteria that may allow an alternate endo-/lysosomal degradation of internalized GJs.

Plasma Membrane-Located GJs are Endocytosed, Resulting in the Formation of Cytoplasmic Double-Membrane GJ Vesicles Termed AGJs or Connexosomes

We reported previously that cells continuously, -and effectively after treatment with natural inflammatory mediators-, internalize and turn over their GJs via a combined endo-/exocytic process (Baker et al. 2008; Falk et al. 2009; Gilleron et al. 2008; Gumpert et al. 2008; Piehl et al. 2007) (Fig. 1, steps 1–5). Internalization was found to occur preferentially into one of two coupled cells, indicating a highly regulated process (Falk et al. 2009; Piehl et al. 2007). The scaffolding protein, ZO-1, a well-known binding partner of Cx43 (Giepmans and Moolenaar 1998; Hunter et al. 2005; Toyofuku et al. 1998), was found to be displaced from GJ plaques on the side of plaque invagination (Baker et al. 2008; Gilleron et al. 2008). This observation suggests that ZO-1, not surprising for a scaffolding protein, may play multiple roles in GJ biosynthesis and function, including regulation of GJ plaque size (Hunter et al. 2005), accrual of channels to GJ plaques (Rhett and Gourdie 2011; Rhett et al. 2011), and defining directionality of GJ plaque internalization (Baker et al. 2008; Gilleron et al. 2008). Further analyses indicated that GJ internalization utilizes well-known components of the clathrin-mediated endocytosis (CME) machinery, including the classical endocytic coat protein clathrin, the clathrin-adaptors AP-2 and Dab2, the GTPase dynamin2, the retrograde actin motor myosin VI (myo6), as well as the process of actin polymerization (Gumpert et al. 2008; Piehl et al. 2007) (Fig. 1, steps 1–4). GJ internalization generates characteristic cytoplasmic double-membrane GJ vesicles, termed annular GJs (AGJs) or connexosomes. Note that the outer membrane of the generated AGJ vesicles corresponds to the plasma membrane of the host-cell, while the inner membrane and the vesicle lumen correspond to plasma membrane and cytoplasm of the neighboring donor cell (Fig. 1, steps 1–5). Others and we further found that internalization is highly regulated and can occur very efficiently. For example, acute GJ internalization can be seen in
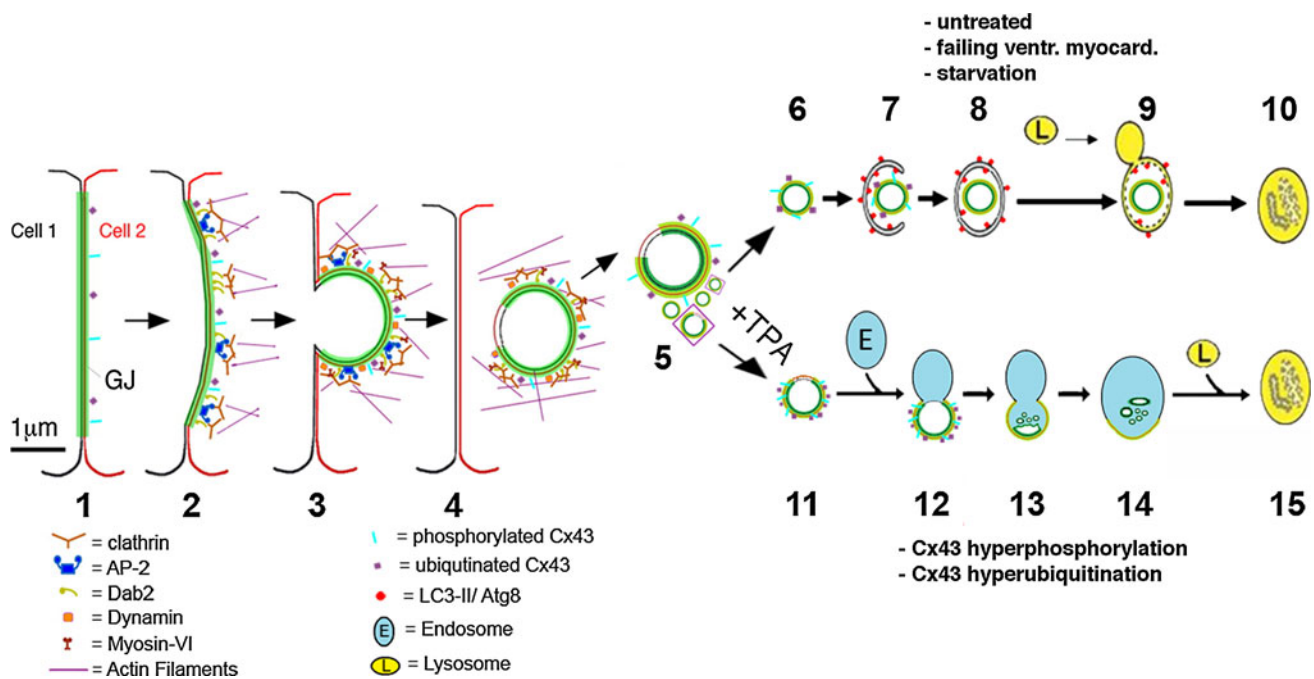
Fig. 1 Schematic representation of proposed steps that lead to GJ internalization (*steps 1–3*), cytoplasmic AGJ vesicle formation and fragmentation (*steps 4, 5*), and AGJ vesicle degradation by phago-/lysosomal (*steps 6–10*) and endo-/lysosomal pathways (*steps 11–15*) based on the previous work by others and by us. Note the proposed nonjunctional membrane domains missing the green GJ label (shown in *steps 4, 5, 11, 12*), and the increased phosphorylation and ubiquitination on AGJ vesicles that fuse with endosomes (*steps 11, 12* vs. *6, 7*). Adapted from Falk et al. (2009) and Fong et al. (2012)

primary porcine pulmonary artery endothelial cells (PAECs) exposed to natural inflammatory mediators such as thrombin and endothelin (Baker et al. 2008), well-known inhibitors of GJIC (Blomstrand et al. 2004; Postma et al. 1998; Spinella et al. 2003; van Zeijl et al. 2007), and in Cx43-GFP expressing NRK cells (Jordan et al. 2001). Efficient internalization of cell–cell junctions reduces/abolishes cell–cell adhesion, most likely allowing the endothelial cells to migrate to the inflamed tissue regions in order to aid in the healing process and to modulate endothelial barrier function (Baldwin and Thurston 2001; Falk 2010; Lum and Malik 1994; Wong et al. 2004). Efficient GJ internalization is also seen in Sertoli cells in response to treatment with the non-genomic carcinogen lindane (Gilleron et al. 2008), and it is seen under pathological conditions such as in the failing canine ventricular myocardium (Hesketh et al. 2010).

Continuous, as well as induced endocytosis of GJ plaques (consisting of double-membrane spanning GJ channels) is supported (I) by numerous earlier ultrastructural and live-cell based analyses that detected AGJ vesicles in the cytoplasm of cells in situ, especially occurring in differentiating tissues and sometimes, in association with lysosomes (Ginzberg and Gilula 1979; Hesketh et al. 2010; Jordan et al. 2001; Larsen et al. 1979; Leach and Oliphant 1984; Mazet et al. 1985; Pfeifer 1980; Severs et al. 1989); (II) the fundamental observation that connexons, once docked, are inseparable under physiological conditions (Ghoshroy et al. 1995; Goodenough and Gilula 1974); and (III) by the typical short half-life of connexins and GJ channels of only 1–5 h (Beardslee et al. 1998; Berthoud et al. 2004; Falk et al. 2009; Fallon and Goodenough 1981; Gaietta et al. 2002).

What Happens to Cytoplasmic AGJ Vesicles After Their Generation?

Four recent studies, Hesketh et al. (2010), Lichtenstein et al. (2011), Fong et al. (2012), and Bejarano et al. (2012) report the degradation of endocytosed AGJ vesicles via autophagy (Fig. 1, steps 6–10), while Leithe and colleagues (Leithe et al. 2009; Leithe and Rivedal 2004b; Fykerud et al. 2012) report degradation of endocytosed AGJ vesicles via the cellular endo-/lysosomal degradation pathway in cells that were treated with the phorbol ester, TPA (12-O-tetradecanoylphorbol 13-acetate), an analog of the secondary messenger DAG (diacylglycerol) (Fig. 1, steps 11–15). Hesketh et al. (2010) report loss of GJs from the plasma membrane, GJ endocytosis, and AGJ degradation by autophagy in pacing-induced failing canine ventricular myocardium. Lichtenstein et al. (2011) report that autophagy contributes to the degradation of endogenously (NRK cells and mouse embryonic fibroblasts) and exogenously (HeLa cells) expressed wild type Cx43 protein, and

of wild type and cataract-associated mutant Cx50 proteins in both un-induced cells and in cells in which autophagy was induced by starvation (Lichtenstein et al. 2011). Fong et al. (2012) report the autophagic degradation of AGJ vesicles in HeLa cells expressing exogenous fluorescently tagged Cx43, and in primary porcine pulmonary artery endothelial cells (PAECs) endogenously expressing Cx43. Bejarano et al. (2012) report the Nedd4-mediated ubiquitin-dependent autophagic degradation of internalized GJs in situ (mouse liver), as well as in starved and fed cultured cells expressing Cx43 endogenously and exogenously (mouse embryonic fibroblasts, NIH3T3, COS7, and NRK cells). In all four studies, cytoplasmic AGJ vesicles were detected inside phagophores by ultrastructural analyses, and AGJs were observed to colocalize with the most commonly used autophagy marker protein, LC3-II/Atg8 (Fig. 2). Autophagosomes exhibit a highly characteristic, clearly recognizable double-membrane structure on ultrathin sections, and thus conventional electron microscopy, as performed by Hesketh et al., Lichtenstein et al., Fong et al., and Bejarano et al. is still one of the best techniques for the characterization of autophagosomes (Mizushima 2004) (Fig. 2D–H). Microtubule-associated protein light chain 3 (LC3, the mammalian homolog of the yeast autophagic protein Atg8) is an abundant soluble cytoplasmic protein. It is proteolytically processed by the removal of a few N-terminal amino acid residues shortly after translation that generates LC3-I. LC3-I is recruited to developing phagophores, is covalently conjugated to phosphatidylethanolamine (PE) of the phagophore membrane (termed LC3-II), and remains on autophagosomes for most of their lifetime (Kabeya et al. 2000; Mizushima 2004). Thus, LC3 protein that was used by all four laboratories in colocalization studies is one of the most useful generic marker-proteins for the characterization of autophagosomes (Kabeya et al. 2000) (Fig. 2A).

Although the studies of Lichtenstein et al. and Bejarano et al. were aimed more broadly at a potential role of autophagy contributing to connexin and GJ degradation in general, the Fong et al., and the Hesketh et al. studies were aimed specifically at investigating the fate of internalized AGJ vesicles that others and we had characterized previously (Baker et al. 2008; Gumpert et al. 2008; Jordan et al. 2001; Piehl et al. 2007). To support their findings, Lichtenstein et al. and Bejarano et al., besides using other approaches, knocked down the autophagy-related proteins Atg5 and Atg7 in cells expressing either endogenous or exogenous Cx43, and used the drugs chloroquine and 3MA to inhibit autophagy. In contrast, Fong et al. knocked down expression of the autophagy related proteins, Beclin-1 (Atg6), LC3 (Atg8), LAMP-2, and p62/sequestosome 1 (SQSTM1) (Fig. 2B, C), and used the drugs 3MA, Wortmannin, and Bafilomycin A1 in Cx43-GFP expressing HeLa cells. Taken together, all four

complementary studies (Bejarano et al. 2012; Fong et al. 2012; Hesketh et al. 2010; Lichtenstein et al. 2011) provide convincing evidence that under physiological, as well as pathological conditions, GJ plaques are endocytosed from the plasma membrane, and the resulting AGJ vesicles are degraded by autophagy (Figs. 1, 2). As mentioned above, in the Lichtenstein et al., Fong et al., and Bejarano et al. studies the ubiquitin-binding protein p62/SQSTM1 was identified as a protein that targets internalized GJs to autophagic degradation. Knocking down p62/SQSTM1 protein levels as performed by Fong et al. resulted in a significantly increased accumulation of cytoplasmic AGJs (av. 55 %, $n = 4$) and a significantly reduced colocalization (av. 69.5 %, $n = 3$) of AGJs with autophagosomes (Fig. 2C). Remarkably, although autophagic degradation of GJs had been described in several classical ultrastructural analyses of various cells and tissues in situ, including heart, dermis, and liver (Leach and Oliphant 1984; Mazet et al. 1985; Pfeifer 1980; Severs et al. 1989) (Fig. 2E, F, H), until recently, not much attention was attributed to this fundamental GJ degradation pathway. Autophagic degradation of GJs plays a significant role in the regulation of GJ function, as inhibition of cellular autophagy increases GJIC, prevents internalization of GJs, slows down the degradation of connexins, and causes cytoplasmic accumulation of internalized GJ vesicles in situ, as well as in cultured cells expressing either endogenous or exogenous connexin proteins (Bejarano et al. 2012; Fong et al. 2012; Lichtenstein et al. 2011). Some characteristics that aid in a better understanding of the autophagic degradation pathway will be described next.

(Macro)Autophagy

Cells have developed three principal degradation pathways: the proteasomal, the endo-/lysosomal, and the phago-/lysosomal system (termed macroautophagy or simply autophagy), and all three have been implicated previously at various steps in the regulation of GJ stability and connexin degradation (Hesketh et al. 2010; Laing et al. 1997; Leach and Oliphant 1984; Leithe and Rivedal 2004a; Musil et al. 2000; Pfeifer 1980; Qin et al. 2003). Although the two latter ones utilize the lysosome for final degradation and are designed for the degradation of protein aggregates, multiprotein complexes, and cytoplasmic organelles, the proteasomal system is designed for the degradation of single polypeptide chains that require unfolding to be inserted into the tubular core of the cytoplasmically located proteasome. Because AGJ vesicles are highly oligomeric multisubunit protein assemblies, their degradation by the proteasome appears unlikely, and to our knowledge, no evidence exists that would suggest proteasome-mediated degradation of assembled GJ plaques or of
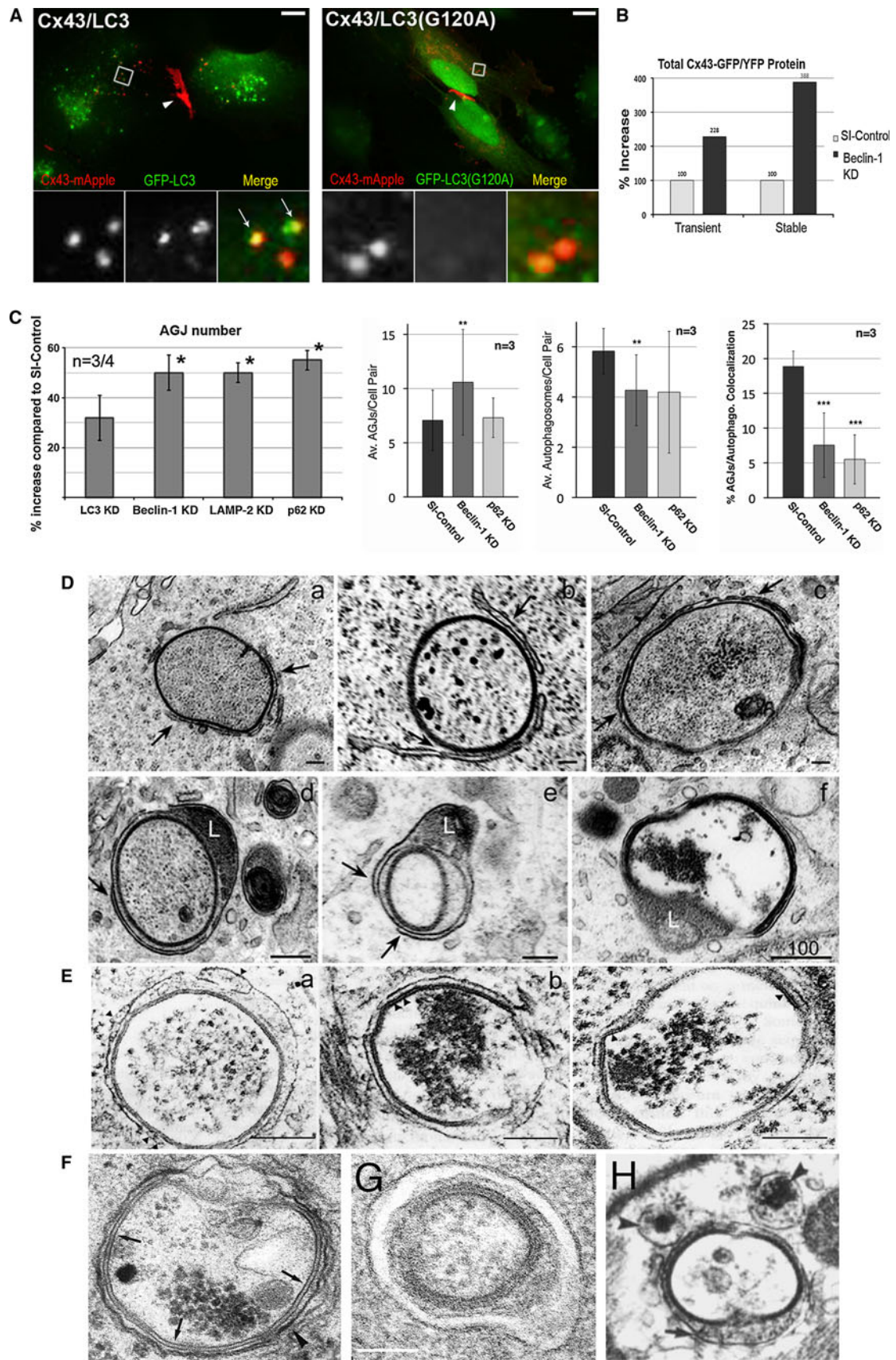
Fig. 2 Evidence for autophagic AGJ vesicle degradation. **A** HeLa cells were cotransfected with Cx43-mApple and the mammalian autophagy marker protein GFP-LC3 (*left*) or the activation-deficient LC3 mutant GFP-LC3 (G120A) (*right*). In cells, a fraction of cytoplasmic LC3 (LC3-I) is covalently conjugated to phagophore membranes (LC3-II) that localizes to autophagosomes; LC3 (G120A) cannot be conjugated and remains cytoplasmic. Representative merged fluorescence images acquired 24 h after transfections are shown. Individual and merged fluorescence signals of the boxed areas are shown below at higher magnification. Robust colocalization of cytoplasmic AGJ vesicles present in Cx43-mApple expressing cells (red puncta) with GFP-LC3-II (green puncta) was observed in GFP-LC3 expressing cells, but not in GFP-LC3 (G120A) expressing cells. Representative colocalizing AGJ vesicles are marked with *arrows*; GJs are marked with *arrowheads*. Scale bars = 10 μm. **B** Western blot analyses of total Cx43-GFP, or Cx43-YFP protein in transiently and stably expressing HeLa cells 72 h after Beclin-1, a crucial autophagy protein, was depleted by RNAi-oligonucleotide transfection. SI control cells were transfected with a scrambled nontargeting RISC-activating control oligonucleotide. Cx43-GFP/YFP was detected by probing with polyclonal anti-Cx43 antibodies. Normalized quantitative analyses revealed a 2- to 3-fold accumulation of Cx43-GFP/YFP protein in Beclin-1-KD over RNAi-control cell. **C** Quantitative AGJ vesicle analyses performed 72 h after RNA oligonucleotide transfection indicated a significant cytoplasmic AGJ accumulation in Beclin-1/ (Atg6), LAMP-2, and p62/SQSTM1 (all autophagy-related proteins) depleted cells (≥50 %, marked with *asterisks*) compared to RNAi control cells (*panel 1, left*). Less pronounced AGJ vesicle-accumulation was observed in LC3-depleted cells (32 %), and this was attributed to sufficient inactive LC3-I that may have remained in the LC3-KD cells and may have been converted into active LC3-II. In addition, quantitative analyses of AGJ vesicles (*panel 2, center left*), LC3-positive autophagosomes (*panel 3, center right*), and colocalizing AGJ/autophagosomes (*panel 4, right*) in Beclin-1 and p62/SQSTM1 knockdown cells revealed a significant increase of AGJs, a significant decrease of autophagosomes, and significantly reduced AGJ/autophagosome colocalization in 3 independent experiments (**$p < 0.01$; ***$p < 0.001$). **D** Multiple stages characteristic of progressive autophagosome formation and maturation that formed around AGJ vesicles revealed by ultrastructural analyses of Cx43-GFP expressing HeLa cell preparations. Double-membrane cisternae (presumably isolation membranes, marked with *arrows*) progressively encircled AGJ vesicles (**a–c**), coalesced into phagophores (**c–e**) and fused with lysosomes (**L, d, e**), resulting in AGJ degradation inside the phagosome (**f**). **A–D** Reproduced from Fong et al. (2012). **E–H** Autophagosomes presumably degrading endogenous AGJs in vivo, identified in the equine stratum spinosum (**E**, reproduced with permission of S. Karger AG, Basel from Leach and Oliphant 1984); rat liver (**F**, reproduced with permission of Elsevier from Pfeifer 1980); mouse embryonic fibroblasts (**G**, reproduced with permission of The Company of Biologists from Lichtenstein et al. 2011); and mammalian cardiomyocytes (**H**, reproduced with permission of Wolters Kluwer Health from Severs et al. 1989). Scale bars = 100 nm

AGJ vesicles. Also, it should be noted here that lysosomal inhibitors such as leupeptin, chloroquine, NH_4Cl, and E-64, that previously have been used to gain evidence for endo-/lysosomal degradation of GJs (Berthoud et al. 2004; Laing et al. 1997; Musil et al. 2000; Qin et al. 2003), will also inhibit autophagic GJ degradation, and thus obtained results may not have been accurately interpreted. Additional, future experiments that specifically target one or the other cellular degradation pathway may be required to

clarify specific roles of both pathways in GJ degradation. GJ endocytosis, postendocytic sorting, and the role of Cx43 ubiquitination for proteasomal and endo-/lysosomal degradation of connexin polypeptides, connexons, nonaggregated GJ channels, and of GJ plaques has recently been extensively reviewed (Kjenseth et al. 2010; Leithe et al. 2011; Su and Lau 2012). Here, we therefore concentrate on the autophagosomal degradation of AGJs, and on addressing a few prerequisites and factors that appear crucial for allowing a potential alternate endo-/lysosomal degradation of AGJ vesicles (Fig. 1).

Historically, autophagy has been known as a lysosomal degradation pathway that is essential for cell survival after nutrient depletion. However, substantial research over the past decade has indicated that autophagy, beside its well-known function in organelle degradation during starvation, represents a much more common and highly conserved lysosome-based cellular degradation pathway that is specifically designed to remove and degrade protein aggregates, multiprotein complexes, organelles, and invading pathogens from the cytoplasm (Bjorkoy et al. 2005; Hung et al. 2009; Pohl and Jentsch 2009; Ravikumar et al. 2008). Recent studies have further shown that protein aggregates, such as the ones formed by huntingtin and β-amyloid protein, and cellular structures such as the midbody ring, a mitotic cytokinesis leftover multiprotein complex, are all degraded by autophagy (Bjorkoy et al. 2005; Hung et al. 2009; Pohl and Jentsch 2009; Ravikumar et al. 2008). Clearly, these cellular structures are degraded by autophagy independent of starvation. In addition, autophagosomal degradation of membranous/vesicular organelles, as for example, malfunctioning mitochondria, is common. Because the catabolic activity of lysosomes is used in this process, degradation-prone structures first need to be separated from the cytoplasm. This is due to the destructive activity of lysosomal enzymes, which cannot be released directly into the cytoplasm. Indeed, cytoplasmic structures targeted for degradation are engulfed in double-membraned vesicles called autophagosomes that allow lysosomal fusion, degradation, and subsequent recycling of the phagosome cargo and the phagosome membrane (Fig. 1, steps 6–8).

Autophagosomes are formed by the elongation and fusion of phagophore membrane cisternae, which are derived from preautophagosomal structures. The membrane origin of phagophores is still unclear and likely involves multiple sources, such as the plasma membrane (Ravikumar et al. 2010), outer mitochondrial membranes (Hailey et al. 2010), the endoplasmic reticulum (Matsunaga et al. 2010), and the Golgi apparatus (Yen et al. 2010; reviewed recently in Mari et al. 2011). A large number of proteins essential or relevant for autophagosome formation and autophagic degradation (termed Atg-proteins) have

been characterized and can be used as reliable markers for autophagic degradation. Of these, the ubiquitin-like proteins Atg12 (that is conjugated to Atg5) and LC3/Atg8, Atg7, and the PI3-kinase complex-component Beclin-1 (BECN1)/Atg6 (essential for phagophore nucleation, as described above) are especially important for autophagosome formation and autophagic degradation. All of them have been targeted in the four above-mentioned GJ/autophagy studies (Bejarano et al. 2012; Fong et al. 2012; Hesketh et al. 2010; Lichtenstein et al. 2011) (Fig. 2A–C).

Autophagosomal Degradation of AGJs

Because cytoplasmic vesicles in general can fuse with endosomes, at first glance, autophagic degradation of AGJ vesicles might not appear intuitive. However, considering the structural organization of AGJ vesicles, including the dense packing of channels that occupy most or even the entire surface of AGJs in a double-membrane arrangement and their cytoplasmic location, autophagic degradation of AGJ vesicles appears much more plausible. In addition, the two tightly bound membranes of AGJ vesicles may not easily allow their fusion with single-membraned endosomes. Because, as explained above, lysosomal enzymes cannot be released into the cytosol, it is likely that the isolation membrane (the phagophore) formed during the initial steps of autophagy is required to sequester and separate the AGJ vesicle from the cytoplasm, thus providing the sealed membrane container that is required for subsequent lysosome fusion and lysosomal-based AGJ degradation. Finally, the unique structural composition of AGJ vesicles with lumen and inner membrane derived from the neighboring cell (being foreign to the AGJ-receiving host cell) may further direct AGJs to autophagic degradation. Also, although cell–cell communication provided by GJs before endocytosis can only accommodate the diffusion of small molecules, ions, and secondary messengers across the connected plasma membranes, endocytosis of GJs and formation of AGJ vesicles could in addition allow the transfer of potentially harmful substances from cell to cell. Such substances, for example, could include unwanted regulatory proteins, other larger molecules (e.g., micro-RNAs), or even cytoplasmic pathogens that could get entrapped in the AGJ vesicle lumen, further requiring efficient AGJ degradation. Taken together, these structural and functional characteristics, in addition with the fact that autophagy serves as the generic pathway for cytoplasmically localized degradation products (organelles and protein-aggregates), renders autophagic degradation the most likely cellular pathway for AGJ degradation.

Signals that May Direct AGJs for Degradation

Posttranslational modification of proteins is a widespread mechanism to fine-tune the structure, function, and localization of proteins. One of the most versatile and intriguing protein-modifications is the covalent attachment of ubiquitin (Ub) or Ub-like modifications to target proteins. Ub is a 76-amino acid protein, and either single or multiple Ub moieties can be conjugated to lysine amino acid residues of target proteins. An incredible diversity of mono- and poly-Ub chains (in which Ub moieties can be linked to each other via the Ub residues Met1-, Lys6-, Lys11-, Lys27-, Lys29-, Lys33-, Lys48-, and Lys63-) conjugated to target proteins have been characterized, and can range in function from protein activation to protein degradation (see Fushman and Wilkinson 2011 for a recent review). Multiple mono-Ubs, and Lys48- and Lys63-linked poly-Ubs have been recognized as important signals for protein degradation. For example, conjugation of Ub moieties to proteins has been recognized as a signal for both proteasomal targeting (addition of Lys48-linked poly-Ub chains) and more recently, as a sorting signal for internalized vesicles of the late endocytic pathway. This is achieved through the addition of multiple mono-Ub moieties or of Lys63-linked poly-Ub chains which ultimately lead to degradation by lysosomes (Hicke 2001; Hicke and Dunn 2003; Schnell and Hebert 2003; Shih et al. 2002; Stahl and Barbieri 2002). In addition, Lys-63-linked poly-ubiquitination can act as an internalization signal for clathrin-mediated endocytosis (CME) (Belouzard and Rouille 2006; Geetha et al. 2005). In this process, multiple mono-Ub moieties are attached to the target protein and are recognized by specific CME-machinery protein-components that associate with a subset of Ub-binding proteins (specifically Epsin1 and Eps15) (Barriere et al. 2006; Hawryluk et al. 2006; Madshus 2006). Further work has shown that the Ub-binding protein, p62/SQSTM1, recognizes and interacts via its UBA-domain with poly-ubiquitinated proteins (Ciani et al. 2003; Seibenhener et al. 2004; Wilkinson et al. 2001) and delivers poly-ubiquitinated (Lys63-linked) oligomeric protein complexes to the autophagic degradation pathway (Bjorkoy et al. 2005; Pankiv et al. 2007). Ubiquitination of Cx43-based GJs has been described previously (Catarino et al. 2011; Girao et al. 2009; Leithe et al. 2009, 2011; Leithe and Rivedal 2004b; reviewed in Kjenseth et al. 2010; Leithe et al. 2011). The findings that Cx43-based GJs can become ubiquitinated, the known affinity of p62/SQSTM1 for ubiquitinated protein complexes, its colocalization with plasma membrane GJs in HeLa, COS7, and PAE cells (Bejarano et al. 2012; Fong et al. 2012; Lichtenstein et al. 2011), and its apparent involvement in targeting AGJ vesicles to autophagic degradation (Fong et al. 2012) suggest that ubiquitination of Cx43 (and at least Cx50), besides serving as a likely signal

for GJ internalization, may also serve as the signal for targeting AGJ vesicles to autophagic degradation. Future research will be required to determine the potentially numerous types (multiple mono-Ubs, Lys48- and Lys63-linked poly-Ubs, etc.) and functions of connexin ubiqitination (see Kjenseth et al. 2010; Leithe et al. 2011; Su and Lau 2012 for recent reviews that discuss Cx ubiqitination). Recently, Kjenseth et al. (2012) described an additional, Ub-like posttranslational modification of Cx43, SUMOylation (SUMO, small ubiquitin-like modifier) that appears to be involved in regulating GJ stability and turnover. The small Ub-like protein SUMO was found to be conjugated to lysines 144 and 237 of the Cx43-C-terminal domain further complicating the role of Ub and Ub-like signals in the maintenance and degradation of GJs.

Alternative, Endo-/lysosomal Degradation of AGJs

Interestingly, a recent paper by Leithe et al. (2009) reports that in TPA-treated cells [a structural analog of the secondary messenger molecule diacylglycerol (DAG)], internalized GJs appear to be degraded by the endo-/lysosomal and not the autophagosomal pathway (Fig. 1, steps 11–15). Very recently, the Leithe lab identified the protein Smurf2 (the HECT E3 ubiquitin ligase *smad ubiquitination regulatory factor-2*) as a critical factor that regulates GJ internalization and endo-/lysosomal targeting in TPA-treated cells (Fykerud et al. 2012). DAG is a known potent activator of protein kinase C (PKC), and PKC is known to phosphorylate and promote ubiquitination of Cx43 (Leithe et al. 2009; Leithe and Rivedal 2004b; Postma et al. 1998). On the basis of these and our own results, it is tempting to speculate that cells might be able to regulate by which pathway (endo-/lysosomal vs. phago-/lysosomal) specific cargo is sequestered and processed (e.g., endo-/lysosomal and phago-/lysosomal pathways might process internalized GJs in different ways). Furthermore, the level of cargo-phosphorylation and/or ubiquitination might determine which of these pathways is ultimately chosen (basal phosphorylation/ubiquitination signaling autophagic AGJ vesicle degradation; elevated phosphorylation/ubiquitination signaling endo-/lysosomal AGJ vesicle degradation) (Fig. 1, steps 6–10 vs. 11–15). Such a regulation dependent on ubiquitin level has for example been shown for the endocytosis of the epidermal growth factor (EGF) receptor (Sigismund et al. 2005).

Endo-/lysosomal degradation of AGJs as observed in TPA-treated cells by Leithe et al. (2009) of course raises an important question: How is it structurally possible for a double-membrane vesicle that consists of tightly bonded membrane layers and densely packed GJ channels to fuse with a single-membrane endosome? The Rivedal and Leithe laboratories suggest that subsequent to GJ internalization

and AGJ formation, the inner AGJ membrane splits and peels away from the outer AGJ membrane, generating a single-membraned cytoplasmic AGJ vesicle that then can fuse with a single-membraned endosome (Kjenseth et al. 2010, 2012; Leithe et al. 2009, 2011). However, because docked GJ channels can not split into undocked connexons under physiological conditions (Ghoshroy et al. 1995; Goodenough and Gilula 1974)—which appears to be the apparent reason for double-membrane GJ endocytosis—it is not clear how membrane separation could be initiated in the AGJ vesicles shortly after their generation. Clearly, low pH (a characteristic of late endosomes and lysosomes, and a potential initiator of GJ splitting), can be excluded because AGJ vesicle membrane-separation needs to occur before AGJ/endosome fusion. Su and Lau (2012) also do not speculate on how cytoplasmic AGJs may end up inside endosomes, as is suggested in their recent review article.

Interestingly, we found that AGJ vesicles examined by electron microscopy may include a small area where the two membranes are void of GJ channels and are not docked or linked to each other (Piehl et al. 2007) (Fig. 3a, and shown schematically in Fig. 1, steps 4, 5, 11 and 12). Similar small AGJ membrane separations were also observed in classical ultrastructural analyses of GJs and AGJ vesicles (see, e.g., Mazet et al. 1985). Possibly, these nonjunctional membrane domains consist of plasma membrane that is derived from both neighboring cells, and we postulate that these areas might originate from plasma membrane regions that were located immediately adjacent to the GJ plaques and were also internalized. To gain further support for this hypothesis, we incubated inducible stably Cx43-YFP expressing HeLa cells (described in Lauf et al. 2002) for 2–4 h with a fluorescently tagged lectin, Alexa594-wheat germ agglutinin (WGA), and examined AGJ vesicles by high-resolution fluorescence microscopy. WGA binds specifically to sialic acid and *N*-acetylglucosaminyl carbohydrate moieties commonly found on extracellular-exposed carbohydrate side-chains of plasma membrane proteins. Due to its relatively large size ($\sim$38 kDa), WGA is not able to traverse the plasma membrane in living cells. However, WGA will label the extracellular surface of plasma membranes and only subsequently will be endocytosed to also label intracellular membrane compartments (Wright 1984). Interestingly we found that a portion of cytoplasmic AGJ vesicles that were likely generated during the WGA-incubation period, exhibited red-fluorescent WGA-puncta (labeled with arrows in Fig. 3b). These results support our hypothesis that the un-docked membrane domains we detected by EM on AGJ vesicles indeed represent plasma membrane that was located in the immediate vicinity of GJ plaques and was concomitantly internalized in the AGJ endocytosis process. For us, it is tempting to speculate that this nonjunctional membrane domain could provide the single membrane area that would
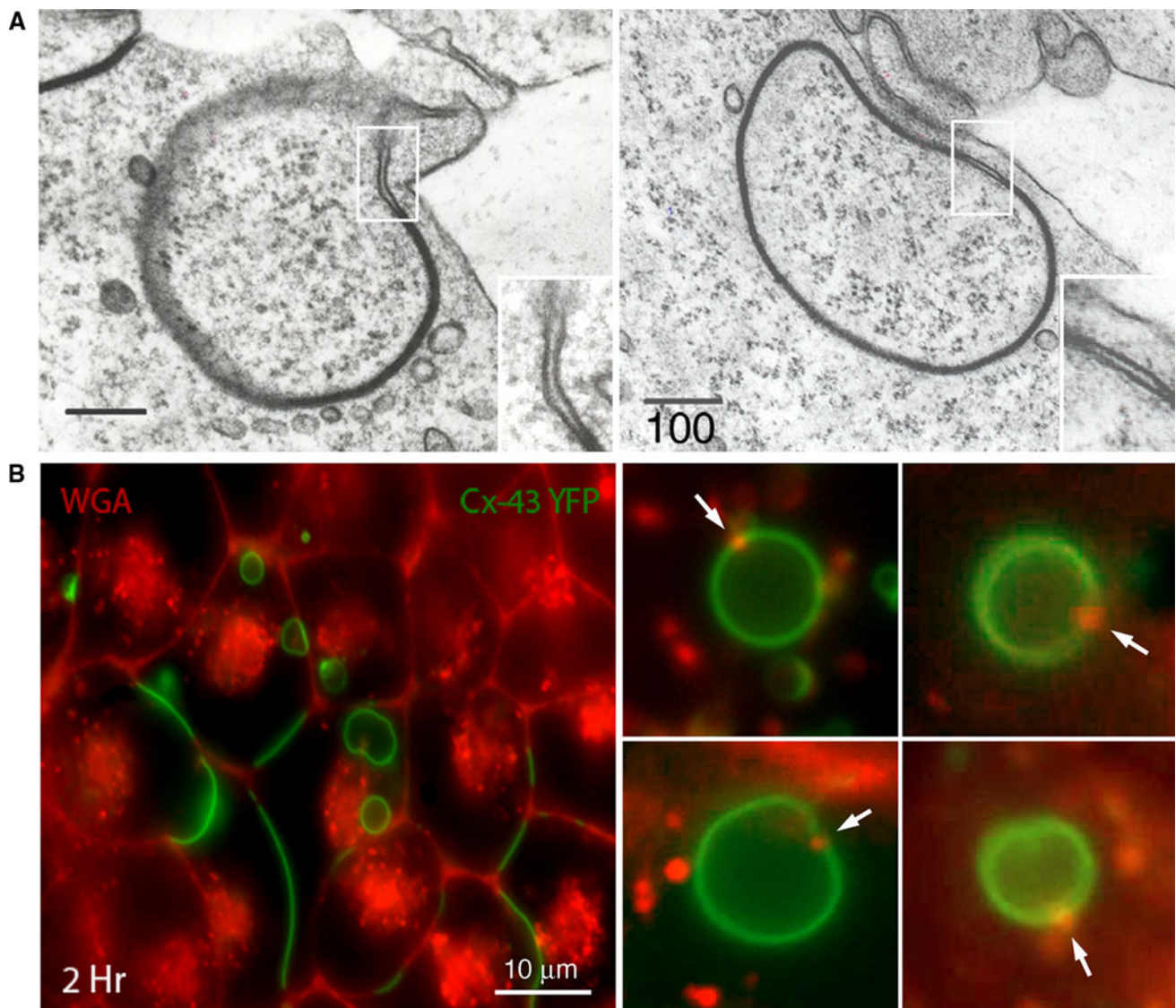
Fig. 3 Fine structure and composition of AGJ vesicles. **a** Double-membrane AGJ vesicles can contain a patch of nonjunctional membrane where the two membrane layers are separated (enlarged in *insets*). These nonjunctional membrane patches appear to be derived from plasma membrane that was located immediately adjacent to the GJ plaque and was concomitantly endocytosed. **b** These nonjunctional AGJ membrane domains label with extracellularly applied, fluorescence-labeled wheat germ agglutinin (WGA) (red puncta on green AGJ vesicles marked with *arrows*) in Cx43-YFP expressing cells. Stable Cx43-YFP expressing HeLa cells were incubated for 2–4 h with Alexa594-labeled WGA and examined by fluorescence microscopy. Low-magnification survey image (*panel 1, left*) and high-resolution images of internalized AGJ vesicles (*panels 2–5, right*) are shown (*scale bars* = nm in **a** and μm in **b**). **a** Adapted from Piehl et al. (2007)

allow double-membrane AGJ vesicles to fuse with single-membrane endosomes.

Conclusion

A number of recent and classic manuscripts describe the endocytosis of GJ plaques as double-membrane spanning structures (Baker et al. 2008; Falk et al. 2009; Ginzberg and Gilula 1979; Gumpert et al. 2008; Jordan et al. 2001; Larsen et al. 1979; Mazet et al. 1985; Piehl et al. 2007) and the autophagosomal, and potentially endo-/lysosomal degradation of the resulting cytoplasmic double-membrane AGJ vesicles (Bejarano et al. 2012; Fong et al. 2012; Hesketh et al. 2010; Leach and Oliphant 1984; Leithe et al. 2009; Lichtenstein et al. 2011; Pfeifer 1980; Severs et al. 1989). On the basis of the recent and classic observations described above, we hypothesize that double-membrane GJ endocytosis is the only practical means of how cells can efficiently remove plasma membrane-localized GJ plaques.

Potential GJ splitting, or GJ dispersion (Lane and Swales 1980) have not been observed by us in any of our multiple live-cell recordings and therefore are not considered efficient mechanisms of GJ removal. Furthermore, on the basis of the recently published evidence suggesting autophagosomal degradation of AGJ vesicles (Fong et al. 2012; Hesketh et al. 2010; Lichtenstein et al. 2011), the knowledge that autophagy serves as the generic pathway for the degradation of cytoplasmically localized organelles and protein-aggregates, and based on the known structural composition of AGJ vesicles consisting of tightly sealed-together membrane layers, we further hypothesize that the default degradation pathway for these cytoplasmic structures is (macro)autophagy. Alternatively, endo-/lysosomal AGJ degradation described to occur in TPA-treated cells may be achieved on the basis of the presence of AGJ membrane-domains where the two membrane-layers are not linked to each other (such as the ones we have characterized and described above, see Fig. 3), providing the structural prerequisite to allow single-membrane endosomes to fuse with double-membrane AGJ vesicles.

Finally, we speculate that the level of connexin phosphorylation and/or ubiquitination might allow cells to regulate by which pathway (endo-/lysosomal versus phago-/lysosomal), endocytosed AGJ vesicles are sequestered and processed; an interesting hypothesis considering that autophagosomal and endo-/lysosomal processing may render different (degradation) products. Future research will elucidate whether our hypotheses are correct, and if there are additional cellular pathways that may dictate the fate of endocytosed GJs.

References

Baker SM, Kim N, Gumpert AM, Segretain D, Falk MM (2008) Acute internalization of gap junctions in vascular endothelial cells in response to inflammatory mediator-induced G-protein coupled receptor activation. FEBS Lett 582:4039–4046

Baldwin AL, Thurston G (2001) Mechanics of endothelial cell architecture and vascular permeability. Crit Rev Biomed Eng 29:247–278

Barriere H, Nemes C, Lechardeur D, Khan-Mohammad M, Fruh K, Lukacs GL (2006) Molecular basis of oligoubiquitin-dependent internalization of membrane proteins in Mammalian cells. Traffic 7:282–297

Beardslee MA, Laing JG, Beyer EC, Saffitz JE (1998) Rapid turnover of connexin43 in the adult rat heart. Circ Res 83:629–635

Bejarano E, Girao H, Yuste A, Patel B, Marques C, Spray DC, Pereira P, Cuervo AM (2012) Autophagy modulates dynamics of connexins at the plasma membrane in a ubiquitin-dependent manner. Mol Biol Cell 23:2156–2169

Belouzard S, Rouille Y (2006) Ubiquitylation of leptin receptor OB-Ra regulates its clathrin-mediated endocytosis. EMBO J 25:932–942

Berthoud VM, Minogue PJ, Laing JG, Beyer EC (2004) Pathways for degradation of connexins and gap junctions. Cardiovasc Res 62:256–267

Bjorkoy G, Lamark T, Brech A, Outzen H, Perander M, Overvatn A, Stenmark H, Johansen T (2005) p62/SQSTM1 forms protein aggregates degraded by autophagy and has a protective effect on huntingtin-induced cell death. J Cell Biol 171:603–614

Blomstrand F, Venance L, Siren AL, Ezan P, Hanse E, Glowinski J, Ehrenreich H, Giaume C (2004) Endothelins regulate astrocyte gap junctions in rat hippocampal slices. Eur J Neurosci 19:1005–1015

Catarino S, Ramalho JS, Marques C, Pereira P, Girao H (2011) Ubiquitin-mediated internalization of connexin43 is independent of the canonical endocytic tyrosine-sorting signal. Biochem J 437:255–267

Ciani B, Layfield R, Cavey JR, Sheppard PW, Searle MS (2003) Structure of the ubiquitin-associated domain of p62 (SQSTM1) and implications for mutations that cause Paget's disease of bone. J Biol Chem 278:37409–37412

Delmar M, Coombs W, Sorgen P, Duffy HS, Taffet SM (2004) Structural bases for the chemical regulation of connexin43 channels. Cardiovasc Res 62:268–275

Falk MM (2010) Adherens junctions remain dynamic. BMC Biol 8:34

Falk MM, Baker SM, Gumpert AM, Segretain D, Buckheit RW 3rd (2009) Gap junction turnover is achieved by the internalization of small endocytic double-membrane vesicles. Mol Biol Cell 20:3342–3352

Fallon RF, Goodenough DA (1981) Five-hour half-life of mouse liver gap-junction protein. J Cell Biol 90:521–526

Fong JT, Kells RM, Gumpert AM, Marzillier JY, Davidson MW, Falk MM (2012) Internalized gap junctions are degraded by autophagy. Autophagy 8:794–811

Fushman D, Wilkinson KD (2011) Structure and recognition of polyubiquitin chains of different lengths and linkage. F1000 Biol Rep 3:26

Fykerud TA, Kjenseth A, Schink KO, Sirnes S, Bruun J, Omori Y, Brech A, Rivedal E, Leithe E (2012) Smad ubiquitination regulatory factor-2 controls gap junction intercellular communication by modulating endocytosis and degradation of connexin43. J Cell Sci doi:10.1242/j cs.093500

Gaietta G, Deerinck TJ, Adams SR, Bouwer J, Tour O, Laird DW, Sosinsky GE, Tsien RY, Ellisman MH (2002) Multicolor and electron microscopic imaging of connexin trafficking. Science 296:503–507

Geetha T, Jiang J, Wooten MW (2005) Lysine 63 polyubiquitination of the nerve growth factor receptor TrkA directs internalization and signaling. Mol Cell 20:301–312

Ghoshroy S, Goodenough DA, Sosinsky GE (1995) Preparation, characterization, and structure of half gap junctional layers split with urea and EGTA. J Membr Biol 146:15–28

Giepmans BN, Moolenaar WH (1998) The gap junction protein connexin43 interacts with the second PDZ domain of the zona occludens-1 protein. Curr Biol 8:931–934

Gilleron J, Fiorini C, Carette D, Avondet C, Falk MM, Segretain D, Pointis G (2008) Molecular reorganization of Cx43, Zo-1 and Src complexes during the endocytosis of gap junction plaques in response to a non-genomic carcinogen. J Cell Sci 121:4069–4078

Ginzberg RD, Gilula NB (1979) Modulation of cell junctions during differentiation of the chicken otocyst sensory epithelium. Dev Biol 68:110–129

Girao H, Catarino S, Pereira P (2009) Eps15 interacts with ubiquitinated Cx43 and mediates its internalization. Exp Cell Res 315:3587–3597

Goodenough DA, Gilula NB (1974) The splitting of hepatocyte gap junctions and zonulae occludentes with hypertonic disaccharides. J Cell Biol 61:575–590

Gumpert AM, Varco JS, Baker SM, Piehl M, Falk MM (2008) Double-membrane gap junction internalization requires the clathrin-mediated endocytic machinery. FEBS Lett 582:2887–2892

Hailey DW, Rambold AS, Satpute-Krishnan P, Mitra K, Sougrat R, Kim PK, Lippincott-Schwartz J (2010) Mitochondria supply membranes for autophagosome biogenesis during starvation. Cell 141:656–667

Hawryluk MJ, Keyel PA, Mishra SK, Watkins SC, Heuser JE, Traub LM (2006) Epsin 1 is a polyubiquitin-selective clathrin-associated sorting protein. Traffic 7:262–281

Hesketh GG, Shah MH, Halperin VL, Cooke CA, Akar FG, Yen TE, Kass DA, Machamer CE, Van Eyk JE, Tomaselli GF (2010) Ultrastructure and regulation of lateralized connexin43 in the failing heart. Circ Res 106:1153–1163

Hicke L (2001) Protein regulation by monoubiquitin. Nat Rev Mol Cell Biol 2:195–201

Hicke L, Dunn R (2003) Regulation of membrane protein transport by ubiquitin and ubiquitin-binding proteins. Annu Rev Cell Dev Biol 19:141–172

Hung SY, Huang WP, Liou HC, Fu WM (2009) Autophagy protects neuron from Abeta-induced cytotoxicity. Autophagy 5:502–510

Hunter AW, Barker RJ, Zhu C, Gourdie RG (2005) Zonula occludens-1 alters connexin43 gap junction size and organization by influencing channel accretion. Mol Biol Cell 16:5686–5698

Jordan K, Chodock R, Hand AR, Laird DW (2001) The origin of annular junctions: a mechanism of gap junction internalization. J Cell Sci 114:763–773

Kabeya Y, Mizushima N, Ueno T, Yamamoto A, Kirisako T, Noda T, Kominami E, Ohsumi Y, Yoshimori T (2000) LC3, a mammalian homologue of yeast Apg8p, is localized in autophagosome membranes after processing. EMBO J 19:5720–5728

Kjenseth A, Fykerud T, Rivedal E, Leithe E (2010) Regulation of gap junction intercellular communication by the ubiquitin system. Cell Signal 22:1267–1273

Kjenseth A, Fykerud TA, Sirnes S, Bruun J, Kolberg M, Yohannes Z, Omori Y, Rivedal E, Leithe E (2012) The gap junction channel protein connexin43 is covalently modified and regulated by SUMOylation. J Biol Chem 287:15851–15861

Laing JG, Tadros PN, Westphale EM, Beyer EC (1997) Degradation of connexin43 gap junctions involves both the proteasome and the lysosome. Exp Cell Res 236:482–492

Laird DW (2005) Connexin phosphorylation as a regulatory event linked to gap junction internalization and degradation. Biochim Biophys Acta 1711:172–182

Lampe PD, Lau AF (2004) The effects of connexin phosphorylation on gap junctional communication. Int J Biochem Cell Biol 36:1171–1186

Lane NJ, Swales LS (1980) Dispersal of junctional particles, not internalization, during the in vivo disappearance of gap junctions. Cell 19:579–586

Larsen WJ, Tung HN, Murray SA, Swenson CA (1979) Evidence for the participation of actin microfilaments and bristle coats in the internalization of gap junction membrane. J Cell Biol 83:576–587

Lauf U, Giepmans BN, Lopez P, Braconnot S, Chen SC, Falk MM (2002) Dynamic trafficking and delivery of connexons to the plasma membrane and accretion to gap junctions in living cells. Proc Natl Acad Sci USA 99:10446–10451

Leach DH, Oliphant LW (1984) Degradation of annular gap junctions of the equine hoof wall. Acta Anat (Basel) 120:214–219

Leithe E, Rivedal E (2004a) Epidermal growth factor regulates ubiquitination, internalization and proteasome-dependent degradation of connexin43. J Cell Sci 117:1211–1220

Leithe E, Rivedal E (2004b) Ubiquitination and down-regulation of gap junction protein connexin-43 in response to 12-O-tetradecanoylphorbol 13-acetate treatment. J Biol Chem 279:50089–50096

Leithe E, Kjenseth A, Sirnes S, Stenmark H, Brech A, Rivedal E (2009) Ubiquitylation of the gap junction protein connexin-43 signals its trafficking from early endosomes to lysosomes in a process mediated by Hrs and Tsg101. J Cell Sci 122:3883–3893

Leithe E, Sirnes S, Fykerud T, Kjenseth A, Rivedal E (2011) Endocytosis and post-endocytic sorting of connexins. Biochim Biophys Acta 1818:1870–1879

Lichtenstein A, Minogue PJ, Beyer EC, Berthoud VM (2011) Autophagy: a pathway that contributes to connexin degradation. J Cell Sci 124:910–920

Lum H, Malik AB (1994) Regulation of vascular endothelial barrier function. Am J Physiol 267:L223–L241

Madshus IH (2006) Ubiquitin binding in endocytosis—how tight should it be and where does it happen? Traffic 7:258–261

Mari M, Tooze SA, Reggiori F (2011) The puzzling origin of the autophagosomal membrane. F1000 Biol Rep 3:25

Matsunaga K, Morita E, Saitoh T, Akira S, Ktistakis NT, Izumi T, Noda T, Yoshimori T (2010) Autophagy requires endoplasmic reticulum targeting of the PI3-kinase complex via Atg14L. J Cell Biol 190:511–521

Mazet F, Wittenberg BA, Spray DC (1985) Fate of intercellular junctions in isolated adult rat cardiac cells. Circ Res 56:195–204

Mizushima N (2004) Methods for monitoring autophagy. Int J Biochem Cell Biol 36:2491–2502

Moreno AP (2005) Connexin phosphorylation as a regulatory event linked to channel gating. Biochim Biophys Acta 1711:164–171

Musil LS, Le AC, VanSlyke JK, Roberts LM (2000) Regulation of connexin degradation as a mechanism to increase gap junction assembly and function. J Biol Chem 275:25207–25215

Pahujaa M, Anikin M, Goldberg GS (2007) Phosphorylation of connexin43 induced by Src: regulation of gap junctional communication between transformed cells. Exp Cell Res 313:4083–4090

Pankiv S, Clausen TH, Lamark T, Brech A, Bruun JA, Outzen H, Overvatn A, Bjorkoy G, Johansen T (2007) p62/SQSTM1 binds directly to Atg8/LC3 to facilitate degradation of ubiquitinated protein aggregates by autophagy. J Biol Chem 282:24131–24145

Pfeifer U (1980) Autophagic sequestration of internalized gap junctions in rat liver. Eur J Cell Biol 21:244–246

Piehl M, Lehmann C, Gumpert A, Denizot JP, Segretain D, Falk MM (2007) Internalization of large double-membrane intercellular vesicles by a clathrin-dependent endocytic process. Mol Biol Cell 18:337–347

Pohl C, Jentsch S (2009) Midbody ring disposal by autophagy is a post-abscission event of cytokinesis. Nat Cell Biol 11:65–70

Postma FR, Hengeveld T, Alblas J, Giepmans BN, Zondag GC, Jalink K, Moolenaar WH (1998) Acute loss of cell–cell communication caused by G protein-coupled receptors: a critical role for c-Src. J Cell Biol 140:1199–1209

Qin H, Shao Q, Igdoura SA, Alaoui-Jamali MA, Laird DW (2003) Lysosomal and proteasomal degradation play distinct roles in the life cycle of Cx43 in gap junctional intercellular communication-deficient and -competent breast tumor cells. J Biol Chem 278:30005–30014

Ravikumar B, Imarisio S, Sarkar S, O'Kane CJ, Rubinsztein DC (2008) Rab5 modulates aggregation and toxicity of mutant

huntingtin through macroautophagy in cell and fly models of Huntington disease. J Cell Sci 121:1649–1660

Ravikumar B, Moreau K, Jahreiss L, Puri C, Rubinsztein DC (2010) Plasma membrane contributes to the formation of pre-autophagosomal structures. Nat Cell Biol 12:747–757

Rhett JM, Gourdie RG (2011) The perinexus: a new feature of Cx43 gap junction organization. Heart Rhythm 9:619–623

Rhett JM, Jourdan J, Gourdie RG (2011) Connexin 43 connexon to gap junction transition is regulated by zonula occludens-1. Mol Biol Cell 22:1516–1528

Schnell DJ, Hebert DN (2003) Protein translocons: multifunctional mediators of protein translocation across membranes. Cell 112:491–505

Seibenhener ML, Babu JR, Geetha T, Wong HC, Krishna NR, Wooten MW (2004) Sequestosome 1/p62 is a polyubiquitin chain binding protein involved in ubiquitin proteasome degradation. Mol Cell Biol 24:8055–8068

Severs NJ, Shovel KS, Slade AM, Powell T, Twist VW, Green CR (1989) Fate of gap junctions in isolated adult mammalian cardiomyocytes. Circ Res 65:22–42

Shih SC, Katzmann DJ, Schnell JD, Sutanto M, Emr SD, Hicke L (2002) Epsins and Vps27p/Hrs contain ubiquitin-binding domains that function in receptor endocytosis. Nat Cell Biol 4:389–393

Sigismund S, Woelk T, Puri C, Maspero E, Tacchetti C, Transidico P, Di Fiore PP, Polo S (2005) Clathrin-independent endocytosis of ubiquitinated cargos. Proc Natl Acad Sci USA 102:2760–2765

Solan JL, Lampe PD (2009) Connexin43 phosphorylation: structural changes and biological effects. Biochem J 419:261–272

Spinella F, Rosano L, Di Castro V, Nicotra MR, Natali PG, Bagnato A (2003) Endothelin-1 decreases gap junctional intercellular communication by inducing phosphorylation of connexin 43 in human ovarian carcinoma cells. J Biol Chem 278:41294–41301

Stahl PD, Barbieri MA (2002) Multivesicular bodies and multivesicular endosomes: the "ins and outs" of endosomal traffic. Sci STKE 2002:pe32

Su V, Lau AF (2012) Ubiquitination, intracellular trafficking, and degradation of connexins. Arch Biochem Biophys 524:16–22

Toyofuku T, Yabuki M, Otsu K, Kuzuya T, Hori M, Tada M (1998) Direct association of the gap junction protein connexin-43 with ZO-1 in cardiac myocytes. J Biol Chem 273:12725–12731

van Zeijl L, Ponsioen B, Giepmans BN, Ariaens A, Postma FR, Varnai P, Balla T, Divecha N, Jalink K, Moolenaar WH (2007) Regulation of connexin43 gap junctional communication by phosphatidylinositol 4,5-bisphosphate. J Cell Biol 177:881–891

Warn-Cramer BJ, Lau AF (2004) Regulation of gap junctions by tyrosine protein kinases. Biochim Biophys Acta 1662:81–95

Wilkinson CR, Seeger M, Hartmann-Petersen R, Stone M, Wallace M, Semple C, Gordon C (2001) Proteins containing the UBA domain are able to bind to multi-ubiquitin chains. Nat Cell Biol 3:939–943

Wong CW, Christen T, Kwak BR (2004) Connexins in leukocytes: shuttling messages? Cardiovasc Res 62:357–367

Wright CS (1984) Structural comparison of the two distinct sugar binding sites in wheat germ agglutinin isolectin II. J Mol Biol 178:91–104

Yen WL, Shintani T, Nair U, Cao Y, Richardson BC, Li Z, Hughson FM, Baba M, Klionsky DJ (2010) The conserved oligomeric Golgi complex is involved in double-membrane vesicle formation during autophagy. J Cell Biol 188:101–114