

GRP78: A Multifunctional Receptor on the Cell Surface

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Abstract

The 78 kDa glucose-regulated protein (GRP78) is an endoplasmic reticulum chaperone, whose function is generally thought to be restricted to controlling the structural maturation of nascent glycoproteins. However, GRP78 also is expressed on the cell surface where it functions as a receptor for a wide variety of ligands, behaving as an autoantigen for several classes of autoantibodies. GRP78 is a signaling receptor for activated α_2 -macroglobulin, plasminogen kringle 5, and microplasminogen, and it plays a critical role in viral entry of coxsackie B, and dengue fever viruses. GRP78 is also implicated in the regulation of tissue factor procoagulant activity and functions as a receptor for angiogenic peptides via a mechanism independent of the VEGF receptor. Cell surface GRP78 is found associated with such diverse proteins as the voltage-dependent anion channel (VDAC), the major histocompatibility complex class I (MHC-I), the teratocarcinoma-derived growth factor I (Cripto), and the DnaJ-like protein MTJ-1. These associations suggest a unique GRP78 cell surface topography, which appears to be compartmentalized to respond differently to agonists that bind to its N- or C-terminal domains. Here, we discuss the significance of these associations, and the possible mechanisms involved in the transportation of GRP78 from the cytosol to the cell surface. *Antioxid. Redox Signal.* 11, 2299–2306.

Introduction

GRP78, A WELL-CHARACTERIZED ENDOPLASMIC RETICULUM (ER) chaperone that belongs to the heat-shock protein (HSP) family, is present in all cells and plays an important role in maintaining cellular homeostasis (18, 23). The primary functions of GRP78 are related to its capacity to bind to hydrophobic patches on nascent polypeptides in the ER and its role as one of the initial components of the signaling cascade that produces the unfolded protein response (UPR) (27, 30). Although best known as an ER luminal protein, GRP78 is also found on the cell plasma membrane where it functions as a cell surface signaling receptor for activated α_2 -macroglobulin (α_2 M*) (34, 35, 68).

Cell-surface GRP78 is a major autoantigen in prostate (33), ovarian (9), and gastric cancer patients (46), and participates in several physiologic processes that include inhibition of tissue factor (TF) procoagulant activity (1, 61), and angiogenesis on endothelial cells (17). It is also found associated with the major histocompatibility complex class I (MHC-I) and is a receptor for coxsackie A9 virus (59, 60) and dengue virus serotype 2 (20) on the cell surface. It is a receptor for plasminogen kringle 5 (K5) and microplasminogen (14) and is found associated to cell surface voltage-dependent anion channel (VDAC) (14).

Autoantibodies against GRP78 isolated from cancer patient sera show different affinities and functions. For example, an anti-GRP78 IgG from the serum of prostate cancer patients, which binds to an N-terminal region of GRP78, enhances cell survival and proliferation (13). However, a mouse monoclonal IgG against the amino acid sequence KDEL, in the C-terminal region of GRP78, inhibits cellular proliferation and induces apoptosis (44). Conversely, a human monoclonal GRP78 antibody against a region in the last C-terminal 20 amino acid residues does not affect cell proliferation or induces apoptosis (19). In contrast, a serum monoclonal anti-GRP78 IgM antibody isolated from gastric cancer patients recognizes an O-linked carbohydrate moiety in GRP78 and induces apoptosis in tumor cells (46).

In cancer cells, adaptation to chronic stress in the tumor microenvironment includes enhanced expression of GRP78 on the cell surface, which helps the tumor to evade immune surveillance while increasing its resistance to apoptosis and tolerance to a wide variety of therapies (26, 27). As discussed above, cell surface GRP78 acts as a receptor or target for a large number of agonists and antibodies. Different physiological responses may occur depending on whether GRP78 is engaged at the N- or C-terminus. In order to perform such diverse functions, the topography of GRP78 on the cell surface must be conditioned to respond to these agonists via specific

pathways controlling the expression of GRP78. In this review, we describe some of the possible mechanisms involved.

The Stress Response and GRP78 Function on the Cell Surface

GRP78 induction plays a critical role in maintaining cell viability against several kinds of stress, including ER Ca^{2+} depletion and accumulation of unglycosylated proteins. ER stress can be chemically induced by agents that inhibit the glycosylation of newly synthesized proteins or by agents that induce ER Ca^{2+} depletion (41, 57, 58). One study using prostate cancer cell lines demonstrated that both the calcium ionophore ionomycin (IM) and the glycosylation inhibitor tunicamycin (TM) induce GRP78 expression (41). However, induction of GRP78 and apoptosis was only observed in response to IM which produces ER Ca^{2+} depletion, but not in response to inhibition of protein glycosylation, suggesting the presence of at least two different pathways mediating the GRP78 stress response.

Thapsigargin (TG), an inhibitor of the ubiquitous sarcoendoplasmic reticulum Ca^{2+} -ATPases, also induces the expression of GRP78 (5). Inhibition of the reticulum Ca^{2+} -ATPases leads to the depletion of intraluminal Ca^{2+} and a concurrent increase of cytosolic free calcium Ca^{2+} ($[\text{Ca}^{2+}]_c$) (57, 58), which plays a critical role in the TG-induced ER stress mechanism (67). Although IM and TG function via different mechanisms, they both induce depletion of Ca^{2+} from ER stores.

The unfolded protein response (UPR) is initiated by a sensitization of the proteins accumulated in the ER lumen to the transmembrane protein kinase/endoribonuclease Ire1(α), the activating transcription factor 6 (ATF6), and the endoplasmic reticulum resident kinase (PERK) (21, 22). Ire1 generates spliced mRNA of the X-box binding protein (XBP1) using its RNase activity, and then the XBP1 protein upregulates the expression of GRP78 (21, 22). ATF6 is cleaved by site 1 protease (S1P) and site 2 protease (S2P) to generate a p50ATF6 fragment that has transcriptional activity. Upon cleavage, the p50ATF6 fragment upregulates the expression of GRP78 through an ER stress response element (ERSE) found in the promoter region of the GRP78 gene (21, 22). PERK has a kinase domain which phosphorylates the translational factor eIF2 α , thereby suppressing most of the *de novo* protein synthesis during ER stress but stimulating the translation of certain mRNAs, including ATF4 (21, 22). All of these processes are necessary to attenuate the accumulation of unfolded proteins during ER stress, especially Ire1 and ATF6 that are critical in the prevention of ER stress-induced apoptosis via upregulation of GRP78 expression (66).

The role of GRP78 in the prevention of apoptosis was indirectly confirmed in a study using nicotine as an antagonistic agent of the ER stress induced by TM and TG (50). As explained above, induction of GRP78 and apoptosis is only observed in response to ER Ca^{2+} depletion, but not in response to inhibition of protein glycosylation. Since nicotine inhibits expression of GRP78 in TM-treated cells, but not in TG-treated cells, the activation of pro-apoptotic caspase-12 was inhibited by nicotine only in TM-treated cells, but not in TG-treated cells (50). The protective effect of nicotine is mediated by a calcium influx activation of the PI 3-kinase/Akt-mediated pathway (50). Nicotine also suppressed the TM-induced, but not TG-induced, splicing of XBP1 mRNA or

production of cleaved ATF6 in PC12 cells (50), suggesting that nicotine halts TM-induced ER stress-mediated apoptosis via mechanisms closely related to the activation of the Ire1-XBP1 and ATF6 pathways, and this protective effect does not occur in TG-treated cells. Nicotine suppresses a common and weak step upstream of both the Ire1-XBP1 and ATF6 pathways which are required for the expression for GRP78 in TM-treated PC12 cells via mechanisms not yet determined (50), but does not affect it in TG-treated PC12 cells (50). This common step may be closely related to the accumulation of unfolded proteins in the ER during ER stress (50). The contribution of caspase-12 to the progression of ER stress induced apoptosis is only marginal in these cells (50). That explains why nicotine completely downregulates the activation of caspase-12 in PC12 cells, while weakly suppressing the TM-induced expression of GRP78 (50).

All these studies help to clarify why GRP78 on the cell surface responds to $\alpha_2\text{M}^*$ in ways that resemble those observed in cells undergoing ER stress (34, 37). First, binding of $\alpha_2\text{M}^*$ to GRP78 initiates a signaling cascade which results in an increase of $[\text{Ca}^{2+}]_c$ and Ire1 α , ATF6, and PERK expression (39). Also, eIF2 α phosphorylation occurs which would inhibit protein synthesis as observed in the UPR (39). ATF4 is also upregulated, leading to GADD34 upregulation which later restores protein synthesis through inhibition of eIF2 α (39). In contrast to what is observed in the UPR, $\alpha_2\text{M}^*$ -induced upregulation of Ire1 α , the apoptosis signal-regulating kinase 1 (ASK1), and the TNF receptor associated factor 2 (TRAF2) does not promote an increase in the c-Jun N-terminal kinase (JNK) or caspase-12 activation which lead to apoptosis (39). The induction of Akt, which phosphorylates and inactivates ASK1 and NF- κ B, upregulates the growth arrest and DNA-damage inducible factor beta (GADD45 β) and inhibits JNK, thereby blocking the pro-apoptotic signaling expected from activation of UPR proteins (39). In the ER, GRP78 and its partners Ire1 α , ATF6, and PERK span the ER membrane to facilitate signal transduction, but they are known to affect phosphatidylinositol-3-kinase (PI 3-kinase) or downstream Akt phosphorylation and NF- κ B induction. However, cell surface GRP78 forms a complex with the ER membrane DnaJ-like protein MTJ-1 and the G-protein- α -11 (G α q11) which facilitates through PI 3-kinase/Akt pathways as well as NF- κ B-dependent mechanisms (38, 40, 63). The result is that plasma membrane GRP78 signaling resembles the signals sent by GRP78 from the ER with the addition of an increase in IP3, Akt phosphorylation, NF- κ B, and a rise in cytosolic Ca^{2+} . The signal transduction cascade components induced by binding of $\alpha_2\text{M}^*$ to GRP78 is summarized in Fig. 1. The net result is an increase in DNA synthesis, protein synthesis, and cellular proliferation.

Topography of Cell Surface GRP78 Is Critical for its Activity as a Multireceptor

Although several reports identified GRP78 on the cell surface (12, 62), the first evidence that GRP78 exhibits the properties of a transmembrane protein was reported by Reddy *et al.* in 2003 (47). A map showing GRP78 transmembrane domains in CHO cell microsomes predicts a pattern suggesting that both N- and C-terminal regions are localized outside of the membrane (48). This topography was later confirmed by studies on human liver HepG2 cells and hepatocellular carcinoma tissue (8, 20). This model reveals that

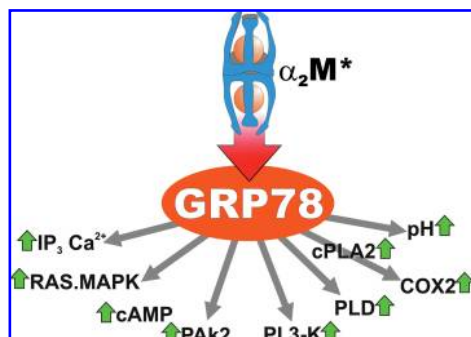


FIG. 1. Signal transduction cascade components induced by binding of α_2M^* to cell-surface GRP78 that result in an increase in DNA synthesis, protein synthesis, and cellular proliferation. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at www.liebertonline.com/ars).

GRP78 contains four hydrophobic domains (I through IV) that may form transmembrane helices (Fig. 2). In this figure we also show the GRP78 regions possibly involved in interactions with several of its ligands and autoantibodies.

Although both the ATP and the peptide binding domains appear to be localized on the extracellular domain of the plasma membrane, there is evidence suggesting that GRP78 functions as a receptor independently from its chaperone activity. For instance, GRP78 on the cell surface inhibits tissue factor procoagulant (TF) activity (61) via physical interaction between the TF extracellular domain and a region localized in the C-terminus of GRP78, distant from either its ATP or peptide binding domain (1).

Also, plasminogen K5 binds to a segment in the N-terminal region of GRP78 and microplasminogen binds to a segment in the C-terminal region of GRP78 (14). A region in microplasminogen including plasminogen amino acid residues Ser⁷⁵⁹–Phe⁷⁷⁸ was identified as the binding segment to GRP78 (14). This segment is homologous to amino acid sequence Gly¹⁰⁰–Phe¹¹⁹ of dengue virus serotype 2 viral protein coat (32). Therefore, a segment in the C-terminal region of GRP78 is the receptor for microplasminogen and dengue virus serotype 2. The peptide CTVLPGGYVRVC, homologous to the plasminogen sequence Ser⁷⁵⁹–Phe⁷⁷⁸ binds to GRP78 on the cell surface and is rapidly internalized via clathrin-mediated endocytosis (24). When conjugated to taxol, this peptide was extremely effective in promoting apoptosis of a human melanoma cell line, thereby demonstrating that the C-terminal region of GRP78 can be used as a target for delivery of peptide–drug conjugates in cancer (29).

Cell surface GRP78 is also an angiogenic receptor on endothelial cells (17). Roy, a 12 amino acid synthetic peptide selected from a phage display library (16), induced *in vitro* angiogenic activity under hypoxic conditions by increasing endothelial cell proliferation, migration, and tube formation (17). This peptide did not induce VEGF receptor gene expression, suggesting a possible VEGF-independent mechanism (16). The angiogenic peptide binds to an N-terminal region of GRP78 (17), thereby suggesting that GRP78-mediated angiogenesis is independent from functions performed by the C-terminal region. Since plasminogen K5 is a potent anti-angiogenic protein (11), and it binds to a site in the N-terminus of GRP78 (14), it is possible that K5 interferes with the binding of proteins normally engaged in angiogenic functions of GRP78.

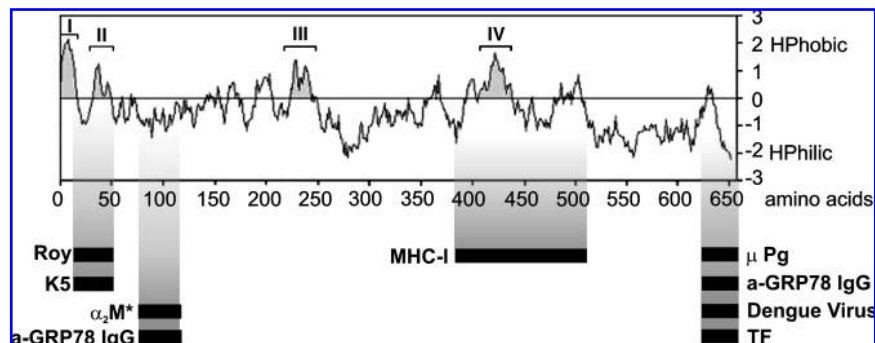
GRP78 also associates with MHC-I on the cell surface (59). Since GRP78 controls the folding of MHC-I (43), its association involves a site in the peptide binding domain, towards the C-terminus of GRP78. The complex between these two proteins serves as a receptor for coxsackie virus A9, which interacts only with GRP78, followed by internalization via MHC-I-associated endocytosis (60).

GRP78 at the cell surface forms a complex with the teratocarcinoma-derived growth factor I (Cripto) with important functions in vertebrate embryogenesis and the progression of human tumors, since it modulates the signaling of transforming growth factor β (TGF- β) superfamily members by forming complexes with some of these ligands and their respective signaling receptors (54). Formation of the GRP78/Cripto complex does not depend on GRP78 ER chaperone function (54), although it is known that a cysteine-rich CFC domain in Cripto is involved in the interaction (54). As discussed above, GRP78 also functions as a cell surface signaling receptor for α_2M^* (35, 36, 55, 68).

Autoimmunity to GRP78

Autoantibodies to GRP78 have been identified in serum from rheumatoid arthritis (2), prostate cancer (32), ovarian (9), and gastric cancer patients (46). The frequently opposite responses of GRP78 to autoantibodies against the N-terminus from prostate cancer (13), the amino acid sequence KDEL on the C-terminus (44), or an IgM from gastric cancer patients, which recognizes an O-linked carbohydrate moiety in GRP78 (46), suggests that the topography of GRP78 on the cell surface is an important factor that modulates its autoimmune response. GRP78 itself does not contain the sequence required for N-linked glycosylation (42). However, using the O-GLYCBASE database provided by SWISS PROT databank (www.expasy.org), we obtained a consensus sequence for the possible

FIG. 2. Hydropathicity transmembrane model of GRP78 using the Kyte–Doolittle method. Four putative hydrophobic domains (I–IV) are identified. Represented below are the ligands and antibodies thus far identified, showing the GRP78 amino acid patches involved in these interactions.



O-glycosylation of GRP78. This was the amino acid residue Thr⁶⁴³ which is preceded by three proline residues, an amino acid commonly found in sequences close to O-glycosylated serine or threonine residues (65). The amino acid Thr⁶⁴³ is localized only 12 amino acid residues upstream from GRP78 C-terminus. Therefore, it is possible to get O-glycosylated GRP78 on the cell surface, but its expression is possibly caused by aberrant glycosylation which is common in cancer cells (15).

We raised a sheep anti-GRP78 polyclonal antibody and purified two IgG populations. The first IgG was similar to the antibody isolated from the serum of prostate cancer patients (13) which recognizes an epitope in the N-terminal region of GRP78, and the second one recognized an epitope in the C-terminal region of GRP78 (13). Both antibodies were tested for their capacity to induce a Ca²⁺ signaling cascade in human prostate 1-LN cells. The antibody against the N-terminal region induced a rise in cytosolic Ca²⁺ which increased for 200 s reaching a peak which gradually decreased thereafter (Fig. 3A), whereas the antibody against the C-terminal region induced a rise in cytosolic Ca²⁺ which increased for 200 s reaching a constant plateau which did not change for up to 300 s (Fig. 3B). To generate different signals, both GRP78 N- or C-terminal regions must be part of separate signaling compartments, readily available to the different autoantibodies. A section of a human prostatic intraepithelial neoplasia (PIN) high grade was stained with the anti-GRP78 IgGs against the N-terminal (Fig. 4A) or the C-terminal regions (Fig. 4B). Both sections demonstrate diffuse staining with the antibodies, thereby confirming the availability of both GRP78 region on the cell surface.

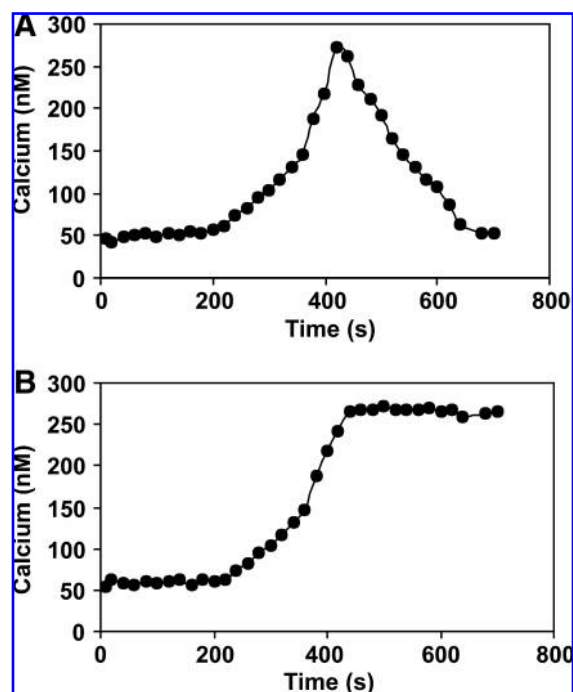


FIG. 3. (A) Changes in intracellular Ca²⁺ of human prostate cancer 1-LN cells exposed to a sheep anti-GRP78 IgG specific for an epitope in the N-terminal region of GRP78. (B) Changes in intracellular Ca²⁺ of human prostate cancer 1-LN cells exposed to a sheep anti-GRP78 IgG specific for an epitope in the C-terminal region of GRP78.

An explanation for the development of autoimmunity to GRP78 in humans can be obtained from animal models. There is evidence suggesting that spreading of humoral autoimmunity from Ro ribonucleoproteins to GRP78 occurs in mice immunized with Ro52 and Ro60 (25). These studies demonstrated the association of GRP78 to a carboxy-terminal region of Ro52 in apoptotic cell membrane blebs. This study was repeated immunizing mice with GRP78 or Ro52 and demonstrated reciprocity in the intermolecular spreading of B cell immunity between Ro52 and GRP78 (45). Humans suffering from two systemic rheumatic diseases, systemic lupus erythematosus and Sjögren's syndrome, show elevated levels of anti-Ro60 autoantibodies (6), but a correlation between these antibodies and autoimmunity to GRP78 remains to be determined.

However, a correlation between the regression of tumors and immunity against heat shock proteins is known (56).

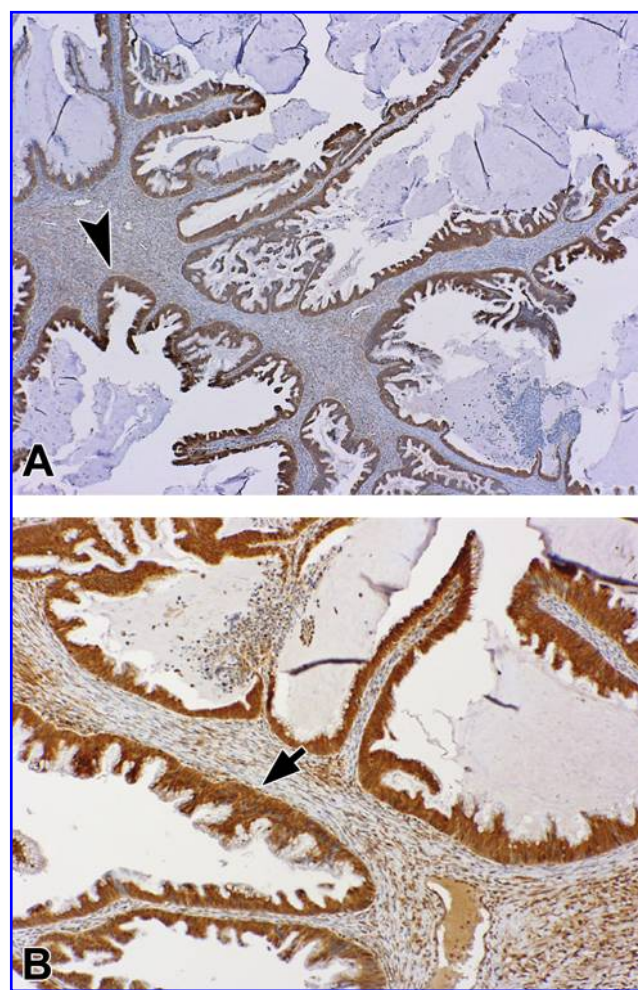


FIG. 4. Prostatic intraepithelial neoplasm (PIN) high grade. (A) Immunostaining of a PIN tissue section with a sheep anti-GRP78 IgG specific for an epitope on its N-terminal region showing diffuse expression of GRP78. (B) Immunostaining of a PIN section with a sheep anti-GRP78 specific for an epitope on its C-terminal region showing a diffuse reactivity (arrow), as observed above. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at www.liebertonline.com/ars).

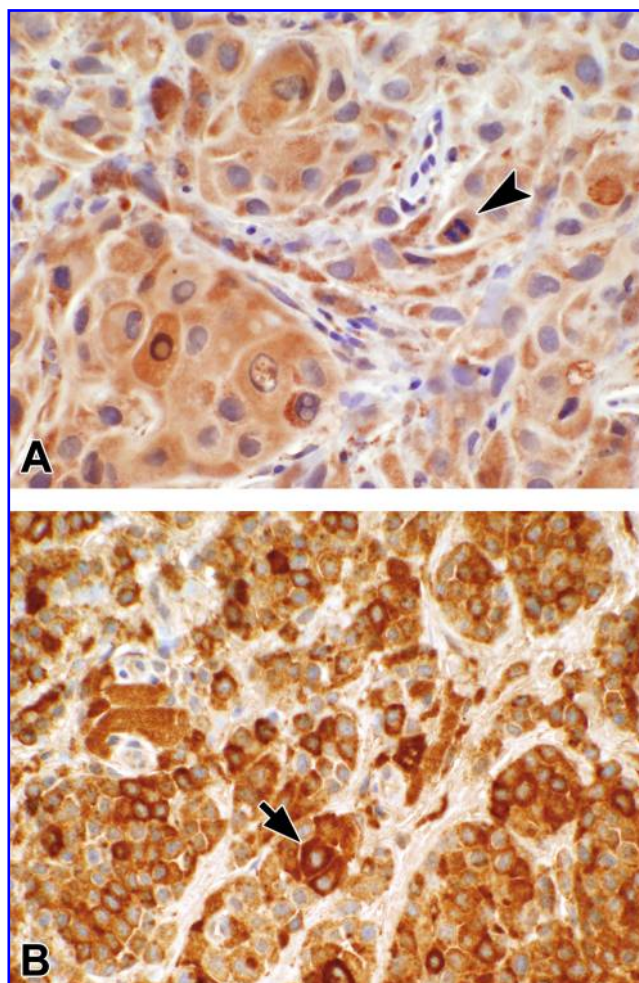


FIG. 5. Immunohistological analyses of sections of invasive nests of malignant human melanoma. (A) Staining with a sheep anti-GRP78 IgG specific for an epitope in the N-terminal region of GRP78 showing diffuse surface staining with some cells demonstrating a more pronounced perinuclear rim of immunoreactivity. There is a mitotic figure off center to the right (*arrow*). (B) Immunostaining of invasive nests of malignant melanoma with a rabbit anti-MTJ1 IGG specific for an epitope in the MTJ1 region comprising amino acids V110AIYEVLKDDERRQRYDDIL129 showing high expression of MTJ-1. There is a coarse, diffuse cytoplasmic staining (*arrow*). The nuclei are negative. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at www.liebertonline.com/ars).

These studies demonstrate that autoimmunity against tumor-derived heat shock proteins protect the host from fatal tumor loads. However, in prostate cancer patients an enhanced immune response against GRP78 increases tumor growth and metastases, and diminishes overall patient survival (33).

To understand this paradox, it will be necessary to understand how expression of GRP78 may assist the tumor cells to evade immune surveillance. One mechanism may involve the association of GRP78 with MHC-I on the cell surface (60). Expression of GRP78 on the surface is not dependent on MHC-I, because in its absence GRP78 expression is upregulated (60). In the absence of functional MHC-I, GRP78 is still

expressed on the cell surface in increased amounts, possibly acting as an alternative antigen-presenting structure, compensating for the loss of MHC-I molecules (60).

MHC-I downregulation is a widespread mechanism used by tumor cells to evade immune surveillance (4, 29, 31, 52, 53). Alterations in the expression of GRP78 may have important implications for MHC-I assembly, peptide loading, and presentation on the tumor cell surface and may be involved in the failure of the immune system to control tumor progression. The downregulation of MHC-I expression in cells overexpressing GRP78 not only protects the tumor cell from immune surveillance, but is also related to its capacity to initiate the signal transduction cascade discussed above. Association of GRP78 with MTJ-1 appears to be critical for this function, and a possible explanation for the appearance of such a protein complex on the cell surface can be inferred from studies using TG (22). The depletion of Ca^{2+} stores in normal cells by TG abolishes the retention of the KDEL-containing GRP78, and results in the appearance of the protein in the surface or the cell culture medium before inducing its synthesis (64). GRP78 is normally associated with the DnaJ protein P58 (IPK) in the ER (49). TG-treated cells showed the GRP78 was transported from the Golgi to p58-containing pre-Golgi intermediate compartment (IC), but was not transported further to the ER. Similarly, p58 that normally cycles between the ER, IC, and cis-Golgi, was largely depleted from the cell periphery and arrested in large-sized IC elements and numerous vesicles in the Golgi region, demonstrating that TG selectively blocks p53 recycling from the IC back to the ER (64). Therefore, the depletion of ER-Ca^{2+} induced by stress signaling facilitates dissociation of GRP78 from p58. At this point GRP78 possibly forms a complex with MTJ-1 (38), a different member of the DnaJ-like protein

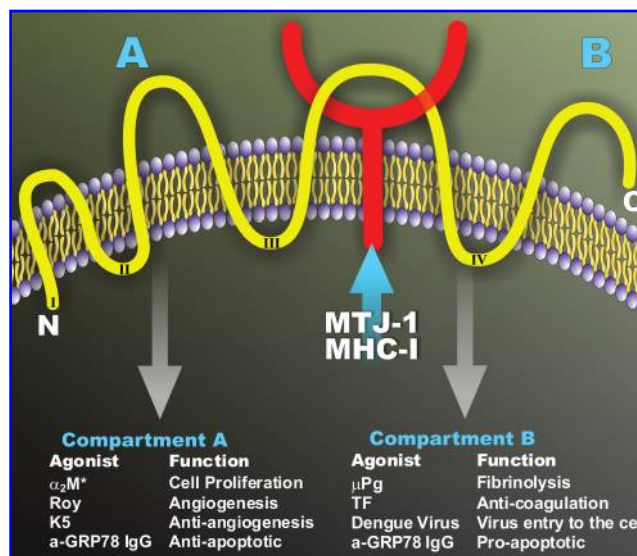


FIG. 6. Model of GRP78 inserted in the cell surface membrane, with its four hydrophobic domains and its two compartments (A) and (B), displaying their known agonists and functions. The function of these compartments would be determined by the co-chaperones MTJ-1 or MHC-I. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at www.liebertonline.com/ars).

family, which binds to a site upstream from its KDEL, C-terminus (7). This association presumably facilitates localization of GRP78 at the cell surface in conjunction with Gxq11 and facilitates signaling through PI 3-kinase, Akt, and NF- κ B (38, 40, 63). Tissue sections from invasive nests of a human malignant melanoma were stained with an antibody against the N-terminal region of GRP78 (Fig. 5A) and an antibody against the MTJ-1 region comprising amino acids V¹¹⁰ AIYEVLKDDERRQRYDDIL129 (Fig. 5B), showing that the GRP78 and MTJ-1 are not only present in highly metastatic human prostate 1-LN cells (67), but they also appear in malignant melanoma.

As discussed above, the topography of cell surface GRP78 adapted to function as a signaling receptor also seems to affect its immunogenicity. This is the case in prostate cancer patients who show high titers of an IgG that binds to the N-terminal region of GRP78 (13). This antibody recognizes a tertiary structure motif containing the amino acid sequence CNVKSDDKC (33). This arrangement is contained within the linear GRP78 primary amino acid sequence L⁹⁸IGRTWND PSVQQDIKFL¹¹⁵ (13). This antibody induces proliferation of several human prostate, breast, and melanoma cancer cell lines, protecting these cells from apoptosis via mechanism mimicking the function of α_2 M* (13). In addition to increasing its antigenic properties, cell surface GRP78 topography also appears to condition its physiological responses, as suggested by the different cytosolic Ca²⁺ wave patterns induced by antibodies against its N- or C-terminal regions.

In summary, expression of GRP78 on the cell surface is adapted for critical functions related to UPR in the normal cell. However, alterations in the pathway of trafficking towards the cell surface, as those observed in tumor cells, may induce changes in its structural topography, thus converting GRP78 into a receptor with additional functions not observed in the ER-linked chaperone. Changes in the surface topography of normal cells occur during their transformation to malignant cells (3), as a result of alterations in the expression of membrane proteins (48). Examples of these changes are the re-appearance in the expression of membrane fetal proteins (51) and alterations in the tertiary structure of cell-surface antigens induced by aberrant glycosylation (15). These changes have been also correlated with tumor progression, metastasis, and low patient survival rates (10), as is observed with GRP78 cell-surface expression in prostate cancer (33). It is clear from the evidence described above that the responses of GRP78 on the cell surface are channeled via two compartments, as demonstrated by the ability of the N- or C-terminal anti-GRP78 antibodies to induce different calcium signaling waves. In a hypothetical model (Fig. 6), we show GRP78 inserted in the cell surface membrane, with its four hydrophobic domains and its two compartments (A and B), displaying some of their agonists and their functions. The function of these compartments would be determined by the co-chaperones MTJ-1 or MHC-I, which bind to areas equidistant from either the N- or C-terminal regions of GRP78. When GRP78 is co-expressed with MHC-I, the C-terminal region of GRP78 may be recognized as an autoantigen by the immune surveillance, being the target of autoantibodies which ultimately induce apoptosis. When GRP78 is co-expressed with MTJ-1, the molecule evades the immune surveillance and becomes a multifunctional receptor whose functions include protection from apoptosis, stimulation of cell proliferation, control of coagu-

lation, and regulation of angiogenesis. The association between GRP78 and MTJ-1 would make also possible the internalization of dengue virus via a binding site specific for microplasminogen (14) in the C-terminal or the GRP78 receptor. Since GRP78 acts primarily as a protective molecule, the evidence suggests that the cell surface GRP78-MTJ-1 complex may play a major role in all these functions.

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Date of first submission to ARS Central, March 11, 2009; date of final revised submission, March 23, 2009; date of acceptance, March 28, 2009.

Abbreviations Used

$\alpha_2\text{M}^*$ = the activated form of α_2 -macroglobulin that binds to cellular receptors
 $[\text{Ca}^{2+}]_c$ = cytosolic free calcium
 ER = endoplasmic reticulum
 GRP78 = the glucose-regulated protein of 78 kDa
 HSP = heat-shock proteins
 IM = ionomycin
 MHC-I = the major histocompatibility complex class I
 MTJ-1 = the ER DnaJ-like protein 1
 p58 = the Golgi DnaJ-like protein p58
 TG = thapsigargin
 TM = tunicamycin
 VDAC = the voltage-dependent anion channel

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