The S100A7-c-Jun Activation Domain Binding Protein 1 Pathway Enhances Prosurvival Pathways in Breast Cancer

Ethan D. Emberley,1,3 Yulian Niu,2,3 Linda Curtis,2,3 Sandra Troup,2,3 Sanat K. Mandal,4 Jeffery N. Myers,1 Spencer B. Gibson,1,3 Leigh C. Murphy,1,3 and Peter H. Watson2,3

Departments of 1Biochemistry and Medical Genetics and 2Pathology, University of Manitoba; 3Manitoba Institute of Cell Biology, Winnipeg, Manitoba, Canada; 4Basic Medical Sciences, Memorial University of Newfoundland and College of the North Atlantic, Clarenville, Newfoundland, Canada; and 5Department of Head and Neck Surgery, University of Texas M.D. Anderson Cancer Center, Houston, Texas

Abstract

S100A7 is among the most highly expressed genes in preinvasive breast cancer, is a marker of poor survival when expressed in invasive disease, and promotes breast tumor progression in experimental models. To explore the mechanism of action, we examined the role of S100A7 in cell survival and found that overexpression of S100A7 in MDA-MB-231 cell lines promotes survival under conditions of anchorage-independent growth. This effect is paralleled by increased activity of nuclear factor-κB (3-fold) and phospho-Akt (4-fold), which are known to mediate prosurvival pathways. S100A7 and phospho-Akt are also correlated in breast tumors examined by immunohistochemistry (n = 142; P < 0.0001; r = 0.34). To explore the underlying mechanism, we examined the role of a putative c-Jun activation domain-binding protein 1 (Jab1)—binding domain within S100A7 using a panel of MDA-MB-231 breast cell lines stably transfected with either S100A7 or S100A7 mutated at the Jab1 domain. Structural analysis by three-dimensional protein modeling, immunoprecipitation, and yeast two-hybrid assay and functional analysis using transfected reporter gene and Western blot assays revealed that the in vitro effects of S100A7 on phospho-Akt and the nuclear factor-κB pathway are dependent on the Jab1-binding site and the interaction with Jab1. Enhanced epidermal growth factor receptor signaling was also found to correlate with the increased phospho-Akt. Furthermore, the Jab1-binding domain is also necessary for the enhanced tumorigenicity conferred by S100A7 expression in murine xenograft tumors in vivo. We conclude that the S100A7-Jab1 pathway acts to enhance survival under conditions of cellular stress, such as anoikis, which may promote progression of breast cancer. (Cancer Res 2005; 65(13): 5696-702)

Introduction

S100A7 is relatively unique among the S100 gene family in terms of structure and its prominent association with early stages of carcinoma (1). Originally associated with abnormally differentiating keratinocytes in psoriasis, "psoriasin" (S100A7) has since been found to be expressed in association with neoplasia in several tissues, including squamous carcinomas in skin (2, 3) and bladder (4), as well as adenocarcinomas of the breast (5, 6). Although the protein is not expressed in normal luminal epithelium, increased expression occurs in parallel with early stages of tumor progression, and S100A7 can be among the most highly expressed proteins in preinvasive carcinoma in situ in both skin (3, 7) and breast (8, 9). With progression to invasive carcinoma, expression is often diminished, but persistent expression can occur in subsets of invasive breast carcinomas where S100A7 is associated with a worse clinical outcome (10).

The action of S100A7 in breast cells may be exerted through an interaction with the multifunctional signaling molecule c-Jun activation domain-binding protein 1 (Jab1). S100A7 expression in the MDA-MB-231 cell model is associated with altered activity of activator protein-1 (AP-1) and hypoxia-inducible factor-1 (HIF-1) transcription factors and their downstream genes, consistent with the downstream pathways believed to be regulated by Jab1 (11). These molecular changes associated with expression of S100A7 are correlated with changes in several biological features in vitro, including decreased adhesion, increased growth, and increased invasiveness. However, the magnitude of these in vitro effects is relatively modest in comparison with a significant overall effect of S100A7 on tumorigenesis in an in vivo xenograft model (11). This suggests that S100A7 may exert other effects that are more important and primarily manifested in the context of the more complex and three-dimensional in vivo environment.

While considering the function of S100A7, we have observed that S100A7 expression can be prominent within areas of tumors that show loss of adhesion and increased apoptosis and necrosis. These are particularly prominent features within high-grade ductal carcinoma in situ (DCIS), but dyskeratosis and loss of cell adhesion are also common features within preinvasive epidermal squamous carcinoma and inflammatory skin lesions, including psoriasis and other idiopathic dermatoses, where S100A7 is highly expressed (12). In breast cells, overexpression is associated with diminished adhesion (11) and S100A7 is induced under conditions of cellular stress, including loss of adhesion (8). In this study, we have examined the relationship between S100A7 and cellular response to stress related to loss of adhesion and the possible role of the S100A7-Jab1 pathway in mediating a prosurvival effect in breast cancer.

Materials and Methods

Mutation of the c-Jun activation domain-binding protein 1—binding site in S100A7 and molecular modeling. The complete open reading frame sequence for S100A7 was cloned previously into the pcDNA3.1 Zeo (Invitrogen, Canada) expression vector (11). Site-directed mutagenesis was done using the Transformer Site-Directed Mutagenesis kit (Clontech, Mountain View, CA) according to the manufacturer's instructions. The three amino acids (Asp58, Leu80, and Gin89) comprising the putative Jab1-binding domain (13) were altered to encode Gly58, Met80, and Lys89, respectively, using mutagenic oligonucleotides to produce the plasmid...
Western blot using a specific polyclonal anti-S100A7 antibody (10, 11) and 231-PTM.14; PTM = psoriasin triple mutant). This was determined by stably expressing mutated S100A7 (S100A7mut) were generated by trans-PCR) and Western blot; data not shown]. MDA-MB-231 clones stably lines MDA-MB-231 and MDA-MB-468 were cultured as described previously (9). The former cell line is negative for S100A7, whereas the latter expresses resulting molecules was optimized using molecular mechanics (MM2) and the residues and to build the three-dimensional models. The energy of the built based on the X-ray structures (Protein Data Bank codes 3PSR and 36x75). Three-dimensional models of S100A7 and mutant S100A7 (S100A7mut) were calculated relative viability reflects the proportion of viable cells for 300 minutes. Tumor cell staining was scored as described (10) to generate a quartile score) were used to define positive status in separate analyses because a wide range of cut points have been used in the literature (17, 18). Statistical analysis was done with Prism GraphPad software and using Spearman correlation and Fisher's exact tests as appropriate.

Reverse transcription-PCR. Total RNA was isolated using TRIzol (Sigma) from each clone. RT-PCR reactions were done as described previously (11). Briefly, total RNA (1 µg) was reverse transcribed in duplicate from triplicate samples. PCR was done using specific primers for EGFR: EGFR-upper (sense) 5'-CACACAACCAAGGCGAAGGAT and EGFR-lower (antisense) 5'-ACATTGGCGTGGACAGGAA or glyceraldehyde-3-phosphate dehydrogenase (GAPDH): GAPDH-upper (sense) 5'-GAGGGTGTAACGACAGGAA and GAPDH-lower (antisense) 5'-CTCTTGTCTTGGTGTTTGG. Reactions were stopped during the log-linear stage of PCR amplification and samples were electrophoresed through a 1% agarose gel that was poststained with ethidium bromide for DNA visualization. Images were captured using a LCD camera and MCID software (Imaging Research, Canada).

**Results**

S100A7 expression is associated with increased survival under anchorage-independent conditions. We observed that S100A7 expression in some lung and breast tumors can be prominent in apparently detached but morphologically viable tumor cells adjacent to and within regions of necrosis and/or increased apoptosis (Fig. 1A). To determine if S100A7 enhanced viability under

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conditions of decreased cellular adhesion, MDA-MB-231 cells expressing S100A7 were assessed after 72 hours of growth under anchorage-independent conditions (Fig. 1B). Two independent cell clones (231-PTM.2 and 231-PTM.14) were characterized and shown to express comparable levels of S100A7mut to the level of S100A7 in the previously established MDA-MB-231 clone 231-HP2 (Fig. 2A), but both S100A7mut clones showed no difference in growth rate when compared with parental cells (data not shown). The two independent clones constitutively expressing S100A7 (231-HP1 and 231-HP2) had a similar 1.32 ± 0.053-fold increase (mean ± SD, n = 3) and 1.34 ± 0.036-fold increase, respectively, in viability compared with nonexpressing control (231-neo) and MDA-MB-231 parental cells (Fig. 1C). Two clones expressing S100A7mut were also assessed under the same conditions. They exhibited a partial increase in their relative viability, with rates that were less than those shown by S100A7-expressing lines (Fig. 1C). The mean ± SD (n = 3) relative loss of viability for 231-PTM.2 and 231-PTM.14 were 1.174 ± 0.034 and 1.193 ± 0.022, respectively. These data suggest that S100A7 confers a survival advantage in cells subjected to anchorage-independent conditions.

Mutation of the c-Jun activation domain-binding protein 1–binding domain of S100A7 abrogates the interaction with c-Jun activation domain-binding protein 1. We have identified previously an interaction between S100A7 and Jab1 and an association between S100A7 expression and alteration of AP-1 and HIF-1 activities. We therefore postulated that the S100A7-Jab1 interaction might be necessary for the effect on survival pathways. Sequence analysis of S100A7 reveals a domain within the COOH-terminal region that is present in other proteins that physically interact with Jab1 (11, 13). To test the role of this putative Jab1-binding domain in mediating the interaction with S100A7, we first did three-dimensional protein modeling of the potential effect of mutation of the three key amino acids within this domain (13) using the known resolved structure for the S100A7 protein (14). Comparison of the three-dimensional models for S100A7 and S100A7mut proteins confirmed that mutation within this domain does not significantly alter the overall protein structure. However, regional changes in conformation are predicted to occur (Fig. 3A). A minimal structural error of 0.1767 as determined by root mean square is calculated when the three residues Asp58/Gly58, Leu80/Met80, and Gin90/Lys90 are superimposed on each other. Similarly, changes occur around the metal sites for Ca2+ and Zn2+ and structural error of 0.3981 is predicted on metal sites when the three metal cations are superimposed (data not shown). These three-dimensional modeling data predict that mutation of the three key amino acids within the Jab1-binding domain would not substantially alter overall protein structure but would result in significant regional changes in conformation.

To next assess the effect of mutation of this domain on the Jab1 interaction, we mutated the putative Jab1-binding domain in both the full-length S100A7 cDNA and a cDNA representing the COOH-terminal portion alone and coexpressed these proteins separately with Jab1 in the yeast two-hybrid assay. We found that in both contexts these mutations abolished the interaction between S100A7 and Jab1 (Fig. 3B). To further test the role of this same domain within human breast cells and to enable subsequent functional analysis, we then developed MDA-MB-231 cells with stable expression of the full-length mutant S100A7 cDNA (S100A7mut). The clones 231-PTM.2 and 231-PTM.14 were then assayed for an interaction between S100A7mut protein and Jab1 by coimmunoprecipitation (Fig. 3C). Under the same conditions whereby endogenous and transgene-derived S100A7 protein could be coimmunoprecipitated with Jab1 from MDA-MB-468 and 231-HP2 cell clones, respectively, mutation of the Jab1-binding domain within S100A7 significantly reduced the association between S100A7mut and Jab1 in the 231-PTM.2 and 231-PTM.14 clones. However, higher levels of expression seen in 231-PTM.14 cells (Fig. 3A) revealed a limited residual interaction (Fig. 3C).

The S100A7-c-Jun activation domain-binding protein 1 interaction can stimulate activation of Akt and nuclear factor-κB activity. The activation of the Akt kinase is thought to be a major factor in promoting survival in epithelial cells under anchorage-independent conditions (19). We therefore assessed Akt expression and phosphorylation status in MDA-MB-231 cell clones expressing S100A7 and S100A7mut proteins by Western blot. Total Akt levels were similar in all cell clones; however, a 4.3 ± 0.4-fold increase (mean ± SD, n = 3) in the relative amount of phospho-Akt (Ser473) was observed in both clones expressing S100A7 when...
Figure 2. S100A7 expression stimulates Akt and NF-κB pathways. A, relative expression of S100A7 or S100A7\textsuperscript{mut} proteins in a panel of MDA-MB-231 cell lines as indicated by the key. S100A7 expression is associated with increased amounts of phospho-Akt (without any change in total Akt or PTEN levels), a reduction in IκBα, and a reduction in p27. S100A7-expressing cells were also found to have higher levels of total and phospho-c-Jun without any change in phospho-JNK levels. In comparison, S100A7\textsuperscript{mut} expression confers no similar changes in the above protein levels. B, relative NF-κB activity in the same panel of MDA-MB-231 cell lines as determined by transient reporter gene transfection assay. Columns, mean of triplicate independent experiments; bars, SD. *P*s were determined by t test.

An intact c-Jun activation domain-binding protein 1–binding domain in S100A7 is required for enhanced tumorigenesis in vivo. To determine if abrogation of the S100A7-Jab1 interaction affects promotion of tumorigenesis in vivo, the S100A7\textsuperscript{mut}-expressing MDA-MB-231 cell lines were injected into the mammary fat pad of nude mice and the generation of tumors was assessed in comparison with S100A7-expressing lines and control parental cells (Fig. 5). All cell lines generated tumors that were detectable in most animals by 3 weeks. However, S100A7 cells developed larger tumors significantly more rapidly than the S100A7\textsuperscript{mut} cells, which in turn developed tumors similarly to and showed no significant difference from parental controls (Fig. 5). At 6 weeks postinjection, tumors >1.5 cm had developed in 5 of 5 and 3 of 5 231-HP1 and 231-HP2 cell-injected mice, respectively, but in 0 of 5, 1 of 5, and 0 of 5 for 231-PTM2, 231-PTM14, and parental control MDA-MB-231 cell-injected mice. This same difference was reflected in a significantly (*P = 0.0039) worse overall survival time for animals injected with S100A7 cells compared with parental control cells as shown previously (11). However, tumors derived from both S100A7\textsuperscript{mut} cells showed no significant difference from the parental control (Fig. 5).

S100A7 induction of phospho-Akt is dependent on phosphatidylinositol 3-kinase activity. Akt activation is typically the consequence of extracellular signals that act through a range of cell surface receptors to stimulate PI3K, the upstream positive regulator of Akt. Alternative mechanisms also exist, including reduced activity of PTEN, a negative regulator of Akt. We observed that PTEN levels were unaffected by the expression of S100A7 or S100A7\textsuperscript{mut} (Fig. 2A), but inhibition of PI3K by LY294002 significantly reduced or abolished the expression of phospho-Akt associated with S100A7 (Fig. 6A). We next considered the possible role of the EGFR signaling pathway that is one of many pathways that might act to stimulate PI3K, because AP-1 is essential for the transcriptional regulation of the EGFR ligand, EGF (23). We observed an increase in EGF mRNA levels associated with S100A7 but not S100A7\textsuperscript{mut} (Fig. 6B) and this correlated with induction of p21 protein, a downstream marker of EGFR signaling in the same cells. Additional experiments confirmed that all cell clones express EGFR at equivalent levels (Fig. 6C). Treatment of the different cell clones with a specific EGFR inhibitor (BPIQ) revealed that both baseline and induced phospho-Akt amounts in all cell clones could be significantly reduced regardless of whether S100A7 was present or was mutated (Fig. 6D). These data suggest that in the MDA-MB-231 cell line model S100A7 induces phospho-Akt compared with parental and 231-neo control cells, but no increase in phospho-Akt was present in either clone expressing S100A7\textsuperscript{mut} (Fig. 2A).

NF-κB is also a major factor in promoting cell survival (20) and Akt can influence NF-κB via phosphorylation of the NF-κB repressor IκBα (21). Western blot analysis of MDA-MB-231 cell clones shows that there is a reduction in IκBα in the presence of S100A7 but not S100A7\textsuperscript{mut} protein expression (Fig. 2A). We then assessed NF-κB activity by transient transfection of a NF-κB reporter plasmid. Cells expressing S100A7 protein show a 3.4 ± 0.7-fold induction (mean ± SD, n = 4) of NF-κB activity (Fig. 2B). By comparison, no such increase is observed in cells expressing S100A7\textsuperscript{mut}.

We have reported previously that S100A7 expression correlates with induction of c-Jun-related AP-1 activity and down-regulation of p27Kip1 (11). We observed similar changes here with reduction in p27Kip1 and induction of phospho-c-Jun associated with S100A7 but not S100A7\textsuperscript{mut} protein expression (Fig. 2A). The increase in phospho-c-Jun in S100A7 clones is paralleled by a similar increase in total c-Jun levels. This is not attributable to an increase in the phosphorylation status of JNK, as JNK is not altered by S100A7 or S100A7\textsuperscript{mut} expression (Fig. 2A), but JNK phosphorylation can be increased in these same cells by transfection of mitogen-activated protein kinase kinase kinase 1 (data not shown). This is compatible with Jab1 stabilization of c-Jun and through direct phosphorylation by a JNK-independent mechanism (22).

These data suggest that S100A7 expression is associated with induction of both phospho-Akt and NF-κB activity and that the induction of these prosurvival pathways as well as AP-1 is dependent on an intact Jab1-binding domain within S100A7.

S100A7 is associated with an increase in phospho-Akt in breast tumors. To examine if a similar relationship between S100A7 and phospho-Akt could be detected in vivo within human breast tumors, we examined their expression within a tumor tissue array. S100A7 expression was seen in 78 of 142 invasive carcinomas and phospho-Akt was expressed in 108 of 142 tumors, comparable with the frequencies observed previously within breast tumors by ourselves (10) and others (17) for these proteins. Overall, there was a significant correlation between levels of expression for S100A7 and phospho-Akt within this cohort (r < 0.0001; r = 0.34; Spearman correlation). The association between S100A7 and phospho-Akt status was also evident in categorical analysis and remained significant (P < 0.0001, Fisher’s exact test) for all of the three cut points used to distinguish positive from negative phospho-Akt status (Fig. 4).
through a classic PI3K-dependent pathway. This may in part be attributable to the autocrine effect of AP-1 induction of EGF leading to an increase in the stimulation of EGFR. When EGFR activity is elevated, it promotes the stimulation of PI3K through phosphorylation events, which in turn result in an enhancement in the phosphorylation status of Akt.

Discussion

In neoplasia, S100A7 is expressed in several tumor types. In addition, S100A7 is induced and sometimes highly expressed with abnormal differentiation in inflammatory dermatoses (12) and in response to diverse stress stimuli, including loss of substrate attachment (8) and UV-B radiation (24) in either breast or skin.

Figure 3. The putative Jab1-binding domain in S100A7 is required for the interaction with Jab1. A, three-dimensional ribbon model to illustrate the overall similarity and regional differences between the predicted molecular structures of S100A7mut compared with S100A7 protein. Structures are aligned in the same orientation. B, yeast two-hybrid control plate (left) shows that the presence of both a bait and a prey plasmid are required for growth in the absence of tryptophan and leucine. However, both the full-length and the COOH-terminal half of S100A7 can interact with Jab1 (middle), but mutation of the Jab1-binding domain prevents an association between these proteins as determined by inactivation of the histidine reporter gene resulting in the absence of growth (middle). Right, plate sector key diagram. C, communoprecipitation reveals that although S100A7 and Jab1 interact in human breast cell lines that express endogenous (MDA-MB-468) or transgene-derived S100A7 (231-HP1 and 231-HP2) no significant interaction is seen in cells expressing S100A7 with mutation of the Jab1-binding domain (231-PTM.2 and 231-PTM.14, respectively).

Figure 4. S100A7 expression is correlated with increased phospho-Akt in human breast tumors. A, histogram representation of the relative levels of phospho-Akt expression (p-Akt immunohistochemistry score) among S100A7-negative (n = 64) and S100A7-positive (n = 78) tumor subgroups as determined by immunohistochemistry in a tumor tissue microarray. B, contingency table analysis of S100A7 and phospho-Akt status. S100A7 and phospho-Akt immunohistochemistry scores of >0 were used to define a tumor as positive and statistical significance was tested by Fisher’s exact test.

Systems. Stress is also a prominent factor within the neoplastic epithelium and particularly in preinvasive lesions where there is cellular crowding, loss of attachment, and necrosis in a restricted but expanding cell population, disconnected from the nutrient and mechanical support of the stroma by an intact basement membrane. We and others (8) have speculated that up-regulation of S100A7 in preinvasive carcinoma is indicative of this stress.

S100A7 may play a role as a secreted chemotactic factor (25), yet more recent data also point to an intracellular action. S100A7 has been associated with several proteins in vitro (11, 26–29). However, only the S100A7-Jab1 interaction has yet been associated with any functional effect (11). Jab1 was originally identified as a factor influencing c-Jun stimulated transcription of AP-1-regulated genes (30). It is now known that Jab1 is a component of a multimeric protein complex (the COP9 signalosome) and that Jab1 interacts with many components of cell signaling pathways (31). This may be in the context of either phosphorylation or proteasomal activities, as Jab1 is also the only known deneddylating protein active in control of the SCF-cullin ubiquitin ligases (32).

We have now shown that S100A7 can promote survival under anchorage-independent conditions in breast cancer cells (33). This survival function, like growth and invasion, is coupled to up-regulation of Jab1 downstream pathways, including AP-1 [as described previously (16)] and NF-κB, and induction of phospho-Akt via a PI3K-dependent mechanism. We have also now established that the above effects are largely dependent on an intact Jab1-binding site within the S100A7 protein. This binding site was originally identified through site-directed mutagenesis as present in both p27 and c-Jun and also necessary for their interaction with Jab1 (13). In p27, triple mutations at the key amino acids within this site (Asp108, Leu130, and Asn140) were shown not to substantially alter the gross protein conformation but reduced the binding ability with Jab1 to 15% of the wild-type (13). Our data here also show that mutation of the three key amino acids that define this same motif in S100A7 leaves the overall predicted three-dimensional protein structure unchanged but causes subtle regional changes in particular around the metal-binding sites. Nevertheless, this is sufficient to significantly reduce the in vitro interaction with Jab1 and significantly diminishes signaling (e.g., induction of phospho-c-Jun, Akt, and NF-κB activity) and biological (e.g., tumorigenesis in mice) effects of S100A7. The difference in tumorigenic capacity observed in vivo between...
S100A7 and S100A7mut-expressing cells is attributable to the intact Jab1-binding domain in the former cells. Whereas S100A7-expressing cells were found previously to have a modest 1.3-fold increase in their growth rate in vitro (11), S100A7mut-expressing cells showed no difference in growth rate compared with MDA-MB-231 parental cells (data not shown). It is therefore likely that the significantly enhanced tumorigenicity related to S100A7 expression that is seen in the in vivo setting is related to other properties than only the increased growth rate. The S100A7-Jab1 interaction results in changes in several signaling pathways and the activation of pro-survival pathways related to Akt and NF-κB may play an important additional role in promoting tumorigenesis under in vivo conditions.

To understand the possible connections between S100A7 expression and survival in breast cancer cells, it may be relevant to consider similar pathways in keratinocytes in the skin under circumstances where S100A7 is also highly expressed. As already noted, these include inflammatory dermatoses (34) and the response to UV-B-related stress (24), resistance to anoikis, and response to wound healing, where altered signaling pathways have been relatively well defined (23, 35–37). In these circumstances, induction of Akt, NF-κB, and AP-1 are often critical components. In breast cells, Akt and NF-κB have also been implicated in cell survival under anoikis conditions (38, 39); however, phosphorylation of Akt may not necessarily be critical for enhanced survival (40).

A link between Jab1 and Akt has not been identified previously. We can speculate that in breast cells S100A7-mediated induction of phospho-Akt is attributable to increased production of AP-1 and possibly also NF-κB-regulated growth factors and cytokines that can act in an autocrine fashion to stimulate PI3K through their cognate receptors. One such pathway, based on our current data, may be the EGF-EGFR-PI3K signaling pathway. A similar autocrine effect has recently been recognized in relation to overexpression of another EGFR ligand in breast cells (41). We have shown here that the in vitro relation between S100A7 and increased phospho-Akt can also be identified in vivo in Erα-negative tumors. Akt activation is known to promote localization of p27 to the cytoplasm (42) and reduced p27 has been observed in Erα-negative tumors (43). We have also shown previously that S100A7 is associated with reduced p27 in DCIS and invasive breast cancer (16). Jab1 might also influence NF-κB activity directly by binding to the Bcl-3 protein, which enhances p50-Bcl-3-DNA complex formation, thereby potentially influencing NF-κB activity (44). The effect of S100A7 on NF-κB is consistent with the known role of NF-κB in promoting cell survival in breast cancer (45). S100A7 expression is strongly correlated with the Erα-negative phenotype in both DCIS and invasive disease (9). In Erα-negative breast cell lines, a critical role for EGFR-NF-κB signaling has been defined in mediating cell cycle progression (46) and resistance to chemotherapeutic agent–induced apoptosis (47). ErbB-2 signaling can also alter NF-κB activity, which correlates with reduced apoptosis. More recently, it has also been shown that an Erα-negative subset of invasive tumors shows increased activation of NF-κB. In this small series (45), 56% of ER-negative invasive tumors manifested higher levels of NF-κB activation, which is similar to the frequency of S100A7 expression in the same tumor phenotype.

Promoting cell survival is a role previously suspected for several other S100 family proteins and S100A7 is one of many similar factors that may influence the balance between survival and apoptosis in breast cancer. However, S100A7 is important because, as several groups have confirmed using distinct technical approaches, S100A7 is among the most highly expressed mRNAs and proteins in DCIS and is frequently differentially expressed during the transition to invasive carcinoma in skin and breast (6–8, 48, 49). The S100A7-Jab1 prosurvival pathway therefore has the potential to have a significant impact in promoting breast cancer at a critical stage in tumor progression.


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