



# Towards molecular mechanisms regulating the expression of galectins in cancer cells under microenvironmental stress conditions

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**Abstract** Galectins, a family of soluble  $\beta$ -galactoside-binding proteins, serve as mediators of fundamental biological processes, such as cell growth, differentiation, adhesion, migration, survival, and death. The purpose of this review is to summarize the current knowledge regarding the ways in which the expression of individual galectins differs in normal and transformed human cells exposed to various stimuli mimicking physiological and pathological microenvironmental stress conditions. A conceptual point is being made and grounded that the modulation of galectin expression profiles is a key aspect of cellular stress responses. Moreover, this modulation might be precisely regulated at transcriptional and post-transcriptional levels in the context of non-overlapping transcription factors and miRNAs specific to galectins.

**Keywords** Galectins · Cellular stress responses · Hypoxia · Cancer · Apoptosis · Cell survival · Transcription factors · miRNA

## Introduction

Animal and human cells respond to exogenous stressors of a chemical and physical nature through a number of specific adaptive stress response pathways that attempt to mitigate damage and maintain or re-establish homeostasis [1]. These pathways are highly conserved in most metazoans, including mammals, highlighting the central and obligatory roles

played by such pathways in organisms' responses to environmental insults. At the molecular level, cells use stress-specific sensors that signal through individual transcriptional factors such as Nrf2 (oxidative stress), HSF-1 (heat shock response), p53 (DNA damage), HIF-1 (hypoxia), MTF-1 (metal stress), NFAT5 (osmotic stress), and NF- $\kappa$ B (inflammation stress). These factors may crosstalk with XBP-1/ATF6/ATF4, controlling unfolded protein response (UPR) due to the accumulation of damaged, aggregated, or misfolded proteins [2]. Although different stress stimuli engage on default own primary sensors, a global remodeling of stressed cells might include a common molecular signature due to the ultimate selection between only two choices: cell death or cell survival. Recent findings indicate that specific glycosylation patterns of cellular proteins, as well as changes in the expression of glycan-binding proteins (lectins), may accompany the stress responses, suggesting the glycobiological mechanisms of such regulation. Animal lectins are central to these mechanisms and consist of at least 15 diverse families of proteins, each with characteristic structural motifs represented by one or several carbohydrate-recognition domains (CRDs) specific to different glycans [3].

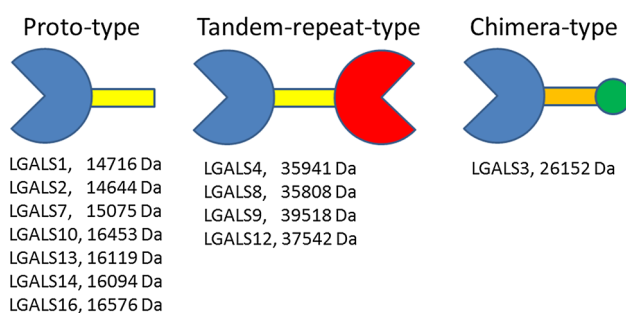
Galectins, a family of soluble  $\beta$ -galactoside-binding proteins, have attracted special attention over the last decade due to the role they play in the regulation of fundamental biological processes, such as cell growth, differentiation, adhesion, migration, survival, and death [4, 5]. The conventional classification of galectins was originally proposed by Hirabayashi and Kasai [6]. This classification considers the structural features of these proteins, distinguishing three subfamilies: proto-type galectins (galectin-1, -2, -5, -7, -10, -11, -13, -14, -15, and -16) with one carbohydrate-recognizing domain (CRD), tandem-repeat galectins (galectin-4, -6, -8, -9, and -12) with two homologous CRDs, and a chimeric galectin-3

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with one CRD linked to a non-lectin N-terminal domain (Fig. 1). Human cells are known to express 12 of these galectins, missing murine galectin-5 and -6 and ruminant galectin-11 and -15. Proto-type galectins are smaller proteins (14–16 kDa) than chimeric (26 kDa) and tandem-repeat galectins (~40 kDa). However, they can form homodimers and multimers and cross-link structures that contain the sugar galactose on the cell surface and within the extracellular matrix, resulting in a variety of specific cellular responses, which regulate cell survival and programmed cell death (apoptosis). For instance, extracellular galectins can stimulate signaling systems, leading to the generation of reactive oxygen species (ROS), the mobilization of intracellular calcium, and the secretion of vascular endothelial growth factors (VEGFs) [7–9]. Galectins can also function intracellularly, controlling apoptosis and mRNA splicing processes in a glycan-independent manner [10, 11]. Most galectins possess multiple cellular stress-related functions, which are associated with stimulatory and inhibitory response mechanisms depending on the cell type and galectin localization (Table 1) [3, 12–15]. Of interest, apoptotic sensitivity of immune cells to tumor-derived galectins has been proposed as a potential mechanism assisting tumor cells to survive and escape from immune surveillance in the body [12].

Galectin expression profiles differ in normal and tumorous tissues [16, 17] and between different cell lines [18–20]; they can undergo a variety of changes under the stress conditions encountered in tumor microenvironments or those associated with inflammation, fibrosis, or cardiovascular and other diseases [21]. For instance, a specific and readily detectable 5- to 30-fold increase in the



**Fig. 1** Basic structure and molecular characteristics of human galectins. Carbohydrate-recognizing domains (CRDs) are schematically presented as *pacman*-like symbols (*purple* and *red*) linked to non-lectin domains (showed as *yellow/orange* bars). Proto-type galectins can form noncovalent homodimers (not shown), while tandem-repeat galectins contain two covalently linked homologous CRDs. CRD of chimera-type galectin-3 is linked to a collagen- $\alpha$ -like sequence (*orange*) followed by a small N-terminal end (*green circle*) mediating the formation of oligomers. Sizes of human galectin molecules were derived from the GeneCards Database at [www.genecards.org](http://www.genecards.org)

circulating levels of several galectins has been reported in the bloodstream of patients with various types of cancers, including breast [22], head and neck [23], bladder [24], melanoma [25], pancreatic [26, 27], and colorectal [28–30] carcinomas. These observations have prompted the development of galectin-targeting drugs, some of which have been tested in clinical trials [31]. In fact, other studies have demonstrated that stress stimuli can induce non-uniform changes in the expression of various galectin genes, which can be tentatively classified as upregulated, downregulated, and constitutive galectins [32]. For instance, the monocytic differentiation of HL-60 cells was accompanied by the upregulation of galectin-3 and the down-regulation of galectin-9 mRNA expression, while no changes or expression were detected with galectins -1, -2, -4, -7, and -8 [33]. This conceptual point has also readily been demonstrated in studies with prostate carcinoma tissues, showing that, as the cancer progressed toward more aggressive stages, the level of galectin-1 increased, the levels of galectins -3, -4, -9, and -12 gradually decreased, and galectin-8 remained stably expressed [34]. As such, many fundamental questions about the cell stress biology of galectin proteins remain insufficiently answered, leaving a number of unresolved issues and limiting the practical application of galectin-based therapies. First, we do not know why cells express as many as 16 different galectins and how/whether these galectins interact with each other. Second, we do not know how a global network of galectins is remodeled in cells under stress conditions and whether these changes can provide a biomarker code or molecular signature of cellular stress responses. Third, we do not know what signaling mechanisms regulate the differential expression of galectin genes in cells and whether a collaboration between common and diverse stress-sensitive signaling pathways is required. Considering recent comprehensive reviews and books on galectins [3, 5, 12–17, 35–37], the main goal of this short review is to focus specifically on the stress-induced changes in the expression of individual galectins in human cells including cancer cell lines and to point out some potential regulatory mechanisms likely deserving of attention in elucidating the crosstalk between various members of the galectin network at the transcriptional and post-transcriptional levels.

## Proto-type galectins

The expression of many human proto-type galectins (-1, -2, -7, -10, and -13), with the exception of the relatively less studied galectins 14 and 16, has been reported to be readily sensitive to a variety of stress stimuli, including hypoxia, redox stress, ER stress, and DNA damage, as well as to stimuli inducing cell differentiation.

**Table 1** Selected cellular stress-related responses and biological functions, which are regulated by galectins (based on reviews [3, 12–15])

Human galectin	Stimulatory effects	Inhibitory effects
LGALS1	Apoptosis of activated T cells Survival of naïve T cells Tumor cells apoptosis (extracellular mechanism) Muscle repair and cell differentiation Tumor cell growth and migration Proliferation of neural stem cells Regeneration of axons Respiratory burst in neutrophils Plasma cell survival and differentiation Angiogenesis Mitogenesis of spleen or lymph node cells, vascular cells, and Hepatic stellate cells	T cell viability B cell proliferation Acute inflammation Nitric oxide release from macrophages Growth of neuroblastoma and stromal bone marrow cells
LGALS2	T cell apoptosis	T cell viability Pro-inflammatory cytokine secretion
LGALS3	T cell and monocyte apoptosis (extracellular mechanism) Tumor growth Re-epithelization of wounded corneas Growth and differentiation of lymphocytes Respiratory burst in macrophages and neutrophils Eosinophil death Angiogenesis Inflammation	T cell apoptosis (intracellular mechanism) T cell viability Inflammation Survival of activated B cells Apoptosis in B cell lymphoma
LGALS4	T cell apoptosis Axon growth	Intestinal inflammation
LGALS7	Tumor cell apoptosis (intracellular mechanism) Keratinocyte differentiation p53-mediated apoptosis of keratinocyte	Cell growth Cell proliferation
LGALS8	Apoptosis of lung carcinoma and synovial fluid cells Respiratory burst of neutrophils Plasma cell differentiation Angiogenesis Autophagy Cell growth arrest	Autoimmune inflammation
LGALS9	Apoptosis of Th1 cells, T cells, thymocytes and NK cells Dendritic cell maturation Tumor cells apoptosis (extracellular mechanism) Respiratory burst in must cells	T cell viability
LGALS10 (CLC)	CD4+ T cells apoptosis Differentiation of promyelocytic cells	Proliferation of T regulatory cells
LGALS12	Tumor cell apoptosis (intracellular mechanism) Adipocyte apoptosis and differentiation	Tumor cell growth
LGALS13	T cell apoptosis Apoptosis promotion in U-937 macrophage cell line	nd
LGALS14	T cell apoptosis	nd
LGALS16	T cell apoptosis	nd

nd no data

## Galectin-1

Since the seminal findings by Le et al. [38], galectin-1 has been recognized as a strong biomarker of hypoxia-induced cellular stress responses with respect to several cell lines (FaDu, SCC4, SQB20, Panc1, and V2P3) associated with head and neck squamous cell carcinoma (HNSCC). It was shown that galectin-1 was upregulated by hypoxia (0.2 and 2 % O<sub>2</sub>), which mimicked the local microenvironmental conditions of tumorous tissues, at both transcriptional and post-translational levels, although global mRNA accumulation surprisingly lagged behind the protein accumulation/secretion [38]. In line with this finding, the level of circulating galectin-1 was found to be elevated in tumor-bearing mice, whereas the expression of galectin-1 in HNSCC tissues was inversely correlated with the T cell marker CD3. Since galectin-1 was originally shown to promote T cell apoptosis [39], as well as to inhibit various aspects of T cell effector functions [40, 41], it was suggested that the hypoxia-induced upregulation of galectin-1 is essential for tumor cells to escape from cellular immune surveillance [38]. Subsequent testing of other cancer cell lines associated with human and mouse melanoma (A375 and B16-F0), mouse breast carcinoma (4T1), and human prostate carcinoma (LNCaP) confirmed the hypoxia-induced expression of galectin-1 at both mRNA and protein levels [42]. In renal cell carcinoma cell line CAK-1, the mimicking of hypoxia stress with CoCl<sub>2</sub>, which inhibits prolyl hydroxylase and HIF-1 $\alpha$  ubiquitination, also resulted in an almost 14-fold, dose-dependent increase in galectin-1 protein expression [43]. Interestingly, the transcriptional control of galectin-1 upregulation under hypoxic conditions seems to be specific to the type of responsive cells and not always dependent on classical hypoxia-induced transcription factors. For example, galectin-1 expression was found to be controlled by HIF-1 $\alpha$  in colorectal carcinoma [44], by C/EBP $\alpha$  in acute myeloid leukemia [45], by AP-1 in classical Hodgkin lymphoma [46], and by ROS and NF- $\kappa$ B in Kaposi's sarcoma [42] cells. Other lines of evidence supporting the hypoxia-induced upregulation of galectin-1 have recently been reported in a model of acute myocardial infarction considering the hypoxic microenvironment in infarcted hearts [47]. In particular, the exposure of HL-1 cardiomyocytes in a cell culture to hypoxia (1 % O<sub>2</sub>, 18 h) or pro-inflammatory cytokines (IL-17, TNF- $\alpha$ , IFN- $\gamma$ ) increased the respective levels of galectin-1 in total cell lysates or cell culture media. Moreover, exogenous and endogenous galectin-1 did not affect the viability of cardiomyocytes, eliminating an apoptotic aspect of its activity. Since galectin-1 is a part of the contractile apparatus of cardiac striated muscles colocalizing with sarcomeric actin on I bands [48], a positive outcome of galectin-1 activity under hypoxic stress has been suggested and considered as

a possible therapeutic mode for preventing heart failure [47].

In addition to hypoxia, the elevation of galectin-1 levels was reported under metabolic stress (glutamine deprivation or ammonia accumulation) in the serum-free cell culture medium of CHO cells [49]. At the organismal level, a rapid (within 1 h) increase of galectin-1 was observed in the serum of rats under restrain stress, which coincided with the increase of corticosterone and was controlled by the sympathetic nervous system [50]. Immunoblot analysis revealed a strong increase of galectin-1 protein in the human glioma cell lines A172 and U118 after a 4-h treatment with a single dose of  $\sim$ 6 Gy ionizing radiation [51]. It is likely that galectin-1 protects glioma cells through its direct role in the UPR, as the siRNA-mediated knockdown of galectin-1 coincided with diminished IRE1 expression and ultimately impaired the ability of human hs683 glioblastoma cells to respond to ER stress [52]. Moreover, decreased galectin-1 expression has been associated with the decreased mRNA level of the hypoxia-related genes implicated in angiogenesis, which confirms a galectin-1-integrated relationship between ER stress and hypoxia [52].

## Galectin-2

A tandem-repeat galectin-2 is a paralog of galectin-1 with a wide range of biological activity. It performs an anti-inflammatory function in the intestine, inducing the apoptosis of specific populations of T cells [53, 54]. This lectin has been shown to move to the nucleus of fibroblastic cells exposed to physical (UV light), chemical (mitomycin C, serum withdrawal), or cell biological (coculture with stromal cells) treatment modalities [55]. These results suggest that changes in the compartmentalization and localization of galectin-2 in cells might be important for regulating stress-induced cellular responses—a mechanism that can also be considered for other galectins. Similar to galectin-4 and galectin-8, the circulating levels of galectin-2 increased in the serum of patients with colon and breast cancer [29], correlating with the ability of these galectins to induce the secretion of cancer-promoting cytokines (G-CSF, IL-6, MCP-1/CCL2, and GRO $\alpha$ /CXCL1) from the vascular endothelium both in vitro and in mice [56]. In gastric cancer, however, an inverse correlation was noticed between the tissue level of galectin-2 and lymph node metastasis [57].

## Galectin-7

Galectin-7 is a proto-type galectin, the expression of which is readily activated by p53 in an association with the apoptotic process, as was initially shown in a model of colorectal cancer cell line DLD-1 [58]. There are several lines of

evidence confirming the pro-apoptotic activity of galectin-7 and its role in genotoxic and oxidative stress responses. For instance, UVB radiation has been found to induce galectin-7 expression in human epidermal keratinocytes, particularly in sunburned apoptotic cells [59] and NHEK neonatal foreskin cells [60]. More specifically, galectin-7 was found to be paired with the anti-apoptotic Bcl-2 protein in mitochondria, but this interaction was disrupted by UVB radiation, which sensitized the apoptotic response of cells [61]. Furthermore, galectin-7 transfectants of HeLa and DLD-1 cells showed enhanced sensitivity to apoptosis induced by UV radiation, actinomycin D, TNF- $\alpha$  plus cycloheximide, etoposide, or camptothecin [62]. The expression of galectin-7 is sensitive to the availability of an antioxidant enzyme Cu/Zn-containing extracellular superoxide dismutase (EC-SOD). In particular, both skin cells from EC-SOD transgenic mice and EC-SOD-transfected keratinocyte cell line HaCaT exhibited a significant upregulation of galectin-7 expression based on the western blotting analysis [63]. Interestingly, Lee et al. [63] claimed that the upregulation of galectin-7 expression occurs in a PGE2-dependent manner as a result of the EC-SOD-mediated activation of COX-2, which leads ultimately to the accumulation of pro-apoptotic molecules, such as caspase-3, caspase-9, Bax, and Bcl-Xs. As to the pathological stress conditions, including cancer, it has been suggested that galectin-7 plays a dual role as a result of its ability to mediate apoptosis and cancer suppression via a p53-dependent pathway and to promote cancer progression via NF- $\kappa$ B-dependent pathway [64]. Since both p53 and NF- $\kappa$ B belong to stress-induced transcription factors, the corresponding upregulation of galectin-7 should be considered in the context of specific cellular stress responses with differential outcomes, which fits perfectly with the conceptual paradigm of stress-induced selection between cell death or cell survival. Indeed, the biological role of galectin-7 cannot be solely related to its pro-apoptotic functions due to the crosstalk between both p53 and NF- $\kappa$ B, as recently demonstrated in MCF7 breast cancer cells [65]. In addition, recent studies have revealed that the upregulation of galectin-7 in breast cancer cell lines MCF7 and MDA-MB-231 is driven by C/EBP $\beta$ -2, which can explain the paradox of concomitant galectin-7 overexpression in cancer cells and p53 mutation [66]. It should be noted that the role of C/EBP transcription factors in cellular responses to stresses, including inflammatory and ER stresses, is well known [67]. As such, the possibility of regulating the galectin-7 gene via the signaling pathway under stress is a very attractive proposition.

### Galectin-10

Galectin-10 belongs to the subfamily of proto-type galectins and has been recognized as a main protein component of the Charcot–Leyden crystals in human

eosinophils [68–70]. The overexpression of this protein has also been detected in regulatory T cells [71] and in differentiated HL-60 cells (a human promyelocytic cell line) [33]. Galectin-10 binds not only  $\beta$ -galactoside sugars [68] but also mannose [69], a feature not found in other galectins. The upregulation of galectin-10 has been reported in several models of physiological and pathological stresses. Bronchial and nasal inflammation is accompanied by the activation and recruitment of eosinophils, and a corresponding accumulation of galectin-10 in peripheral blood [72], samples of sputum [73], and nasal lavage [74]. Elevated levels of galectin-10 have also been reported in gut biopsies of patients with celiac disease, an autoimmune disorder of the intestine caused by an allergy to gluten [75]. Lastly, a drastic time-dependent increase in the expression of galectin-10 at the mRNA and protein levels was reported in the process of the myeloid differentiation of HL-60 cells into neutrophilic or eosinophilic lineages, as induced by DMSO or sodium butyrate, respectively [33]. Since no expression of galectin-10 has been observed in undifferentiated HL-60 cells, this galectin deserves attention as a potential biomarker of cellular stress responses in other models. In particular, the presence of binding sites for redox-sensitive transcription factors Sp1 and Oct1 in the promoter region of the galectin-10 gene [76] may explain its high expression in ROS-producing granulocytes.

### Galectin-13

Galectin-13 (placenta tissue protein 13, PP13) is a proto-type galectin, which forms stable homodimers through disulfide bonds [77–79]. These dimers were not observed in a Laemmli solution containing 10 % 2-mercaptoethanol, and the galactoside-binding activity and haemagglutination were impaired in the presence of 1 mM dithiothreitol [79]. These properties of galectin-13 might be important for the redox regulation of its biological activity. What is interesting in this context is that the 48-h treatment of a choriocarcinoma cell line BeWo with vitamin C, a reducing agent, was found to increase the PP13 protein expression at protein level in a dose-dependent manner [80]. The available information about galectin-13 expression has been limited largely to placental tissue and more specifically to syncytiotrophoblasts, although initial findings have detected the protein in a few other normal (spleen, fetal kidney, and adult bladder) and tumorous tissues [81]. In terms of reproductive biology, galectin-13/PP13 is specifically known and recognized to be one of biomarkers of preeclampsia [82, 83], as it shows different expression dynamics compared to control subjects [84, 85].



## Galectin-14 and galectin-16

Human galectin-14 and galectin-16 genes are expressed predominantly in placental tissues, together with galectin-13 in the Chr19 cluster. These three galectins have been proposed to contribute to immunosuppression at the maternal–fetal interface mostly by inducing T cell apoptosis [86]. Ovine galectin-14 has been studied in more detail and detected primarily in eosinophils [87]. Eosinophils likely serve as a source of secreted galectin-14, which has been detected in bronchoalveolar lavage fluid, mammary gland lavage, and gastrointestinal tract mucus following allergen or parasite challenge [88, 89], indicating a relationship to inflammatory stress response.

## Chimeric type galectin-3

The overexpression of galectin-3 has been well documented in different cancer cell models and tumorous tissues under hypoxic conditions. Indeed, the promoter region of chimeric type galectin-3 gene contains binding sites for the transcription factor HIF-1, which drives hypoxia-induced galectin-3 mRNA and protein expression, as observed in HeLa cells and mouse embryonic fibroblasts from HIF-1 $\alpha$  wild-type, but not HIF-1 $\alpha$  null mice [90]. The expression of galectin-3 gene was also strongly upregulated by hypoxia in the murine melanoma cell line BF-F10 [91]; however, this effect could be cell-specific because subsequent studies revealed no significant changes in five out of six human melanoma cell lines [92]. It is interesting to note that the combined hypoxia-induced upregulation of galectin-3 and epidermal growth factor receptor has been proposed to enhance the invasive potential of tumor cells that are exposed to stressed microenvironmental conditions [93]. Proteomic analysis also revealed the upregulation of galectin-3 in human placental cell line BeWo, which was associated with trophoblast syncytialization [94]. This species- or cell-specific variability needs further examination considering complex galectin networks in cells. Nevertheless, the weak but significant hypoxia-induced upregulation of galectin-3 gene in the WM278 human melanoma cell line [92] and the strong immunostaining for galectin-3 in hypoxic regions of cancer tissue biopsies from patients diagnosed with breast DCIS [95] suggest a potential application for this molecule with anti-apoptotic activity [96] in protecting cancer cells from hypoxia stress. The accumulation of cancer cells with high levels of galectin-3 protein has also been confirmed in a xenotransplant model of glioblastoma multiformes in specific hypoxic areas, which histochemically appeared as so-called pseudopalisades representing hypercellular zones around the necrotic tissues [97]. In cell culture, the NG97ht hybrid

glioblastoma cells showed a very strong upregulation of galectin-3 in a HIF-1 $\alpha$  and NF- $\kappa$ B-dependent manner under conditions mimicking the tumor's microenvironment, i.e., combined hypoxia and nutrient deprivation. This galectin-3 upregulation was essential for cell survival because the siRNA-mediated galectin-3 knockdown sensitized transfected cells to the cell death [97]. However, the role of galectin-3 in hypoxia-mediated responses can be more complex and tissue-specific, because it can serve as a multifunctional inflammatory mediator. For instance, in a mice neonate model, hypoxia–ischemia treatment led to the upregulation of galectin-3 in microglia/macrophages associated with specific brain injuries in the deep gray matter areas [98]. As such, the ability of galectin-3 to contribute to various inflammatory responses (chemotaxis, phagocytosis, stimulation of cytokines, and ROS) [99–103] may explain the extent of tissue damage.

Hyperthermic and hypothermic conditions were found to have opposite effects, stimulation vs inhibition, on the expression of galectin-3 in the microglial cells of hippocampal brain tissues from gerbils following experimental ischemia [104, 105]. Interestingly, the increased levels of galectin-3 at a high temperature (39 °C) were associated with less severe apoptotic damage in brain tissues, suggesting that galectin-3 plays a protective role. In a different context, interaction between galectin-3 and IL-10 was required to protect human breast carcinoma BT549 cells against liver ischemia–reperfusion-induced cytotoxicity [106]. Oxidative stress induced by ozone exposure was also associated with the rapid (within 3 h) and prolonged (up to 72 h) accumulation of galectin-3 in the bronchiolar epithelium and alveolar macrophages of rats [107, 108]. Since galectin-3 has been found to have a positive effect on the re-epithelialization of wounds [109], it is anticipated that this effect may be involved in both the protection against the oxidative damage of lungs and wound repair [107]. Galectin-3 upregulation has also been found to be a feature of different types of acute and chronic inflammatory responses associated with microbial infection, asthma, liver injuries, and fibrosis [110]. The increased level of circulating galectin-3 has also been recognized as one of the biomarkers of chronic and acute heart failure [111–113]. Since heart failure as a clinical syndrome deals largely with oxidative stress [114], a related mechanism could be responsible for the upregulation of galectin-3.

Silencing galectin-3 in HeLa cells has resulted in the increased resistance of transfected cells to DNA-damaging agents, such as ionizing radiation (10–40 Gy), etoposide, carboplatin, and mitomycin C [115]. Galectin-3 protein levels in glioblastoma cells increased in response to UV-C radiation and treatments with alkylating reagents, and required the involvement of such transcription factors as NF- $\kappa$ B and Jun [116]. However, it should be noted that

under certain stress conditions, e.g., immobilization stress in mice, the levels of galectin-3 in alveolar macrophages and spleen and liver tissues decreased. The same trend was observed in human glioblastoma A1235 cells under hyperthermic conditions, the mechanisms of which are still uncertain [117]. Such non-uniform changes in the expression of galectin-3 under stress conditions underscore the need for a more comprehensive analysis of galectin protein networks in cells and the interactions between different galectin members.

### Tandem-repeat type galectins

Human tandem-repeat galectins (4-, -8, -9, and -12) have been relatively less studied with respect to their participation in cellular stress responses. However, the alterations in the expression of these galectins have been reported in relation to inflammation and cancer.

#### Galectin-4

Tandem-repeat galectin-4 is expressed chiefly in the intestine tissue and contributes substantially to the regulation of inflammation, the activation of immune cells, the expansion of memory T cells in mucosal tissue [118–121], and the stabilization of lipid rafts in cells [122, 123]. Although no data are available on the effects of environmental stress on the expression of galectin-4 in mammalian cells, the level of this galectin is known to be drastically elevated (11–25 folds) in the sera of patients with colorectal and breast cancer in comparison with healthy subjects. This elevation occurs concurrently with galectin-2, galectin-3 and galectin-8 [29], all enhancing the production of cytokines and chemokines by endothelial cells, which are involved in processes of angiogenesis and metastasis [56]. The upstream regulatory elements of the galectin-4 gene include the binding sites for HNF-4, MyoD, c-Rel, HNF-3 $\beta$ , C/EBP, and HFH-2 [124], which might be indirectly involved in a variety of cellular stress responses.

#### Galectin-8

Galectin-8 is a tandem-repeat galectin with one of the longest 3'UTR regions among mRNA transcripts, which indicates the complex mechanisms of its expression regulation [125]. Therefore, it is not surprising that, despite the massive amount of information regarding the expression of galectin-8 in tumors and its up- and down-regulation compared to healthy tissues [126], the details of galectin-8's transcriptional and translational machinery remain unexplored and in need of in-depth study based on stress-

induced cellular models. The ability of galectin-8 to induce strong superoxide production in human neutrophils [127] indicates the potential significance of oxidative stress in this context. In addition, the fact that several splicing variants of galectin-8 with different biological activity exist [128, 129] provides an exciting direction of research in the context of the stress-dependent regulation of alternative pre-mRNA splicing in cells [130].

#### Galectin-9

Galectin-9 is a tandem-repeat galectin that serves as a distinctive regulator of adaptive and innate immunity, which is able to weaken the immune system in hyper-immune conditions (autoimmune disease, asthma, infection, allograft rejection) and enhance it in immune-compromised conditions (e.g., cancer) [131]. These immunomodulatory effects of galectin-9 result from the elimination or activation of specific subpopulations of immune cells, which shifts the immune response in the required direction. It is not surprising that, with respect to pathological stress conditions, tumors and especially metastatic sites have mostly shown lower levels of galectin-9 than normal tissues [132]. At the same time, the exposure of host cells to bacterial or viral infections has been found to induce galectin-9 expression [131]. Moreover, individual factors mimicking or associated with inflammatory stress, such as LPS, IFN- $\gamma$ , TNF, and IL-1 $\beta$ , are powerful stimuli for galectin-9 expression in a variety of cells, including vascular endothelial cells [133, 134], monocytes [135], macrophages [136], fibroblasts [137], multipotent mesenchymal stromal cells [138], and astrocytes [139, 140]. A variety of transcription factors and related signaling pathways have been reported to be essential for the upregulation of galectin-9, including a redox-sensitive JNK/c-Jun signaling pathway in astrocytes [140], the phosphorylation of STAT-1 in HUVEC cells [141], and Smad3 in regulatory T cells [142]. Although it remains unclear how galectin-9 collaborates with other galectins, the administration of the recombinant galectin-9 seems to be a very promising strategy for treating immune and cancer diseases [131].

#### Galectin-12

Galectin-12 is a tandem-repeat galectin that is expressed variably in different tissues, but relatively strongly in peripheral blood leukocytes, myeloid cell lines [143], and adipocytes [144]. The intracellular level of galectin-12 mRNA is upregulated by reagents that synchronize cells at the G1 phase (theophylline plus dibutyryl-cAMP) or G1/S boundary (hydroxyurea or thymidine) of the cell cycle [143]. The time-dependent increase of the galectin-12

mRNA transcripts over a 7-day period was found to accompany the differentiation of preadipocyte mouse 3T3-L1 cells into mature adipocytes [145]. A detectable amount of galectin-12 has also been associated with lipid droplets in cells and involved in the regulation of lipid metabolism and energy homeostasis [146]—an interesting aspect with important consequences for cell stress biology.

### **The complexity of the transcriptional and post-transcriptional regulation of galectin networks, and suggestions for future studies**

Galectins represent a complex family of glycan-binding proteins with defining specificity to  $\beta$ -galactoside sugars due to the quite similar structural and dynamic properties of carbohydrate-recognizing domains [147]. By comparison, the promoter regions of the genes encoding galectins and the 3' untranslated regions of galectin mRNAs are very different, explaining the variety of patterns of galectin expression in cells treated with stress. Indeed, a robust bioinformatics analysis of human galectin genes demonstrates very few overlaps between tentative transcription factors and between miRNAs targeting mRNA transcripts (Table 2). A detailed systems biology approach is required to establish galectin regulatory networks that integrate stimulatory and inhibitory pathways. The role of different transcription factors has been addressed in many studies, as highlighted in the previous sections. However, the details of how signaling mechanisms control the expression of stress-sensitive galectins still need elaboration. Furthermore, the role of galectin-specific miRNAs cannot be overlooked because of the very well-known upregulation of non-protein coding genes in cells under stress [148]. The current experimental findings related to the miRNA-mediated regulation of galectin expression have been limited to few studies. In particular, the transfection of a renal carcinoma cell line CAK-1 miR-22 was found to be very efficient in inhibiting both galectin-1 and HIF-1 $\alpha$  [43]. A sequence called miR-322 was claimed to recognize human galectin-3 3'UTR, and the silencing of miR-322 with antisense oligo was found to upregulate galectin-3 mRNA transcripts in several cancer cell lines [149]. The list of potential galectin-specific miRNAs (Table 1), which has been retrieved using a DIANA microT algorithm for microRNA target prediction [150, 151], makes it evident that this regulation can vary dramatically between the various galectins, utilizing multiple miRNAs (galectins -3, -8, -9, -12, -13), very few (galectins -1, -4, -7, -10), or none (galectin-2). Remarkably, galectin-8 stands out against other galectins by overwhelming number of potential target miRNAs ( $\sim$ 120), which is due to the longest 3'-UTR

among all galectins. The biological significance of this diversity remains obscure and awaits further studies with different cell stress models.

The network of galectins in cells represents a well-balanced system that is sensitive to a variety of stress stimuli mimicking, for instance, the physiological cues for cell differentiation or the pathological microenvironment of tumorous tissues. The alteration of galectin expression profiles seems to be a very delicate mechanism that contributes to cell survival or cell death in the context of cellular stress responses. It is evident that the exposure of cells to stress remodels the galectin expression profiles, including the up- and down-regulation of certain galectins [27]. However, we are still far from gaining an ultimate understanding of the biological significance of galectin networks in cells, especially since some galectins, e.g., galectins -1, -3, and -8, are abundantly expressed in a variety of cell lines, while others are either tissue-specific or silent [18, 152]. Although the activation of stress-specific transcription factors can explain some aspects of the remodeling of galectin networks, additional global molecular mechanisms must be taken into account, including the epigenetic regulation of galectin gene expression and the destabilizing effects of miRNAs targeting galectin mRNAs. For instance, it has been reported that, in cancerous tissues, the promoter regions of all galectin genes contain multiple CpG sites available for the methylation and DNA methylation/demethylation of galectin genes [153]. Accordingly, an efficient way to activate the expression of silent galectins is by inhibiting DNA methylation. This approach has been demonstrated to be efficient in the case of galectin-1 [154] and was recently confirmed in the case of the low expressing galectin-7 in various cell lines, using a specific DNA methylation inhibitor 5-aza-2'-deoxycytidine [155]. The application of this strategy to examining cellular stress responses deserves more attention in the context of galectin expression in cells and tissues with different DNA methylation statuses.

In sum, the differential expression of galectins in tissues and individual cell lines requires the thorough examination of galectin expression profiles and galectin networking in the context of cellular stress responses. Knowledge of the galectin signatures of stressed cells can provide a platform for understanding the functional differences between upregulated and downregulated galectins and the potential value of these galectins as biomarkers or new molecular targets for stress-associated cellular disorders. As such, a comprehensive profiling of galectin expression and subsequent combined inhibition of multiple stress-inducible galectins rather than individual galectins might be a promising strategy for developing new anti-cancer therapies.



**Table 2** The list of tentative transcription factors and miRNAs that may regulate the expression of galectins in human cells

Human galectin	Transcription factors	hsa-miRNAs <sup>a</sup>
LGALS1	AP-1, c-Jun, p53, SEF-1(1), ATF-2, MyoD, YY1, HEN1, E2F, E2F-1	4635, 22-3p, 4717-5p
LGALS2	AP-1, PPAR- $\gamma$ 1, PPAR- $\gamma$ 2, c-Fos, c-Jun, HNF-4 $\alpha$ 1, HNF-4 $\alpha$ 2, COUP, COUP-TF, COUP-TF1, ATF-2, ATF6	No predictions
LGALS3	NF- $\kappa$ B, NF- $\kappa$ B1, AML1a, AP-1, c-Jun, Sp1, HNF-4 $\alpha$ 1, HNF-4 $\alpha$ 2	612, 548at-5p, 3187-5p, 5189, 1285-3p, 3190-5p, 3622b-5p, 4253, 24-3p
LGALS4	CBF-A, NF-Y, NF-YA, c/EBP $\alpha$ , TBP, TFIID, RelA, PPAR- $\gamma$ 1, PPAR- $\gamma$ 2, CREB, AML1a, AP-1, ATF-2, $\delta$ CREB, c-Jun	4688, 27a-5p, 185-3p, 4278
LGALS7	P53, CREB, NF-1, HSF2, $\delta$ CREB, HSF1 (long), Amt	3194-5p, 3972
LGALS8	NF-E2, NF-E2 p45, Nkx5-1, ROR $\alpha$ 2, Bach2, CUTL1, ER- $\alpha$	3065-3p, 388-5p, 300, 1913, 4742-3p, 607, 381, 196a-5p, 3662, 431-5p, 196b-5p, 5096, 148a-3p, 573, 3671, 152, 889, 545-5p, 3616-5p, 148b-3p, 29c-3p, 5003-3p, 29b-3p, 2054, 890, 29a-3p, 5008-3p, 3922-3p, 522-3p, 3672, 4775, 105-5p, 3129-3p, 507, 1910, 664-5p, 4778-5p, 29b-2-5p, 892b, 651, 4794, 557, 506-5p, 205-3p, 324-3p, 4666a-5p, 499a-5p, 4533, 3646, 5583-5p, 548c-3p, 4307, 5701, 1272, 4291, 3680-3p, 4670-3p, 27b-3p, 4263, 3152-5p, 2681-5p, 130a-5p, 10a-3p, 562, 3129-5p, 27a-3p, 3613-3p, 4729, 4711-3p, 9-5p, 7-5p, 876-3p, 4802-3p, 2052, 224-3p, 508-5p, 5692a, 33a-3p, 5589-3p, 606, 5700, 579, 3163, 302c-5p, 512-3p, 4747-5p, 320e, 3617, 551b-5p, 3611, 2355-5p, 335-3p, 3159, 4276, 1285-5p, 18b-3p, 1301, 644b-3p, 320c, 5047, 3140-3p, 320b, 3185, 320a, 4282, 582-3p, 5585-5p, 4693-5p, 524-5p, 4708-5p, 136-5p, 5480-3p, 320d, 374b-3p, 4760-3p, 3134, 499a-3p, 19b-1-5p, 1277-5p, 4694-3p, 520d-5p, 4429
LGALS9	NRSF form 1/form 2, STAT1, STAT1 $\alpha$ , STAT1 $\beta$ , POU2F2 (Oct-2.1), Oct-B1, Oct-B3, Oct-B2, CUTL1, POU2F2C, POU2F1, POU2F1a, POU2F2B	764, 3190-3p, 1197, 3202, 541-3p, 3934, 654-5p, 4657, 486-3p, 4477b, 4459, 505-5p, 548an, 4646-5p, 5090, 665, 4447, 4787-5p, 4314, 4736, 4793-3p, 4472
LGALS10 (CLC)	STAT3, p53, FOXJ1, HFH-3, HFH-1, FOXL1	573, 3616-5p
LGALS12	SREBP-1a, SREBP-1b, SREBP-1c, c/EBP $\alpha$ , c/EBP $\beta$ , PPAR- $\gamma$ 1, PPAR- $\gamma$ 2	5692a, 5590-3p, 1291, 765, 3928, 4719, 4650-5p, 484
LGALS13	NRSF form 1, NRSF form 2, Bach2	4314, 204-3p, 4646-5p, 4778-5p, 3192, 374b-3p, 4690-5p, 3927, 657, 4650-3p
LGALS14	No predictions	4778-5p, 4779, 3927, 204-3p, 4646-5p, 4650-3p, 330-5p, 4314, 4320, 326
LGALS16	No predictions	4779, 4778-5p, 5196-5p, 3927, 3155a, 3155b, 4689, 4650-3p, 4652-3p

The results represent the search for the specific information on the following websites: GeneCards (<http://www.genecards.org/>), SABioscience (most relevant regulatory transcription binding sites, <http://www.sabiosciences.com>), and miRNA target prediction software microT-CDS at Diana Tools (<http://diana.imis.athena-innovation.gr/DianaTools/>)

<sup>a</sup> The predicted miRNAs are listed in order of the overall miRNA target gene (miTG) score decreasing. The miTG score is supposed to correlate with fold changes in protein expression [146] and its threshold was set up to 0.7 as per default option of the microT-CDS search

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