NRF2 transcriptionally activates the heat shock factor 1 promoter under oxidative stress and affects survival and migration potential of MCF7 cells

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Abstract

Functional up-regulation of heat shock factor 1 (HSF1) activity through different post-translational modifications has been implicated in the survival and proliferation of various cancers. It is increasingly recognized that the HSF1 gene is also up-regulated at the transcriptional level, a phenomenon correlated with poor prognosis for patients with different cancers, including breast cancer. Here, we analyzed the transcriptional up-regulation of HSF1 in human cells upon arsenite- or peroxide-induced oxidative stress. Sequential promoter truncation coupled with bioinformatics analysis revealed that this activation is mediated by two antioxidant response elements (AREs) located between 1707 and 1530 base pairs upstream of the transcription start site of the HSF1 gene. Using shRNA-mediated down-regulation, chromatin immunoprecipitation of NRF2, site-directed mutagenesis of the AREs, and DNaseI footprinting of the HSF1 promoter, we confirmed that Nuclear factor erythroid-derived 2-like 2 (NRF2, also known as NFE2L2) interacts with these AREs and up-regulates HSF1 expression. We also found that BRM/SWI2-related gene 1 (BRG1), a catalytic subunit of SWI2/SNF2-like chromatin remodeler, is involved in this process. We further show that NRF2-dependent HSF1 gene regulation plays a crucial role in cancer cell biology, as interference with NRF2-mediated HSF1 activation compromised survival, migration potential, and the epithelial-to-mesenchymal transition and autophagy in MCF7 breast cancer cells exposed to oxidative stress. Taken together, our findings unravel the mechanistic basis of HSF1 gene regulation in cancer cells and provide molecular evidence supporting a direct interaction between HSF1 and NRF2, critical regulators of two cytoprotective mechanisms exploited by cancer cells.

Introduction

Healthy cells upregulate heat shock factor 1 (HSF1) activity when challenged with a stress such as oxidative stress to protect its normal protein structure and function (1). HSF1 drives expression of a group of inducible heat shock protein chaperones (HSPs) such as HSP70 and HSP90 to refold the affected proteins to their native conformation or drive the removal of aggregates (1-3). HSF1 also controls the upregulation of many genes associated with different cellular processes other than the HSPs (4-6).

HSF1 exists in unstressed cells in an inactive state within an HSP90-immunophilin-p23 complex (7,8). Per a current model, a misfolded protein generated under stress titrates away the chaperones from the inactive complex, thereby freeing HSF1 to form a homotrimer. The trimeric complex binds to its recognition sequence, heat shock elements (HSEs) consisting of inverted 5'-nGAAn-3' motifs on the promoters of its target genes (9). Furthermore, various post-translational modifications (PTMs) such as phosphorylation, acetylation, and sumoylation regulate the activity of HSF1. A noncoding RNA was shown to play an important role in regulating HSF1 function (10,11). Studies also suggested that HSF1 engages a distinct set of coactivators or corepressors to regulate genes in a stress-specific manner (12).

Normally, cellular HSF1 is inactivated as the stress is ameliorated. In contrast, cancer cells maintain HSF1 in a constitutively activated state to sustain their proliferative potential (13). This event is driven by the relatively higher level of oxidative stress in cancer cells caused by higher NADPH oxidase activity, and higher mitochondrial rate of respiration associated with enhanced aerobic glycolysis and a defective antioxidant response (14). Many cancer cells, in particular, maintain an elevated level of the HSPs such as HSP90, -70, -40 and -27 due to overexpression of various oncoproteins. In fact, mice devoid of the HSF1 gene (hsf1/-) are much less susceptible to chemical induced transformation (15).

An upregulated state of the HSF1 gene in different types of human cancers has been reported (16). HSF1 mRNA level was significantly upregulated in oral squamous cell carcinoma, correlating the tumor size with a relatively higher level of HSF1 in the nuclear compartment (17). HSF1 was found to be overexpressed in the malignant prostate and in pancreatic cancer cells as well (13). Furthermore, HSF1 gene amplification and higher HSF1 levels were reported in hepatocellular carcinoma (18).
Elevated HSF1 mRNA levels were correlated with higher grades of breast tumors (19). While all these studies supported transcriptional upregulation of HSF1 with cancer growth and proliferation, little is known about the underlying mechanism of this cancer cell-specific HSF1 regulatory mechanism.

Nuclear factor erythroid-derived 2-like 2 (also named NRF2) controls cellular redox potential in response to oxidative stress (20-22). NRF2 in a healthy cell is constantly degraded through ubiquitination and proteasomal degradation by its association with KEAP1, a substrate adapter protein for the E3 ubiquitin ligase complex. Disruption of its binding with KEAP1 leads to stabilization and nuclear translocation of NRF2. NRF2 binds to the antioxidant response element (AREs) on the promoter of its target antioxidant responsive genes as a heterodimer with a small Maf protein (20,23-25).

Both NRF2 and HSF1 were reported to control certain genes such as heme oxygenase (26,27) and HSP70 (28) associated with cytoprotection. Increasing body of evidence suggested that these two factors also engage in mutual compensatory activities (20). However, it remains to be understood how these activities are precisely regulated.

We investigated HSF1 promoter regulation under oxidative stress in human cells induced by arsenite treatment as a model (condition) to obtain insight into the phenomenon observed in cancer cells. We identified two anti-oxidant response elements (AREs) in the promoter of the HSF1 gene responsible for its sensitivity to oxidative stress. We have further shown that the AREs engage in a multiprotein activation complex with NRF2 and the chromatin-modifier BRG1 to mediate HSF1 transcription under arsenic stress. Furthermore, MCF7 cells appear to depend on this NRF2-dependent HSF1 transcription for their growth and proliferation.

**Results**

**Transcription of the HSF1 gene is upregulated by a proteotoxic stressor**

Upregulation of the HSF1 gene was tested in cells in response to two forms of a proteotoxic stressor, heat shock or arsenite treatment. HT1080 cells were either grown at 37°C (control) or subjected to heat shock at 42°C for 1 h (HS) or treated with 20 µM sodium arsenite for 2 h. The treated samples were then analyzed for HSP70, HSF1, and GAPDH levels by real time RT-PCR (qRT-PCR). These two treatment conditions led to a significant induction of HSP70 both at mRNA and protein levels (Fig. 1A, right panel). An increase in HSF1 expression notably occurred in arsenite-treated samples only (Fig. 1A). Further experimentation will be required to better understand this HSP70 upregulation but activation of HSF1 function by differential signalling pathways under these stressors has been reported (12). Notably, HSP70 was shown to be regulated by a few factors other than HSF1 under HS such as NF-Y, CREB and NF-kB (29,30). Upregulation of HSF1 (and also its target HSP70 gene) both at mRNA and protein levels in different cancer cell lines, HeLa, MCF7, and PC3 but not in immortalized cell lines HEK293 and NKE under those treatment conditions measured by qRT-PCR (Fig. 1B) and immunoblotting (Fig. 1C), respectively suggested that this is not specific to a particular cancer cell type. ROS, estimated by DCFDA fluorescence (Fig. 1B, right panel) in response to arsenite treatment, is also higher in MCF7 and HT1080 as compared to HEK293 and NKE cells.

To test whether the increase in HSF1 mRNA is due to its de-novo RNA synthesis, and not due to an increased stability, we blocked transcription by treating cells with actinomycin D (ACTD), followed by HS or arsenite treatment as described above. Abrogation of arsenite induced upregulation of HSF1 and HSP70 mRNA and protein levels upon ACTD treatment suggested that HSF1 was indeed upregulated at the transcriptional level by arsenite (Fig. 1D).

**Identification of sequence elements present in the HSF1 gene promoter responsible for its upregulation by arsenite treatment**

To locate the enhancer element, several truncated versions of HSF1 gene promoter DNA, along with the full-length version were cloned upstream of the renilla-luciferase reporter in a promoter-less pGL4.79 vector (Fig. 2A, left panel). The full-length promoter construct carries the HSF1 promoter sequence from -1931 to +78, (+1, transcriptional start site) (pHSF1-FL [-1931/+78]). A reporter construct pHSP70[-450/+91] carrying from -450 to +91 bp of the
HSP70A1A promoter in the same vector was used as a positive control. The empty vector was used as a negative control. As revealed by luciferase mRNA level measured by qRT-PCR, cells transfected with pHSF1-FL [-1931/+78] construct showed >7-fold induction with arsenite treatment (Fig. 2A, right panel). HT1080 cells were chosen for this study because of a relatively low basal level of HSF1 mRNA in them. Assay of other constructs upon an identical treatment condition revealed that the region between -1720 and -1360 is responsible for the observed effect (Fig. 2A, right panel). To identify transcription factors that can bind this region, the nucleotide sequence of HSF1 promoter spanning from -1931 to -1360 nucleotides was subjected to transcription factor binding site analysis by rVista (rVista 2.0; https://rvista.dcode.org). This analysis predicted binding sites for hundreds of transcription factors including three putative binding site of NRF2, a transcription factor reported to be upregulated with oxidative stress (22,31-33). However, there was no prediction for the presence of any HSE motif with confidence (data not shown). NRF2, a basic-leucine zipper (bZIP) protein binds to anti-oxidant response elements (ARE) upon oxidative stress in the upstream promoter region of many anti-oxidative phase-II genes like NQO1, HO-1, and TRX (34). The putative NRF2 binding sites ARE-A, ARE-B and ARE-C on the HSF1 promoter including their predicted scores are shown (Fig. 2B). The nucleotide sequence in capital letters highlights the core-binding regions. Comparison of the consensus ARE sequence with those of HSF1, NQO1 and HO-1 gene promoters using Clustal Omega multiple sequence alignment tool identified distinct types of HSF1 AREs (Fig. 2C) (35-39).

**Effect of NRF2 knockdown on HSF1 expression**

To check the dependence of NRF2 for HSF1 induction by arsenite, HT1080 cells were transiently transfected with shRNA against NRF2 or a scramble (pLKO.1-shNRF2 vs pLKO.1-scr) to knockdown endogenous NRF2. qRT-PCR analysis suggested that downregulation of NRF2 prevented induction of HSF1 expression by arsenite (Fig. 3A). Efficient knockdown of NRF2 as determined by immunoblot (Fig. 3B) was reflected in inhibition of HO-1 gene expression (Fig. 3A, lower panel). Inhibition of arsenite induced HSF1 expression under this condition was also shown by immunoblotting (Fig. 3C). Interestingly, the HSP70 transcript level under the same treatment condition was decreased to a lesser extent which may reflect compensatory role of HSF1 for NRF2 (see Discussion).

**Functional validation of putative NRF2 binding sites in the HSF1 promoter**

To functionally validate the importance of three putative ARE motifs on HSF1 promoter activity, reporter constructs were made in pGL4.79-mCMV vector, where one of these motifs (ARE-A, -B or -C) was deleted one at a time (Fig. 3D). The NQO1-ARE was cloned in the same vector and used as an NRF2 sensitive positive control. HSP70 promoter cloned in the same vector was also used in the assay. Luciferase expression obtained (by assaying the luciferase mRNA levels) from these ARE-carrying constructs were then compared with a pHSF1-FL construct (Fig. 3D, left panel). As shown (Fig 3D, middle panel), ARE-B and ARE-C are important for NRF2-dependent HSF1 upregulation. When compared with the full-length reporter expression, deletion of ARE-B (compare pHSF1-ARE-C with pHSF1-FL, also compare pHSF1-ARE-C with pHSF1-ARE-BC) or ARE-C (compare pHSF1-ARE-AB with pHSF1-FL) reduced luciferase expression most, whereas deletion of ARE-A (compare pHSF1-ARE-BC with pHSF1-FL) did not significantly affect reporter induction by arsenite. Deletion of either ARE-B or ARE-C reduced the reporter expression level by ~49% and ~46%, respectively (Fig. 3D, middle panel). Notably, cells with downregulated NRF2 showed a significant loss of reporter expression in all of the HSF1-promoter constructs (Fig. 3D, middle and right panels, open arrow) like NQO1-ARE-Luc construct (Fig. 3D, middle and right panels, solid arrow). These results suggest that NRF2 is involved in the induction of HSF1 gene expression by arsenite which acts through the ARE-B and ARE-C motifs.

**NRF2 binds to predicted AREs of the HSF1 promoter in vitro**

Electrophoretic mobility shift assay (EMSA) was carried out to examine the binding of NRF2 to ARE-A, ARE-B, and ARE-C elements of the HSF1 promoter. These motifs, along with their
mutant versions were synthesized individually as 26-bp double-stranded oligonucleotides and labelled at their 5’-ends with γ-[32P] ATP (used as probes). Nuclear extract (Nuc) isolated from HT1080 cells, untreated or pretreated with arsenite, were used as the source of NRF2 protein. Formation of arsenite-induced DNA-protein complex could be detected only with wild type ARE-B and ARE-C (compare Fig. 4A, lane 5 with lane 7, and lane 9 with lane 11; arrowhead). Both ARE-B and ARE-C, like NQO1-ARE (positive control), formed DNA-protein complexes only with arsenite-treated nuclear extract (Fig. 4B, lanes 3, 7 and 11; arrowhead). As expected, all three ARE-B, ARE-C, and NQO1 ARE formed similar complexes as suggested by their similar mobility. Addition of a 100-fold molar excess of respective unlabeled probes abolished the formation of complexes (Fig. 4B, lanes 5, 9 and 13). An inclusion of NRF2-specific antibody in the reaction resulted in supershifting of the labeled complexes (Fig. 4B lanes 4, 8 and 12, compare the filled arrowhead with an open one). Addition of a nonspecific IgG instead of α-NRF2 antibody in the reaction did not produce any effect on the mobility of the complex (Fig. S2).

NRF2 binds an ARE as a heterodimer with a small Maf protein to elicit its trans-activation function (31,33). Binding to an ARE sequence was tested with a purified his₆-NRF2 and his₆-MafG protein mixed together in varying molar ratios. NRF2 with MafG in the molar ratio of 1:2 resulted in a visible complex with all the AREs (Fig. 4C, lanes 4, 7 and 10, arrowhead). The complexes formed on NQO1-ARE (using this ratio of NRF2 and MafG) was challenged with increasing concentrations of unlabelled NQO1-ARE, ARE-B and ARE-C. As revealed, complex assembled on the ARE-C was less stable than that on the NQO1 and ARE-B (Fig. 4D). Direct measurement of the equilibrium dissociation constant (Kₒ) suggested the complex formed on ARE-B is of higher stability compared to that on ARE-C with Kₒ of 0.983 μM and 1.847 μM, respectively, while the Kₒ of the complex formed on the NQO1ARE was 0.672 μM (Fig. 4E).

A direct association of NRF2-MafG with the AREs is also reflected in the DNaseI footprinting assay. As revealed, protection by the complex to DNaseI digestion extended to nucleotides beyond the core motifs of all three AREs including the NQO1 (Fig. 4F). Interestingly, binding of NRF2-MafG complex induced DNaseI hypersensitivity only at the ARE-B (asterisk).

NRF2 interacts with HSF1 promoter AREs in cells

Redox imbalance activates NRF2 in a cell which should in principle be neutralized by a ROS quencher, n-acetyl cysteine (NAC). This was essentially found when internal ROS levels were measured (Fig. 5A).

To test if NRF2 is recruited to the AREs on the HSF1 promoter, chromatin immunoprecipitation (ChIP) analysis was performed in cells pretreated or untreated with arsenite in the presence or absence of NAC. For convenience, cells overexpressing FLAG-NRF2 was used. In the assay, ChIP-enriched DNA carried ARE-B and ARE-C regions only and NQO1-ARE (positive control), but not that of ARE-A. This was greatly reduced by NAC pre-treatment. This indicated that NRF2 associates only with ARE-B and ARE-C upon arsenite treatment. Results are summarised by bar graphs where enrichment of the untreated control samples was defined as 1 (Fig. 5B).

Increase in arsenite induced HSF1 mRNA expression was dependent on ROS generation. Expression of HO-1, an NRF2 target gene, was monitored as a positive control in the experiment (Fig. 5C). Tertiary butylhydroquinone (TBHQ), an inducer of mitochondrial oxidative stress and NRF2 activity (40), effectively induced HSF1 promoter activity as tested by assaying the sensitivity of the HSF1 promoter directed reporter and endogenous HSF1 mRNA levels (Fig. 5D). Azadiradione, an inducer of HSF1 activity (41), had little effect on HSF1 mRNA and HO-1 levels although it significantly induces HSP70 mRNA (Fig. 5D). HSF1 mRNA induction is, therefore, a direct consequence of NRF2 activity caused by oxidative stress.

Arsenite-induced HSF1 upregulation requires chromatin remodeler BRG1

NRF2, a member of the cap-N-collar family of transcription factors, recruits CBP coactivator to its target gene promoters through cooperative interaction of its two domains Neh4 and Neh5 in a stress-independent manner (42,43). The Neh3 domain of NRF2 was shown to recruit CHD6 to
the NQO1 gene both under basal and tert-butylhydroquinone induction (44). A BRG1-containing coactivator was shown to be required for NRF2-dependent activation of the HO-1, but not NQO1 gene (45). A possible involvement of a chromatin-remodeling complex on the HSF1 promoter was tested by measuring the effect of downregulation of subunits of different chromatin-remodeling complexes such as SSRP1 of the FACT complex, BRG1 (SMARCA4) of the SWI2/SNF2 complex, and SMARCA3 of the SWI/SNF complex (HLTF) using corresponding si- or sh-RNAs (Fig. 6A). Among these, only BRG1 downregulation affected arsenite-mediated HSF1 expression to a significant level (Fig. 6B). Reduced recruitment of RNA-polymerase II specifically to the promoter region of HSF1 (HSF1-pr) upon BRG1 inhibition, is indicative of NRF2 dependence on BRG1 for its function in response to arsenite stress (Fig. 6C).

**Effect of NRF2-dependent HSF1 expression on proliferation and epithelial to mesenchymal transition of MCF7 cells induced by oxidative stress**

Upregulation of HSF1 gene expression at the levels of protein and mRNA was reported in breast cancer patients by a cohort study (19,46). Therefore, MCF7 cells were selected to validate the importance of NRF2-dependent HSF1 expression in a cellular function. HSF1 and NRF2 functions were downregulated by shRNA or all-trans retinoic acid (RA), respectively, alone or in combination, to assess their effects on cell morphology, proliferation, viability as well as epithelial-mesenchymal transition (EMT) of MCF7 cells in response to arsenite treatment. NRF2 in the presence of RA is defective in ARE binding, because, it preferably forms complex with retinoic acid receptor α (RARα) when RA is present (47). The optimum concentration of RA on NRF2 function inhibition was determined by its dose-dependent activity, i.e., inhibition versus toxicity study (Fig. S1). Dependence of MCF7 cells to NRF2-dependent HSF1 transcription demonstrated a drastic change in their morphology; MCF7 developed apoptotic vesicles when exposed to arsenite as well as when treated with HSF1 shRNA and RA (Fig. S3, arrows). Inhibition of the factors NRF2 and HSF1, alone or in combination also resulted in a marked alteration in the proliferation (Fig. 7A) and the viability (Fig. 7B) of the cells (Figs. 7C, S3). Similar effect on HO-1 expression by arsenite treatment in cells pre-treated with RA or NRF2 shRNA suggested that these two treatments are functionally comparable (Fig. 7C). EMT, a crucial developmental event in cells, has been shown to correlate with the aggressiveness of cancer (48). To further assess the effect of HSF1 and NRF2 inhibition on tumorigenicity, the expression levels of two important EMT markers, E-cadherin and N-cadherin, were determined by immunoblotting (49,50). After four days of arsenite exposure, E-cadherin, an epithelial marker, decreased in the arsenite treated set, but not so when both HSF1 and NRF2 were inhibited (Fig. 7D). The arsenite-induced upregulation of mesenchymal marker N-cadherin, in contrast, was abrogated following inhibition of HSF1 and NRF2 (Fig. 7D).

Autophagy was earlier shown to help cancer cell survival and migration through overcoming intracellular stress (51). To examine if autophagy has any role in this case, immunoblot was carried out to estimate the level of LC3II, a marker of autophagy activation (52). The level of ATG7, a HSF1 target (53) and an E1 ubiquitin ligase involved in the autophagosome formation (54) was also monitored. Inhibition of HSF1 and NRF2 alone or in combination appeared to affect the levels of LC3II (Fig. 7D). Next, role of ATG7 and HSF1 alone and in combination was analyzed. The results suggested that downregulation of these factors which inhibit autophagy also impairs EMT (Fig. 7E).

Involvement of NRF2 and HSF1 in cell migration in response to arsenite treatment was monitored by wound healing assay. Significant block in migration/wound healing of cells was observed when both the factors were inhibited (Fig. 7F). Induction of HSF1 by peroxide treatment was found to be similarly dependent on NRF2, as RA treatment reduced HSF1 mRNA transcription similar to that in the HO-1 gene (Figs. 7G, S1B). The role of HSF1 and NRF2 on cell viability was also measured in response to hydrogen peroxide treatment yielding results similar to that of arsenite (Fig. 7H).

**Discussion**

Results presented here have unraveled a molecular basis of transcriptional upregulation of cellular HSF1 gene by NRF2 upon oxidative stress induced by sodium arsenite or hydrogen
peroxide (Figs. 1 and 7G-H). Two AREs located between 1707 and 1517 base pairs upstream of the HSF1 promoter were identified to be responsible for mediating the NRF2 function (Figs. 2-3). We also showed that this event plays an important role in survival, proliferation and migration of breast cancer cells (Fig. 7). Constitutive activation of NRF2 has been implicated by earlier studies in cancer cell survival and proliferation (32,55).

An important finding of this study is the identification of two unique AREs by comparison with an up-to-date consensus ARE-sequences. Although the sequence analysis software identified ARE-A, ARE-B and ARE-C, functional assays validated only ARE-B and ARE-C as the functional AREs. These two AREs differed from that of the NQO1 or HO-1 gene (Fig. 2C). For example, the ARE-B element matched the upstream TGA present in both NQO1 and HO-1 AREs but not downstream. The ARE-C element matched the downstream AGC present in both NQO1 and HO-1 AREs but it carries TTA instead of TGA upstream. Assembly of the complex with nuclear extracts on the ARE-B and ARE-C, with mobility similar to that of NQO1, suggests the formation of a complex involving similar players (Fig. 4C). The KD value of ARE-C, however, was measured to be two and three times of that of ARE-B and NQO1, respectively (Fig. 4E). The KD of NRF2-MafG heterodimer binding to ARE-B with a higher affinity than that of ARE-C suggests that the requirement of GC at 9, 10 position of an ARE may not be essential in all ARE sequence context (36). Although it remains to be experimentally verified, the presence of T at position 3 of ARE-C (which is less conserved in the consensus ARE) may be responsible for its lower affinity to bind the NRF2-MafG heterodimer (Fig. 4E). Mismatch in positions 4 and 10 may have rendered putative ARE-A inactive (although r-VISTA scored it higher than ARE-C. (Fig. 2B left panel and Fig. 2C).

The sensitivity of both NRF2- and HSF1-guided pathways to a proteotoxic stressor is known; HSF1 and NRF2 were shown to activate a common set of genes with overlapping functions in heat shock and antioxidant response pathways (56). NRF2 and HSF1 were reported to compensate for each others’ activity (20). NRF2 increase HSP70 expression during methionine deprivation in a process independent of HSF1 function, suggesting that inhibition of HSF1 activity can be in part bypassed by NRF2-dependent anti-oxidant response (57). NRF2 knockout mice showed a higher level of unfolded protein response, thus a higher level of HSF1 activation (58). This compensatory function may be responsible for failure to detect any significant change of HSP70 transcription induction in cells with downregulated NRF2 (Fig. 3A). HSP70 was also regulated by factors other than HSF1(29).

While this study convincingly showed that cellular HSF1 is a target of NRF2, especially under oxidative stress, it remains to be determined why earlier ChIP sequencing studies did not detect NRF2 presence on the HSF1 promoter (35,36,38). Studies here suggest that HSF1 transcription was differentially regulated by oxidative stress in different cells. For example, it was induced 8-fold more in HT1080 compared to the NKE cells (Fig. 1B). Additional investigation is necessary to conclude that the extent of dependence on NRF2 is determined in a cell by its endogenous ROS level. This study shows that HSF1 gene is upregulated in cells by oxidative stress in proportion to their endogenous ROS levels (Fig. 1B). Efficient neutralization of the effect of arsenite by n-acetyl cysteine suggested that a major mediator of arsenite action was through increasing the level of cellular ROS (Fig. 5C).

We also found that NRF2 requires BRG1 to regulate HSF1 promoter activity (Fig. 6). Downregulation of FACT and helicase-like transcription factor (HLTF) did not affect arsenite-induced HSF1 transcription. An association of P-TEFb, Mediator and DNA-bending protein is anticipated in the process. MED16 was shown to be required in NRF2 target gene expression (59). Future studies will show how NRF2, recruited at the identified ARE-B and –C, communicates with RNA polymerase II at the core promoter (60).

This study highlighted an important role of NRF2 and HSF1 collaboration in cancer cells survival and progression. Our results suggested that both NRF2 and HSF1 alone or in combination play positive role in arsenite-induced EMT and migration in MCF7 cells (Figs. 7D-H) (61). These two factors may support these processes by enhancing autophagy (Figs. 7D-E), an important process many cancer cells utilize for their benefit (20,51,53,62).
Many cancer cells have an elevated level of oxidative stress (63). An activated ROS signaling supports prosurvival pathways through facilitating several cellular processes such as inactivating tumor suppressor genes, enhancing glucose consumption, the rate of oncogenic mutation, and anaerobic respiration (64). NRF2 plays a crucial role in maintaining higher ROS in cells. Oncogenes can direct increased NRF2 expression (65). This gain of function in NRF2-controlled interactome has been reported in lung, breast, skin, esophageal, gallbladder, renal, pancreatic and endometrial cancer (66,67). NRF2 exerts checks and balances on the cellular ROS level by upregulating expression of its target genes such as glutathione peroxidase, and peroxiredoxin (20,64). At the same time, cancer cells exhibit an elevated level of HSF1 activity, i.e., upregulated levels of HSPs to support their prosurvival property (15,16). The role of various post-translational modifications modulating HSF1 activity has been under extensive investigation (5). Altogether, the results presented here shed light on the molecular basis of transcriptional upregulation of the HSF1 gene for adaptation to oxidative stress and its correlation with aggressiveness of cancer.

**Experimental procedures**

**Cell culture**

The mammalian cell lines used in this study, HT1080 (human fibrosarcoma), HeLa (cervical carcinoma), MCF7 (breast adenocarcinoma), PC3 (prostate adenocarcinoma), HEK293 (immortalized human embryonic kidney) and NKE (normal kidney epithelium), were a kind gift from Dr. Andrei Gudkov. All cells were grown in complete DMEM (Gibco) supplemented with 10% FBS (Gibco), 2 mM L-glutamine (Himedia), 100 U/ml penicillin-streptomycin (Himedia), 2.5 µg/ml amphotericin B (Himedia) and non-essential amino acids (Himedia). Cells were cultured in 37°C in a humidified atmosphere containing 5% CO2. Cells grown to no more than 90% confluence were distributed in new plates by trypsinization as required.

**Reagents and antibodies**

All the reagents were of analytical grade and were purchased from SRL India, Merck or Sigma-Aldrich. All primers and oligonucleotides used were procured from Sigma. Restriction enzymes were bought from NEB. The antibodies used anti-HSF1 - Biobharati Lifesciences (AB 0220); anti-HSP70 - Biobharati Lifesciences (AB 0210); anti-NRF2 - CST (# 12721); anti-beta actin-HRP secondary - Abcam (ab20272); anti-HO-1 - CST (#5853); anti-HLTF (SMARCA3) - Novus (NB100-280); anti-BRG1 - CST (#3508); anti-SSRP1 - Biolegend (609702); anti-E Cadherin - CST (#3195); anti-N Cadherin - CST (#13116); anti-ATG7 - CST (#2631) and anti-LC3B – CST (#3868).

**Heat shock and arsenite treatments**

The cells were plated the day before for treatment. Heat shock was conducted by submerging the plate of cells (grown to ~70% confluency) in water bath pre-warmed at 42°C for 1 h. The temperature in the media reached 42°C within 5 min. The growth media was not replaced either before or after heat shock. Treatment with sodium arsenite (20 µM) was carried out for 2 h unless otherwise indicated.

**Preparation of whole cell extracts and Western blot analysis**

The cells were harvested from culture plates with a cell-scaper on ice in ice cold PBS and rinsed twice with PBS. Whole cell extracts (WCE) were prepared essentially using the procedure described earlier (29). Cell extracts containing 20-50 µg total protein or as appropriate, was electrophoresed in 10% (acrylamide:bisacrylamide 29:1) denaturing PAGE and the resolved proteins were transferred to PVDF membrane (Millipore). The membrane was blocked with 3% BSA or 5% fat-free milk in PBST (137 mM NaCl, 2.7 mM KCl, 10 mM Na2HPO4, 1.8 mM KH2PO4, pH 7.4, supplemented with 0.1% Tween 20) for 30 min at room temperature and incubated with a desired primary antibody at an optimized dilution for overnight at 4°C. The next day, the membrane was washed 3-4 times with PBST followed by incubation with secondary antibody for 1 h at room temperature. The membrane was then washed as before and developed by chemiluminescent detection (Clarity-BioRad) according to manufacturer's instructions. For quantification of the immunoblots, band-intensities were measured using ImageJ software considering β-actin as normalization control and values were plotted using GraphPad Prism 6.0.
RNA isolation, semiquantitative RT-PCR (sqRT-PCR) and quantitative/real-time PCR (qRT-PCR)

Total RNA was isolated from cultured cells using TRIzol reagent as per manufacturer’s protocol (Life Technologies). Isolated RNA was dissolved in ultrapure water and quantified using BioSpectrometer (Eppendorf). For cDNA preparation, 1 μg total RNA was reverse transcribed using i-script cDNA synthesis kit (BioRad) in 10 μl reaction volume. For semiquantitative RT-PCR, a 10-fold (or as appropriate) diluted cDNA was probed with gene-specific primers using Taq polymerase. Expression of GAPDH mRNA in the same sample under analysis was considered as endogenous control. Quantitative real-time PCR (qRT-PCR) was performed using SYBR green (Hot Jumpstart SYBR green) according to the manufacturer’s protocol (Sigma). Results were expressed as the ratio of treated samples to untreated samples normalized to their GAPDH levels. Measured numbers of threshold were converted to relative fold change using $2^{ΔΔCT}$ method (68). The primer sets used for estimation of transcript levels for different genes are described in Supporting Information (Table S1).

Plasmid Constructs

The human HSP70 promoter (pHSP70[-450/+/91]) and 5'-deletion fragments of the human HSF1 promoter (Fig. 2) were generated by PCR from human genomic DNA using primers containing restriction sites. A Xhol and HindIII recognition site was added to the PCR product through 5'-ends of forward and reverse primers, respectively. Amplified fragments were subsequently cloned into the pGL4.79[hRluc/neo] reporter vector (Promega) pre-digested with the same restriction enzymes. Cloning of the ARE site from NQO1 gene promoter [5'-TCCGCAGTCACAGTCAGCAGAATCTG-3'] and HSF1 promoter versions were done in pGL4.79-mCMV between Acc65I and BglIII sites. The pGL4.79-mCMV vector is a modified pGL4.79[hRluc/neo] vector with a minimal CMV (mCMV) enhancer element (5'-TAGAGGTATATAATGGAAGCTCGACTTCAG-3') cloned between BglIII and HindIII sites. Nucleotide sequences of PCR primers used are listed in Supporting Information (Table S2).

Luciferase reporter assay

HT1080 cells grown in 12-well plates to ~70% confluence were transfected with different reporter constructs carrying the HSF1 promoter variants using Lipofectamine 2000 (29). Next day, cells were distributed into two wells and treated with or without 20 μM arsenite for 2 h, followed by isolating the RNAs by TRIzol reagent. Expression levels of different genes were measured by sqRT-PCR and qRT-PCR from the cDNA prepared from the total RNA pretreated with DNase I. Relative fold increase in Renilla-luciferase (RLuc) mRNA levels in the presence of arsenite was calculated with respect to the untreated control as well as carrier internal vector control. The levels of Rluc mRNA in samples transfected with promoter-less pGL4.79 [hRluc/neo] vector was considered as 1. Unless otherwise stated, reporter gene assays were carried out in three parallel experiments or repeated at least three times.

Construction of shNRF2-pLKO.1-puro vector

shRNA [5'-TGGCATCACCAGAACACTCAGTGGAATCTCAGTGGAAATCT-3'] against the NRF2 gene was cloned at AgeI/EcoR1 sites in pLKO.1-puro (a 3rd generation lentiviral vector constructed in Bob Weinberg Lab - Addgene plasmid # 8453) with the help of RNAi Consortium (TRC) portal (http://www.broadinstitute.org/rnaipublic/)(47). For stable knockdown of NRF2, cells were transduced by lentiviral particles made from shNRF2-pLKO.1 vector using psPAX2 (Addgene#12260) and pMD2.G (Addgene#12259) as packaging plasmids following the protocol described in the Supporting Information (69).

Electrophoretic mobility shift assay (EMSA)

Nuclear extracts (NE) were prepared from HT1080 cells with NE-buffer (25 mM HEPES pH 7.8, 420 mM NaCl, 10% glycerol, 0.5 mM EDTA and 1% NP-40) supplemented with protease and phosphatase inhibitors. ARE-A [5'-CTGGGGGCTGG AAGAGAAATGGGTCC-3'], ARE-B [5'-GGATTGGCTGAAGAGTCACAGGAATG-3'], ARE-C [5'-TAGACTCTTGAAGCAGTTCAGCGATG-3'] regions of the HSF1 promoter or their mutated forms - ARE-mB [5'-
GGATTGGCcacAGAGTCACAGGAATG-3'],
ARE-mC [5'- TAGACTCTcacG
AAGCAGTTGAAGGC-3'] and human NQO1-
ARE regions [5'-
TCCGCAATCGACTGACACTGA
GCAGAATCTG-3'], after annealing with their
complementary strands, were end-labelled
with [γ-32P]ATP using T4 polynucleotide kinase. Six
nanogram of a probe was incubated with 20 μg
of NE on ice for 30 min in a 20 μl reaction in
binding buffer (20 mM HEPES (pH 7.9), 100
mM NaCl, 10% glycerol, 0.5 mM EDTA, 2 μg
BSA, 2.5 μg salmon sperm DNA, 1 mM PMSF,
1 mM NaF and 1 mM Na3VO4). For competitive
binding, a 100-fold excess of respective
unlabeled double stranded wild type or mutant
oligonucleotides was added to the reaction
mixture. For super-shift analysis, anti-NRF2
antibody (1 μg), or anti-his6 antibody (1 μg) or an
IgG antibody (1 μg) was added to the reaction
mixture. The reaction products were analyzed on
a 4% non-denaturating polyacrylamide
(acrylamide:bisacrylamide::29:1) gel in TBE
buffer (45 mM Tris-borate with 1 mM EDTA,
pH 8.0). The dried gel was visualized using a
Typhoon Trio+ PhosphorImager (GE
Healthcare). DNase I footprinting was performed
as described (70).

Chromatin immunoprecipitation (ChIP) assay

HT1080 cells transfected with a FLAG-tagged
NRF2 over expression plasmid (NC16
pCDNA3.1 FLAG, Addgene plasmid # 36971)
were treated with 20 μM sodium arsenite or
mock for 2 h. Treatment with n-acetyl cysteine
(5 mM) was carried out for 3 h prior to
treatment with arsenite. Preparation of sheared chromatin,
incubation with anti-FLAG antibody (Sigma
#F7425) for collecting the associated DNA, and
PCR was carried out (31). The DNA was
quantified by quantitative PCR using the primers
listed in Supporting Information (Table S3).
ChIP against RNA Polymerase II was performed
with anti-RNA Polymerase II antibody (Abcam
#ab817).

Cell proliferation analysis

Cell proliferation was measured by viability
determination using 3-(4,5-dimethylthiazol-2-yl)-
2,5-diphenyltetrazolium bromide (MTT) assay or
by direct cell counting. Cells were seeded at
0.5x10^5 cells per well in 12-well plates and
incubated under standard conditions. After the
experiment, cells were incubated with 0.5 mg/ml
MTT solution (Himedia-RM1131) at 37°C,
5%CO2 for 4 h in the dark. After 4h incubation
the MTT solution was removed and DMSO was
added to the plates. OD_{570} value was measured
with Biospectrometer (Eppendorf). For counting,
cells were trypsinized after washing with PBS.
After making thorough suspension, samples
were counted using haemocytometer.

Wound healing assay

Cells (2x10^5) were grown in complete medium in
6-well plates until cells are 80-90% confluent.
The under-surface of each well was marked with
three parallel straight lines. A scratch was made
across the surface of the plate using sterilized
disposable 200 μl pipette tip to remove the
complete layer of cells within the scratch area at
90° to the orientation lines. Each well was then
washed twice with PBS, replaced with growth
medium supplemented with 5% serum and
handled as mentioned. The width of the scratch
was imaged using a microscope with camera
(Leica), immediately (0 h) or after 24 h or 48 h
of treatment at same magnification settings.
Scratch-gap area was measured using ImageJ
software and values were plotted using GraphPad
Prism 6.0.

ROS quantification by DCFDA assay

Cells pre-treated as appropriate were incubated
with 5 μM DCFDA (2',7'-dichlorodihydrofluorescein diacetate) for 30 min.
After removing the DCFDA by washing twice
with ice-cold PBS, the labelled cells were
trypsinized, rinsed and finally resuspended in
PBS. Oxidation of DCFDA to the highly
fluorescent 2',7'-dichlorofluorescein (DCF)
proportional to ROS generation was analysed by
measuring 10,000 events/sample using FACS
(FACSVERSER, BD Biosciences).

Bioinformatics analysis

Transcription factor-binding site analysis was
done by rVista (rVista 2.0;
https://rvista.dcode.org). WebLogo program
(http:// weblogo.berkeley.edu) was used for
generating the sequence logo of the ARE-motif
from a curated list of known AREs as described
(39).

Statistical analysis
All experiments were performed at least three times. Plotting of graphs and statistical analysis was performed by one-way ANOVA with appropriate post-hoc tests, using GraphPad Prism 6.0 software. Scatter plots represent individual data points combined with means ± SD. Values were considered to be statistically significant when $P < 0.05$.

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**Conflict of interest** - Authors declares no conflict of interest.

**Author contribution** - SP and MP designed the experiments. SP carried out promoter cloning, mutational analyses, reporter assays, EMSA, si/sh RNA knockdown experiments. SG purified his$_6$-NRF2 and MafG proteins, SP and SG carried out experiments with MCF7 cells. SM and SP performed DNase I-footprinting experiments with guidance from SS. SP and MP wrote the paper. MP conceptualized, planned, supervised the study, edited and communicated the manuscript.
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independent importance for the progress of prostate cancer. Clinical cancer research: an official journal of the American Association for Cancer Research 13, 7003-7011


Figure 1. Transcriptional upregulation of HSF1 and HSP70 genes in cells of different organ origin upon arsenite treatment. (A) qRT-PCR analysis of HSF1 and HSP70 mRNA levels in HT1080 cells upon heat shock at 42°C for 1 h (HS) or exposure to 20 µM arsenite for 2 h (Ars) represented by scatter plots. Bar, mean ± SD (n=4), ***P < 0.001 compared with Ctrl (control). Representative immunoblots showing the upregulation HSF1 and HSP70 in HT1080 cells as indicated with estimation of their levels shown on the right. Bar, mean ± SD (n=3), **P < 0.01; ***P < 0.001. (B) qRT-PCR analysis of HSF1 and HSP70 mRNA levels upon arsenite treatment in different cell lines as indicated (left and middle panels). Estimation of relative ROS levels induced in different cell lines under conditions indicated as determined by DCFDA assay, performed after 2 h of arsenite treatment (right panel). Bar, mean ± SD (n=3), **P < 0.01, ***P < 0.001, compared with Ctrl. (C) Representative immunoblots showing the upregulation HSF1 and HSP70 in different cell lines as indicated with estimations of their levels on the right. Bar, mean ± SD (n=3), *P < 0.05; ***P < 0.001; ns, not significant. (D) qRT-PCR analysis of HSF1 and HSP70 mRNA in HT1080 cells pre-treated with or without 1 µg/ml actinomycin D (ACTD) for 2 h followed by treatment with HS or arsenite. In all assays, GAPDH mRNA level was used as normalization control. Representative immunoblots showing the upregulation HSF1 and HSP70 as indicated with estimation of their levels shown on the right. In all immunoblot experiments β-actin was used as internal reference. Bar, mean ± SD (n=3), ***P < 0.001; **δδδP < 0.01; δδδδP < 0.001; ns, not significant.

Figure 2. Analysis of HSF1 gene promoter elements responsible for its sensitivity to arsenite treatment.

(A) Luciferase reporter assay was performed in HT1080 cells using full-length and different truncated versions of the HSF1 promoter as indicated by schematic drawing. Numbers indicate nucleotide positions with respect to +1 as the transcriptional start site. qRT-PCR analysis of promoter activity (fold increase in luciferase mRNA level) in arsenite treated vs. untreated samples expressed as relative luciferase mRNA levels represented by scatter plots. Bar, mean ± SD (n=3), ***P < 0.001; ns, not significant. RLA was normalized by measuring GFP mRNA level from a vector cotransfected with the reporter vector as a transfection control. (B) Putative antioxidant response elements (AREs) with corresponding scores, locations and core sequences on the HSF1 promoter as revealed by rVISTA analysis (left panel). Schematic showing putative AREs with their relative positions on the HSF1 promoter (right panel). (C) Clustal Omega alignment of nucleotide sequences of HSF1 promoter AREs with those of NQO1 and HO-1 promoters. The nucleotides matching the logo generated by the WebLogo program are marked by asterisks.

Figure 3. NRF2 regulates HSF1 transcription by arsenite treatment in HT1080 cells.

(A) qRT-PCR analysis of the effect of shRNA-mediated NRF2 knockdown on arsenite (Ars)-induced HSF1 expression and other genes as indicated. Bar, mean ± SD (n=3), ***P < 0.001 compared with (Ctrl-NRF2-scr). (B) Representative immunoblots showing the levels of NRF2 along with estimation of their levels as indicated. Bar, mean ± SD (n=3), ***P < 0.001 compared with Ctrl-NRF2-scr. (C) Representative immunoblots showing the levels of HSF1 along with estimation of their levels as indicated. Bar, mean ± SD (n=3), **P < 0.01 compared with Ctrl-NRF2-scr column. (D) Schematic showing HSF1 promoter-luciferase constructs employed to functionally validate each of the putative AREs located on the HSF1 promoter (left panel), and their dependence on NRF2 by luciferase reporter assay (right panels). Relative promoter activity is expressed as the ratio between the mRNA levels of luciferase and GFP mRNAs, with or without NRF2 knockdown (NRF2-sh). Solid arrow and open arrows point the effect on NQO1-promoter and HSF1-promoter activities, respectively. Bar, mean ± SD (n=3), ***P < 0.001 compared with pHSF1-FL+ars column; ns, not significant.

Figure 4. NRF2 binds putative ARE-regions identified in the HSF1 gene promoter.
Figure 5. NRF2 binds HSF1 AREs in cells.

(A) Electrophoretic mobility shift assay (EMSA) demonstrating the formation of protein-DNA complex (arrowhead) only with wild-type HSF1 ARE-B and ARE-C oligonucleotides as probes, but not with ARE-A or with mutated AREs (ARE-mB and ARE-mC). Nuclear extract (Nuc) isolated from HT1080 cells pretreated with arsenite (Ars) was used in the experiment. (B) EMSA showing complex formation on ARE-B and ARE-C with the same Nuc used in panel A along with NQO1-ARE used as positive control. One-hundred fold excess of unlabelled oligonucleotide over its labelled counterpart was used in the cold competition experiment (cold comp). Complexes super-shifted with NRF2 antibody are indicated (open arrowhead). (C) EMSA showing the effect of different molar ratios of purified NRF2 and MafG proteins used in the formation of the complex on the indicated AREs. (D) EMSA for comparison of the relative affinity of the AREs for complex formation. Complexes were formed on NQO1-ARE by purified NRF2:MafG and challenged by different molar excess of the unlabelled corresponding double stranded oligonucleotides (cold probe) as indicated. (Lower panel) Plots showing the sensitivity of the complexes (estimated by densitometric scanning of corresponding bands) to increasing doses of unlabelled AREs as indicated. Error-bar, SD (n=3). (E) EMSA and corresponding plots showing measurement of the equilibrium dissociation constant (Kd). The percentage of bound complex formed on each of NQO1-ARE, ARE-B and ARE-C DNA is plotted as a function of the monomeric concentration of purified NRF2. The Kd of each complex is indicated. Error-bar, SD (n=3). (F) Autoradiogram showing DNase I footprints of NRF2 binding on the top strands of NQO1-ARE, ARE-B, and ARE-C motifs. DNase I-protected regions are shaded with the ARE sequence shown in bold letters. Lanes A+G and G contain the products of Maxam-Gilbert chemical sequencing reactions for dA and dG residues that served as sequence markers. Asterisk, hypersensitive site.

Figure 6. Arsenite-induced HSF1 transcription requires BRG1, but not HLTF or SSRP1, in MCF7 cells.

(A) Representative immunobots showing knockdown levels of the indicated factors with their corresponding si/sh-RNA. (B) qRT-PCR analysis showing the levels of HSF1 mRNA by arsenite treatment with the indicated factors downregulated. Bar, mean ± SD (n=3), ***P < 0.001. (C) ChIP qPCR analysis of RNAP II recruitment by arsenite treatment on the HSF1 promoter (HSF1-pr) in cells pretreated with si-BRG1. The position of the primers used in the ChIP experiment was shown on the top. Bar, mean ± SD (n=3), ***P < 0.001 compared with -siBRG1-Ars; δδδP < 0.001 compared with -siBRG1+Ars. Bar, mean ± SD; ns, not significant. HSF1-pr, HSF1 gene promoter; HSF1-gb, gene body.

Figure 7. NRF2 regulation of HSF1 is required for biology in MCF7 cells upon stress induced by arsenite and peroxide treatment.
(A and B) Levels of growth and viability of MCF7 cells upon HSF1 inhibition by shRNA (HSF1-KD) and NRF2 inhibition by all-trans retinoic acid (RA) determined by cell counting (A) and MTT assay (B), respectively. Bar, mean ± SD (n=3), ***P < 0.001. (C) Representative immunoblots along with estimation of their levels showing relative efficiency of RA and NRF2-shRNA in inhibiting NRF2 function. (D) Representative immunoblots along with estimation of their levels showing the roles of HSF1 and NRF2 in epithelial-mesenchymal transition (EMT). The EMT markers and efficacy of HSF1-KD are indicated. Cells were pre-treated with 1 µM arsenite for four days before EMT markers were checked. (E) Representative immunoblots along with estimation of their levels showing the effect of ATG7 and HSF1 on autophagy and EMT. (F) Effect of ablation of HSF1 and NRF2 functions on cell migration and wound healing. Cells were treated with HSF1 shRNA and RA as described above for 24 h before scratch was created with a sterile tip to introduce gaps. Cells were incubated with fresh medium without or with arsenite up to 48 h when wound healing was estimated. Representative phase-contrast images with corresponding treatments as indicated. Rectangles represent initial wound boundary. Levels of wound healing with corresponding treatments as indicated on the right. Bar, mean ± SD (n=3), ***P < 0.001; ns, non significant. (G) qRT-PCR analysis of the cellular levels of HSF1, HO-1 and HSP70 (positive control) mRNA induced by H2O2 (100 µM, 3 h). Bar, mean ± SD (n=3). (H) Viability of cells determined by MTT assay under treatment conditions as indicated. Bar, mean ± SD (n=3), **P < 0.01.
Figure - 1
Relative luciferase mRNA level [Luc/GFP]

A

B

<table>
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<tr>
<th>Region</th>
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<td>NRF2_Q4_01</td>
<td>0.61</td>
<td>-1530 to 1517</td>
<td>cTTAGGAAGGgG</td>
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</tbody>
</table>

C

mARE consensus

mARE consensus

Figure - 2
Figure - 5
Figure - 6