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Heterotrimerization of Heat-Shock Factors 1 and 2 Provides a Transcriptional Switch in Response to Distinct Stimuli

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Organisms respond to circumstances threatening the cellular protein homeostasis by activation of heat-shock transcription factors (HSFs), which play important roles in stress resistance, development, and longevity. Of the four HSFs in vertebrates (HSF1-4), HSF1 is activated by stress, whereas HSF2 lacks intrinsic stress responsiveness. The mechanism by which HSF2 is recruited to stress-inducible promoters and how HSF2 is activated is not known. However, changes in the HSF2 expression occur, coinciding with the functions of HSF2 in development. Here, we demonstrate that HSF1 and HSF2 form heterotrimers when bound to satellite III DNA in nuclear stress bodies, subnuclear structures in which HSF1 induces transcription. By depleting HSF2, we show that HSF1-HSF2 heterotrimerization is a mechanism regulating transcription. Upon stress, HSF2 DNA binding is HSF1 dependent. Intriguingly, when the elevated expression of HSF2 during development is mimicked, HSF2 binds to DNA and becomes transcriptionally competent. HSF2 activation leads to activation of also HSF1, revealing a functional interdependency that is mediated through the conserved trimerization domains of these factors. We propose that heterotrimerization of HSF1 and HSF2 integrates transcriptional activation in response to distinct stress and developmental stimuli.

INTRODUCTION

Cells react to stressful conditions by activation of heat-shock factors (HSFs), of which there are three mammalian isoforms: HSF1, HSF2, and HSF4 (Pirkkala et al., 2001). Activated HSFs bind to heat-shock elements (HSEs) within the promoters of their target genes and induce synthesis of protective molecular chaperones called heat-shock proteins (Hsps). Hsps prevent protein misfolding and are required for stress resistance and healthy cell growth, development, and aging (Bukau et al., 2006, Morimoto, 2008). They also protect against metabolic, neurodegenerative and cardiovascular disorders (Balch et al., 2008). In addition to Hsps, HSFs are associated with expression of noncoding satellite III (sat III) RNA in nuclear stress bodies (nSBs) (Jolly et al., 2004, Rizzi et al., 2004), to which HSF1 and HSF2 translocate upon stress (Jolly et al., 1997, Alastalo et al., 2003). The nSBs form on the locus 9q12 consisting of pericentromeric heterochromatin, and the sat III transcripts provide scaffolds for docking of other nSB components, as shown for the splicing factor ASF/SF2 (Chiodi et al., 2004, Metz et al., 2004). Besides ASF/SF2, the RNA processing factors heterogeneous nuclear ribonucleoprotein (hnRNP) A1-associated protein (HAP), hnRNPM, Sam68, and SRp30c localize to the nSBs (Weighardt et al., 1999, Denegri et al., 2001).

HSF1 is activated by classical stresses such as heat shock and heavy metals and responds to elevated temperatures in vitro (Ahn et al., 2001, Ancker and Sistonen, 2007). HSF1 is also involved in development and has critical roles in longevity and cancer (Xiao et al., 1999, Hsu et al., 2003, Morley and Morimoto, 2004, Dai et al., 2007). Unlike HSF1, HSF2 lacks intrinsic stress responsiveness (Ahn et al., 2001). Another major difference between these factors is that while HSF1 is evenly expressed, the levels of HSF2 fluctuate. These changes in expression coincide temporally with HSF2 DNA binding activity during developmental processes (Rallu et al., 1997, Min et al., 2000). The function of HSF2 in development was revealed by hsf2−/− mice, which display neurological and reproductive abnormalities in both genders (Kallio et al., 2002, Wang et al., 2003, Chang et al., 2006, Åkerfelt et al., 2008). In addition, the stress-induced expression of hspm in hsf2−/− cells is altered (Östling et al., 2007). However, the mechanism by which HSF2 is recruited to stress-inducible promoters is not known. How HSF2 is activated, and the functional relationship between HSF1 and HSF2 also remain to be elucidated.

In this study, we use the nSBs as a model system to show that HSF1 and HSF2 interact as DNA-bound heterotrimers. When HSF1-HSF2 heterotrimerization is inhibited by depletion of HSF2, the transcription of sat III DNA is enhanced, indicating that HSF1-HSF2 heterotrimeriza-

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Abbreviations used: HSF, heat-shock factor; Hsp, heat-shock protein; nSB, nuclear stress body; sat III, satellite III.
acquired using a Plan-Apochromat 63×/1.4 oil differential interference contrast objective and further processed using Adobe Photoshop (Adobe Systems, Mountain View, CA) and CorelDRAW software.

Western Blot Analysis
Soluble cell extracts were prepared and subjected to SDS-polyacrylamide gel electrophoresis (PAGE) followed by transfer to nitrocellulose membrane (Protran nitrocellulose; Whatman Schleicher and Schuell, Dassel, Germany). HSF1 was detected by polyclonal anti-HSF1 antibodies (Sarge et al., 1993; Holmberg et al., 2000). HSF2 by polyclonal anti-HSF2 antibodies (Sarge et al., 1993; Ostling et al., 2007) and Hsc70 by SPA-815 (Nventa Biopharmaceuticals). Secondary antibodies were horseradish peroxidase conjugated and purchased from Promega (Madison, WI) or GE Healthcare (Little Chalfont, Buckinghamshire, United Kingdom). The immunoblots were developed with an enhanced chemiluminescence method (ECL kit; GE Healthcare).

Immunoprecipitation
Male hybrid mice of the B6129S/FJ strain were used in coimmunoprecipitation experiments. HSF2 knockout mice were obtained by matings of heterozygous mice that have been described previously (Kallio et al., 2002) and were maintained in a C57BL/6N background. The pathogen-free mice were housed under controlled environmental conditions and fed with complete pellet chow and allowed tap water. The mice were killed by CO₂ asphyxiation. All mice were handled in accordance with the institutional animal care guidelines of the California Institute of Technology. For coimmunoprecipitation experiments, testes were isolated from 60- to 80-d-old mice and lysed in 2 ml of lysis buffer (Alastalo et al., 2003). The precleared cellular lysate was incubated with anti-HSF1 (NeoMarkers), anti-HSF2 (NeoMarkers), or polyclonal FLAG2M2 (Sigma-Aldrich, St. Louis, MO) antibodies. The supernatant was removed by centrifugation for 1 h at 4 °C under rotation. After centrifugation, the Sepharose beads were washed with supplemented TEG buffer, and the immunoprecipitated proteins were run on 8% SDS-PAGE and transferred to nitrocellulose filter for immunoblotting as described above.

Semiquantitative Reverse Transcription (RT)-PCR and Real-Time RT-PCR
RNA was isolated with the RNAeasy kit (QIAGEN). Contaminating genomic DNA was removed with two DNase I treatments according to the RNAeasy protocol (QIAGEN). Of each sample, 1 μg of RNA was subjected to reverse transcription using the High Capacity cDNA Reverse Transcription kit (Applied Biosystems, Foster City, CA). For semiquantitative RT-PCR, Absolute Rox mix (Advanced Biotechnologies, Epsom, United Kingdom) was used and the PCR was run 40 cycles. The same sat III primers as for ChIP were used. The glyceraldehyde-3-phosphate dehydrogenase (GAPDH) primers were GAPDH For 5′-ACC CCC TCC TCC ACC TTG GA-3′, GAPDH Rev 5′-TTG CTC TAG CCA AAT TCG TTG T-3′. Real-time RT-PCR analyses were performed with Absolute cybgreen mix (Advanced Biotechnologies) and the ABI Prism 5700 and 7900 (Applied Biosystems). Relative RNA quantities were normalized to GAPDH. For real-time RT-PCR, the following primers and probes were used: sat III For 5′-AAT GCA ATG CAA TGT AGC-3′, sat III Rev 5′-CCT GTA CTC GGG TTG ATT CC-3′, GAPDH For 5′-ACC CCC TCC TCC ACC TTG GA-3′, and GAPDH Rev 5′-CTG TCT CTC TAG CCA AAT TCG TTG T-3′ (Shumaker et al., 2006); and hsp70 Probe 5′-FAM TTACACACCT CCTGCTTCTCTTT TAMRA-3′, hsp70 For 5′-GCCGAGACGAGCAGTGTGA-3′, hsp70 Rev 5′-CCTGGTACAGTCCGCTGATGA-3′, and GAPDH Rev 5′-GGAATTTGC- CATGGGTGGA-3′.

Structural Modeling
The structural model of the human HSF heterotrimer of two HSF1 (amino acids [aa] 16-205) molecules and one HSF2 (aa 8-194) was done in three steps. First, a template of the DNA binding domain of six Kynureninases (K. lactis) HSF monomers bound to a 32-base pair DNA was generated using SYBYL 7.3 (Tripos, St. Louis, MO) by aligning three dimers of the crystal structure of K. lactis HSF bound to DNA to each other as suggested by Littlefield and Nelson (1999). Second, the HR-A domain was aligned with the alpha-helix in the K. lactis HSF in a β-barrel structure. The H-R-A-B domain was aligned with the mHSF1 protein (Batchelor et al., 1998); K. lactis HSF bound to DNA next to each other as suggested by Littlefield and Nelson (1999). The HR-A domain was aligned also with the alpha-helix of the K. lactis HSF in a β-barrel structure. The H-R-A-B domain was aligned with the mHSF1 protein (Batchelor et al., 1998).
et al., 2004). Ten models were generated with Modeler (Sali and Blundell, 1993), and the model with the lowest objective function was chosen. Sequence alignment in Supplemental Figure 3 was done with ALSCRIPT (Barton, 1993), and Figure 2, A and B, were created with the PYMOL Molecular Graphics System (Delano Scientific, Palo Alto, CA).

Confocal Microscopy and Two-Photon Fluorescence Lifetime Imaging

The two-photon and confocal microscopy on HeLa cells was performed with an inverted two-photon laser scanning microscope Axiovert 200M (LSM510 NLO META; Carl Zeiss). During the experiment, cells were maintained at 37°C in a humidified atmosphere containing 5% CO2 by using an on-stage incubator (PeCon, Frankfurt, Germany). All measurements were performed using a 63×/1.4 oil immersion plan-apochromat objective. In the fluorescence lifetime imaging (FLIM) experiments, the fluorescence decays were measured by the time-correlated single photon counting technique. Fluorescence decays were fitted using a biexponential model and the corresponding mean decay time in each pixel was color coded to obtain FLIM images (SPCImage software; Becker & Hickl, Berlin, Germany). Fluorescence resonance energy transfer (FRET) was identified by the shorter lifetime of donor (CFP) in the presence of acceptor (τ_{DA}) as compared with that (τ_D) in the control donor-only cells. The FLIM/FRET efficiency was calculated as 

\[ E_{\text{FLIM-FRET}} = \frac{\tau_D}{\tau_D + \tau_{DA}} \]

Additional acceptor photobleaching experiments were carried out on the same cell and completed with FLIM measurements to confirm FRET. At least five cells were measured for each experimental condition.

RESULTS

Stress-induced Translocation of HSF2 in the nSBs Is HSF1 Dependent

The colocalization of HSF1 and HSF2 into the nSBs (Alastalo et al., 2003) prompted us to further investigate their functional relationship. HSF1 binds to DNA in the nSBs (Jolly et al., 2002), and we performed ChIP in K562 cells to examine the binding of HSF2 to sat III DNA. Heat shock induced binding of HSF1 and HSF2 was detected (Figure 1A), indicating that both HSFs occupy the same sat III DNA sequences (also see Supplemental Figure 1). To investigate how HSF1 affects the localization of HSF2, we generated a HeLa cell line stably down-regulating HSF1 by using vector-based RNAi (Figure 1C). In HSF1-depleted cells, the localization of both HSF1 and HSF2 into nSBs was abrogated (Figure 1B; for additional times, see Supplemental Figure 2A), inferring that stress-induced HSF2 DNA binding activity is dependent on HSF1. This result is supported by the finding that transient down-regulation of HSF1 by shRNAs in HEK293T cells (Figure 1E) abolishes sat III transcription (Figure 1D and Supplemental Figure 2B).

HSF1 and HSF2 Interact as DNA-bound Heterotrimers

The dependence of HSF2 on HSF1 activity for localization to the nSBs (Figure 1B) raised the question of the underlying mechanism. Upon activation, both HSF1 and HSF2 form heterotrimers through their trimerization domain consisting of the heptad repeats A and B (HR-A/B) (Sarge et al., 1993). Because HSF2 interacts with HSF1 via the HR-A/B domain (Alastalo et al., 2003), we studied whether HSF1 and HSF2 can form heterotrimers. We aligned the HR-A/B sequences of HSF1 and HSF2 and found that the amino acids involved in trimerization are conserved, especially well within the midsection of the HR-A/B domains of HSF1 and HSF2 (Supplemental Figure 3). Using two HSF1 HR-A/B helices and one HSF2 HR-A/B, we made a structural model of the left-handed coiled coil that constitutes the trimer interface (Figure 2A). All buried polar residues, which have been suggested to play a role in partner verification, are conserved in the HSF1-HSF2 coiled coil structure (Figure 2A). Based on the crystal structure of DNA-bound K. lactis (KLUEL) HSF (Littlefield et al., 1999), we generated a model of a human HSF1-HSF2 heterotrimer. The heterotrimer is bound to DNA and composed of the DNA binding and HR-A/B domains of HSF1 and HSF2 (Figure 2B). Adjacent to the HSF1-HSF2 heterotrimer, an HSF1 homotrimer is shown. The trimers are bound to a 32-base pair DNA double-stranded helix, with two nucleotide spacers as in a canonical HSE. We measured a distance of ~40 Å between the HR-A/B coiled coils of two HSF trimers (Figure 2B). Noncovalent contacts require proximities of <4 Å (Laberge, 1998), and at a distance of 40 Å, electrostatic interactions are unlikely to occur (Creighton, 1993), excluding interactions between separate trimers. This suggests that interactions between HSF1 and HSF2 on DNA are mediated through heterotrimerization.

FLIM-FRET was used to investigate whether HSF1 and HSF2 interact on DNA within the nSBs. We could not detect FRET when fusing CFP and YFP to the C termini of full-length HSF1 and HSF2, presumably because the C termini of HSF1 and HSF2 are highly mobile, preventing FRET. Therefore, to facilitate the proper positioning of the CFP and YFP moieties, we used HSF1 and HSF2 C-terminal deletion constructs (Figure 2C), that translocate into nSBs spontaneously (Supplemental Figure 4A; Jolly et al., 2004). These C-terminal deletion constructs contain the DNA binding and HR-A/B domains of HSF1 and HSF2 and should be apt for the study of interaction between the proteins as HSF1 and HSF2 interact through the HR-A/B domains (Alastalo et al., 2003). Upon transfection of HeLa cells with the HSF1 and HSF2 constructs, the fluorescence lifetime of the donor (HSF1-CFP) was shorter in the presence of acceptor (HSF2-YFP) compared with that in cells with only HSF1-CFP (Figure 2D), indicating that FRET occurs. The FRET signal was predominantly localized to the nSBs with a mean FRET efficiency of 10%, a significant number considering that the FRET efficiency of an HSF1-CFP/HSF1-YFP pair representing HSF1 homotrimers was 14% (Figure 2E). Additional FACS-FRET (Supplemental Figure 4B) and acceptor photo-bleaching experiments (data not shown) confirmed the FRET results, showing that HSF1 and HSF2 interact as DNA-bound heterotrimers.

Stress-induced HSF Activity is Regulated through HSF1-HSF2 Heterotrimerization

To investigate the impact of HSF1-HSF2 heterotrimerization on stress-induced transcription, we abrogated heterotrimer formation by depleting HSF2. HSF2-specific siRNAs were transfected to HEK293T cells (Figure 3B), and the transcription of sat III DNA was measured by real-time RT-PCR. A robust increase in the accumulation of sat III transcripts was evident when HSF2 was depleted (Figure 3A), demonstrating that HSF1-HSF2 heterotrimerization regulates HSF-mediated transcription. As expected, HSF2 knockdown did not alter the stress-induced relocalization of HSF1 to the nSBs (Figure 3C).

Elevated HSF2 Expression Induces HSF1-HSF2 Heterotrimerization and Activates Transcription

HSF2 is involved in development, and several reports show a correlation between increased HSF2 expression and DNA binding activity (Murphy et al., 1994, Rallu et al., 1997, Min et al., 2000, Chang et al., 2006, Åkerfelt et al., 2008). Abrogation of HSF2 DNA binding in the nSBs was associated with reduced HSF2 protein levels (Figure 1C), indicating that HSF2 is regulated in a concentration-dependent manner. We investigated the impact of elevated HSF2 expression on sat III transcription in HeLa and HEK293T cells by real-time RT-PCR, and we found that...
increased HSF2 concentration (Figure 4C and Supplemental Figure 5C) led to a prominent induction (~500-fold in HeLa cells; ~150-fold in HEK293T cells) of sat III transcription in the absence of stress (Figure 4A and Supplemental Figure 5A). To extend the study to other HSF targets, we measured the impact of HSF2 overexpression on the transcription of hsp70. In HeLa cells, transcription of also hsp70 was induced approximately twofold (Figure 4B), suggesting that HSF2 is activated when abundantly expressed. No similar induction of hsp70 was detected in HEK293T cells (Supplemental Figure 5B), which is probably due to the constitutive HSF activity in these cells, caused by the adenoviral transactivator E1A (Phillips et al., 1991).

The effect of elevated HSF2 expression on the localization of HSF1 was studied with immunofluorescence in HeLa and HEK293T cells. When abundantly expressed, HSF2 translocated to the nSBs (Figure 4D and Supplemental Figure 5D), whereas it remained dispersed in the nucleoplasm of moderately over-expressing HeLa cells (Figure 4E), further suggesting that HSF2 is regulated by its concentration. Intriguingly, HSF2 recruited also HSF1 to the nSBs (Figure 4D), implying that the increased expression of HSF2 seen during development leads to activation of HSF1.

To provide more evidence for HSF1-HSF2 heterotrimerization as a regulatory mechanism of transcription during developmental processes, we chose to investigate interaction between HSF1 and HSF2 in mouse testis, a tissue undergo-
ing active differentiation. Moreover, HSF2 is abundantly expressed in testis and has been shown to be active during spermatogenesis (Sarge et al., 1994, Fiorenza et al., 1995, Alastalo et al., 1998, Kallio et al., 2002, Wang et al., 2003, Åkerfelt et al., 2008). We performed coimmunoprecipitation of HSF1 and HSF2 in both wild-type and HSF2 knockout testis, and we found that HSF2 could be coimmunoprecipitated with HSF1 antibodies and vice versa (Figure 4F). These results indicate that HSF1 and HSF2 form heterotrimers during spermatogenesis.

Figure 3. Stress-induced HSF activity is regulated through HSF1-HSF2 heterotrimerization. (A) Real-time RT-PCR was used to assess the impact of HSF2 down-regulation on the transcriptional activity during heat shock (HS) in the nSBs. The fold induction was calculated by comparing the induction in HSF2 RNAi (+) samples to the induction in Scr. (−) samples, which were arbitrarily set to 1. The data represent three biological samples, and relative quantities of sat III RNA were normalized to GAPDH. Error bars indicate SD. (B) Western blot analysis of Scr. (−) and HSF2 RNAi (+) HEK293T cells. HS indicates a 1-h heat shock. (C) The localization of HSF1 (green) and HSF2 (red) to nSBs in Scrambled (Scr.) or HSF2– down-regulating cells (HSF2 RNAi) was followed by staining. The settings used for acquiring images of HSF1 and HSF2 in Scr. cells were reused for HSF2 RNAi cells. For staining, polyclonal and monoclonal antibodies were used against HSF1 and HSF2, respectively. The nucleus is shown in blue by staining of DNA with DAPI. Heat shock and control are indicated by HS and C, respectively.
Figure 4. Elevated HSF2 expression activates transcription and induces HSF1- HSF2 heterotrimerization. (A) Real-time RT-PCR analysis of sat III transcription upon HSF2 over-expression (+) in untreated HeLa cells. To exclude the possibility of unspecific activation of the heat shock response, GFP was over-expressed as a control (−). (B) hsp70 transcription upon HSF2 overexpression (+) was measured in untreated HeLa cells by real-time RT-PCR. GFP was over-expressed as a control (−). In A and B, fold induction was calculated by comparing transcription in the HSF2-over-expressing cells to the control cells, in which transcription was arbitrarily set to 1. The data represent three (A) and five (B) biological samples, and the relative quantities of RNA were normalized to GAPDH. Error bars indicate SD. (C) Western blot analysis of HSF1 (top) and HSF2 (bottom) in control (−) and HSF2-over-expressing (+) HeLa cells. (D) HSF2 was over-expressed in HeLa cells and the localization of HSF1 (green) and HSF2 (red) was monitored in the absence of stress. The arrow marks a cell over-expressing HSF2. (E) HSF1 and HSF2 localization in untreated HSF2-over-expressing HeLa cells. Moderate and robust HSF2 expression is indicated by a thick and thin arrow, respectively. In D and E, monoclonal anti-myc and polyclonal anti-HSF1 antibodies were used for staining. The nucleus is shown in blue by staining of DNA with DAPI. (F) Coimmunoprecipitation of endogenous HSF1 and HSF2 in mouse wild-type testis (HSF2 WT). To show interaction during spermatogenesis, antibodies against HSF1 and HSF2 were used for immunoprecipitation. In HSF2 knockout testis (HSF2 KO), no interaction could be detected. As a negative control, anti-FLAG antibodies were used. The asterisk indicates small molecular weight isoforms of HSF2, as described in Alastalo et al. (1998).

DISCUSSION

Integration of HSF Activity in Response to Stress and Developmental Stimuli

Trimerization is a crucial step in the activation process of HSFs that greatly increases the affinity for DNA (Xiao et al., 1991). In this study, we show that HSF1 and HSF2 form heterotrimers and propose that HSF1-HSF2 heterotrimerization provides a switch that integrates transcriptional activation in response to stress and developmental stimuli (Figure 5). HSF1 is known to be activated by stress and responds to elevated temperatures in vivo and in vitro. We suggest that when activated, HSF1 does not only form homotrimers but also trimersizes with HSF2, which itself is inert to stress. This model explains why the translocation of HSF2 into the nSBs is abrogated when HSF1 is depleted and also the previously suggested dependence of HSF2 on HSF1 for stress-induced DNA binding activity (Ostling et al., 2007). Moreover, we show that elevated expression of HSF2 leads to its activation, suggesting that concentration regulates HSF2 during development (Figure 5). When activated, HSF2 incorporates HSF1 into a transcriptionally competent heterotrimer, illustrating the capacity of HSFs to initiate heterotrimerization. This shows, for the first time, an interdependent cooperation between HSF1 and HSF2 that is mediated through the conserved HR-A/B domains. We propose that HSF1 needs cooperation from HSF2 in responding to developmental stimuli and that some of the functions during development earlier ascribed to HSF1 are in fact a consequence of HSF1-HSF2 heterotrimer activity.

Implications of HSF1-HSF2 Heterotrimerization

Our results show that HSF1-HSF2 heterotrimerization regulates stress-induced transcription, as demonstrated by increased expression of sat III transcripts when HSF2 is depleted. Also, the positive impact on hsp70 and hsp25, and the negative impact on hsp40 and hsp110 transcription seen in hsf2−/− cells (Ostling et al., 2007), can now be explained by HSF1-HSF2 heterotrimerization. HSF1 and HSF2 prefer architecturally different HSEs (Kroeger et al., 1993). This suggests that HSF1-HSF2 heterotrimers bind DNA differently than homotrimers and that the distinct regulation of HSF
target genes could arise from binding of HSF1-HSF2 heterotrimers to specific sites. Another possibility is that HSF1-HSF2 heterotrimers compete with homotrimers for common binding sites. For example, the clusterin promoter contains an HSE which binds only one trimer, and on which HSF1-HSF2 heterotrimerization has been proposed to occur (Loison et al., 2006). However, no formal proof for HSF1-HSF2 heterotrimerization on the clusterin promoter has yet been provided.

Another example of a protein family using heterotrimerization is the matrins. The matrin heterotrimers have a variable stoichiometry that has been suggested to be determined by the concentration of the individual monomers (Frank et al., 2002). Our model does not exclude variations in the stoichiometry of the HSF1-HSF2 heterotrimers, which may change similarly to that of the matrin analogs. Because the expression of HSF2 varies between different cell types and tissues (Rallu et al., 1997, Fiorenza et al., 1995), the HSF1-HSF2 heterotrimer stoichiometry could be modified accordingly, allowing tissue-specific regulation of HSF-mediated transcription.

Interestingly, HSF2 levels are reduced when HSF1 is down-regulated (Figure 1C), a phenomenon that has been noted also by others (Rossi et al., 2006) and is not due to unspecific down-regulation by RNAi (Supplemental Figure 6). Besides HSF1 down-regulation, heat shock reduces the levels of HSF2 (Figure 3B). It is plausible that the HSF-mediated stress-induced transcription upon prolonged stress is determined by the receding amounts of HSF2 available for heterotrimerization with HSF1 and that HSF1-HSF2 heterotrimerization regulates transcription in a temporal manner.

The nSBs: Versatile Centers for Regulation of Gene Expression?

The localization of HSF1 and HSF2 to the locus 9q12 is followed by expression of sat III transcripts and formation of nSBs. Transcription of sat III DNA is a general response to stress (Valgardsdottir et al., 2008) and the sat III transcripts are noncoding and heterogenous in size (Jolly et al., 2004, Rizzi et al., 2004). The transcripts bind a subset of mRNA-processing factors that localize to the nSBs (Weighardt et al., 1999, Denegri et al., 2001). Because the ratio between splicing factors determines the choice of splicing site, the nSBs are thought to induce alternative splicing upon stress (Jolly and Lakhota, 2006). However, the nSBs may have multiple functions. The sat III transcripts could be involved in genomic silencing by incorporation into the RNAi system (Biamonti, 2004). Possibly, the sat III transcripts may play a role in the regulation of gene expression. In Drosophila, noncoding RNAs (ncRNAs) can activate transcription (Sanchez-Elsner et al., 2006). Interestingly, this regulation is mediated via binding of Ash1 to the ncRNA molecules, which bind to the same sequences from which they are transcribed, a feature they share with the sat III transcripts in the nSBs. Moreover, it has been proposed that the expression of human and chick coding mRNAs containing a-like sequences in their untranslated regions is controlled by small and developmentally expressed ncRNAs derived from α-satellite DNA (Li and Kirby, 2003). In human genes, segments of sat III DNA have been detected in the flanking regions and introns (Borstnik et al., 1994). It is tempting to speculate that an analogous control system of gene expression, involving the sat III transcripts and regulated by HSF1 and HSF2 in response to distinct stimuli, is used in humans.

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1346 Molecular Biology of the Cell


