Small heat shock proteins
Vos, Michel

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2009

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Download date: 10-06-2020
HSPB7 is a SC35 speckle resident small heat shock protein

Michel J Vos, Bart Kanon & Harm H Kampinga

Department of Cell Biology, Section of Radiation and Stress Cell Biology, University Medical Center Groningen, Groningen, The Netherlands

In revision for Biochimica et Biophysica Acta – Molecular Cell Research.
Abstract

The HSPB family is one of the more diverse families within the group of HSP families. Some members have chaperone-like activities and/or play a role in cytoskeletal stabilization. Some members also show a dynamic, stress-induced translocation to SC35 splicing speckles. If and how these features are interrelated and if they are shared by all members is yet unknown. Tissue expression data and interaction and co-regulated gene expression data of the human HSPB members was analysed using bioinformatics. Using a gene expression library, sub-cellular distribution of the diverse members was analyzed by confocal microscopy. Chaperone activity was measured using a cellular luciferase refolding assay.

Results: Online databases did not accurately predict the sub-cellular distribution of all the HSPB members. A novel and non-predicted finding was that HSPB7 constitutively localized to SC35 splicing speckles, driven by its N-terminus. Unlike HSPB1 and HSPB5, that chaperoned heat unfolded substrates and kept them folding competent, HSPB7 did not support refolding. Our data suggest a non-chaperone-like role of HSPB7 at SC35 speckles. The functional divergence between HSPB members seems larger than previously expected and also includes non-canonical members lacking classical chaperone-like functions.
Introduction

The human small heat shock protein (small HSP, HSPB) family of chaperones contains a total of eleven family members (1;2). All HSPB proteins are characterized by a conserved crystallin domain flanked by a variable sized N- and C-terminus resulting in a molecular size of approximately 16-40kDa. Another well-described characteristic is their ability to oligomerize into large, spherical and symmetrical structures (3). The main feature of many small HSPs is their ability to interact with components of the cytoskeleton (4-8) and to protect the cytoskeleton during stress (9). In cells, HSPB1 has been found to affect cell motility and morphology, related to its interaction with cytoskeletal elements (10). Furthermore, HSPB1 seems to fulfill a protective roles in heart diseases like ischemia (11;12) and atrial fibrillation (13) preventing contractile elements against becoming dysfunctional.

One other well-defined molecular function of HSPB proteins is their ability to prevent aggregate formation of denatured proteins in vitro (14;15). In vivo, this basic function is part of the cellular pathways accommodating protein folding and degradation (16;17). Active processing of HSPB bound substrates occurs in collaboration with HSPA (HSP70) members which can lead to either the refolding or degradation of the substrate (2;17).

The vital role of HSPB members as chaperones and/or protectors of the cytoskeleton is also apparent from several genetically inherited diseases. Mutation in both HSPB1 and HSPB8 have been reported to be causative in the development of Charcot-Marie-Tooth disease and distal hereditary motor neuropathy (18;19). Mutated HSPB4 and HSPB5 can both cause cataract (20;21) while desmin-related myopathy is caused by specific mutation in HSPB5 (22).

Another feature of certain HSPB proteins is their involvement in RNA splicing: e.g. HSPB1 up-regulation was found to enhance the recovery of splicing after heat stress (23) which may relate to early findings of enhanced recovery of translation arrest after stress when HSPB1 was over-expressed (24). This has been associated with findings that, upon a combination of stress and (stress-induced) phosphorylation, HSPB1 associates with nuclear splicing speckles (or SC35 speckles) (25), which are nuclear domains involved in RNA splicing. Also HSPB5 has been reported to associate with these nuclear speckles in a phosphorylation dependent manner (26). Interestingly, this HSPB member was shown to recruit the F-box protein FBX4 to the speckles, suggesting a role for HSPB5 in facilitating ubiquitination of speckle components (26;27). We also found that heat denatured substrates associate with these nuclear speckles together with HSPB1 and indirect evidence indicated that this was not associated with refolding of denatured substrates (28). Rather, a hypothetical model was proposed that these nuclear splicing speckles would be used during stress for temporal storage of unfolded proteins to target them for degradation upon stress relief. This model was supported by findings that these speckles largely overlapped with sites for protein degradation (29).

Whether cytoskeleton-related functions, splicing-related functions and chaperone activity are distinct features of the various HSPB proteins or whether they all are phenotypical manifestations of a single conserved function remains unclear. Also, to what extend the various HSPB members differ in these functional aspects remains to be elucidated. Therefore, we initiated a systematic study on the HSPB1-HSPB10 members of the human HSPB family (HSPB11 was not investigated as it was discovered (30) after we had completed our studies). In this MS, we provide the first part of these data, starting with a general overview, mainly based on bioinformatics, on the tissue specific expression, intracellular localization patterns, interactions partners and co-regulated genes of the HSPB1-10 members. Using a human HSPB plasmid library, we initially focused on the sub-cellular localization patterns of the HSPB family. Interestingly, we show that one of the least investigated HSPB members, HSPB7, is a SC35-speckle associated protein under non-stressful conditions. Association of HSPB7 with nuclear speckles is dependent on the N-terminus of HSPB7. While HSPB1 can assist in the refolding of heat denatured
proteins, HSPB7 is ineffective in doing so. Moreover, targeting HSPB1 to the nuclear speckles using the HSPB7 speckle localization signal abolishes its refolding enhancing capacity, strongly suggesting that association with speckles is not associated with chaperone-assisted refolding.

**Experimental procedures**

**Reagents and antibodies**

Tetracycline, MOPS and cycloheximide were obtained from Sigma, beetle luciferin from Promega. Antibodies against the V5 tag (Invitrogen) and SC35 (Abcam) were mouse monoclonal. The antibody against the MYC tag (Abcam) was rabbit-polyclonal.

**Molecular techniques**

Standard recombinant DNA techniques were carried out essentially as described by Sambrook et al. (31) Oligonucleotide primers (Biolegio) and plasmids used in this study are listed in Table S1 and Table S2 respectively. Restriction enzymes were used according to the manufacturer’s instructions (Invitrogen, New England Biolabs). Preparative polymerase chain reactions (PCR) were carried out using Vent DNA polymerase (New England Biolabs) according to the manufacturer’s instructions. DNA sequencing reactions were carried out by ServiceXS. HSPB protein sequences were retrieved from the NCBI database and analysed by ClustalX (32) and visualized using Treeview (33).

**HSPB plasmid generation**

The human HSPB family members were isolated from both mixed cell line cDNA and commercially available cDNA clones (Open Biosystems) (Table S1). PCR products were cloned into the pCDNA5/FRT/TO-MV plasmid (Invitrogen) (Figure S1) and sequence verified. Modification of the pcDNA5/FRT/TO plasmid was performed by cloning of oligonucleotides. This vector is designed to allow, in combination with a tetracycline repressor, for tetracycline-regulated expression (Figure S1). The HSPB encoding cDNAs were subsequently sub-cloned in frame with either a HIS tag, V5 tag, EGFP, MYC or mRFP tag (for availability see Figure S1). As such, the resulting library is tailored to a large set of research topics. Deletion of the N-terminus of HSPB7 was performed using the Quickchange kit (Stratagene). Generation of chimeric constructs was performed as described before (34).

**Growth conditions and DNA transfections**

Flp-In T-Rex HEK293 cells expressing the Tet repressor (Invitrogen) and HeLa cells were cultured in Dulbecco’s modified Eagle’s medium (Gibco; Invitrogen) supplemented with 10% fetal calf serum (Griener Bio-one) at 37 °C under a humidified atmosphere containing 5% CO2. Mouse HL-1 atrial cardiomyocytes were maintained in Claycomb Medium (Sigma) supplemented with 100 μM norepinephrine (Sigma) dissolved in 0.3 mM l-ascorbic acid (Sigma), 4 mM l-glutamine (Gibco; Invitrogen) and 10% fetal calf serum (Griener Bio-one) at 37 °C under a humidified atmosphere containing 5% CO2. HEK293 cells and mouse HL-1 cells were transfected using Lipofectamine (Invitrogen) according to the manufacturer’s instructions using 1ug of plasmid DNA per 35-mm dish. HeLa cells were transfected using Effectene (Qiagen) according to the manufacturer’s instructions using 0.6 ug of plasmid DNA per 35-mm dish. Gene expression in Flp-In T-Rex HEK293 cells was induced with a final concentration of 1 μg/mL tetracycline.

**Microscopy**

For microscopy, cells were plated 24 hours before transfection. For fixation, the coverslips were washed with cold PBS and fixed for 15 minutes with methanol (-20 °C). Cells were permea-
bilized in blocking solution (100 mM glycine, 3% BSA, 0.1% triton) for 1 hour followed by 1 hour incubation with the primary antibody (V5 anti-mouse, 1:200, SC-35 anti-mouse, 1:10000, MYC anti-rabbit 1:200). After three washing steps, coverslips were incubated for 1h with CY3-conjugated anti-rabbit secondary antibody (Amersham Biosciences) at 1:200 dilution or with FITC-conjugated anti-mouse secondary antibody (Jackson) at 1:200 dilution. After three washing steps, the coverslips were mounted using Citifluor mounting medium (Citifluor Ltd). Images were obtained using an inverted confocal laser scanning microscope (TCS SP2, DM RXE, Leica, Rijswijk, The Netherlands) with a 63x/1.32 NA oil objective. The mRFPRuby fusion protein (35;36) was excited with a 543-nm helium–neon laser line and emission was recorded between 571 and 626 nm using a DD 488/543 dichroic filter.

Luciferase refolding assay
Chaperone activity of HSPB members was assessed by using the luciferase refolding assay (37). Briefly, HEK293 cells were co-transfected with nuclear targeted luciferase (Nuc-superluc-EGFP) (38) together with HSPB encoding plasmids (1:9 ratio). Two hours after transfection, expression was induced by addition of tetracycline. After 24 hours, cells were resuspended and divided into 1 mL portions in tissue-grade 10 mL tubes. The following day, cells were given a heat-shock (30 minutes at 43 °C) in the presence of cycloheximide (20 µg/mL) and 4-morpholino propane sulfonic acid (MOPS; 20mM, pH7.0) in order to inhibit protein synthesis and increase the buffer capacity of the medium respectively. After heat-treatment, cells were allowed to recover before luciferase activity was determined (3 hours at 37 °C). Luciferase activity measurements were performed using a Berthold Lumat 9510 luminometer (Berthold Technologies).

Results

Bioinformatical analysis
Compared to other HSP families, small HSPs show a rather large sequence divergence, in particular in both the N- and C-terminal regions. A nearest neighbor analysis using the full sequences (Figure 1a) in order to link functional properties of the diverse member will thus likely be prone to wrong interpretations. And although the two functionally related and interactive members HSPB4 and HSPB5 (39) cluster together in such an analysis (figure 1a), HSPB1 does not, despite the fact that it shares many functional features with HSPB4 and HSPB5, amongst others of chaperone activity (15). Rather, in such an analysis HSPB1 clusters together with the non-functionally related HSPB8. Therefore, we repeated the nearest neighbor analysis using only the conserved crystallin domains (Figure 1b). Now, HSPB1 did group together with its functionally related family members HSPB4 and HSPB5. In addition, HSPB2 and HSPB3, which are reported to form functional hetero-oligomers during muscle differentiation (40), now also appear as a (separate) group within the tree, suggesting that this nearest neighbor analysis based on the crystalline domain only might be more informative for function. If correct, this nearest neighbor analysis would than suggest a possible functional overlap between HSPB8/HSPB10 and HSPB7/HSPB9 (Figure 1b). We have indeed observed a functional overlap between HSPB7 and HSPB9 in handling aggregated substrates (data submitted elsewhere). A functional overlap between HSPB8 and HSPB10 remains to be tested experimentally.

Next, we extracted data from online databases to analyze both interaction data (41) and co-expression data (42) to provide information on interaction partners and co-regulated genes. HSPB members show an extensive set of interaction partners including other HSPB members (Figure 2a). When looking at gene-networks, HSPB members show co-regulated expression with numerous genes, again including other HSB genes (Figure 2a). Clearly these data are yet far from complete as many HSB members have only been poorly studied. Moreover, part of
the data only come from cell free studies and yet have to be verified in living cells. But, as can be derived from Figure 2b, there is a likely complex and extensive interactive network within the HSPB family suggesting that they cooperate in several processes.

In addition to differences in functionality, individual HSPB members show large differences in tissue-specific expression (Figure 3). HSPB4 for instance, is found at high concentrations in the eye lens, while its expression is almost absent in other tissues (43). Compiling data from the UniGene EST ProfileViewer (NCBI) (Figure 3a) for total messenger levels reveals that in the human body as a whole, the most abundant
HSPB7 localizes to SC35 speckles

HSPB member is HSPB1, followed by HSPB5 and interestingly also HSPB7 (Figure 3a top row). Although reported to be expressed almost exclusively in heart tissue (44), messenger RNA for HSPB7 can also be found in adipose tissue, connective tissue and the parathyroid gland. HSPB9, that clusters together with HSPB7 in the nearest neighbor tree (Figure 1b) has been referred to as a testis specific HSPB member (45). But, HSPB9 expression is also found in lung and pancreas tissue.

When comparing HSPB messenger composition for a selection of organs, HSPB1 and HSPB5 represent the most abundant HSPB messengers in brain, muscle and eye tissue (Figure 3b). Looking at heart tissue, HSPB7 is indeed transcribed at very high levels in comparison to the other HSPB members (Figure 3b). HSPB messenger composition in the testis shows that HSPB7 and HSPB1 are the most abundant in this organ and not HSPB9. The most restricted members in view of tissue specific expression are HSPB4 (eye), HSPB9 (lung, pancreas, testis) and HSPB10 (testis) (Figure 3a).

Subcellular localization

The small HSPs are known to be widely distributed throughout eukaryotic cellular compartments. Herein, plants take a special place, with the most widely known organelle specific distribution pattern (46). In Drosophila at least one small HSP, the mitochondrial HSP22, shows compartment specific localization besides the cytosol and nucleus (47). As a complete picture of HSPB protein localization is currently unavailable, we combined web-based prediction programs and subcellular localization databases together with confocal microscopy imaging of the V5-tagged HSPB library to generate a complete overview. In silico prediction of subcellular localization was performed using PSORT, Ptarget and Multiloc (48-50) (Figure 4a). There was a surprisingly large disagreement between the predictions made by these different programs especially with regards to a tentative mitochondrial localization signal. Using MITOPRED (51), a web server dedicated specifically for the prediction of mitochondrial localized proteins, HSPB5 and HSPB7 were predicted to be mitochondrial with high confidence, while the other members were not predicted to localize to mitochondria. For HSPB5, a mitochondrial localization was indeed recently experimentally verified (52). However, nor the LOCATE database (53) nor the Human Protein Reference (HPR) database (54) indicated the mitochondrial localization of HSPB5 and large differences in the predicted localization and experimentally verified localizations were seen, especially when using the Ptarget server.

To investigate and directly compare the localization of HSPB proteins experimentally, we expressed the V5-tagged HSPB members in human HEK-293 cells (Figure 4b). Endogenous HSPB1, the most extensively investigated HSPB member is known to be mostly cytosolic under non-stress conditions and only enters the nucleus upon stress-induced phosphorylation and changes in oligomeric size after which it co-localizes with SC35 positive nuclear speckles (17;25). Using MCF-7 cells that express high levels of HSPB1, endogenous HSPB1 indeed showed mainly cytoplasmatic staining in unstressed cells and a heat-induced localization to nuclear speckles (Figure 4c). Staining of the ectopically expressed V5-HSPB1 in HEK293 cells, showed a similar pattern of expression during control and heat-shocked conditions (Figure 4d), showing that the V5-tag did not interfere with its physiological localization patterns. Also several experimental data are available for HSPB4 and HSPB5. Like HSPB1, HSPB4 was reported to be localized in the cytoplasm (55;56). A similar pattern is seen for the ectopically expressed V5-tagged HSPB4 (Figure 4b). HSPB5 has been reported to be a cytosolic and nuclear protein where it can specifically localize to SC-35 positive nuclear speckles (57;58) in a phosphorylation dependent manner (26;59). Again, the transiently expressed V5-tagged HSPB5 confirmed the cytosolic staining representative for non-phosphorylated HSPB5. Also a faint signal of nuclear foci could be detected, confirming that like untagged HSPB5, also V5-HSPB5 in part associates with nuclear domains. The findings on these three well-studied and closely related HSPB mem-
HSPB members (Figure 1b) show that their cellular compartmentalization is highly comparable and also show that V5-tagging does not interfere with their intracellular localization. Also, V5-tagging of HSPB1, HSPB4 or HSPB5 did not affect their function as chaperone in cells to support refolding of heat denatured luciferase (Figure 8a). Apparently for these members tagging does not affect biological activity. The V5-tagged HSPB2 was found to be present in the nucleus and cytoplasm, consistent with the data from LOCATE. In addition, HSPB2 was present in foci throughout both cellular compartments. HSPB2 has been shown previously to localize to mitochondria (60), we were however unable to detect overlap of the cytosolic HSPB2 foci and the mitochondrial marker Cox8-dsRED (data not shown) suggesting either errors in the predictive programs or a inhibitory effect of the V5 tag on mitochondrial import. The nature of the nuclear foci was not elucidated.

To date, no experimental data are available on the localization of HSPB3, the protein that is most closely related to HSPB2 (Figure 1b). Unlike HSPB2, however, but consistent with the database
HSPB7 localizes to SC35 speckles

predictions, V5-HSPB3 showed mainly a cytosolic localization with some minor nuclear staining. No clear localization to specific other organelles or sub-nuclear domains was seen. Also for the intracellular localization of HSPB6 experimental data are lacking. The V5-HSPB6 confirmed the predicted cytosolic distribution but could not confirm the mitochondrial localization as predicted by Ptarget.

Figure 4. Intracellular distribution of the human HSPB. (A) Several databases were used to extract the predicted intracellular distribution and published intracellular distribution. (B) Intracellular distribution of V5-tagged human HSPB proteins in HEK293 cells. Arrows indicate bright foci in both the nucleus and the cytoplasm (V5-HSPB2), nuclear foci (V5-HSPB7) and aggresome formation (V5-HSPB10). The nucleus was visualized by expression of the human Histone-2B fused to the monomeric red fluorescent protein ruby (36;83). This signal was traced in Adobe photoshop and depicted as a dashed line. (C) Redistribution of endogenous HSPB1 to nuclear speckles after a heat shock in MCF-7 cells. (D) Redistribution of exogenous V5-HSPB1 to nuclear speckles after a heat shock in HEK293 cells.
HSPB8 has been reported to be an exclusively cytosolic protein (61) although others also have suggested that it is localized to the nucleus in some cells (18). The ectopically expressed V5-HSPB8 shows a predominant cytosolic staining, with some intense staining in cytosolic foci. These foci could potentially represent autophagosomes, consistent with the suggested function of HSPB8 in autophagy (62). Its closest homologue HSPB10, known to be a structural protein in sperm tails (63), also mainly localized to the cytosol with minor nuclear staining. The expression was however accompanied by the appearance of many cytoplasmic foci and the formation of an aggresome, suggesting misfolding and/or failed clearance of the ectopically expressed V5-tagged protein (64).

The V5-tagged HSPB9 showed a diffuse cytosolic and nuclear distribution (Figure 3b), whereas in vivo HSPB9 shows mainly a nuclear localization in testis and a cytosolic/nuclear distribution in tumor cells (65). Again this localization was not predicted correctly by the in silico prediction programs (Figure 3a). Staining of HSPB7 showed a rather striking distribution. HSPB7 was reported to interact with α-Filamin, an actin-binding protein (44), suggesting a cytoskeletal localization. The V5-HSPB7 showed cytosolic staining (Figure 3b). In addition, however, bright nuclear foci could be detected, that suggested association with nuclear sub-domains in the absence of stress.

During stress, several heat shock proteins are known to be re-allocated within the cells and especially move to the nucleus, including to nuclear speckles (25;66-68). Therefore, we analysed heat-induced alterations in intracellular localization for all the individual HSPB members. Interestingly, most members appeared after heat shock in nuclear foci or showed an enhanced nuclear foci signal in comparison to control conditions (Figure S2a). The clearest change in subcellular distribution was found for HSPB1 and HSPB4, which both entered the nucleus after heat shock treatment and appeared at nuclear foci (Figure S2a, b).

**HSPB7 specifically associates with Cajal bodies and SC35 speckles**

Because of the association of HSPB1 with splicing and the stress-induced reallocations of HSPB1 and HSPB5 to SC35 splicing speckles, we decided to identify to which specific nuclear structure(s) HSPB7 localizes. Hereto, we co-expressed different nuclear sub-domain markers tagged with EGFP or EYFP with MYC tagged HSPB7. EGFP tagged SP100 was used to visualize promyelocytic leukaemia (PML) nuclear bodies which play a role in transcriptional regulation, programmed cell death, tumor suppression, and antiviral defense (69;70). These structures were in close proximity to MYC-HSPB7-containing bodies, but did not overlap (Figure 5a). EGFP-tagged Coilin, marking the Cajal bodies, implied in spliceosomal snRNP assembly and various other functions (71) showed partial overlap with the MYC-HSPB7 signal (Figure 5b), indicating that the HSPB7 can localize to Cajal bodies. Splicing speckles were visualized using SC35 and ASF/SF2; two members of the serine/arginine (SR) rich protein family. These proteins form a group of structurally and functionally related splicing factors which are essential for constitutive and alternative splicing regulation in higher eukaryotes (72;73). Expression of EGFP tagged alternative splicing factor/splicing factor 2 (ASF/SF2) showed complete co-localization with MYC-HSPB7 (Figure 5c). Similarly, EGFP tagged SC35 also completely co-localized to MYC-HSPB7 (Figure 5c). Finally, staining of endogenous SC35 confirmed co-localization with MYC-HSPB7 (Figure 5c).

So, in contrast to HSPB1 and HSPB5 that enter the nucleus and associate with speckles only after stress, HSPB7 localizes to these splicing factories also in non-stressed human HEK293 cells (Figure 4b). To test whether this localization is not restricted to HEK293 cells only, we also expressed V5-HSPB7 in mouse HL-1 cardiac myocytes and human HeLa cells. Also in these
HSPB7 localizes to SC35 speckles

Two cell types HSPB7 localized to nuclear speckles (Figure 6a,b), whereas V5-HSPB1 was largely cytosolic in both cell types under non-stressed conditions (Figure 6c,d).

The N-terminus of HSPB7 is required and sufficient for localization to SC35 splicing speckles

As the conserved crystallin domain is the conserved motif for the HSPB members, it is likely that sub-cellular localization is regulated by targeting sequences present in the N-terminal or C-terminal domain. Indeed, for Drosophila HSP27 and HSP22 a nuclear localization signal and a mitochondrial targeting sequence respectively have been identified in the N-terminal domains (47;74). To analyze if the N-terminus of HSPB7 is required for speckle association, we deleted the first 71 amino acids of HSPB7 (the ΔN-HSPB7 mutant, Figure 7a). Compared to the full length HSPB7 (Figure 7b1, b1'), the ΔN-HSPB7 mutant showed less nuclear staining with a complete loss of speckle-association (Figure 7b2, b2'). To test whether the N-terminus of HSPB7 indeed drives speckle localization, we generated HSPB chimera by switching the N-
terminal domains between HSPB1 and HSPB7 (Figure 7a). When expressed in cells, HSPB7 containing the N-terminus of HSPB1 (NB1-ΔNB7) was present in both the cytoplasm and nucleus but completely lacked any detectable association with sub-nuclear domains (Figure 7b3, b3'). HSPB1 containing the N-terminus of HSPB7 (NB7-ΔNB1) on the other hand showed staining of sub-nuclear structures resembling wildtype HSPB7 (Figure 7b4, b4'). Staining of endogenous SC-35 indeed confirmed association of NB7-ΔNB1 with speckles (Figure 7c). Thus it seems that speckle association of HSPB7 is indeed dependent on the N-terminal domain. To test whether the N-terminus of HSPB7 can also target proteins without a crystallin domain to SC35 speckles,
HSPB7 localizes to SC35 speckles

we fused the N-terminus of HSPB7 to the red fluorescent protein mRFPruby (NB7-mRFPruby). The NB7-mRFPruby chimeric protein indeed co-localized with EGP tagged SC35 (Figure 7d), proving that the N-terminus of HSPB7 contains a novel nuclear speckle localization signal which functions independently of HSPB domain architecture.

**Speckle association of HSPB1 and HSPB7 in not linked to chaperone activity**

In previous studies (17;28) it was found that after heat shock, not only chaperones like HSPB1 are reallocated to SC35 speckles, but also heat-denatured proteins. Although HSPB1 overexpression could enhance refolding of heat denatured nuclear model substrates like firefly luciferase, indirect evidence, including the absence of HSP70 family members in these foci (75), suggested that the association of HSPB1 and denatured luciferase in SC35 speckles was not associated with refolding activity. To further look into the relevance of the presence of both HSPB7, HSPB1 and unfolded luciferase in SC35 speckles for the storage and subsequent processing of unfolded nuclear proteins, we first tested whether the constitutively SC35-associated HSPB7 also could assist in the refolding of heat-denatured nuclear localized luciferase. Overexpression of either V5-tagged HSPB1, HSPB4 or HSPB5 indeed resulted in enhanced refolding (Figure 8a) as described before for the untagged versions in vitro (15;76). Refolding activity of HSPB4 towards nuclear luciferase was due to a translocation of HSPB4 towards the nucleus upon heat shock (Figure S2a, S3). Under these conditions, NLS tagged luciferase was
found exclusively in the nucleus (Figure S3), suggesting that the cytosolic fraction of HSPB4 does not contribute to refolding of heat-denatured nuclear luciferase. Overexpression of the SC35-associated V5-HSPB7 did however not show any refolding promoting activity (Figure 8a). The NB1-ΔNB7 mutant, harboring the crystallin domain of HSPB7 and devoid of nuclear speckle association also did not show refolding promoting activity (Figure 8b), in line with the complete lack of chaperone activity of the full length HSPB7. The NB7-ΔNB1 mutant, harboring the crystallin domain of HSPB1, but now associated with SC35 speckles via the N-terminus of HSPB7, lost refolding promoting activity (Figure 8b), suggesting that localization in part results in loss of refolding capacity.

Finally, we asked whether speckle-associated HSPB proteins with no folding activity could affect the wildtype HSPB1 folding capacity via e.g. co-oligomerization or induced association with splicing speckles or by competitive substrate binding. Hereto, we co-expressed HSPB7 with HSPB1 and nuclear luciferase. This however did not affect the capacity of HSPB1 to assist in refolding heat denatured luciferase (Figure 8c). Next, we co-expressed the NB7-HSPB1 (NB7-ΔNB1) mutant, which is targeted to nuclear speckles, together with wildtype HSPB1. Again, HSPB1 refolding capacity was not negatively influenced by co-expression of a speckle-associated (mutant) HSPB protein (Figure 8c). This highly suggests that NB7-ΔNB1, lacking folding activity, does not interfere with the folding-active wildtype HSPB1.

Discussion

We have presented an overview on several aspects and properties of the human HSPB family using a variety of specialized databases and focused subsequently on sub-cellular localization patterns. Apart from their cytoskeletal localization, some HSP members have been reported to reside in the nucleus during non-stressed states or after a heat-shock. Inside the nuclear compartment, HSPB1 and HSPB5 can furthermore associate with sub-nuclear structures called SC35- or splicing speckles. Using the V5-tagged HSPB plasmid library we confirmed these data for HSPB1 and for the first time show that HSPB7 contains a speckle targeting sequences in its N-terminus that is capable of driving it and other proteins to splicing speckles under non-stressful conditions.

**HSPB7 is a resident component of SC35-speckles containing a speckle targeting sequence in its N-terminal domain**

SC35 speckles (also known as nuclear splicing speckles) are sub-nuclear structures involved in the storage and assembly of the splicing machinery and contain pre-mRNA splicing factors, transcription factors, snRNAs and ribosomal proteins (77). Furthermore, modulation in splicing factor concentrations appears to link SC35 speckles to alternative splicing (78). The SC35 speckle resident splicing factors primarily belong to the serine/arginine-rich (SR) protein family (79;80).

In general, little is known on how proteins are able to associate with SC35 speckles. One known SC35 speckle targeting signal consists of the SR motif itself, as was shown for the SC35 protein (73), although the presence of an SR motif not always drives proteins to SC35 speckles, meaning that other elements or the context around SR motifs may also play a role (81). Until now, only one non-SR motif has been reported to function as a targeting signal for SC35 speckles. Cdk9, an elongation factor for RNA polymerase II-directed transcription and DYRK1A, a protein kinase (78;82), both contain a histidine-rich region which was shown to be sufficient to target EGFP to SC35 speckles. HSPB1, HSPB5 and HSPB7 however lack such a SR motif and histidine-rich region, suggesting that other elements in the HSPB sequences are required for speckle association. The dependency on a specific sequence needed for SC35 speckle association
was reported for the Drosophila HSP27 (74). The authors showed that speckles association in HeLa cells was dependent on two leucine residues (L50, L52) located in the N-terminus. Although leucines are present in the N-termini of HSPB1, HSPB5 and HSPB7, their contribution to speckle association have yet to be established (Figure S4).

In this study we showed that the N-terminus of HSPB7 functions as a unique and novel SC35 targeting sequence. Deletion of the N-terminus of HSPB7 or replacement by the N-terminus of HSPB1, abrogated HSPB7 speckle association. We furthermore showed that the N-terminus alone is sufficient to target either a crystallin domain or mRFPruby to SC35 speckles. HSPB7 contains a serine-rich region, which shows homology to the SR motif. Deletion of the serine stretch did however not result in dissociation of HSPB7 from SC35 speckles (data not shown). This suggests that the N-terminus of HSPB7 contains additional elements allowing for speckle association, which have yet to be determined.

Functional implications of HSPB speckle associations

HSPB1 is known to associate with SC35 speckles during heat stress. When luciferase is over-expressed under these conditions, it also associates with SC35 speckles (28). In view of this, SC35 speckles might function as storage sites for HSPB-luciferase complexes, ready to be refolded upon stress relief. Could SC35 speckles indeed act as a depot for unfolded proteins, and does the association of HSPB proteins with SC35 speckles reflect a role in chaperoning of protein refolding? We showed that the SC35 speckle resident HSPB7 is not active in refolding of heat-denatured luciferase in contrast to HSPB1 and HSPB5. This suggests that at least for HSPB7, association to SC35 speckles is unrelated to protein refolding. By exchanging the N-terminus of HSPB1 for the N-terminus of HSPB7, we were able to target the HSPB1 crystallin domain to SC35 speckles which resulted in loss of refolding activity. This suggest either that speckles association of HSPB1 is not related to refolding activity or that the HSPB1 N-terminus in required together with the HSPB1 crystallin domain to form a functional unit in assisting protein refolding activity. While co-expression of HSPB5 and luciferase clearly showed that this HSPB member is a chaperone capable of refolding heat-denatured luciferase, the direct association of HSPB5 with SC35 speckles has been suggested to relate to protein ubiquitination and degradation rather than protein refolding (26;27). In conclusion, data on HSPB association with SC35 speckles hint to other functions than specific refolding of denatured proteins in situ.

As HSPB1 has been shown to enhance recovery of splicing after a heat shock, a role in splicing of HSPB7 at SC35 speckles should be addressed. A possible function of the SC35 speckle-resident HSPB7 herein could be to fulfill a function in splicing under normal conditions while accumulation of HSPB1 at SC35 speckles during stress indicates a requirement to protect the splicing machinery and accelerate splicing recovery. This idea is under current investigation.

Acknowledgements

This work was supported by Innovatiegerichte Onderzoeksprogramma Genomics. Grant IGE03018.
References


Supplemental tables and figures

Table S1 Primers used in this study

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Alternative name</th>
<th>Human Gene ID</th>
<th>Origien</th>
<th>Primer Name</th>
<th>Primers sequence 5' - 3'</th>
<th>Restriction site</th>
</tr>
</thead>
<tbody>
<tr>
<td>HSPB1</td>
<td>HSP27, Hsp25</td>
<td>3315</td>
<td>cDNA mix</td>
<td>B1-F</td>
<td>ACAACTCGAGAAAGCATGACGAGCGCCGCGTC</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B1-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB2</td>
<td>MKBP; HSP27</td>
<td>3316</td>
<td>Open Biosystems</td>
<td>B2-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B2-R</td>
<td>ATAAACGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB3</td>
<td>HSPL27</td>
<td>8888</td>
<td>cDNA mix</td>
<td>B3-F</td>
<td>ACAAGGCCGCCAACAATGAAAAATACCTTTGAGG</td>
<td>NotI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B3-R</td>
<td>ACCACCGGTTTTCTGACGACGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB4</td>
<td>crystallin alpha A</td>
<td>1409</td>
<td>cDNA mix</td>
<td>B4-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B4-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB5</td>
<td>crystallin alpha B</td>
<td>1410</td>
<td>cDNA mix</td>
<td>B5-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B5-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB6</td>
<td>HSP20</td>
<td>126393</td>
<td>Open Biosystems</td>
<td>B6-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B6-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB7</td>
<td>cvHSP</td>
<td>129</td>
<td>Open Biosystems</td>
<td>B7-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B7-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB8</td>
<td>H11; HMM2; HSP22</td>
<td>26353</td>
<td>Open Biosystems</td>
<td>B8-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B8-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
<tr>
<td>HSPB9</td>
<td>FL27437</td>
<td>90486</td>
<td>Open Biosystems</td>
<td>B9-F</td>
<td>ACAACTCGAGAACATGCGGGCTCTAGTCCTCA</td>
<td>XhoI</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>B9-R</td>
<td>AAAACCGGTTTTCTTGGAGCCGCTTCTAT</td>
<td>Mil</td>
</tr>
</tbody>
</table>

Table S2 Plasmids used in this study

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
<th>Origen</th>
</tr>
</thead>
<tbody>
<tr>
<td>pCDNA5/FRT/TO Mammalian expression vector; tetracycline regulatable expression</td>
<td>Invitrogen</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1 Adapted multiple cloning site: Xhol-Agel-Ascl</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV2 Adapted multiple cloning site: Notl-Agel-Ascl</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1 Contains N-terminal V5 tag sequence</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV2 Contains N-terminal V5 tag sequence</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-EFGP-MV1 Contains N-terminal EFGP sequence</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-EFGP-MV2 Contains N-terminal EFGP sequence</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-HIS-MV1 Contains N-terminal HIS sequence</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-HIS-MV2 Contains N-terminal HIS sequence</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-HSPB1 V5 tagged human HSPB1</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV2-HSVP1 V5 tagged human HSPB2</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-HSPB3 V5 tagged human HSPB3</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV2-HSBP4 V5 tagged human HSBP4</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-HSBP5 V5 tagged human HSBP5</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV2-HSBP6 V5 tagged human HSBP6</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-HSBP7 V5 tagged human HSBP7</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-HSBP8 V5 tagged human HSBP8</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV2-HSBP9 V5 tagged human HSBP9</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-HSBP10 V5 tagged human HSBP10</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-MV1-NB7 V5 tagged human HSPB7 lacking N-termins (Δ1-73)</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-NB1-NB7 V5 tagged human HSBP7 with N-terminus of HSBP1</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-V5-NB7-V5NB1 V5 tagged human HSBP7 with N-terminus of HSBP7</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-H2B-mRFPruby Human histone 2B fused to monomeric red fluorescent protein ruby</td>
<td>[65]</td>
<td></td>
</tr>
<tr>
<td>pCDNA5/FRT/TO-NB7-mRFPruby N-terminus of HSB7 fused to mRFPruby</td>
<td>This study</td>
<td></td>
</tr>
<tr>
<td>pSV2-EYFP-SP100 EYFP tagged SP100; PML body marker</td>
<td>Spector Laboratory</td>
<td></td>
</tr>
<tr>
<td>pEYFP-SF2A5 EYFP tagged sf2A5; SR marker</td>
<td>Spector Laboratory</td>
<td></td>
</tr>
<tr>
<td>pTRE-GFP-collin EGFP tagged human Collin; Caji body marker</td>
<td>Matera Laboratory</td>
<td></td>
</tr>
<tr>
<td>SC35-eGFP EGFP tagged SC35; SR marker</td>
<td>Tazi Laboratory</td>
<td></td>
</tr>
</tbody>
</table>
Figure S1. The human HSPB plasmid library. (A) The human HSPB family was cloned into an adapted pCDNA5/FRT/TO vector backbone containing two different multiple cloning sites (MCS). Subsequently, the HSPB members were subcloned into pCDNA5/FRT/MV vectors containing various tags. (B) In combination with the Tet repressor, this library can be used for tetracycline regulated expression.

Figure S2. Intracellular distribution of the human HSPB family after heat shock. (A) Intracellular distribution of V5-tagged human HSPB proteins in HEK293 cells either directly after a 30 minute heat shock treatment (43°C) or combined with a recovery period of 45 minutes at 37°C. (B) Summary of HSPB localization at control conditions or after heat shock treatment. Grey boxes indicate nuclear foci which have been found positive for SC35 staining. The DAPI signal for nuclear staining was traced in Adobe photoshop and depicted as a dashed line.
HSPB7 localizes to SC35 speckles

Figure S3. Localization of V5-HSPB4 and nuclear luciferase during heat shock. HEK293 cells over-expressing V5-HSPB4 and EGFP tagged nuclear luciferase were heat shocked (30 minutes, 43°C) and allowed to recover for 45 minutes at 37°C after which cells were fixed and analysed by confocal microscopy. See Appendix 4 for colour print.

Figure S4. Protein alignment of N-terminal regions of SC35 speckle associated small heat shock proteins. The N-termini of Drosophila HSP27 and human HSPB1, HSPB5 and HSPB7 were aligned using the BLOSUM 62 scoring matrix. Leucines are indicated in bold and the percentage of leucines present in the N-terminal sequences are indicated. The protein sequence required for Drosophila HSP27 to associate with SC35 splicing speckles is indicated by a box.