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Functional overlap between conserved and diverged KH domains in *Saccharomyces cerevisiae* SCP160

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**ABSTRACT**

The K homology (KH) domain is a remarkably versatile and highly conserved RNA-binding motif. Classical KH domains include a characteristic pattern of hydrophobic residues, a Gly-X-X-Gly (GXXG) segment, and a variable loop. KH domains typically occur in clusters, with some retaining their GXXG sequence (conserved), while others do not (diverged). As a first step towards addressing whether GXXG is essential for KH-domain function, we explored the roles of conserved and diverged KH domains in Scp160p, a multiple-KH-domain-containing protein in *Saccharomyces cerevisiae*. We specifically wanted to know (1) whether diverged KH domains were essential for Scp160p function, and (2) whether diverged KH domains could functionally replace conserved KH domains. To address these questions, we deleted and/or interchanged conserved and diverged KH domains of Scp160p and expressed the mutated alleles in yeast. Our results demonstrated that the answer to each question was yes. Both conserved and diverged KH domains are essential for Scp160p function, and diverged KH domains can function in place of conserved KH domains. These findings challenge the prevailing notions about the requisite features of a KH domain and raise the possibility that there may be more functional KH domains in the proteome than previously appreciated.

**INTRODUCTION**

Proper gene expression depends on precisely orchestrated interactions between nucleic acids and nucleic acid-binding proteins. In fact, virtually every step of gene expression involves the activities of both sequence-specific and general nucleic acid-binding proteins. For example, transcription of DNA to RNA employs helicases, transcription factors, RNA polymerase, 5'-capping enzymes, poly (A) polymerase and numerous other proteins required to process the nascent mRNA transcript (1,2). All of these factors must recognize nucleic acids in some manner. Then numerous mRNA-binding proteins are required to escort transcripts out of the nucleus and, ultimately, to coordinate protein translation (3). Thus, gene expression relies heavily on nucleic acid-binding proteins, with major roles for proteins that bind to mRNA. In keeping with this workload, proteins have evolved a vast array of domains that mediate interactions with RNA, including but not limited to the hnRNP K homology (KH) domain, RNA recognition motifs (RRMs), arginine-rich motifs, and zinc-finger motifs (4).

Many RNA-binding domains are abundant and highly conserved across species. In fact, Chen and Varani have estimated that about 1.5–2% of the human genome is composed of proteins that contain RRM domains, the most abundant and well-characterized of the RNA-binding domains (4). RNA-binding motifs are typically recognized and defined on the basis of their conserved primary amino acid sequence, but the degree of sequence conservation among different motifs varies widely (4). Although some major residues are defined functionally, others have been identified strictly on the basis of sequence conservation or homology (5,6). A key question is whether these conserved residues are actually critical for protein function, and therefore whether sequence conservation alone can be used as a measure of functional significance.

One remarkably versatile and highly conserved RNA-binding motif is the KH domain (7). KH domains, which were originally identified as a repeated sequence in the hnRNP K protein (7), are ~70 amino acids in length, with a characteristic pattern of hydrophobic residues, a GXXG segment and a variable loop. KH domains are often found in multiple copies per protein. There is strong evidence that KH domains are critically important to the function of those proteins that contain them. For example, fragile X syndrome, a leading cause of inherited mental retardation, can arise from a missense mutation of Ile304Asn in...
the second KH domain of the FMRP protein (8). Indeed, the Ile304Asn mutation is associated with a severe clinical phenotype (8). Thus, there is evidence that mutations in KH domains can cause human disease, which underscores the importance of defining what constitutes a functional KH domain.

Some proteins contain both conserved KH domains that include the GXXG motif, as well as what have been termed diverged KH domains, in which the GXXG motif is interrupted or altered (9). Although the structures of a number of conserved KH domains have been solved (10–14), there has been little functional analysis of diverged KH domains. Recent evidence suggests possible synergetic binding to mRNA targets by the three KH domains of hnRNP K protein (15), thereby enhancing interaction with the nucleic acid substrate. Chmiel and colleagues (16) drew a similar conclusion from their work with the Drosophila PSI protein, which contains four KH domains. While these findings do shed light on the functional importance of KH domain clustering in proteins, they fail to address the functional significance of KH domain sequence conservation or divergence.

As a first step towards addressing whether GXXG is essential for KH domain function, we explored the roles of conserved and diverged KH domains in Scp160p, a multiple KH domain protein in S. cerevisiae. Scp160p includes 14 KH domains (17), only seven of which contain a strictly conserved GXXG motif (KH 2, 8–12 and 14). The other seven KH domains are diverged, with interruptions or alterations of the GXXG motif. Although the exact function of Scp160p and its orthologs, known as vigilins in higher eukaryotes, is not known, recent work suggests a role for this protein in modulating the metabolism of specific mRNA targets in the cytoplasm (18,19). Consistent with this postulated function, much of Scp160p is found in large protein complexes associated with soluble or membrane-bound polyribosomes (17,20–25). The goal of the present study was to explore two questions. First, are diverged KH domains essential for Scp160p function? Second, can diverged KH domains functionally replace conserved KH domains? To address these questions, we deleted and/or interchanged conserved and diverged KH domains of Scp160p, then expressed these variant alleles in yeast. We applied a combination of previously defined genetic (23) and biochemical (17,20–25) assays to the strains expressing these mutated alleles to discern the functional capacity of each encoded Scp160p protein.

Our results demonstrated that the answer to each of our two questions was yes. Both conserved and diverged KH domains were essential for Scp160p function, and diverged KH domains were capable of functioning in place of conserved KH domains.

MATERIALS AND METHODS

Yeast strains and manipulations

All yeast manipulations were performed according to standard protocols. The strains used for this study are listed in Supplemental Table 1 and, unless otherwise noted, were derived by two-step gene replacement (26) at the SCP160 locus from the haploid parent strain W303 [MATa ade2-1 his3-11,15 leu2-3,112 ura3-1 trpl-1 can1-100 RAD5+], a gift from Dr. R. Rothstein, Columbia University, NY.

Construction of FLAG.scp160 variant alleles

Unless otherwise noted, all recombinant DNA manipulations were performed according to standard procedures (27) using the XL10-Gold® (Stratagene) strain of Escherichia coli. To facilitate site-directed mutagenesis of SCP160, a 2.2 kb PstI/EcoRI fragment containing sequence from the beginning of SCP160 KH8 through approximately 430 bp downstream of the stop codon was gel purified and ligated into pGEM3-zf(+) using T4 DNA Ligase (Invitrogen) according to the manufacturer’s instructions. The resulting plasmid (JF4566, pGEM3zf+.SCP160.Eco.Pst) was confirmed by restriction analysis and sequencing and used as a template for the generation of all subsequent modified alleles, as detailed below.

To create scp160 alleles individually depleted for KH13 and KH14, we used the QuikChange™ Site-Directed Mutagenesis Kit (Stratagene) according to the manufacturer’s instructions, with one exception: we increased the number of PCR cycles from 18 to 28. Relevant primer sequences are listed in Supplemental Table 2. Each initial deletion was designed to remove the appropriate KH domain precisely, but also to leave in its place a short “scar sequence” that would facilitate subsequent replacement by an alternate KH domain sequence via gap repair homologous recombination. Primers scpdelKH13.stu.xho.f1 and scpdelKH13.stu.xho.r2 were used to replace KH13 with a StuI-linker-XhoI scar, resulting in the allele FLAG.scp160Δ13.scar. Similarly, primers scpdelKH14.stu.xho.f2 and scpdelKH14.stu.xho.r2 were used to replace KH14 with a StuI-linker-XhoI scar, resulting in the allele FLAG.scp160Δ14.scar. Finally, alleles intended to carry either a clean deletion or KH domain replacement of KH13 or KH14 were generated by gap repair of the corresponding scar construct with an appropriate fragment, as described below. The gapped backbone fragment for each recombination procedure was generated from the appropriate plasmid (pGEM3-zf(+).FLAG.Scp160Δ14.scar or pGEM3-zf(+).FLAG.Scp160Δ13.scar) by digestion with StuI and XhoI, followed by gel purification.

The inserts for scar replacement were generated as follows: (a) to remove the StuI-linker-XhoI scar from each deletion template, the indicated oligonucleotides in Supplemental Table 2 were annealed and extended in a single round of polymerization using the TripleMaster PCR System (Eppendorf) in a thermocycler, (b) to create FLAG.scp160Δ14.11, a fragment encoding KH11 was amplified from a wild-type SCP160 template using primers scpdelKH14.addback.KH11.f1 and scpdelKH14.addback.KH11.r1, (c) to create FLAG.scp160Δ14.13, the replacement sequence was generated by PCR using the primers scpdelKH14.addback.13.f1 and scpdelKH14.addback.13.r1, (d) to create FLAG.scp160Δ13.6,
the replacement sequence was generated by PCR using the primers scpdelKH13.addback.KH6.f1 and scpdelKH13.addback.KH6.r1, and finally (e) to create FLAG.scp160Δ13.14, the replacement sequence was generated by PCR using the primers SCP.KH14.addback.f1 and SCP.KH14.addback.r1. All DNA fragments were gel purified using the QIAquick® Gel Extraction Kit (Qiagen), according to the manufacturer’s instructions.

To accomplish gap repair homologous recombination, the appropriate purified PCR fragments were individually cotransformed into competent *E. coli* with gel-purified, gapped plasmid backbone. Transformants were cultured and the plasmids isolated using the Qiaprep Spin® Miniprep Kit (Qiagen). All resultant alleles were verified by restriction analysis and DNA sequencing across the entire region that had been generated by PCR to ensure sequence integrity.

Once the desired sequence manipulations were completed and verified, we next moved the relevant *SCP160* sequences into yeast-integrating plasmids via gap repair homologous recombination for subsequent insertion into the *SCP160* locus of the yeast genome. Towards that end, all verified plasmids were digested with PstI and EcoRI. The ~2.2 kb band from each construct was gel purified and individually cotransformed into competent *E. coli* with pJF2147 (YIp1ac211.FLAG: *SCP160*) that had been gapped by digestion with AflIII and XbaI. Resultant constructs were confirmed by restriction digestion, linearized by digestion with PstI, and transformed into the yeast strain JFY4943. Appropriate integration was confirmed by genomic PCR, followed by direct sequence analysis of each *SCP160* locus from KH12 to 600 bp downstream of the stop codon.

**Analyses of the ability of FLAG.SCP160 and modified alleles to complement scp160Δ eap1Δ synthetic lethality**

We assessed the ability of all modified alleles listed in Figure 1 to function *in vivo* by quantifying the ability of each to complement scp160Δ eap1Δ synthetic lethality (23). Briefly, *scp160Δ eap1Δ* cells carrying both an *SCP160 URA3* “maintenance” plasmid and an *scp160* variant allele in a LEU2 “test” plasmid were inoculated into liquid medium lacking both uracil and leucine, to enable loss of the *URA3* maintenance plasmid. When this culture reached an OD 600 of ~2.0, again 300,000 cells were inoculated into synthetic media lacking only leucine, to enable loss of the *URA3* maintenance plasmid. When this culture reached an OD 600 of ~2.0, again 300,000 cells were inoculated into synthetic medium lacking leucine and grown to an OD 600 of 1.5–2.0. Finally, cells were counted, and appropriate dilutions were plated to synthetic medium lacking leucine ±5-fluoro-orotic acid (5-FOA). 5-FOA is toxic only to cells that contain a functional *URA3* gene (28); therefore, the number of colonies that grew on the 5-FOA medium relative to the number of colonies that grew on medium lacking 5-FOA was a measure of the proportion of cells in the culture that had lost the *URA3* maintenance plasmid. This proportion, in turn, was a measure of the ability of the variant *scp160* test plasmid to complement loss of the wild-type *SCP160* maintenance plasmid. Empty test plasmid backbone served as the negative control, and test plasmid encoding wild-type FLAG.Scp160p served as the positive control. For comparison between experiments, the proportion of cells that lost the *URA3* plasmid in each strain was normalized to the corresponding proportion from the positive control strain. Therefore, the final values calculated indicated how effectively, relative to wild-type *SCP160*, each modified allele of *scp160* functioned *in vivo*. Since the *URA3* maintenance plasmid was the same in all strains and all experiments, any issues of plasmid replication efficiency or distribution, independent of *SCP160* sequence, should have cancelled out.

**Biochemical analyses of Scp160p**

All cell lysates and subcellular fractionations were performed as described previously (21,22,25). Briefly, mid-log-phase cultures were incubated with cycloheximide at a final concentration of 100 μg/ml for 1 min at 30°C, and then for 15 min on ice with swirling. Cells were washed in cold water, then lysed in cold buffer (25), each containing 100 μg/ml cycloheximide. All cell lysis procedures were accomplished using a multihed vortex mixer that was set to the highest speed at 4°C for 20 min. The supernatant from the lysis was centrifuged at 3000 rpm at 4°C for 5 min in a tabletop microfuge. The supernatant from this step was transferred to a fresh tube and centrifuged at 12000 rpm, 4°C, for 8 min in a tabletop microfuge. The supernatant from this final spin was the soluble lysate. The protein concentration of this soluble lysate was quantified using the Bio-Rad Protein Assay (cat #500-0006) according to the manufacturer’s instructions. Next, 15 μg of soluble protein from untagged
wild-type, FLAG-tagged wild-type, and FLAG-tagged Scp160p variants were each run on a gel for subsequent Western blot analysis. FLAG.Scp160p band intensity, for the wild-type protein and all variants, was quantified by scanning densitometry, and FLAG.Scp160p signal was normalized to the intensity of a previously reported endogenous protein also recognized by the anti-FLAG M2 antibody (21).

For analyses of polysome association, 200 µl of soluble lysate were loaded onto a 15–45% sucrose gradient and centrifuged at 39,000 rpm in an ultracentrifuge for 2.5 h at 4°C, as described previously (25). Fractions (1 ml) were collected from the sucrose gradients and 400 µl of each were concentrated for Western blot analysis. In brief, samples were mixed with 400 µl MeOH and 100 µl chloroform and agitated vigorously. Precipitated proteins were pelleted by centrifugation at 13,000 rpm for 2 min in a tabletop microfuge; the top phase was discarded, and 400 µl MeOH was added to the pellet. Each sample was inverted to mix and then re-centrifuged at 13,000 rpm for another 5 min. This supernatant was discarded, and samples were dried in a speed vac with no heat for ~20 min until no remaining liquid was visible. The protein pellet was resuspended in 1× loading buffer and applied onto a 10% SDS-PAGE gel for subsequent Western blot analysis using the monoclonal ANTI-FLAG M2 antibody (Sigma-Aldrich) to detect FLAG-tagged Scp160p, as described previously (25). Controls involved preincubation of lysates with either 50 units/ml tagged Scp160p, as described previously (25). Controls and 400 µl of each were concentrated for Western blot analysis. In brief, samples were mixed with 400 µl MeOH and 100 µl chloroform and agitated vigorously. Precipitated proteins were pelleted by centrifugation at 13,000 rpm for 2 min in a tabletop microfuge; the top phase was discarded, and 400 µl MeOH was added to the pellet. Each sample was inverted to mix and then re-centrifuged at 13,000 rpm for another 5 min. This supernatant was discarded, and samples were dried in a speed vac with no heat for ~20 min until no remaining liquid was visible. The protein pellet was resuspended in 1× loading buffer and applied onto a 10% SDS-PAGE gel for subsequent Western blot analysis using the monoclonal ANTI-FLAG M2 antibody (Sigma-Aldrich) to detect FLAG-tagged Scp160p.

RESULTS

Expression of FLAG-tagged wild-type and variant Scp160p proteins in yeast

As a first step to delineate the distinct versus potentially overlapping functions of conserved and diverged KH domains in Scp160p, we generated alleles encoding two modified variants: FLAG.Scp160pΔ14p, in which conserved KH14 was deleted, and FLAG.Scp160pΔ13p, in which diverged KH13 was deleted (Figure 1). While previous studies from our lab and others (24,25) had tested the function of Scp160p missing KH14 or KH13+14, the _FLAG.scp160pΔ13_ allele created here was novel. From the _FLAG.scp160pΔ14_ and _FLAG.scp160pΔ13_ templates, we then generated an additional four modified alleles; two in which the deleted KH domains were replaced by the same class of KH domain (i.e., conserved for conserved, or diverged for diverged), and two in which the deleted KH domains were replaced by the opposite class of KH domain. The encoded proteins were designated FLAG.Scp160pΔ14.11p, in which conserved KH11 replaced conserved KH14, FLAG.Scp160pΔ14.13p, in which diverged KH13 replaced conserved KH14, FLAG.Scp160pΔ13.6p, in which diverged KH6 replaced diverged KH13, and FLAG.Scp160pΔ13.14p, in which conserved KH14 replaced diverged KH13 (Figure 1). As a result of these manipulations, two of the modified proteins, FLAG.Scp160pΔ14p and FLAG.Scp160pΔ13p, each carried a total of 13 KH domains, and four of the modified proteins, FLAG.Scp160pΔ14.11p, FLAG.Scp160pΔ14.13p, FLAG.Scp160pΔ13.6p, and FLAG.Scp160pΔ13.14p, each carried a total of 14 KH domains. Each modified allele was sequence confirmed and introduced into the appropriate yeast genomic locus in place of the wild-type SCP160 allele by two-step gene replacement, as described in the Materials and Methods section.

To confirm the expression of each variant Scp160p protein, soluble lysates from mid-log-phase cultures of the appropriate strains were subjected to Western blot analysis with the M2 anti-FLAG monoclonal antibody. Representative results are presented in Figure 2A. Due to the different lengths of the KH domains deleted or...
replaced, the protein sizes varied from about 70 amino acids larger than the wild-type protein (FLAG.Scp160 Δ14.13p), to about 140 amino acids smaller than the wild-type protein (FLAG.Scp160Δ13p). Yeast expressing untagged Scp160p served as a negative control for specificity of the antibody, and a ~100 kDa endogenous yeast protein that cross-reacts with the M2 antibody (21,22,25) served as a convenient internal control for loading (Figure 2A, bottom-most band in each lane). As illustrated in Figure 2A (open circles), each modified protein was expressed and displayed the expected migration pattern relative to the wild-type FLAG-tagged protein. Furthermore, quantitation of the Scp160p signal in each lane, relative to the corresponding loading control, for this and replicate experiments, demonstrated that each modified isoform was expressed at a level indistinguishable from that of the wild-type protein (Figure 2B).

In vivo function of Sbp160p KH domain variants

To test the impact of KH domain loss or substitution on Sbp160p function, we first assessed the ability of each variant allele illustrated in Figure 1 to replace SCP160 in vivo (23). As a control, we analyzed the SCP160 variants that lacked either conserved KH14 or diverged KH13 in parallel with the other variants. Previous studies from our lab (25) had demonstrated the functional significance of KH14, and previous studies from Seedorf and colleagues (24) had demonstrated the functional importance of KH13 + 14 combined. For genetic testing, each modified scp160 allele was subcloned into a plasmid and transformed into scp160Δ eap1Δ cells maintained by a URA3 maintenance plasmid. Although SCP160 is not itself essential in yeast (29), deletion of SCP160 in combination with deletion of EAP1 is synthetically lethal (23).

To assess how well each modified scp160 allele functioned in vivo, we applied a previously validated quantitative complementation assay (23). As explained in Materials and Methods, this assay measures the frequency with which a scp160Δ eap1Δ mutant strain loses a wild-type SCP160 maintenance plasmid in the presence of a modified scp160 test plasmid. Results are calculated as the relative percentage of maintenance plasmid loss, and the calculated value gives an indication of the functional capacity of the tested allele. For example, a poorly complementing sequence or empty test backbone will have a very low percentage maintenance plasmid loss, because few if any cells will survive loss of the SCP160 URA3 maintenance plasmid. In contrast, strains that carry an SCP160 test sequence that functions well in vivo will have a very high degree of maintenance plasmid loss, because most if not all cells will survive loss of the maintenance plasmid. As explained earlier, because the URA3 maintenance plasmid was the same in all strains, any issues of plasmid replication efficiency or distribution, independent of SCP160 sequence, should have cancelled out. Further, given that each of the wild-type and variant SCP160 test sequences was expressed from the same wild-type SCP160 promoter and plasmid backbone, and that all of these alleles were demonstrated to express comparable levels of Scp160p protein when genomic (Figure 2), there should have been no disparities in Scp160p expression levels for this experiment.

Results of these analyses for the control strains confirmed that both KH domains 13 and 14 are essential for Sbp160p function. As illustrated in Figure 3, the FLAG.scp160Δ14 allele (conserved KH domain deleted) enabled only ~14% wild-type levels of maintenance plasmid loss, and the FLAG.scp160Δ13 allele (diverged KH domain deleted) enabled only ~10% wild-type levels of maintenance plasmid loss. While the ΔKH14 allele provided an anticipated result (25), this was the first demonstration that loss of KH13 alone also compromised Scp160p function. Together, these results provide a foundation for the remainder of the study, which involved testing various add-back alleles for restoration of function.

As illustrated in Figure 3, both of the add-back alleles derived from FLAG.scp160Δ14, namely FLAG.scp160Δ14.11, in which a conserved KH11 replaced a conserved KH14, and FLAG.scp160Δ14.13, in which a diverged KH13 replaced a conserved KH14, demonstrated significant complementation. In fact, FLAG.scp160Δ14.13 demonstrated the highest degree of complementation of any of the modified scp160 alleles tested here. In contrast, while the FLAG.scp160Δ13.14 add-back allele, in which a conserved KH14 replaced a diverged KH13, demonstrated significant complementation compared to the ΔKH13 variant, the FLAG.scp160Δ13.6 allele, in which a diverged KH6 replaced a diverged KH13, did not. Indeed, the FLAG.scp160Δ13.6 allele performed even more poorly than did either deletion variant alone.

Impact of KH domain loss and substitution on macromolecular interactions of Sbp160p

Scp160p exists as a component of large mRNA/protein complexes (mRNPs) in yeast (21). To assess whether
conserved and diverged KH domains make specific contributions to these interactions, we tested whether the Scp160p variants created here could form mRNPs. For these analyses, soluble lysates prepared from mid-log-phase cultures of yeast expressing each Scp160p variant were size-fractionated over an S300 Sephacryl column, as described in the Materials and Methods section. The resulting fractions were subjected to Western blot analysis using the anti-FLAG M2 antibody. Each panel represents one lysate fractionated into twenty 2-ml samples, as indicated at the top of the figure. The elution positions of the void volume (≥1300 kDa) and other size markers are indicated. (B) Signal intensity of each fraction in (A) was quantitated by scanning densitometry and used to calculate the fraction of each variant Scp160p present in samples 1–5 (shaded bars representing the large complexes characteristic of wild-type Scp160p) vs. samples 6–20 (open bars representing smaller complexes). Values plotted are also listed above each corresponding bar.

Lysetes from yeast expressing full-length FLAG.Scp160p protein were analyzed in parallel as a positive control. To facilitate quantitative comparison among the elution profiles of the different Scp160p variants, the signal intensity in each lane was quantified by scanning densitometry, and the fraction of total signal detected for each protein in the first 5 lanes versus the last 15 lanes is presented in Figure 4B. These studies were replicated at least three times to ensure reproducibility.
As illustrated in Figure 4, wild-type FLAG.Scp160p migrated through the column predominantly with the void volume, demonstrating that most of the protein existed as part of a large complex (≥1.3 MDa). Previous studies have confirmed that these large complexes are mRNPs by virtue of their sensitivity to RNase digestion and the presence of both poly (A) binding protein Pab1p (21) and polyadenylated RNA (18, 21, 22).

Deletion of either conserved KH14 or diverged KH13 significantly shifted the Scp160p signal from the void volume to fractions representing smaller complexes, or even monomeric Scp160p (Figure 4), which comigrates with globular proteins of ~450 kDa (21). While both variant migration patterns were clearly different from that observed for wild-type Scp160p, FLAG.Scp160Δ13p migrated even more aberrantly than did FLAG.Scp160Δ14p (Figure 4B), suggesting that loss of diverged KH13 was even more disruptive to macromolecular interactions than was loss of conserved KH14.

When the missing conserved KH14 sequence was replaced, either by conserved KH11 or by diverged KH13 (Figure 4), close to half of each add-back protein migrated correctly as a large complex, although a ‘tail’ of smaller complexes extended beyond the normal limit in both profiles. Similarly, when the missing diverged KH13 sequence was replaced, either by diverged KH6 or by conserved KH14, the majority of signal representing each modified protein again migrated as expected (Figure 4). Indeed, the FLAG.Scp160ΔKH13.14p protein showed an S300 elution profile that was almost indistinguishable from that of wild-type Scp160p (Figure 4B). Thus, the conserved and diverged KH domains studied here appear to be functionally interchangeable to a large extent for protein complex formation.

Impact of KH domain loss or substitution on Scp160p association with polyribosomes

Scp160p has been implicated in the cytoplasmic metabolism of specific transcripts (18). Consistent with this presumed function, Scp160p associates with polyribosomes (21, 22, 24, 25). To examine this more specific aspect of Scp160p macromolecular interaction in the context of KH domain contribution, we assessed the migration through a sucrose gradient of each Scp160p variant from Figure 1. Sucrose gradients enable the size separation of large complexes, such as ribosomal subunits, monosomes, and polyribosomes. Western blot analyses of the fractions collected from these gradients revealed the distribution profile for each Scp160p variant protein relative to the migration pattern of the FLAG.Scp160p wild-type control. Finally, to test whether co-migration with polyribosomes reflected association of each variant Scp160p with polyribosomes, as opposed to non-specific aggregation, we pretreated relevant samples with RNase or EDTA, as described below. To facilitate comparison between the different profiles, the FLAG-Scp160p signal intensity in each lane was quantified by scanning densitometry and plotted as the fraction of total signal migrating in samples 1–4 (complexes smaller than monosomes) versus fractions 5–11 (monosomes and polysomes).

As expected (21, 22, 25), a majority (>80%) of the wild-type FLAG.Scp160p protein migrated with monosomes and polyribosomes near the bottom of the gradient, while more than half of the FLAG.Scp160Δ14p variant protein migrated near the top of the gradient (Figure 5A), indicating a loss of association with polyribosomes. Loss of diverged KH13 produced an even more striking shift of Scp160p signal from the bottom to the top of the gradient (Figure 5A), reconfirming the functional significance of this domain. Of note, although neither wild-type Scp160p nor any of the ΔKH13 variant proteins showed any signal in the top-most gradient fraction, representing free proteins and small complexes, all three ΔKH14 proteins did show signal in this fraction. The simplest explanation for this disparity is that the wild-type and ΔKH13 Scp160p proteins assembled entirely into complexes larger than those found in the first gradient fraction, while the three ΔKH14 Scp160p proteins each maintained at least a subpopulation that did not.

Add-back of conserved KH11 to the ΔKH14 protein had little if any impact on polyribosome association, although add-back of diverged KH13 restored monosome or polyribosome comigration to more than half of the molecules (Figure 5A). A similar ‘partial rescue’ was seen following add-back of diverged KH6 to the ΔKH13 protein, such that more than half of the FLAG.Scp160Δ13.6p protein migrated with the denser gradient fractions. Finally, add-back of conserved KH14 in place of the missing diverged KH13 completely normalized the sucrose gradient profile of the variant protein (Figure 5A).

To confirm that the pattern of Scp160p migration evident in these experiments corresponded to association with ribosomes, samples were either treated with EDTA, which dissociates polyribosomes and monosomes into small and large ribosomal subunits, or RNase, which dissociates polyribosomes into monosomes. Both treatments caused the signals for all Scp160p variants tested to migrate predominantly at the top of the gradient (Figure 5B and C), confirming that the pattern in the absence of pretreatment was due largely to association with polyribosomes, and not simply to aggregation. For all three variant proteins, however, especially Scp160Δ13.6p, a portion of the signal did remain in the denser fractions even after treatment with EDTA or RNase (Figure 5B and C), indicating that these proteins may have aggregated to some extent. By extension, these results suggest that while the data presented in Figure 4 reflect predominantly mRNP formation by the variant Scp160p proteins, some degree of aggregation may also have occurred.

DISCUSSION

The goal of this study was to explore whether diverged KH domains are as important for Scp160p function as conserved domains, and also whether diverged KH domains can functionally replace conserved KH domains in Scp160p. Our results yielded two important conclusions. First, diverged KH domains can be as critical for function as conserved KH domains. Specifically,
Figure 5. Sucrose gradient fractionation of Sca160p-containing complexes. (A) The upper panel illustrates a representative sucrose gradient profile monitored by absorbance at 254 nm, indicating positions of the small and large ribosomal subunits, monosomes, and polyribosomes. A254 profiles of lysates derived from yeast expressing wild-type and Sca160p variants were indistinguishable. The lower seven panels in (A) present anti-FLAG Western blot analyses of gradient fractions from yeast expressing each of the indicated Sca160p variants. Fractionation experiments were repeated at least three times for each strain, with indistinguishable results. The bar graph presents a quantitative assessment of the data illustrated above. In particular, signal intensity of each sample was quantified by scanning densitometry and used to calculate the fraction of each variant Sca160p present in samples 1–4 (shaded bars representing proteins migrating with complexes smaller than monosomes) versus samples 5–11 (open bars representing Sca160p proteins migrating with monosomes or polysomes). Values plotted are also listed above each corresponding bar. (B) Impact of RNase pretreatment on migration of wild-type and variant Sca160p proteins through a sucrose gradient. (C) Impact of EDTA pretreatment on migration of wild-type and variant Sca160p proteins through a sucrose gradient.
we demonstrated, as others have hypothesized (24), that at least one diverged KH domain in Scp160p, KH13, is essential for Scp160p function, despite its lack of the GXXG motif. Second, there can be considerable functional overlap between diverged and conserved KH domains. In particular, we observed that add-back of the diverged KH13 domain sequence to an Scp160p variant missing conserved KH14 partially restored both presumed mRNP formation and polyribosome association, and also restored close to 50% wild-type complementation. It is also important to note, however, that no ‘add-back’ variant was able to restore fully wild-type levels of SCP160 function when measured by our biochemical or quantitative complementation assays. Furthermore, the variants studied here showed differing levels of biochemical function with regard to presumed mRNP formation and polyribosome association. These results highlight the distinction between the shared and unique roles of individual KH domains in a multi-KH-domain protein; though they may be repeated, these units are not simply interchangeable.

Size alone is not the answer

Another noteworthy conclusion from our results is that neither the sheer number of KH domains nor the total protein size defines Scp160p function. For example, each of the add-back alleles included a total of 14 KH domains, yet there was enormous disparity in their degrees of function. Furthermore, as illustrated in Figure 2, the variant Scp160p proteins were not all the same size, even after add-back, because KH domain 13 is almost twice the size of any of the other KH domains. This disparity means that the variants missing KH13 with either a KH6 add-back or a KH14 add-back were both approximately the same size as the variant protein that was simply missing KH14, with no add-back, and yet the function of these proteins differed dramatically (Figures 3–5). Clearly, size alone does not define Scp160p function.

Uncoupling aspects of Scp160p function

One of the interesting observations from the data we present here is that SCP160 function is not binary; the variants we have created and tested clearly uncouple different aspects of Scp160p function. For example, all four of the add-back alleles we tested restored at least partial ability of Scp160p to form presumed mRNP, but only three restored at least partial ability of the protein to associate with polyribosomes. Finally, of all the variant alleles tested, only one, SCP160Δ14.13, restored significant function as measured using our genetic complementation assay. The simplest interpretation of these results would be that SCP160 function, as measured by the complementation assay, is a complex variable. An ability to form presumed mRNP appears to be a prerequisite for polyribosome association, and polyribosome association appears to be necessary but not sufficient for full function in vivo. It is also interesting to note that the allele demonstrating the strongest ability to complement scp160Δ eap1Δ synthetic lethality (SCP160Δ14.13) was not the same allele that showed the greatest association with polyribosomes (SCP160Δ13.14). Furthermore, the most genetically functional of all of the add-back alleles tested was SCP160Δ14.13, in which a conserved KH domain was replaced by a diverged KH domain. These data clearly demonstrate that the GXXG motif cannot be essential for the function of every KH domain in Scp160p.

Scp160p and the vigilins

Here we have used Scp160p in yeast as a model to study conserved and diverged KH motifs within a multi-KH-domain protein. Scp160p is most closely related to a KH-domain protein; Scp160p: yeast multi-KH-domain protein. Solid line represents N-terminal and C-terminal protein sequence not predicted to contain KH domain sequences.

In silico predictions

The KH domain models of two commonly used protein domain databases, SMART and Pfam (34,35), were capable of recognizing all the conserved KH domains in Scp160p, but only a subset of the diverged KH domains, which were not confidently predicted because the scores fell below the allowed significance threshold. Nevertheless, these in silico systems were capable of recognizing all the diverged KH domains of most vigilins. It is interesting to note that, while Scp160p KH6 was not recognized by either program, this domain was still able to restore some
biochemical function to the FLAG.Scp160Δ13p variant protein.

By calling into question a disparity between sequence and function among KH domains, our results raise the possibility that there may be more functional KH domains in the proteome than previously appreciated. By extension, these results would suggest that more RNA-binding proteins may exist, as well. Finally, these data clearly imply the need for in vivo validation of other sequence motifs defined by in silico methods.

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