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The stem–loop binding protein stimulates histone translation at an early step in the initiation pathway

BARBARA GORGONI,1,4 STUART ANDREWS,2,4,5 ANDRÉ SCHALLER,3,6 DANIEL SCHÜMPERLI,3 NICOLA K. GRAY,1 and BERNDT MÜLLER2

1MRC Human Genetics Unit, Western General Hospital, Crewe Road, Edinburgh EH4 2XU, Scotland, United Kingdom
2School of Medical Sciences, Institute of Medical Sciences, University of Aberdeen, Foresterhill, Aberdeen AB25 2ZD, Scotland, United Kingdom
3Institute for Cell Biology, University of Bern, Baltzerstrasse 4, CH-3012 Bern, Switzerland

ABSTRACT

Metazoan replication-dependent histone mRNAs do not have a poly(A) tail but end instead in a conserved stem–loop structure. Efficient translation of these mRNAs is dependent on the stem–loop binding protein (SLBP). Here we explore the mechanism by which SLBP stimulates translation in vertebrate cells, using the tethered function assay and analyzing protein–protein interactions. We show for the first time that translational stimulation by SLBP increases during oocyte maturation and that SLBP stimulates translation at the level of initiation. We demonstrate that SLBP can interact directly with subunit h of eIF3 and with Paip1; however, neither of these interactions is sufficient to mediate its effects on translation. We find that Xenopus SLBP1 functions primarily at an early stage in the cap-dependent initiation pathway, targeting small ribosomal subunit recruitment. Analysis of IRES-driven translation in Xenopus oocytes suggests that SLBP activity requires eIF4E. We propose a model in which a novel factor contacts eIF4E bound to the 5′ cap and SLBP bound to the 3′ end simultaneously, mediating formation of an alternative end-to-end complex.

Keywords: histone mRNA; histone hairpin-binding protein (HBP); translation initiation; oocyte maturation; translational control; poly(A) tail

INTRODUCTION

The stem–loop binding protein (SLBP), or histone hairpin-binding protein (HBP), is an RNA-binding protein essential for the coordination of histone gene expression with DNA synthesis. A failure to ensure appropriate replication-dependent histone gene expression in somatic cells results in the inhibition of cell-cycle progression, defects in cell division, and changes in gene expression. SLBP binds to the conserved stem–loop structure located in the 3′ untranslated region (3′ UTR) of histone mRNA (Wang et al. 1996; Martin et al. 1997). SLBP is an essential protein (Sullivan et al. 2001; Kodama et al. 2002; Pettitt et al. 2002; Zhao et al. 2004) that is part of a multifactor complex that binds to the histone mRNA 3′ UTR and contains the U7 snRNP and the zinc-finger protein ZFP100 (Müller and Schümperli 1997; Marzluff and Duronio 2002). This complex mediates histone-specific mRNA processing that results in mature mRNAs that do not contain a poly(A) tail but end in the stem–loop structure. The stem–loop and SLBP are also involved in translation of histone mRNAs (Gallie et al. 1996; Ling et al. 2002; Sanchez and Marzluff 2002). SLBP is associated with polyribosomes, dependent on the presence of intact histone mRNA (Whitfield et al. 2004; S. Andrews and B. Müller, unpubl. results), and can activate the translation of reporter mRNAs containing the stem–loop structure (Ling et al. 2002; Sanchez and Marzluff 2002).

Interestingly, the production of SLBP and histones is also regulated during development but, in contrast to regulation in somatic tissues, it is not coupled to DNA replication (Wang et al. 1999; Allard et al. 2002). In Xenopus laevis, replication-dependent histone mRNAs are accumulated during the early stages of oogenesis and are maintained in an inactive state. During oocyte maturation, translation of these stored mRNAs ensures that sufficient histones are present prior to the midblastula transition (Woodland 1980), when zygotic transcription begins. Xenopus oocytes express two SLBP species
xSLBP1 is the homolog of mammalian SLBP, can stimulate translation (Sanchez and Marzluff 2002), and is present throughout oogenesis, increasing approximately twofold at oocyte maturation (Wang et al. 1999). xSLBP2 is similar to xSLBP1 only in the RNA-binding domain, is degraded at oocyte maturation, and is not present in somatic cells. Histone mRNAs are mainly bound to xSLBP2 during oogenesis and since it cannot stimulate translation (Sanchez and Marzluff 2002), it is thought to maintain them in a translationally silent state. Upon maturation, xSLBP2 is exchanged for xSLBP1, which is released from the nucleus and activates translation of histone mRNAs (Wang et al. 1999; Sanchez and Marzluff 2002).

It is well established that the translation of polyadenylated mRNAs is stimulated by the interaction of poly(A)-binding proteins such as PABP1 and ePABP with the poly(A) tail (Gorgoni and Gray 2004; Wilkie et al. 2005). It is proposed that PABP contacts factors at the 5’ end of the mRNA, thereby increasing the recruitment of ribosomal subunits. One important interaction is between PABP and the scaffolding factor elf4G, which in turn interacts with the cap-binding protein elf4E. This interaction is thought to simultaneously increase the affinity of elf4E for the cap and of PABP for the poly(A) tail. elf4G then recruits the small ribosomal subunit by binding elf3 (for reviews, see Mangus et al. 2003; Gorgoni and Gray 2004). PABP also interacts with termination factors, suggesting a role for PABP in ribosome recycling (Mangus et al. 2003; Gorgoni and Gray 2004). SLBP may fulfill a role similar to PABP in the translation of histone mRNAs. However, the mechanism by which SLBP stimulates translation is not yet clear. In a heterologous yeast system, human SLBP stimulates translation of reporter genes dependent on the presence of initiation factors elf4G and elf3 (Ling et al. 2002). An interaction between elf4G and SLBP was also detected in mammalian cell extracts. Additionally, sequences in the N terminus and in the C terminus have been suggested to be required for SLBP activity (Ling et al. 2002; Sanchez and Marzluff 2002).

Here we investigate the mechanism by which SLBP stimulates translation in Xenopus oocytes. We show that SLBP affects translation initiation and that its ability to stimulate translation increases dramatically during oocyte maturation. Using a directed yeast two-hybrid approach we found that it interacts with translation factors elf3 and Paip1. We confirmed these interactions in mammalian cell extracts and mapped the interaction with elf3h to the SLBP RNA-binding domain and with Paip1 to the C-terminal domain. However, the N-terminal region is sufficient for stimulation of translation. This, together with an IRES-based approach, indicates that other factors are required for SLBP-mediated histone mRNA translation. We present experimental evidence that these factors act early in translation initiation and propose that this may be mediated by a novel specific factor that functions through elf4E.

RESULTS

SLBP translational activity is increased by oocyte maturation

It has been previously reported that Xenopus SLBP1 (xSLBP1) and human SLBP (hSLBP) can stimulate translation in Xenopus stage VI oocytes and in yeast, respectively (Ling et al. 2002; Sanchez and Marzluff 2002). Since histone mRNA translation is normally activated during oocyte maturation (Woodland 1980), we compared the translational activity of both human and Xenopus SLBP1 in stage VI versus mature Xenopus oocytes, using the tethered function assay (Gray et al. 2000; Fig. 1A). This eliminates interference from the endogenous xSLBP proteins present in oocytes (xSLBP1 and xSLBP2). A fusion of MS2 to the RNA-binding protein U1A, which does not activate translation, was used as a negative control. Figure 1B shows that tethered xSLBP1 stimulates expression of an mGpppG (m7G)-capped luciferase reporter approximately threefold compared to MS2-U1A in stage VI oocytes. The injected reporter mRNAs remain stable throughout the time course of this assay (Gray et al. 2000), indicating that the effects of xSLBP1 occur at the level of translation, consistent with previous results (Ling et al. 2002; Sanchez and Marzluff 2002). While weaker, the effect of tethered hSLBP was reproducible, stimulating translation between 1.4 and 1.7 times compared to MS2-U1A. Interestingly, the translational activity of both hSLBP and xSLBP1 increased significantly when oocytes were matured by treatment with progesterone: up to threefold for the human and sevenfold for the Xenopus protein (Fig. 1B). This increase is specific, since no stimulation of a luciferase reporter lacking the MS2 RNA-binding sites was observed in mature oocytes, as shown for MS2-xSLBP1 (Fig. 1C). Importantly, translation of the polyadenylated β-galactosidase control reporter did not notably change during maturation (average of β-galactosidase activity of progesterone-treated samples is 0.93 times that of untreated samples; data not shown), and the increase in stimulation was not due to increased expression of the fusion proteins (Fig. 1D). Interestingly, the mobility of SLBPs was reduced in progesterone-treated samples, presumably due to protein phosphorylation (Müller et al. 2000). Taken together these results suggest that SLBP translational activity is upregulated during oocyte maturation.

SLBP stimulates translation initiation

Although it is established that SLBP can stimulate translation, the mechanism by which this is achieved is less clear. In order to determine whether SLBP affects translation initiation or a downstream event, we compared translation stimulation by xSLBP1 of an m7G-capped luciferase reporter with a reporter containing the Cricket Paralysis Virus internal ribosome entry site (CrPV IRES). This IRES is
known to bind the ribosome directly, without a requirement for any of the canonical translation initiation factors, by interacting with the P-site of the ribosome (Wilson et al. 2000). Although the CrPV IRES mRNA is translated less efficiently than m$^7$G-capped mRNA in oocytes, luciferase activity of both reporters in oocytes expressing MS2-U1A was normalized to 1, allowing for direct comparison of SLBP-mediated translational activation. As shown in Figure 2, tethered xSLBP1 stimulates translation of m$^7$G-capped luciferase but, in contrast, does not stimulate translation of the CrPV IRES reporter. This suggests that xSLBP1 functions at the level of translation initiation and that it requires the activity of translation initiation factors.

**SLBP interacts with eIF3 and Paip1**

Our results suggest that one or more canonical translation initiation factors is required for SLBP-mediated translation stimulation. To identify the factors that may be involved, we performed a directed yeast two-hybrid screen using hSLBP and xSLBP1 as bait and a panel of vertebrate translation factors, including eIF4G and eIF3 subunits, and also eIF1, eIF2, eIF3, and Paip1.
SLBP stimulates an early step in translation

eIF1A, eIF2, eIF4A, eIF4B, eIF4E, eIF4H, eIF5, eIF5A, and eIF5B (data not shown). Since SLBP showed a degree of self-activation of the lacZ reporter, we selected for interaction on media lacking histidine and containing 25 mM 3-AT. The iron regulatory protein 1 (IRP1), an RNA-binding protein with a defined role in mRNA specific translation repression, was used as a negative control. The growth pattern on 3-AT-containing media indicated a clear interaction between both human and *Xenopus* SLBP and subunit h (or p40) of eIF3 (Fig. 3A). Importantly, this protein was also isolated in a yeast two-hybrid screen of a human cDNA library using hSLBP as bait (data not shown), highlighting the potential importance of this interaction. We performed GST-pulldown assays with purified GST-eIF3h and SLBP proteins to confirm the interaction between the SLBPs and eIF3h. Figure 3B and 3C show that both human and *Xenopus* SLBPs were specifically enriched when GST-eIF3h was coupled to glutathione beads, but not when GST-eIF3h was omitted or replaced by GST alone. Importantly, this shows that the interaction between eIF3h and SLBP is direct and does not require the presence of other proteins. To determine whether eIF3 and SLBP interact in mammalian cell extracts, a GST-based approach was taken. HA-tagged human SLBP was expressed in HEK293 cells and whole-cell extracts were incubated in the presence of GST-eIF3h. Figure 3D shows that hSLBP is specifically co-isolated with GST-eIF3h. The interaction between eIF3h and hSLBP in cell extracts is not mediated by RNA, as treatment of the extract with RNase A did not abrogate the interaction (Fig. 3E).

Interestingly, yeast eIF4G was shown to be genetically required for hSLBP to stimulate the translation of reporter mRNAs in yeast and human eIF4G was found in complexes with SLBP in mammalian extracts (Ling et al. 2002). However, these studies did not address whether the co-isolation of these proteins was mediated by other factors. Surprisingly, no interaction between SLBP and eIF4G was identified in the directed yeast two-hybrid analysis, despite experimental controls indicating that the proteins were active in the yeast two-hybrid system (Fig. 4A). This suggests that eIF4G and SLBP do not interact directly, although they may be present in the same complex. However, vertebrate cells contain an additional protein, Paip1, which shares considerable homology with the C-terminal two thirds of eIF4G and has been proposed to mediate the translation of polyadenylated mRNAs, similar to the role of eIF4G (Craig et al. 1998). We therefore examined whether Paip1, which is not present in yeast but is expressed in *Xenopus* oocytes (Gray et al. 2000), could interact with SLBP. Figure 4B shows that, in contrast to eIF4G, Paip1 interacts with both human and *Xenopus* SLBP. This interaction is direct as it can be detected in pulldown assays using yeast two-hybrid assays.
purified proteins (Fig. 4C). Furthermore, the hSLBP-Paip1 interaction can be detected in mammalian whole-cell extracts. hSLBP was specifically enriched with GST-Paip1 (Fig. 4D) and this interaction was not mediated by RNA (Fig. 4E).

eIF3 and Paip1 bind to different regions of SLBP

The interaction of hSLBP with eIF3h and Paip1 was mapped to determine whether it corresponds to the same domains that were previously implicated in the activation of translation (Ling et al. 2002; Sanchez and Marzluff 2002). The human SLBP protein was divided in three portions: N terminus (Nt, amino acids 1–120), RNA-binding domain (RBD, amino acids 121–203), and C terminus (Ct, amino acids 204–270). Directed yeast two-hybrid analysis with eIF3h revealed that this subunit specifically binds the RBD of hSLBP (Fig. 5A). In contrast, Paip1 was found to interact with the C-terminal region of hSLBP (Fig. 5A). The interaction between the RBD of hSLBP and eIF3h was confirmed in GST-pulldown assays, using 35S-methionine-labeled hSLBP domains and GST-eIF3h. Figure 5B shows that all domains containing the RBD were enriched in pulldown assays with GST-eIF3h, whereas the N-terminal or C-terminal domain alone showed no enrichment, mirroring the results of the yeast two-hybrid analysis. Thus the interaction of eIF3 and Paip1 with SLBP does not correlate with regions of SLBP previously ascribed to stimulate translation in Xenopus.

The N terminus of xSLBP1 is required to activate translation

A sequence of 10 residues in the N-terminal domain of xSLBP1 (residues 70–79) was described as necessary to activate translation of reporter RNAs in vitro and in Xenopus stage VI oocytes (Sanchez and Marzluff 2002), although a requirement for the C terminus of hSLBP in yeast has also been suggested (Ling et al. 2002). The finding that interactions with neither eIF3 nor Paip1 apparently explain the function of the N-terminal domain led us to re-examine the regions required for translation. Since increased activity of SLBP was observed in mature oocytes compared to stage VI, the ability of different domains to stimulate translation was examined in mature oocytes, where histone mRNAs are normally translated. The tethered function assay was utilized, as it allows separation of the role of protein domains in translation from their RNA-binding activity. The Xenopus SLBP1 protein was divided into the three main domains, Nt, RBD, and Ct, and MS2 fusions were constructed (Fig. 6A). When analyzed in mature oocytes, MS2-NtRBD maintained an activity similar to full-length xSLBP1, while RBD-Ct was unable to appreciably stimulate translation of the luciferase reporter (Fig. 6B). A further analysis of Nt and RBD revealed that full translational activity was retained by Nt, while RBD showed no activity. These data are in agreement with data reported previously in stage VI oocytes (Sanchez and Marzluff 2002). To further investigate whether the N-terminal region identified by Marzluff and colleagues also represents the only active region in mature oocytes, a construct was created taking advantage of a natural splice isoform of SLBP, which is present in human and mouse (Modrek et al. 2001; A. Schaller, D. Schümerli, and B. Müller, unpubl. observation). This splice form deletes exon 3, which contains the 10 amino acid activation domain, while maintaining the open reading frame. An MS2-xSLBP1 fusion with an exon 3 deletion, encompassing amino acids 57–92 (Fig. 6A), was constructed and tested in the tethered function assay. As shown in Figure
6B, this construct was unable to stimulate translation of the luciferase reporter. This supports the idea that exon 3 in the N terminus is required for translation stimulation by xSLBP1 and confirms that interactions with eIF3 and Paip1 are not sufficient for translational activity in either mature or immature oocytes. Furthermore, as deletion of exon 3 does not interfere with the binding to histone mRNA (data not shown), it is possible that this SLBP form may act as an inhibitor of histone gene expression.

**xSLBP1 stimulates an early step in translation initiation**

The above results do not completely exclude a role for Paip1 and eIF3 in SLBP-mediated translation; however, they reveal that different factor(s) that interact with the N-terminal domain must have a more dominant function. Our results with the CrPV IRES implicate an important role of an initiation factor in this process. To determine the step in translation initiation at which SLBP acts and to gain insights into which initiation factors are involved, we performed tethered function assays in stage VI oocytes expressing MS2-xSLBP1 with luciferase reporters containing viral IRESs that show different factor requirements (Ostareck et al. 2001). The experiments were also performed in mature oocytes and equivalent results were obtained (data not shown). Initially, we analyzed the classical swine fever virus (CSFV) IRES, whose activation does not require eIF4E, eIF4G, eIF4A, eIF4B, eIF1, and eIF1A (Pestova et al. 1998). We found that MS2-xSLBP1 was unable to stimulate translation directed by this IRES (Fig. 7A), suggesting that one or more of these factors are required and that 40S recruitment or scanning is promoted by SLBP. To further delineate the requirements for SLBP-mediated stimulation, two additional reporter mRNAs were tested, which contained either the poliovirus (PV) IRES or a nonfunctional ApppG (ApG) cap. The analysis of PV IRES showed that xSLBP1-mediated activation of this reporter was completely abrogated (Fig. 7B). Since this IRES utilizes all the canonical initiation factors except eIF4E (Belsham and Jackson 2000), this implies that xSLBP1 affects 40S joining through eIF4E. This is consistent with a marked reduction in the level of stimulation of ApG-capped reporter mRNA by xSLBP1 (data not shown). However, we were unable to detect a direct interaction between SLBP and eIF4E in the yeast two-hybrid approach, despite these proteins being expressed and active in the experimental system (Fig. 7C).

**DISCUSSION**

Replication-dependent histone mRNAs differ from other metazoan mRNAs in that they do not end in a poly(A) tail but in a conserved stem–loop structure. This structure binds the protein SLBP that stimulates translation of histone mRNAs (Ling et al. 2002; Sanchez and Marzluff 2002). An attractive hypothesis is that SLBP could be the functional homolog of PABP, directing circularization of histone mRNAs through the interaction with factors at the 5’ end. This idea is supported by the genetic requirement of eIF4G and eIF3 for its activity in yeast (Ling et al. 2002). In this article we have shown that SLBP targets translation initiation and investigated the physical interaction of SLBP with translation initiation factors. We found that it interacts with eIF3 and with the eIF4G-homolog Paip1. However, interactions with neither Paip1 nor eIF3 seem to underlie the effects of SLBP in translation. Importantly, translation regulation by xSLBP1 appears to target the initial cap-binding step, which is critical for recruitment of the small ribosomal subunit.

**Interaction of SLBP with eIF3 and Paip1**

Our investigation of the interaction between SLBP and human eIF3 extends previous observations (Ling et al.
We show that this interaction is direct and identify the subunit of eIF3 involved as subunit h (previously called p40 in human) (Fig. 3). This subunit is not part of the core eIF3 complex conserved in yeast, suggesting that it may have a regulatory function (Hershey and Merrick 2000). It is tempting to speculate that one of its possible roles is in the regulation of specific mRNAs. However, our mapping of the region of interaction between eIF3h and hSLBP shows that it binds to the RBD (Fig. 5), a domain that is not sufficient for translation activation (Fig. 6; Ling et al. 2002). Paip1 is not conserved in yeast and shares considerable homology with the C-terminal two thirds of eIF4G. Given the hypothesis of SLBP being a functional homolog of PABP, an interaction with Paip1 appears interesting, as this protein has been suggested to play a role in poly(A)-mediated translation and mRNA stability by contributing to the circularization of mRNA (Craig et al. 1998). The SLBP Paip1-binding domain is in the C-terminal region (Fig. 5), which had been suggested to contribute to the translational activity of human SLBP (Ling et al. 2002). However, this domain cannot stimulate translation in Xenopus oocytes (Fig. 6; Sanchez and Marzluff 2002).

Previous work had suggested a genetic requirement for eIF4G and shown eIF4G to be present in complexes with hSLBP (Ling et al. 2002). However, we could not detect a direct interaction between eIF4GI and hSLBP or xSLBP1. Although a negative result in the yeast two-hybrid system cannot formally rule out a direct interaction with eIF4GI, it is noteworthy that both SLBP and eIF4GI fusion proteins used in this analysis were capable of mediating protein–protein interactions with other factors (Fig. 4). A second eIF4G, eIF4GII, has been described (Gradi et al. 1998) and we cannot exclude an interaction with this protein. However, the functional homology between eIF4GI and eIF4GII and the failure of SLBP to stimulate a PV IRES makes this unlikely. Conversely, a direct interaction with Paip1 was detected by yeast two-hybrid and confirmed in whole-cell extracts (Fig. 4). Paip1 is not conserved in yeast and shares considerable homology with the C-terminal two thirds of eIF4G. Given the hypothesis of SLBP being a functional homolog of PABP, an interaction with Paip1 appears interesting, as this protein has been suggested to play a role in poly(A)-mediated translation and mRNA stability by contributing to the circularization of mRNA (Craig et al. 1998). The SLBP Paip1-binding domain is in the C-terminal region (Fig. 5), which had been suggested to contribute to the translational activity of human SLBP (Ling et al. 2002). However, this domain cannot stimulate translation in Xenopus oocytes (Fig. 6; Sanchez and Marzluff 2002).
Characterization of SLBP activity during oogenesis

Previous analysis in yeast had indicated that both N- and C-terminal sequences contributed to the translational activity of hSLBP (Ling et al. 2002), whereas analysis in stage VI oocytes suggested that sequences in the N terminus were sufficient (Sanchez and Marzluff 2002). In our analysis, the use of the tethered function assay allowed the dissection of the domain functions, separating those required for RNA binding from those required for translational activation per se. We were therefore able to examine the role of each domain singularly.

Histone mRNAs are normally stored inactive in the late stages of oogenesis and their translation is activated at meiotic maturation (Woodland 1980). Interestingly, when the activity of full-length SLBP in stage VI and mature oocytes was compared, a significant increase in SLBP activity was found (Fig. 1). Although overall translation rate rises following oocyte maturation (Richter et al. 1982), the tethered function assay and relative controls ensure that the effects we observe are specific for SLBP. Xenopus oocytes express a second SLBP protein, xSLBP2. During oogenesis xSLBP2 is the main protein bound to histone mRNAs in the cytoplasm and it maintains them in a repressed state (Wang et al. 1999; Sanchez and Marzluff 2002). At maturation, xSLBP2 is degraded, xSLBP1 is released from the nucleus, and it substitutes xSLBP2 on histone mRNAs, activating their translation (Wang et al. 1999; Sanchez and Marzluff 2002). Our results suggest that in addition to the presence or localization of a specific SLBP protein, translation of histone mRNAs may be regulated also by an increased activity of xSLBP1. Since this increase cannot be due to changes in RNA binding of SLBP, it may be explained by modification of the translational activity of the protein or of its partner(s) or by de novo expression of a new partner at maturation. Our analysis of xSLBP1 domains in mature oocytes (Fig. 6), combined with that of Marzluff and colleagues in stage VI oocytes (Sanchez and Marzluff 2002), indicates that the N-terminal domain mediates translation by xSLBP1 in both stages. This suggests that the same translation factor(s) are likely to be utilized in both developmental time points and that a variation of their expression levels or activity may occur. Meiotic maturation involves the activation of various signal transduction pathways that activate kinases (Schmitt and Nehruda 2002). Phosphorylation of SLBP has been described during the cell cycle, where it targets the protein for degradation in mammalian cells (Zheng et al. 2003) and for nuclear relocation in Drosophila embryos (Lanzotti et al. 2004). Mouse SLBP appears to be phosphorylated during oocyte maturation (Allard et al. 2002) and xSLBP1 can be phosphorylated in Xenopus egg extracts by addition of cyclinB/cdc2, of which it is a substrate in vitro (Müller et al. 2000). This modification does not appear to alter binding to the stem–loop or RNA processing but it is currently unknown whether it can alter its translational activity. The small mobility shift of both MS2-hSLBP and MS2-xSLBP1 following progesterone treatment indicates that the MS2 fusion proteins retain the ability to be phosphorylated (Fig. 1D). This raises the possibility that the increase in their translational activity may be due to this modification. Additionally, it is interesting to note that phosphorylation of translation factors, including eIF4E, has been described during oocyte maturation, and phosphorylation of eIF4E is associated with an increase in its activity (Morley and Pain 1995). It is therefore reasonable to imagine that modification of eIF4E and/or xSLBP1 during oocyte maturation contributes to the increase in histone mRNA translation.

A model for SLBP-mediated stimulation

SLBP has been suggested to be a molecular mimic of PABP (Ling et al. 2002; Sanchez and Marzluff 2002). Cytoplasmic polyadenylation during oocyte maturation is thought to enhance translation by providing an extended scaffold for the recruitment of additional molecules of PABP, thus increasing end-to-end complex formation. As a consequence, regulators that activate translation through PABP and whose target mRNAs are thought to contain multiple binding sites are responsive to the number of MS2 sites in tethered function assays (B. Collier, B. Gorgoni, C. Loveridge, H. Cooke, and N.K. Gray, in prep.). In contrast, stimulation by hSLBP and xSLBP1 is not enhanced by the presence of multiple MS2 binding sites, as a reporter mRNA containing only one MS2 binding site was not stimulated less efficiently than a reporter with three MS2 sites (data not shown). Consistent with this observation, PABP and SLBP appear to stimulate translation by different mechanisms.

While we show that SLBP can interact with eIF3 and Paip1, these interactions are not sufficient to stimulate translation and may even play no role. First, the tethering of deletion constructs containing the interaction domains (RBD, Δexon 3, RBD-Ct) fails to stimulate translation (Fig. 6). We cannot formally exclude defects in structural folding of these deletion mutants, although the mimic of the natural isoform missing exon 3 is likely to be correctly folded. Additionally, SLBP fails to stimulate translation of IRESs that utilize eIF3 but do not utilize eIF4E, specifically PV and CSFV IRESs (Fig. 7; Pestova et al. 1998; Belsham and Jackson 2000). Nevertheless, these results do not rule out a contribution of eIF3, for instance by stabilizing interactions formed between SLBP and other factors at the 5′ end (see below and Fig. 8). Likewise, Paip1 functions by interacting with eIF4A (Craig et al. 1998), which is required for PV IRES translation (Pause et al. 1994), suggesting that it does not play a predominant role in SLBP-mediated translation. Moreover, unlike eIF3, the role of Paip1 in translation is less clear and recent results have suggested an important function of this protein in mediating mRNA
stability (Grosset et al. 2000). Thus, Paip1 might play a role in stabilizing histone mRNAs.

Analyses of IRES-containing reporters suggest that SLBP targets an early stage in the translation initiation pathway (Figs. 2, 7). SLBP was not able to stimulate translation through any of the IRESs tested, including PV, indicating that it utilizes factors involved in cap-dependent rather than cap-independent pathways. The finding that translation driven by an ApG cap is reduced compared to mG-capped messages is consistent with this idea (data not shown). These pathways vary mainly in the way the small ribosomal subunit is recruited; thus SLBP influences the initial cap-binding step that facilitates the binding of the small ribosomal subunit.

We propose that SLBP stimulates translation through eIF4E. SLBP however does not appear to contact eIF4E directly (Fig. 7C). We therefore favor a model in which a protein factor interacts simultaneously with both SLBP and eIF4E linking the two ends of the mRNA (Fig. 8). Several lines of evidence suggest that this factor is unlikely to be eIF4G, in contrast to PABP-mediated translation, first, we were unable to detect a direct interaction between SLBP and eIF4E (Fig. 4A). Second, PV IRES translation is dependent on the presence of eIF4G (Belshaw and Jackson 2000; Svitkin et al. 2001) but SLBP is unable to stimulate PV IRES-mediated translation, indicating that this factor does not play a predominant role. This is in contrast to PABP1, which is known to function through eIF4E and can stimulate translation through the PV IRES (N.K. Gray, unpubl. results), supporting the idea that neither eIF4G I nor II is involved in SLBP activity. Although Paip1 is a homolog of eIF4G, it does not interact with eIF4E (Craig et al. 1998) and cannot therefore be the factor bridging SLBP and eIF4E. These indications lead us to conclude that the functional interaction between SLBP and eIF4E in translation initiation is mediated by a yet unidentified protein factor.

Several proteins that interact with eIF4E have been described including eIF4G, 4E-BPs, and mRNA-specific regulators such as maskin and Cup (von der Haar et al. 2004). These proteins share a common 4E-binding motif and bind to the same region of eIF4E. One possibility is that the proposed factor contains this motif, although this may preclude interactions with eIF4G that are important in recruiting the small ribosomal subunit via eIF3. However, SLBP can bind directly to eIF3 and Paip1, and these factors or the novel factor may allow small ribosomal subunit recruitment in the absence of eIF4G. Alternatively, the proposed factor may interact with a different region of eIF4E, allowing its normal interaction with eIF4G, and the SLBP-eIF3 interaction may serve to stabilize complexes formed at the 5′ end, as depicted in Figure 8. The identification of this factor is a priority of future investigations, enabling a more complete understanding of the mechanism by which SLBP stimulates translation.

MATERIALS AND METHODS

Plasmids

MS2-fusion proteins

pMS2-U1A (Gray et al. 2000) and pMSPN (Wilkie et al. 2005) have been previously described. For production of MS2-SLBP fusion proteins, the Xenopus SLBP1 open reading frame was amplified by PCR with primers upstream of initiation and downstream of termination codon: 5′-GAAACCTCAAGCGAGGCTGACAA-3′ and 5′-CTCAGCTGTCTGTAAGGCAAG-3′. After insertion into pGEM-T easy, the xSLBP1 fragment was released using NheI and XhoI and inserted into pMSPN. The hSLBP open reading frame was inserted into a modified version of pMS2, obtained by replacing the XbaI-NcoI fragment with TCTAGAAATTTTGGTTAACTT and CTCGAGCTTCTGGTAAAGGACTGTGC. After insertion into pMS2-U1A (Gray et al. 2000) and pMSPN (Wilkie et al. 2005) Plasmids

MATERIALS AND METHODS

Plasmids

MS2-fusion proteins

pMS2-U1A (Gray et al. 2000) and pMSPN (Wilkie et al. 2005) have been previously described. For production of MS2-SLBP fusion proteins, the Xenopus SLBP1 open reading frame was amplified by PCR with primers upstream of initiation and downstream of termination codon: 5′-GAAACCTCAAGCGAGGCTGACAA-3′ and 5′-CTCAGCTGTCTGTAAGGCAAG-3′. After insertion into pGEM-T easy, the xSLBP1 fragment was released using NheI and XhoI and inserted into pMSPN. The hSLBP open reading frame was inserted into a modified version of pMS2, obtained by replacing the XbaI-NcoI fragment with TCTAGAAATTTTGGTTAACTT and CTCGAGCTTCTGGTAAAGGACTGTGC. After insertion into pMS2-U1A (Gray et al. 2000) and pMSPN (Wilkie et al. 2005) Plasmids

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IRES) (Bergamini et al. 2000) and pCSFV-CAT (classical swine fever virus IRES) (Ostareck et al. 2001) were a gift from Dr. Matthias Hentze (EMBL, Heidelberg), and pEJ4 (cricket paralysis virus IRES-luciferase) was a gift from Drs. Eric Jan and Peter Sarnow (Stanford University). To generate IRES-luciferase-MS2 reporter constructs, the PV IRES was amplified from pPV. IRES-luc with oligonucleotide primers ATCATAAGGTGAGCAGAAAAA GCTGGGATACCCGGG and TTCCTGGGATCGGAAATCTGAGC and the PCR product was digested with HindIII and Sphl and ligated into pLG-MS2 cut HindIII and Sphl. The CSFV-IRES was amplified from pCSFV-CAT with CAGTCAGTTGATCACTGAGAAGGATGTGATTTGCAAGA and TAGTTGTTGTATTCTTAAGAGCCTGGGCC. The PCR product was digested with BclI and BamHI and ligated into the PV IRES reporter that does not contain MS2-binding sites and acts as a control for variations in injection efficiency or in translational activity between oocytes. Oocytes were incubated overnight before collection. For maturation experiments, after the second microinjection stage VI oocytes were treated overnight with 10 µg/mL progesterone (Sigma) and maturation was scored by the appearance of a white spot on the animal pole. Luciferase activity was normalized for β-galactosidase activity and values obtained with the different SLBP fusions were divided by values of MS2-U1A, CrPV-luciferase-MS2 or CrPV-luciferase-MS2 reporter constructs, the PV IRES was amplified from pPV. IRES-luciferase-MS2 reporter mRNAs were co-injected with a polyadenylated β-galactosidase reporter that does not contain MS2-binding sites and acts as a control for variations in injection efficiency or in translational activity between oocytes. Oocytes were incubated overnight before collection. For maturation experiments, after the second microinjection stage VI oocytes were treated overnight with 10 µg/mL progesterone (Sigma) and maturation was scored by the appearance of a white spot on the animal pole. Luciferase activity was normalized for β-galactosidase activity and values obtained with the different SLBP fusions were divided by values of MS2-U1A, thus obtaining the fold of translational activation. Error bars on graphs represent standard error in all cases.

**Antibodies**

Polyclonal anti-SLBP antibodies have been previously described (Zhao et al. 2004). Polyclonal anti-MS2 antibody was a gift from Professor Peter Stockley (University of Leeds). Mouse monoclonal anti-(His)_6 antibody was from Promega. Anti-rabbit and anti-mouse IgGs coupled to horseradish peroxidase were from Sigma and Amersham Biosciences.

**Immunoprecipitation**

*Xenopus* oocytes were incubated overnight with 50 µCi/mL of 35S-methionine (ICN) in the absence or presence of 10 µg/mL progesterone. Oocytes were lysed in IP lysis buffer (10µL/oocyte; 150 mM NaCl, 50 mM Tris–HCl at pH 8, 1% NP40, protease inhibitors). Extracts were cleared by centrifugation and 20 µL of lysate were added to 200 µL of lysis buffer and incubated for 1 h at 4°C with an anti-MS2 antibody (1:100). Thirty microliters of Protein-G sepharose beads (Amersham Pharmacia Biotech) were added to the lysate and mixed for 1 h at 4°C. Beads were washed three times with IP lysis buffer and bound material eluted in 20 µL of SDS gel loading dye prior to SDS-PAGE analysis.

**Tethered function assays**

Tethered function assays were performed as described (Gray et al. 2000). Briefly, in vitro transcribed mG-Capped RNAs encoding MS2-fusion proteins were micro-injected into *Xenopus* stage VI oocytes. After 6 h incubation, the mG-Capped luciferase-MS2 or luciferase-ΔMS2, or the ApG-Capped luciferase-MS2, PV-luciferase-MS2, CSFV-luciferase-MS2 or CrPV-luciferase-MS2 reporter mRNAs were co-injected with a polyadenylated β-galactosidase reporter that does not contain MS2-binding sites and acts as a control for variations in injection efficiency or in translational activity between oocytes. Oocytes were incubated overnight before collection. For maturation experiments, after the second microinjection stage VI oocytes were treated overnight with 10 µg/mL progesterone (Sigma) and maturation was scored by the appearance of a white spot on the animal pole. Luciferase activity was normalized for β-galactosidase activity and values obtained with the different SLBP fusions were divided by values of MS2-U1A, thus obtaining the fold of translational activation. Error bars on graphs represent standard error in all cases.
SDS-PAGE and Western blotting

Samples were separated by 8% (for MS2-fusion proteins) or 10% SDS-PAGE. Proteins were detected either by staining with Coomassie brilliant blue or by chemiluminescence (Amersham Pharmacia Biotech) after electro-transfer to Hybond-P membrane (Amersham Pharmacia Biotech) and probing, with anti-hSLBP (1/5000) or anti-His (1/1000). Horseradish peroxidase-conjugated anti-rabbit and anti-mouse IgGs were used as secondary antibodies (1/5000). 35S-methionine-labeled proteins were detected by fluorography using 2'-5'-diphenyloxazol.

Yeast two-hybrid analysis

Yeast two-hybrid analyses were performed with strain MaV99 (Vidal et al. 1996) and L40ura+ as described (Zhang et al. 1999). Transformed yeast cells were diluted and plated on media lacking leucine, tryptophan, and histidine and supplemented with 10 or 25 mM 3-AT.

Production of recombinant SLBP proteins

The production and purification of M(H)6-LEA-tagged recombinant hSLBP using Ni-NTA resin (Qiagen) was described earlier (Michel et al. 2000). For the expression of His-tagged xSLBP1 the cDNA was amplified using CAGGGCTCGAGGTCATGTC and TAAAGGACTCGAGTACTAACC, and the amplification product was cleaved with XhoI and inserted into pFASTBAc modified to express CTCGGAGTTAACTAACG, and the amplification product was amplified using CAGGGCTCGAGGTCATGTC and TAAAGGACTCGAGTACTAACC. The production and purification of M(H)6-LEA tagged recombinant hSLBP or xSLBP1, 300 μL of 0.4–0.6 at 37°C yeast strains, respectively. J. Cell Sci. 25 mM 3-AT.

GST-pulldown assays

BL21 pGEX-elF3h were grown to an OD600 of 0.4–0.6 at 37°C and then expression was induced with 0.1 mM IPTG for 90 min. Two milliliters bacteria were harvested by centrifugation and stored at −80°C. Cell pellets were resuspended in buffer A (PBS with 1 mM phenyl methyl sulfonyl fluoride, 0.5 mM dithiothreitol, protease inhibitor cocktail [Roche]) and cells were lysed by sonication at 4°C and supplemented with 0.5% Triton X-100 (v/v). The insoluble protein was enriched by 10 min centrifugation at 10,000g at 4°C. Protein was resuspended in 300 μL 8 M urea/PBS and the urea concentration was then reduced stepwise by addition of 1/4 volumes of buffer A at room temperature until it was below 2.5 M. This was then added to glutathione sepharose beads. BL21 pGEXHMK-PAIP1 was grown and induced as described except that induction with 0.2 mM IPTG was for 3 h. GST was expressed in BL21 pGEX-4T-1 as described. Cells were lysed and soluble proteins separated from debris by centrifugation as above and proteins from 2-ML aliquots were used in pulldown assays. GST or GST-fusion proteins were mixed with 100 μL of 50% (v/v) glutathione 4B sepharose beads (Amersham Biosciences) in PBS for 1 h at room temperature. The beads were washed three times with 300 μL buffer A and then mixed with 300 μL buffer A containing either 1 μg recombinant hSLBP or xSLBP1, 300 μg HEK293 extract, or 30–40 μL 35S protein premixed with 300 μg BL21 lysate for 30 min at 4°C. Reactions were incubated for 1 h at room temperature. Subsequently the beads were washed three times with buffer A and resuspended in 25 μL SDS-PAGE loading buffer.

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