2002

One-step affinity purification of the yeast ribosome and its associated proteins and mRNAs

Toshifumi Inada

Eric Winstall

Salvador Zipagun Tarun Jr.

John R. Yates III

Dave Schieltz

See next page for additional authors

Recommended Citation

Inada T., Winstall E., Tarun Jr. S.Z., Yates III J.R., Schieltz D., Sachs A.B. (2002) One-step affinity purification of the yeast ribosome and its associated proteins and mRNAs. RNA 8: 948-958. doi: 10.1017/S1355838202026018

RNA (2002), *8*:948–958. Cambridge University Press. Printed in the USA.

DOI: 10.1017.S1355838202026018

METHOD

One-step affinity purification of the yeast ribosome and its associated proteins and mRNAs

TOSHIFUMI INADA,[1,3] ERIC WINSTALL,[1,4] SALVADOR Z. TARUN, JR.,[1] JOHN R. YATES, III,[2] DAVE SCHIELTZ,[2] and ALAN B. SACHS[1]

[1]Department of Molecular and Cell Biology, University of California at Berkeley, Berkeley, California 94720, USA
[2]Department of Cell Biology SR11, The Scripps Research Institute, La Jolla, California 92037, USA

ABSTRACT

We describe a one-step affinity method for purifying ribosomes from the budding yeast *Saccharomyces cerevisiae*. Extracts from yeast strains expressing only C-terminally tagged Rpl25 protein or overexpressing this protein in the presence of endogenous Rpl25p were used as the starting materials. The purification was specific for tagged 60S subunits, and resulted in the copurification of 80S subunits and polysomes, as well as ribosome-associated proteins and mRNAs. Two of these associated proteins, Mpt4p and Asc1p, were nearly stoichiometrically bound to the ribosome. In addition, the degree of mRNA association with the purified ribosomes was found to reflect the mRNA's translational status within the cell. The one-step purification of ribosome and its associated components from a crude extract should provide an important tool for future structural and biochemical studies of the ribosome, as well as for expression profiling of translated mRNAs.

Keywords: 60S subunit; FLAG tag; polysome; ribosome-associated protein; Rpl25p; translation

INTRODUCTION

Composed of at least 80 proteins, four ribosomal RNAs (rRNA), messenger RNA (mRNA), and transfer RNA (tRNA), the eucaryotic ribosome and polysome particles are among the most complicated ribonucleoprotein (RNP) complexes. The composition of the eucaryotic 80S ribosome has been analyzed in many studies (reviewed in Warner, 1982; Woolford & Warner, 1991). Most of these have relied on conventional density gradient centrifugation for ribosome purification, followed by one- or two-dimensional gel electrophoresis and sequence analysis of the individual polypeptides (Lee, 1990). These analyses have defined a core set of ribosomal proteins. However, an extensive proteomic and genomic analysis of ribosome-associated factors has been delayed due to the lack of a fast, reliable, and efficient purification method. An example of such an approach using epitope tagging and immuno-affinity purification to study ribosome biogenesis in *Saccharomyces cerevisiae* has recently been reported (Bassler et al., 2001; Harnpicharnchai et al., 2001).

Immuno-affinity purification of DNA- and RNA-binding proteins, coupled with the use of DNA microarrays, has also been shown to be valuable for genome-wide identification of associated nucleic acid components (Ren et al., 2000; Tenenbaum et al., 2000). For instance, immuno-affinity purification of FMRP, an RNA-binding protein mutated in individuals with Fragile X Syndrome, allowed for the identification of mRNAs enriched in the FMRP-mRNP complex. This complex was found to be associated with about 4% of the mRNAs expressed in the mouse brain, many of which encode proteins involved in synaptic or developmental neurobiology (Brown et al., 2001; Darnell et al., 2001).

Translational control is now recognized as a major mechanism regulating gene expression (Sonenberg et al., 2000). Therefore, to gain a global understanding of how translational control contributes to cellular phenotypes, it has become important to determine both the overall amount and the translation status of each mRNA within a cell. To achieve this goal, high-throughput approaches have recently been developed (Carter et al., 2000; Pradet-Balade et al., 2001). DNA microarrays can accurately quantify the amount of mRNA in a prep-

Reprint requests to: Alan B. Sachs, Department of Molecular and Cell Biology, University of California at Berkeley, Berkeley, California 94720, USA; e-mail: asachs@uclink4.berkeley.edu.
[3]Present address: Division of Biological Science, Graduate School of Science, Nagoya University, Chikusa, Nagoya 464-8602, Japan.
[4]Present address: Centre Protéomique de l'est du Québec, Centre de recherche du CHUL, Université Laval, Québec, G1V 4G2, Canada.

aration. The translational status of an mRNA can be determined by methods that rely on the sedimentation rate difference between heavily translated (many ribosomes bound) and poorly translated (few to no ribosomes bound) mRNAs in a sucrose gradient. Although highly informative (Johannes et al., 1999; Zong et al., 1999; Kuhn et al., 2001), this type of analysis requires a large amount of starting biological material, and thus cannot be routinely performed on large numbers of small samples or on samples of limited quantity.

We have created an *S. cerevisiae* strain expressing a FlagHis_6 epitope (FH)-tagged version of the ribosomal protein Rpl25p, and developed a method using extracts from this strain that can purify ribosome-associated proteins and mRNAs with high throughput and small sample requirements. A more detailed analysis of these associated components revealed the presence of abundant proteins bound to the ribosome in a salt-labile manner. In addition, the amount of mRNA associated with the purified ribosomes was found to reflect its translational status within the cell.

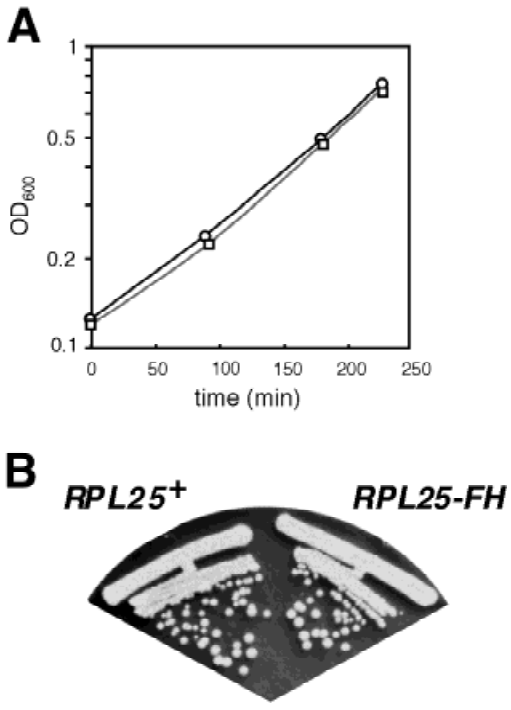

FIGURE 1. Growth characteristics of strains CB012 and YIT613. **A:** Growth curves for yeast strains CB012 (*RPL25*$^+$; circle) and YIT613 (*RPL25-FH*; square) in liquid YPD medium at 30 °C. **B:** Growth of yeast strains CB012 and YIT613 on solid YPD medium. The plate was incubated at 30 °C for 3 days.

RESULTS

Affinity purification of the yeast ribosome

The gene encoding Rpl25p in *S. cerevisiae* was modified to encode a protein tagged at its C-terminus with an FH epitope. We selected *RPL25* for several reasons. First, because a Rpl25p-GFP fusion could partially complement a *rpl25*::*HIS3* mutation (Hurt et al., 1999), it was anticipated that the small FH tag would not seriously affect Rpl25p activity. This proved to be correct, as a yeast strain harboring only *RPL25-FH* was viable (see Materials and Methods for strain construction details). Second, we chose *RPL25* because it is essential in *S. cerevisiae*, and therefore the activity of a modified *RPL25-FH* gene could be easily estimated by its ability to support growth of a strain lacking wild-type *RPL25*. As shown in Figure 1, the growth rate of the *RPL25-FH* recombinant strain YIT613 was equivalent to that of the parental strain, indicating the tag did not seriously compromise Rpl25p function. The last reason Rpl25p was selected as a target for epitope tagging was that its procaryotic homolog, Rpl23p, is located on the surface of the large ribosomal subunit (Ban et al., 2000). Therefore, it seemed likely that the epitope tag would be accessible to affinity-capture reagents.

To test this last hypothesis, crude extracts from YIT613 cells (see Table 1 for strain details) were incubated with an anti-Flag antibody affinity resin. After extensive washing, bound proteins were eluted with high concentrations of the Flag peptide. By a variety of criteria, the single-step affinity method yielded highly purified ribosomes. First, a subset of the polypeptides found in the affinity-purified ribosomes (Fig. 2A, lanes 2, 3) were similar in mass to those observed in 80S ribosome purified by a multistep conventional centrifugation method (Fig. 2A, lane 5). A significant number of proteins associated with the ribosome in the low salt IXA-100 buffer (asterisks in Fig. 2A, lane 2) were eluted from the immobilized particles with the higher ionic strength IXA-500 buffer (Fig. 2A, lane 3). This suggested that ribosome-associated proteins could also be purified by this affinity technique (see below for more detail).

A second indication that the affinity method yielded intact ribosomes was derived from an examination of the rRNA in the purified material. Both the 18S and 25S rRNAs within the purified preparation were intact, whereas little tRNA was detectable (Fig. 2B). Both the integrity of the rRNA and the near absence of tRNA suggested a significant purification of intact ribosomes had occurred.

A third indication of the success of the purification was the near absence of free 40S subunits in the eluate from the affinity resin (Fig. 3A, lower panel). This suggested a specific purification of 60S and 80S particles. In addition, polyribosomes were also present in the eluted material (Fig. 3A, lower panel). This suggested that intact mRNA would also be present in the purified material, as intact mRNA tethers the individual ribosomes in the polyribosome particle (see below).

We note that larger polyribosomes were missing from this purified material. As the unbound fraction still con-

TABLE 1. Yeast strains used in this study.[a]

Strain[b]	Genotype [plasmid] (plasmid no.)[c]	Source
CB012	MATa *ade2-1 his3-11,15 leu2-3,112 trp1-1 ura3-1 pep4Δ::HIS3 prbΔ::his3 prc1Δ::hisG*	Sachs strain collection
YAV129	*trp1 leu2 ura3 his4 lys2 cup1:: LEU2PGKMFA2 rex1::TRP1 rex2::LYS2 rex3::HIS4 rex4::NEO*	van Hoof et al. (2000)
YIT613	CB012 *rpl25::LEU2* [p*RPL25-FH-URA3CEN*] (BIT700)	This study
YIT623	CB012 [p*GAL1-RPL25-FH-LEU2CEN*] (BIT751)	This study
YIT722	YIT613 [p*X3-LUC-TRP1CEN*] (BIT757)	This study
YIT723	YIT613 [p*B3-LUC-TRP1CEN*] (BIT758)	This study
YIT724	YIT613 [p*LUC-TRP1CEN*] (BIT759)	This study

[a] Strain requests should be sent to Toshi Inada (p47294a@nucc.cc.nagoya-u.ac.jp).
[b] Strain number to be used when making requests.
[c] Bacterial strain containing indicated plasmid and number to be used when making plasmid requests.

tained large polyribosomes (Fig. 3A, middle vs. lower panel), we exclude the possibility that these were lost during the procedure due to RNase activity. Instead, we hypothesize that these large polysomes have a unique feature that prevents their purification. One possibility is that their large size prevents them from entering into the matrix of the antibody-coated agarose affinity media. In support of this hypothesis, preliminary results suggest that the use of impermeable superparamagnetic uniform monodisperse polymer beads (Dynabeads, Dynal) allow for a more representative purification of the polyribosomes in the extract (E. Winstall & A.B. Sachs, unpubl. observations).

We also created a yeast strain containing *GAL1:RPL25-FH*, which expresses the tagged protein in a galactose-inducible and glucose-repressible manner. This strain allows for several additional experimental features to be added to a study design. First, it permits the high level, inducible synthesis of a tagged ribosome in a strain containing the endogenous *RPL25* by having galactose in the growth medium. This synthesis can be rapidly inhibited by the addition of glucose. One example of the utility of this inducible/repressible system is in the study of ribosomes synthesized prior to some cellular challenge, such as the addition of a nutrient or a radiolabeled compound. By repressing the synthesis of the tagged subunit by the addition of glucose to the growth medium at the time of the challenge, a stable pool of presynthesized ribosomes can be experimentally distinguished from the newly synthesized ribosomes. Alternatively, the system could allow for the study of ribosomes synthesized after a challenge by inducing the synthesis of the tagged protein with galactose at the time of the challenge.

Several simple experiments were performed to validate the utility of this inducible *RPL25-FH* strain (YIT623), whose growth rate in galactose was indistinguishable from its wild-type parent. First, the expression level of ribosomes containing Rpl25p-FH produced by the *GAL1:RPL25-FH* gene in a *RPL25*$^+$ background was examined by immunoblot analysis. The level of FH-tagged Rpl25p in YIT623 cells (*RPL25*$^+$ [p*GAL1-RPL25-FH*]) grown on galactose medium was nearly half of that in YIT613 cells (*rpl25*::*LEU2* [p*RPL25-FH*]; Fig. 4A, lanes 1, 3, 4). This indicates that high level expression could be obtained. Furthermore, the expression of *GAL1*:*RPL25-FH* was efficiently repressed in cells grown in glucose medium (Fig. 4A, lanes 1, 2). The rapid repression of *RPL25-FH* synthesis after transfer from galactose medium to glucose medium was confirmed by northern blot analysis (Fig. 4B, lanes 3, 4).

Analysis of proteins associated with the affinity-purified ribosomes

Tagged ribosomes were purified using extracts of YIT623 cells (*RPL25*$^+$ [p*GAL1-RPL25-FH*]) grown on galactose medium. Several of the ribosomal proteins and ribosome-associated proteins were identified in this mixture by tryptic digestion and mass spectrometry (Link et al., 1999). We initially focused on two proteins bound to the ribosome in near stoichiometric quantities (Fig. 2C). One of these abundant proteins was Asc1p (Fig. 2C; see Materials and Methods for protein identification). Asc1p has previously been reported to be a novel ribosomal component (Link et al., 1999). We also found Asc1p to be purified with 40S subunits using a more conventional purification (Fig. 2A,

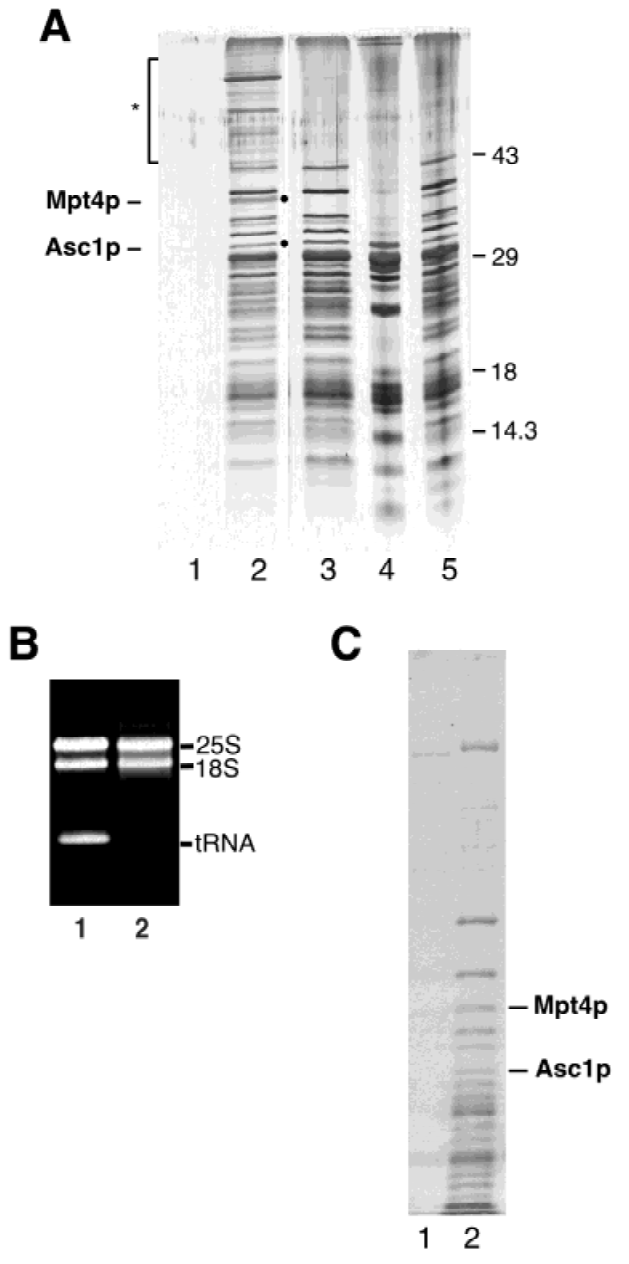

FIGURE 2. Purification of yeast ribosomes. **A:** Proteins associated with purified ribosomes. Tagged ribosomes were purified as described in Materials and Methods. Lane 1: purification from strain CB012 in IXA-100 buffer. Lane 2: purification from strain YIT613 in IXA-100 buffer. Lane 3: purification from strain YIT613 in 500 mM KCl buffer. Lane 4: purified 40S subunits. Lane 5: purified 80S ribosomes. Material shown in lanes 4 and 5 was derived from a conventional purification method (see Materials and Methods). Proteins were resolved on 12% SDS-PAGE and visualized by silver staining. Asterisks indicate high molecular weight ribosome-associated proteins within the sample shown in lane 2. **B:** RNA associated with purified ribosomes. RNA samples were prepared from YIT613 crude extracts (lane 1) or affinity-purified ribosomes (lane 2), resolved on a 1.0% agarose gel, and visualized by ethidium bromide staining. **C:** Identification of Asc1p and Mpt4p. Lane 1: purification from strain CB012 in IXA-100 buffer. Lane 2: purification from strain YIT613 in IXA-100 buffer. The positions of Asc1p and Mpt4p are indicated. Proteins were resolved on 12% SDS-PAGE and visualized by Coomassie Brilliant Blue staining.

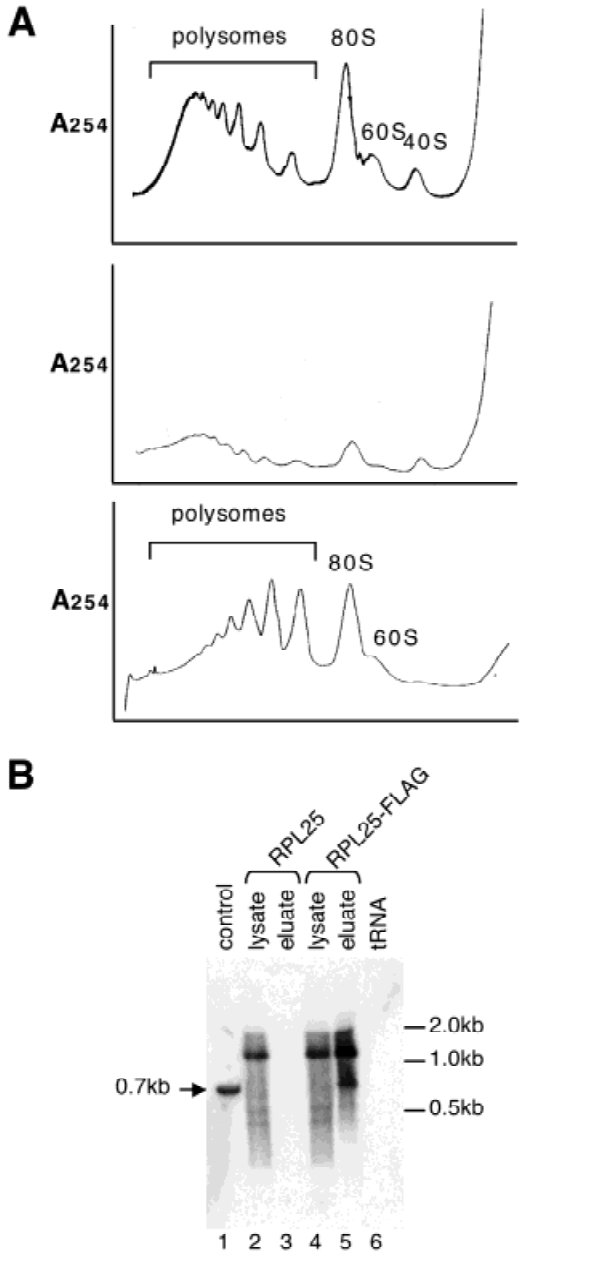

FIGURE 3. Analysis of mRNAs associated with affinity purified ribosomes. **A:** Polysome profiles of affinity-purified material. Tagged ribosomes were purified from 15 A_{260} units of YIT613 crude extract (upper panel). This and the unbound fraction (middle panel) and the elution fraction (lower panel) were resolved by velocity sedimentation on 15–50% sucrose gradients. The positions of 40S and 60S subunits, 80S subunits, and polysomes are indicated. The top of each gradient is on the right. **B:** Poly(A)$^+$ RNAs are copurified with the tagged ribosomes. Lane 1: in vitro transcribed poly(A)$^+$ control RNA. Lanes 2, 4, 5: total RNA (5 μg) isolated from the indicated sample. Lane 3: total RNA isolated from the eluate of the untagged *RPL25* strain. Lane 6: yeast tRNA (5 μg). RNA samples were hybridized to oligo-dT, and then reverse transcribed in the presence of [α^{32}P]-dCTP. Following electrophoresis of the samples along with DNA size markers on a formaldehyde-1.5% agarose gel, radioactive signals were obtained and analyzed by phosphorimaging. The arrow indicates the position of the 700-bp cDNA fragment generated by a control poly(A)$^+$ RNA. The positions of fragments of the DNA ladder within the gel are indicated to the right.

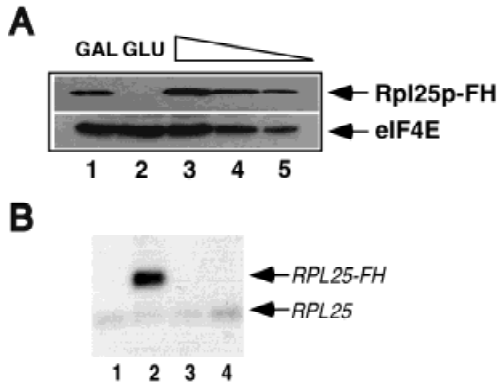

FIGURE 4. Inducible synthesis of Flag-tagged ribosomes. **A:** Expression levels of *RPL25-FH* controlled by the *GAL1* promoter. YIT623 (*RPL25*$^+$ [p*GAL1-RPL25-FH*]; lanes 1 and 2) and YIT613 (*rpl25*::*LEU2* [p*RPL25-FH*]; lanes 3–5) were grown on YM medium containing galactose (lane 1) or glucose (lanes 2–5). Proteins from cell extracts equivalent to 0.3 OD_{600} (lanes 1–3), 0.15 OD_{600} (lane 4) and 0.075 OD_{600} units (lane 5) were resolved by 12% SDS-PAGE and visualized by western analysis. **B:** Rapid repression of *RPL25* mRNA synthesis. Yeast strain YIT623 grown in SC medium containing 2% galactose was shifted to SC medium containing 2% glucose medium, and total RNA was prepared 30 min (lane 3) or 60 min (lane 4) after the medium change. Lane 1: RNA samples prepared from cells grown in glucose. Lane 2: RNA samples from cells grown in galactose. RNA samples were analyzed by northern blot analysis using a radioactive *RPL25* probe.

lanes 4, 5), and the binding of Asc1p is not salt labile (Fig. 2A, lanes 1, 2). *ASC1* has also been identified as *CPC2*, whose deletion leads to an accumulation of half-mer polyribosomes (Chantrel et al., 1998). Together with our purification data, these data suggest the involvement of Asc1p in translation or ribosome biosynthesis.

We also identified Mpt4p as a salt-labile ribosome-associated protein (Fig. 2C). Mpt4p has previously been identified in *S. cerevisiae* as a purine motif triple-helical binding protein (G4p2) that has high affinity and specificity for quadruplex nucleic acid (Frantz & Gilbert, 1995). The gene *STM1/MPT4* has also been isolated as a multicopy suppressor for temperature-sensitive mutations of *TOM1*, *HTR1*, and *POP2* (Hata et al., 1998). In addition, Ray38p, the homolog of Mpt4p in *Candida maltosa*, was recently shown to be a ribosome-associated protein (Takaku et al., 2001). Interestingly, Ray38p became phosphorylated and dissociated from the ribosome after cycloheximide treatment. The phenotype of a *ray38* null mutant indicates that the dissociation of Ray38p from ribosome facilitates the induction of cycloheximide resistance in *C. maltosa* (Takaku et al., 2001). Although all of these data suggest a distinct role for Mpt4p in nucleic acid binding and ribosome function, no clear assignment of function of Mpt4p has yet been made.

The identity of the remainder of the salt-labile, ribosome-associated proteins in these preparations is currently being examined.

Analysis of the mRNAs copurifying with the ribosome

The fact that polysomal particles were efficiently purified using the anti-FLAG affinity matrix (see Fig. 3A) strongly suggested that intact or near intact ribosome-associated mRNAs were recovered upon elution from the resin. To test this hypothesis, we performed oligo-dT-primed reverse transcription reactions on total RNA isolated from affinity purified samples. Specifically, total RNA prepared from crude extracts or the eluate obtained after FLAG affinity purification was used for reverse transcription in the presence of ^{32}P-labeled dCTP. As specificity controls, yeast tRNA or RNA isolated from a strain lacking the FLAG-tagged RPL25p were also used in this analysis. Following primer extension, equal volumes of reaction were subjected to electrophoresis in a denaturing agarose gel.

As expected, the material from the crude extract RNA preparation appeared as a smear ranging from 0.3 kb to about 2 kb in size, consistent with the average range of length of yeast mRNAs (Fig. 3B, lanes 2, 4). Discrete bands of about 1 kb most probably reflect the high abundance of specific pol II transcripts in yeast, such as *TDH2/TDH3* or the *TEF1/TEF2* genes (Velculescu et al., 1997). A similar reverse transcription profile was found for RNA prepared from the affinity purified material derived from an extract containing Rpl25p-FH tagged ribosomes (Fig. 3B, lane 5). In contrast, no signal could be detected in the eluate obtained from lysates lacking tagged ribosomes or from tRNA (Fig. 3B, lanes 3, 6). From these results, we conclude that poly(A)$^+$ mRNAs are specifically copurified with the tagged ribosomes.

We next wanted to test whether the amount of a specific mRNA copurifying with the ribosomes changed according to its translational status. To test this, we used a set of very well characterized in vivo reporter mRNAs encoding firefly luciferase (*LUC*) with or without stable stem-loop structures in their 5′ untranslated region (5′ UTR; Oliveira et al., 1993). It has been shown that a stem-loop in the 5′ UTR inhibits translation, and that the extent of inhibition depends upon the thermodynamic stability of the stem (Oliveira et al., 1993). Figure 5A illustrates the structure of the three reporter mRNAs that were tested. Plasmids expressing each of these *LUC* mRNAs were transformed into yeast strain YIT613, which expresses Rpl25p-FH protein as its sole source of Rpl25p.

To confirm the inhibitory effect of the 5′ UTR stem-loop structure on translation initiation of the reporter mRNAs, we first examined the sedimentation profile of each of the *LUC* transcripts. Extracts were sedimented on 15% to 50% sucrose gradients that were then fractionated into 12 fractions of equal volume. Polysome profiles were generated during fractionation by continuous measurement of the absorbance at 254 nm. A

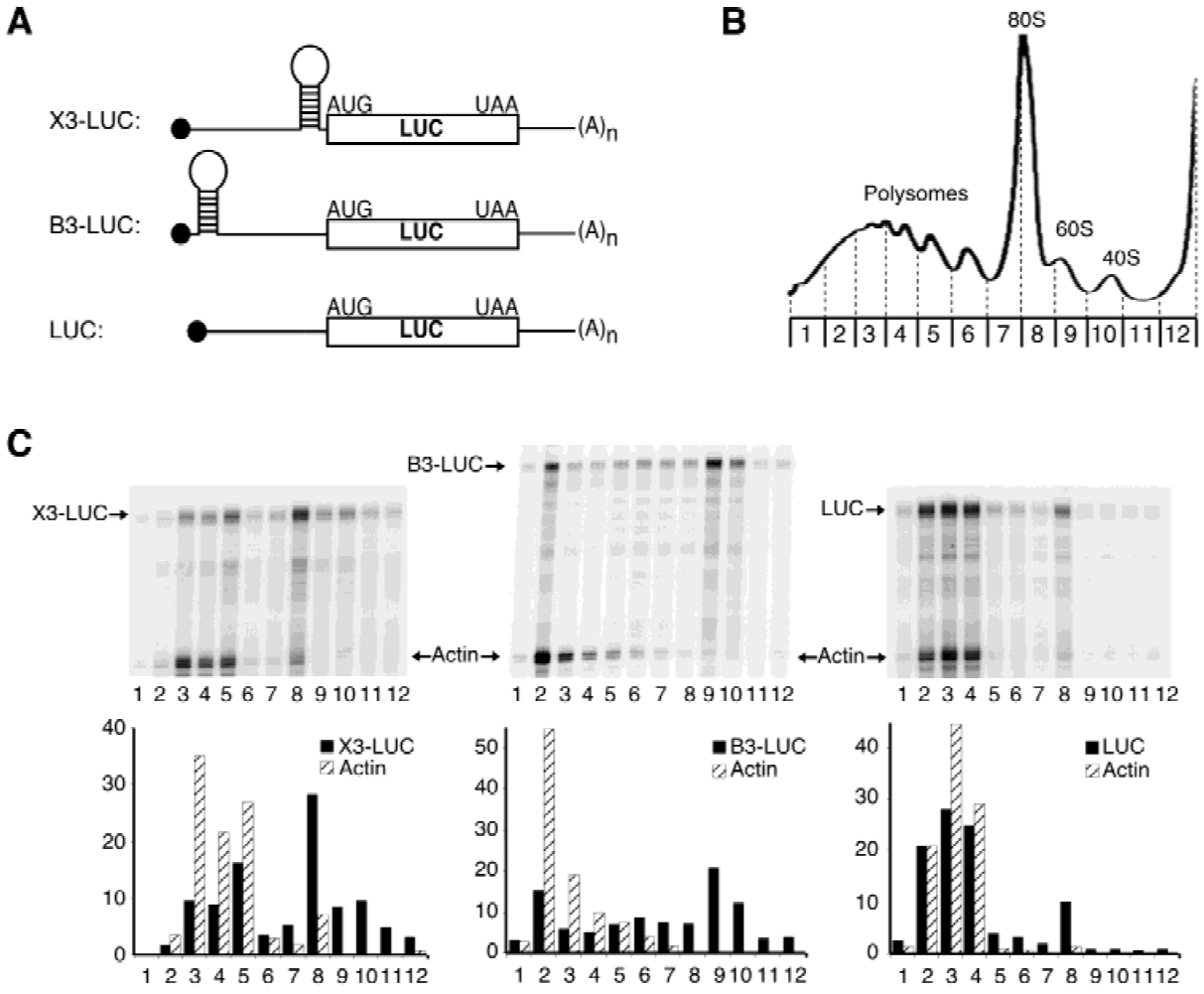

FIGURE 5. Differential ribosome association of various *LUC* mRNAs **A:** Structure of the different reporter mRNAs used in this study. Plasmids expressing these transcripts have been described in detail by Oliveira et al. (1993). Expression of each mRNA is directed by the same modular *GAL1-PGK1* promoter and is induced upon growth in medium containing galactose as the carbon source. The X3-*LUC* and B3-*LUC* mRNA contain a stable stem-loop structure (~−17 kcal/mol) near the AUG initiating codon or near the 5′ cap structure, respectively. **B:** A typical polysome profile obtained following sedimentation of yeast extracts through 15–50% sucrose gradients. Yeast strains carrying the different reporter plasmid were grown to log phase on SC glucose medium. Expression of the *LUC* reporter mRNAs was induced by transferring the cells to SC galactose medium and allowing them to grow to mid-log phase. Extracts were prepared and sedimented in the absence of cycloheximide as described in Materials and Methods. The top of the gradient is on the right. The positions of polysomes, the 80S ribosome, and the 60S and 40S ribosomal subunits are indicated. Each gradient was fractionated from the bottom into 12 fractions of equal volume. Dashed lines on the polysome profile indicate the boundaries of each fraction. **C:** Quantitation of *LUC* reporter mRNAs in each fraction. Total RNA was isolated from each fraction and analyzed by RNase protection analysis as described in Materials and Methods. The protected fragments generated by the X3-*LUC* mRNA (193 nt), the B3-*LUC* mRNA (225 nt), the *LUC* mRNA (193 nt), and the endogenous actin mRNA (118 nt) are indicated by arrows. Images were acquired and analyzed by phosphorimaging. The intensities of the *LUC*- or the *ACT1*-protected fragments in each fraction are represented on the graph as the percentage of the total signal intensity in all of the fractions.

typical polysome profile is shown in Figure 5B. Total RNA was isolated from each fraction, and hybridized simultaneously to radiolabeled RNA probes complementary to the *LUC* reporter and *ACT1* transcripts. Following digestion with RNases A and T1, the protected fragments were resolved by gel electrophoresis and detected by phosphorimaging. As shown in Figure 5C, *LUC* mRNAs without any stem-loop in their 5′ UTR (right panel) were mostly found (>70%) in fractions cosedimenting with polysomes (Fig. 5B). This sedimentation profile and the one observed for the control actin mRNA (Fig. 5C, all three panels) are expected for transcripts that are efficiently recruited to the ribosomes. In contrast, both *LUC* mRNAs with stable stem-loop structures (−17 kcal/mol) in their 5′ UTR were diffusely distributed across the gradient, with about 60% of the transcripts being present in fractions lighter than those with a single 80S ribosome.

Luciferase activity was then assayed in extracts expressing the different reporter mRNAs. As expected, *LUC* mRNAs bearing a stem-loop near the 5′ cap structure (B3-*LUC*) or close to the first AUG codon (X3-*LUC*) produced 5% to 10% of the luciferase activity detected in the extract expressing a *LUC* mRNA with an unstructured leader sequence (Fig. 6A). This decrease in *LUC* activity is thought to be mostly the result of a decrease in the efficiency of translation initiation, as the steady-state levels of each reporter transcript have been found to be highly comparable (Oliveira et al., 1993; Fig. 6B).

Given the above results, we hypothesized that following affinity purification of the tagged ribosome, the amount of *LUC* mRNAs detected in the eluate (bound fraction) should reflect the translational status of the mRNA. To test this hypothesis, extracts were incubated with the anti-FLAG affinity resin under conditions that were designed to avoid mRNA degradation (see Materials and Methods). Following the washing steps, tagged ribosomal particles were eluted using the FLAG peptide. Total RNA was purified from the eluted fractions and then quantitated. Equal amounts of total RNA isolated either from the crude extract or from the anti-FLAG resin eluate were then hybridized in solution to radiolabeled RNA probes complementary to the 5′ end of the *LUC* reporter mRNA or to the *ACT1* mRNA. The amount of probe used in the assay was in large excess over the target sequence in the RNA samples, as these assays were found to respond linearly to the amount of input RNA (data not shown).

As shown in Figure 6B, lanes 1–3, similar levels of the different *LUC* reporter mRNAs were found in the total extract, confirming that the different leader sequences do not substantially affect the steady-state level of the transcript (Oliveira et al., 1993). *LUC* mRNA can also be detected in the ribosome-associated fraction (Fig. 6B, lanes 4–6). However, the amount of *LUC* mRNA with a stem-loop in its leader region that was bound to ribosomes was at least four times less than that found for the *LUC* mRNA with an unstructured leader sequence (Fig. 6B, compare lanes 4 and 5 to lane 6). These results show that the level of *LUC* mRNA that is copurified with the tagged ribosome reflects its translational efficiency within the cell.

We note that because very large polysomes (>5 ribosomes) are not effectively purified using the affinity resin (see Fig. 3A), those mRNAs associated with more than five ribosomes (such as longer mRNAs) would be underrepresented in the ribosome-bound fraction. Consequently, the purification method reported here does not allow for the direct prediction of the translational status of an mRNA, and could significantly underestimate the translatability of mRNAs bound to large numbers of ribosomes. To overcome this limitation, the technical difficulties of purifying very large polyribosomes will have to be solved.

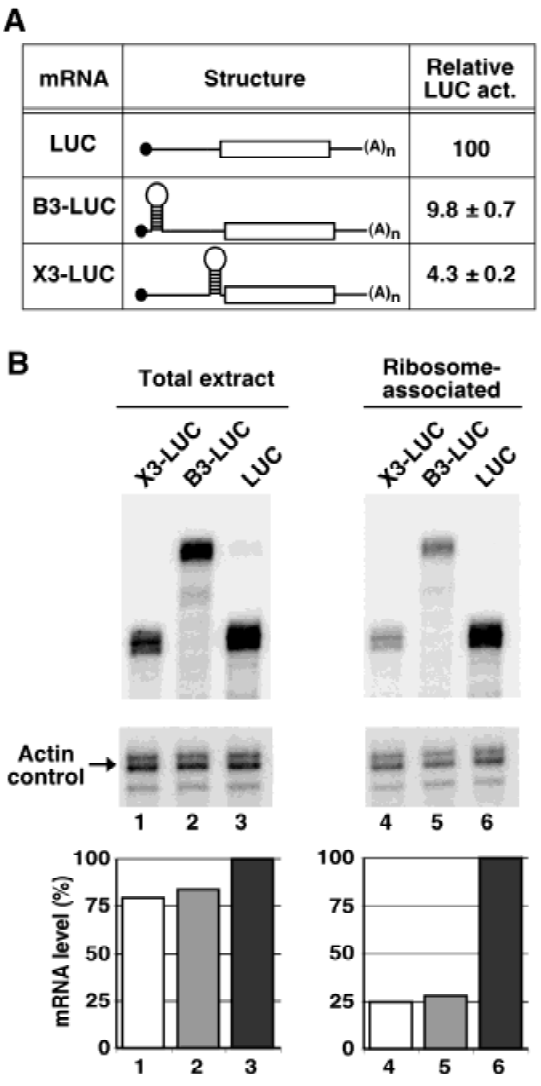

FIGURE 6. Differential purification of various *LUC* mRNAs with the ribosome. **A:** Structure of the different *LUC* reporter transcripts and relative luciferase activity measured in extracts. The luciferase activity (and the standard deviation) is expressed as the percentage of the activity measured in the extract versus that in the control (*LUC* mRNA with no stem-loop) extract. **B:** Quantitation of *LUC* reporter mRNAs in the total extract and in the ribosome-associated fraction. Tagged ribosomes were purified from extracts expressing each of the reporter mRNAs as described in Materials and Methods. Total RNA was prepared from the crude extract and from the fraction eluted from the affinity resin. Equal amounts (2.5 μg) of total RNA were hybridized to radiolabeled RNA probe complementary to portion of the *LUC* and the *ACT1* mRNA. Following RNase digestion, the protected fragments were separated by gel electrophoresis and quantitated by phosphorimaging. For each sample, the intensity of the luciferase mRNA-protected fragment was normalized using the actin mRNA signal, and is represented as the percentage of the *LUC* mRNA signal found in the crude extract.

DISCUSSION

We report here the successful development of a simple affinity purification strategy for yeast ribosomes. Material purified with this procedure contains 60S subunits, 80S monosomes, and small polyribosomes. Associated with these are many proteins, including Asc1p and

Mpt4p, as well as intact mRNAs. The degree to which the mRNA is purified correlates well with its translational activity within the cell.

Our results suggest that the affinity purification of ribosome-bound mRNA could be used as a fast and easy high-throughput screening procedure to identify subsets of mRNAs that change their translational activity in different yeast mutants or under different growth conditions. Preliminary experiments in which mRNAs copurifying with the tagged ribosome were hybridized to yeast cDNA microarray were, in fact, able to identify transcripts that have been previously shown by sedimentation analysis to be translationally regulated following changes in the nutritional status of the yeast (E. Winstall & A.B. Sachs, unpubl. observation; Hinnebusch, 1984; Kuhn et al., 2001).

There are several advantages of using affinity-purified ribosomes over centrifugation techniques to analyze ribosome-associated proteins and mRNAs. Copurification on an immobilized resin represents a more direct means than cosedimentation for assessing ribosome association. The purification procedure is simple and rapid, so that a large number of different samples can be processed at the same time. The amount of starting biological material needed to analyze associated proteins and mRNAs can be scaled down, thereby allowing experiments designed to assess the consequences of multiple conditions on ribosome association to be performed. Finally, coupled to mRNA amplification methods, the procedure described here can theoretically allow for the determination of the translation status of mRNAs at the single- or near single-cell level.

For now, affinity purification of the ribosome is restricted to small polyribosomes carrying a tagged ribosomal protein. Future development milestones will include optimizing methods to purify the larger polyribosomes and obtaining monoclonal antibodies directed against epitopes on the ribosome in higher cells. With these advances, expression profiling of mRNAs in translationally active and inactive pools in mammalian cells should be greatly simplified. In addition, efficient scaling of the preparation is possible (T. Aragon & A.B. Sachs, unpubl. observations), and this should allow for the very rapid purification of large amounts of intact ribosomes for structural studies. Many other applications of this technology are certainly imaginable, and each of these should further advance studies on the ribosome and on translational control processes.

MATERIALS AND METHODS

Strains and growth conditions

S. cerevisiae strains and oligonucleotides used in this study are listed in Tables 1 and 2. Strains were grown in rich medium (YP) or synthetic complete (SC) yeast medium supplemented with 2% carbon source, as described (Guthrie & Fink, 1991).

TABLE 2. Oligonucleotides in this study.

Oligo	Sequence (5′–3′)
OIT39	ATCGGCCGCGGCGACTACAAGGACGACGATGACAAG GGCAGCGGCCATCATCATCATCATCATTAAGGATCCA
OIT40	AGCTTGGATCCTTAATGATGATGATGATGATGGCCGC TGCCCTTGTCATCGTCGTCCTTGTAGTCGCCGCGG CCGAT
OIT57	GCTCTAGAGATAAAATGGCTCCATCTGGT
OIT58	CCCAAGCTTCGAAGCATAAGAATGCAGCA

YIT613 was created from parental strain CB012. CB012 was transformed with p*RPL25-FH* (see below), and then the chromosomal *RPL25* was disrupted by transformation with the *Not*I-*Xho*I fragment used to construct the *rpl25*::*HIS3* (pL25-GFP) strain (Hurt et al., 1999), with the *LEU2* gene replacing the *HIS3* gene. Recombinants containing *rpl25::LEU2* were identified by standard methods.

Plasmids construction

p*RPL25-FH* (BIT751) was constructed as follows. Two complementary oligonucleotides, OIT39 and OIT40, encoding the FLAG-$(His)_6$ epitope were annealed and inserted into pBluescript KS+ using *Eco*RV-*Hin*dIII sites to create pBluescriptFH. The *Bam*HI-*Eco*RV fragment of pSB32::L25-TAG (Hurt et al., 1999) containing *RPL25* was inserted into the corresponding sites of pBluescriptFH to create p*RPL25*+FH. Both the *Bam*HI-*Hin*dIII fragment containing the 3′ UTR region of *RPL25* and the *Xba*I-*Bam*HI fragment containing 5′ UTR region of *RPL25* (Hurt et al., 1999) were inserted into the corresponding sites of the yeast centromeric vector YCplac33 (Gietz & Sugino, 1988) to create p*RPL25*/5′+3′UTR. The *Bam*HI-*Bam*HI fragment of p*RPL25*+FH was inserted into *Bam*HI site of p*RPL25*/5′+3′UTR plasmid. The resulting plasmid p*RPL25-FH* contains the *RPL25* promoter and the open reading frame, fused in frame to sequences that encode the FLAG-$(His)_6$ epitope followed by the transcriptional terminator from the *RPL25* gene.

To construct p*GAL1-RPL25-FH* (BIT757), the full-length C-terminal FH-tagged form of *RPL25* was first obtained by amplifying *RPL25* DNA fragments from p*RPL25-FH* with primers OIT57 and OIT58. PCR product was cloned into p415*GAL1* (Mumberg et al., 1994) using *Xba*I and *Eco*RI sites, and the DNA sequence of the resulting plasmid p*GAL1-RPL25-FH* was checked by standard sequencing procedures. The resulting plasmid contains the *RPL25* open reading frame transcribed by the *GAL1* promoter, fused in frame to sequences that encode the FH tag, followed by the transcriptional terminator from the *CYC1* gene.

The plasmids YCpLUCEX1, YCpB3LUCEX1, and YCpX3LUCEX1 used to generate luciferase reporter mRNA are a kind gift of John E.G. McCarthy, and have been described in details by Oliveira et al. (1993). For the purpose of our study, the *LUC* expression modules had to be excised

from YCpX3LUCEX1, YCpB3LUCEX1, and YCpLUCEX1 (all *URA3CEN* vectors) as *Hin*dIII fragments and were then introduced into *Hin*dIII–digested Ycplac22 (Gietz & Sugino, 1988) to produce plasmids BIT757, BIT758, and BIT759, respectively (*TRP1CEN* vectors). The plasmid BIT760, used to generate the *LUC* antisense RNA probe, was constructed by introducing a 225-bp *Bam*H1-*Bsa*AI fragment from BIT758 into *Bam*H1-*Eco*RV-digested pBluescript KS+. This insert contains the B3 stem-loop leader sequence (see Fig. 3A) and 153 nt of the *LUC* ORF. The plasmid BIT761 used to synthesized the *ACT1* antisense RNA probe was generated by introducing a 1-kb *Hin*dIII–*Xho*I fragment from p*YACT1* (a pBR322-based plasmid containing an *Eco*RI yeast genomic fragment encompassing the *ACT1* gene; Ng & Abelson, 1980) into *Hin*dIII-*Xho*I-digested pBluescript KS+.

Purification of ribosomes by conventional centrifugation methods

Yeast strain yAV129 (van Hoof et al., 2000) was grown in 500 mL YPD to an OD_{600} of 2.0. The 80S ribosomes were purified on discontinuous sucrose gradients. The pelleted ribosome complexes were washed twice with IXA-500 buffer (50 mM Tris-HCl, pH 7.5, 500 mM KCl, 12 mM $Mg(OAc)_2$, 1 mM DTT, 1 mM PMSF) and then resuspended for 15 min at 37 °C in IXA-800 containing 10 mM puromycin. After recentrifugation, pellets were dissolved in buffer E (50 mM Tris-HCl, pH 7.5, 5 mM $MgCl_2$, 100 mM KCl, 0.1 mM EDTA, 1 mM DTT, 50% glycerol) and the resulting solution was sedimented on a 15–25% sucrose gradient to separate and fractionate the 60S and 40S ribosomal subunits. Each of the fractions was mixed with the equal volume of IXA dilution buffer (50 mM Tris-HCl, pH 7.5, 12 mM $Mg(OAc)_2$, 12 mM β-mercaptoethanol), and pelleted at 40,000 rpm for 12 h. The pellets were dissolved in buffer E and analyzed for protein and RNA content as described.

Extract preparation for ribosomal protein and ribosome-associated protein analysis

Yeast strain YIT613 was grown in 200 mL YPD at 30 °C to an OD_{600} of 0.8. Cells were pelleted for 3 min with the use of a clinical centrifuge, resuspended in 400 μL of lysis buffer (20 mM HEPES, pH 7.4, 2 mM $Mg(OAc)_2$, 100 mM KOAc, 100 μg/mL cycloheximide, 0.5 mM DTT) on ice, and transferred to 1.5-mL microcentrifuge tubes. After pelleting for 5 min at 7,000 rpm in 1.5-mL microcentrifuge tubes, cells were resuspended in an equal volume of lysis buffer containing a protease inhibitor cocktail (complete mini-EDTA free; Roche), and lysed in the presence of 1 vol of glass beads by vortexing six times for 20 s at 40-s intervals. Lysates were cleared briefly at 10,000 rpm for 5 min, followed by a 20-min 10,000-rpm centrifugation to give the final lysate.

Extract preparation for mRNA analysis

Yeast strains expressing the Rpl25p-FH fusion protein were grown in 500 mL of rich (YPD) or synthetic complete (SC) medium containing 2% (w/v) of the appropriate carbon source to an OD_{600} of 0.8. Cells were pelleted at 30 °C for 10 min at 6,000 rpm in a GSA rotor (Sorvall) prewarmed at 30 °C. Cells were then resuspended in 50 mL of washing buffer (20 mM HEPES, pH 7.4, 2 mM $Mg(OAc)_2$, 100 mM KOAc, 2% glucose or galactose, 1× amino acids) equilibrated at 30 °C, and transferred to a 50-mL conical tube in which they were pelleted for 3 min at room temperature in a clinical centrifuge. The cell pellet was snap-frozen in liquid nitrogen and then ground in liquid nitrogen using a mortar and a pestle. The resulting cell powder was then resuspended on ice in 4 mL of lysis buffer (20 mM HEPES-KOH, pH 7.4, 2 mM $Mg(OAc)_2$, 100 mM KOAc, 1 mM DTT, 1 mM PMSF) supplemented with a protease inhibitor cocktail (Complete tablets; Roche Biochemicals) and an RNase inhibitor (50 U/mL RNasin; Promega). Extracts were then transferred to 1.5-mL Eppendorf tubes and clarified by centrifugation at 4 °C for 5 min at 5,000 × *g*. Supernatant was recovered and centrifuge at 4 °C for 10 min at 9,000 × *g* to remove membranes and insoluble material. Extracts were kept in aliquots at −80 °C until ready to use.

Affinity purification of the ribosome

For ribosome purification, about 15 A_{260} units of extract were mixed with an equal volume of ice-cold 2× binding buffer (100 mM Tris-HCl, pH 7.5, 24 mM $Mg(OAc)_2$, 1 mM DTT, 1 mM PMSF, 50 U/mL RNAsin) and with 400 μL (bead volume) of anti-FLAG M2-agarose affinity resin (Sigma) in a 2-mL Eppendorf tube. Binding was allowed for 2 h at 4 °C with constant and gentle rocking. Resin was then washed five times with 0.8 mL of ice-cold IXA-100 buffer (50 mM Tris-HCl, pH 7.5, 100 mM KCl, 12 mM $Mg(OAc)_2$, 1 mM DTT, 1 mM PMSF). Elution was achieved by incubating the resin in 0.4 mL of IXA-100 buffer containing the FLAG peptide at 100 μg/mL for 20 min at 4 °C with gentle rocking. Eluate was either frozen in liquid nitrogen and stored at −80 °C for future use or processed immediately for total RNA purification or protein analysis.

Total RNA preparation

Total extracts, eluates, or sucrose gradient fractions were mixed with an equal volume of 2× proteinase K buffer (0.2 M Tris-HCl, pH 7.5, 0.3 M NaCl, 2% SDS, 25 mM EDTA) and digested with 0.1 mg/mL proteinase K for 45 min at 37 °C. Samples were then extracted twice with 1 vol of phenol:chloroform:isoamyl alcohol (25:24:1) and extracted once with 1 vol of chloroform:isoamyl alcohol (24:1). RNA in the aqueous phase was then precipitated with 1 vol of isopropanol and resuspended in DEPC-treated water after washing the RNA pellet with 70% ethanol.

For the experiments described in Figures 5 and 6, yeast strains YIT722-724 (containing the galactose-inducible *LUC* mRNAs described in Table 1) were first grown to log phase in selective medium with glucose as the carbon source, and then diluted into medium with galactose to induce expression of the *LUC* reporter mRNAs. Cells were then allowed to grow to mid-log phase, and extracts were prepared as described above.

cDNA synthesis

Total RNA isolated from the eluate of the control, untagged *RPL25* strain and 5 μg of total RNA isolated from each of the other fractions were allowed to hybridize to oligo-dT, and were then reverse transcribed in the presence of [α^{32}P]-dCTP according to standard protocols (Sambrook et al., 1989). Unincorporated nucleotides and oligo-dT were removed using Qiaquick microspin column (Qiagen). Equal volumes of each sample were then loaded on a 1.5% denaturing agarose gel. Following electrophoresis, the gel was dried and analyzed using a Typhoon 9400 phosphorimager (Amersham Pharmacia Biotech) coupled to the software ImageQuant version 5.2 (Amersham Pharmacia Biotech).

Sedimentation on sucrose gradient and polysome profiling

Sucrose gradients (15–50% sucrose in 10 mM Tris-acetate, pH 7.4, 70 mM ammonium acetate, 4 mM magnesium acetate) were prepared in 14 $\times$ 89 mm polyallomer tubes (Beckman Coulter) by the freezing and thawing method described by Luthe (1983). Crude extracts or eluates (maximum of 9 A_{260} units) were layered on top of the sucrose gradients and centrifuged at 40,000 rpm in a SW41 rotor (Beckman) for 2.5 h at 4 °C. Gradients were then fractionated from the bottom at a flow rate of 1 mL/min using a peristaltic pump. Polysome profiles were generated by continuous absorbance measurement at 254 nm using a single path UV-1 optical unit (Pharmacia) connected to a Pharmacia LKB-REC2 chart recorder. Where indicated, equal volume fractions (0.95 mL) were collected and processed for total RNA purification as described above. RNA was then resuspended in RNA hybridization buffer (80% (v/v) formamide, 40 mM PIPES, pH 6.7, 400 mM NaCl, 1 mM EDTA) and used for RNase protection analysis as described below.

RNase protection analysis

A gel-purified 673-bp *Pvu*II fragment from plasmid BIT760 was used for the synthesis of the *LUC* riboprobe with T3 RNA polymerase. The *ACT1* riboprobe was synthesized from a 3.4-kb *Sty*I fragment from plasmid BIT761 with T7 RNA polymerase. Full-length RNA probes (*LUC*: 446 nt, *ACT1*: 195 nt) were synthesized in the presence of [α^{32}P]-UTP (800 Ci/mmol; NEN/Perkin Elmer) and gel purified according to established protocols (Ausubel et al., 1987). Total RNA (2.5 μg) and yeast tRNA (48.5 μg) in RNA hybridization buffer were mixed with probes, denatured at 85 °C, and allowed to hybridize at 50 °C for at least 15 h. RNase treatment was then performed with 12.5 U of RNase A/mL and 500 U of RNase T1/mL (RNase Cocktail; Ambion) for 45 min at 37 °C. Nuclease-resistant fragments were separated on urea-6% polyacrylamide sequencing gels. As approximate DNA size markers, ^{32}P-labeled *Msp*I-digested fragments of pBR322 were run on all analytical gels. Protected fragments are as follows: *B3-LUC* mRNA leaves a 225-nt fragment, *X3-LUC* and *LUC* transcripts leave a 193-nt fragment, and *ACT1* mRNA generates a 118-nt fragment. Image acquisition and signal quantitation were performed using the phosphorimaging device described above.

Luciferase assays

Protein concentration was determined in each extract by the method of Bradford (1976) using the Bio-Rad Protein Assay reagent (Bio-Rad). Extracts were then serially diluted from 1:100 to 1:1,000 in Buffer A (30 mM HEPES-KOH, pH 7.4, 100 mM KOAc, 2 mM $Mg(OAc)_2$) supplemented with 1 mg/mL bovine serum albumin. Ten microliters of the diluted extract were then mixed with 50 μL of the reconstituted luciferase assay substrate (Promega) and luminescence was immediately counted for 15 s on a TD-20/20 luminometer (Turner Designs). Each sample was analyzed in triplicate and the signal obtained was normalized using the protein concentration in the extract.

Northern blot analysis

Yeast strain YIT623 was grown in 200 mL SC-Galactose to an OD_{600} of 0.1. Cells were pelleted in a clinical centrifuge for 3 min and resuspended immediately in fresh chase medium containing 0.1 mg/mL methionine and 2% glucose (SCD-leu). Samples (50 mL) were withdrawn at the indicated time points, and the pellets were frozen. Total RNA samples were extracted from the frozen pellets and used for northern blot analysis as described (Ashe et al., 2000). The *Bam*HI-*Eco*RV fragment of pSB32-L25::TAG (Tollervey et al., 1993) containing *RPL25* gene was used as a probe.

Protein analysis

Mass spectrometry was performed as described (Link et al., 1999).

Tryptic peptides identified from Mpt4p were (frequency of peptide): EAQADAAAEIAEDAAEAEDAGKPK (1), EAYVPATK, EYLEFDATFVESNTR (1), KADVPPPSADPSK (1), TAQLSL QDYLNQQANNQFNK (1), VNQGWGDDKK (1), KGNN TANATNSANTVQK (2), NIDVSNLPSLA, PSGNEGAIR, SKDVTDSATTK (2).

Tryptic peptides identified from Asc1p were: AAEPHAVS LAWSADGQTLF (1), ADDDSVTIISAGNDK (1), DGEIMLWN LAAK, SDVMSVDIDKK (1), VFSLDPQYLVDDLRPEFAGYSK (1), GTLEGHNGWVTSLATSAGQPN (1), LWDVATGETYQR (1), YWLAAATATGIK (1), AMYTLSAQDEVFSLAFSPNR (2), AAEPHAVSLAWSADGQTLFAGYTDNVIR (3), VFSLDPQYL VDDLRPEFAGY(3), AWNLNQFQIEADFIGHNSNINTLTASP DGTLIASAGK(8).

ACKNOWLEDGMENTS

We thank Ed Hurt for pSB32::L25-TA*G* and the plasmid to construct *rpl25::LEU2*, Roy Parker for the strain yAV129, and John E.G. McCarthy for the YCpLUCEX plasmids. This work was supported by the Japan Society for the Promotion of Science to T.I., National Institutes of Health grant GM 50308 to A.B.S., and grant RR11823 from the Yeast Resource Center to J.R.Y.. E.W. was supported by a postdoctoral fellowship from The Natural Sciences and Engineering Research Council of Canada (NSERC).

Received March 26, 2002; returned for revision
April 5, 2002; revised manuscript received April 26, 2002

REFERENCES

Ashe MP, De Long SK, Sachs AB. 2000. Glucose depletion rapidly inhibits translation initiation in yeast. *Mol Biol Cell 11*:833–848.

Ausubel FM, Brent R, Kingston RE, Moore DD, Seidman JG, Smith JA, Struhl K, eds. 1987. *Current protocols in molecular biology*. New York: Greene Publishing Associates and Wiley-Interscience.

Ban N, Nissen P, Hansen J, Moore PB, Steitz TA. 2000. The complete atomic structure of the large ribosomal subunit at 2.4 Å resolution. *Science 289*:905–920.

Bassler J, Grandi P, Gadal O, Lessmann T, Petfalski E, Tollervey D, Lechner J, Hurt E. 2001. Identification of a 60S preribosomal particle that is closely linked to nuclear export. *Mol Cell 8*:517–529.

Bradford MM. 1976. A rapid and sensitive method for the quantification of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal Biochem 72*:248–254.

Brown V, Jin P, Ceman S, Darnell JC, O'Donnell WT, Tenenbaum SA, Jin X, Feng Y, Wilkinson KD, Keene JD, Darnell RB, Warren ST. 2001. Microarray identification of FMRP-associated brain mRNAs and altered mRNA translational profiles in fragile X syndrome. *Cell 107*:477–487.

Carter MS, Kuhn KM, Sarnow P. 2000. Cellular internal ribosomes entry site elements and the use of cDNA microarrays in their investigation. In: Sonenberg N, Hershey JWB, Mathews MB, eds. *Translational control of gene expression*. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press. pp 615–635.

Chantrel Y, Gaisne M, Lions C, Verdiere J. 1998. The transcriptional regulator Hap1p (Cyp1p) is essential for anaerobic or heme-deficient growth of *Saccharomyces cerevisiae*: Genetic and molecular characterization of an extragenic suppressor that encodes a WD repeat protein. *Genetics 148*:559–569.

Darnell JC, Jensen KB, Jin P, Brown V, Warren ST, Darnell RB. 2001. Fragile X mental retardation protein targets G quartet mRNAs important for neuronal function. *Cell 107*:489–499.

Frantz JD, Gilbert W. 1995. A yeast gene product, G4p2, with a specific affinity for quadruplex nucleic acids. *J Biol Chem 270*: 9413–9419.

Gietz RD, Sugino A. 1988. New yeast–*Escherichia coli* shuttle vectors constructed with in vitro mutagenized yeast genes lacking six-base-pair restriction sites. *Gene 74*:527–534.

Guthrie C, Fink G. 1991. *Guide to yeast genetics and molecular biology.* San Diego, California: Academic Press.

Harnpicharnchai P, Jakovljevic J, Horsey E, Miles T, Roman J, Rout M, Meagher D, Imai B, Guo Y, Brame CJ, Shabanowitz J, Hunt DF, Woolford JL Jr. 2001. Composition and functional characterization of yeast 66S ribosome assembly intermediates. *Mol Cell 8*:505–515.

Hata H, Mitsui H, Liu H, Bai Y, Denis CL, Shimizu Y, Sakai A. 1998. Dhh1p, a putative RNA helicase, associates with the general transcription factors Pop2p and Ccr4p from *Saccharomyces cerevisiae*. *Genetics 148*:571–579.

Hinnebusch AG. 1984. Evidence for translational regulation of the activator of general amino acid control in yeast. *Proc Natl Acad Sci USA 81*:6442–6446.

Hurt E, Hannus S, Schmelzl B, Lau D, Tollervey D, Simos G. 1999. A novel in vivo assay reveals inhibition of ribosomal nuclear export in ran-cycle and nucleoporin mutants. *J Cell Biol 144*:389–401.

Johannes G, Carter MS, Eisen MB, Brown PO, Sarnow P. 1999. Identification of eukaryotic mRNAs that are translated at reduced cap binding complex eIF4F concentrations using a cDNA microarray. *Proc Natl Acad Sci USA 96*:13118–13123.

Kuhn KM, DeRisi JL, Brown PO, Sarnow P. 2001. Global and specific translational regulation in the genomic response of *Saccharomyces cerevisiae* to a rapid transfer from a fermentable to a nonfermentable carbon source. *Mol Cell Biol 21*:916–927.

Lee JC. 1990. Ribosomes from *Saccharomyces cerevisiae*. In: Rose, AH, Harrison JS, eds. *The yeasts*. New York: Academic Press. pp 489–539.

Link AJ, Eng J, Schieltz DM, Carmack E, Mize GJ, Morris DR, Garvik BM, Yates JR 3rd. 1999. Direct analysis of protein complexes using mass spectrometry. *Nat Biotechnol 17*:676–682.

Luthe DS. 1983. A simple technique for the preparation and storage of sucrose gradients. *Anal Biochem 135*:230–232.

Mumberg D, Muller R, Funk M. 1994. Regulatable promoters of *Saccharomyces cerevisiae*: Comparison of transcriptional activity and their use for heterologous expression. *Nucleic Acids Res 22*: 5767–5768.

Ng R, Abelson J. 1980. Isolation and sequence of the gene for actin in *Saccharomyces cerevisiae*. *Proc Natl Acad Sci USA 77*:3912–3916.

Oliveira CC, van den Heuvel JJ, McCarthy JE. 1993. Inhibition of translation initiation in *Saccharomyces cerevisiae* by secondary structure: The roles of the stability and position of stem-loops in the mRNA leader. *Mol Microbiol 9*:521–532.

Pradet-Balade B, Boulme F, Beug H, Mullner EW, Garcia-Sanz JA. 2001. Translation control: Bridging the gap between genomics and proteomics? *Trends Biochem Sci 26*:225–229.

Ren B, Robert F, Wyrick JJ, Aparicio O, Jennings EG, Simon I, Zeitlinger J, Schreiber J, Hannett N, Kanin E, Volkert TL, Wilson CJ, Bell SP, Young RA. 2000. Genome-wide location and function of DNA binding proteins. *Science 290*:2306–2309.

Sambrook J, Fritsch EF, Maniatis T. 1989. *Molecular cloning: A laboratory manual*. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press.

Sonenberg N, Hershey JWB, Mathews MB, eds. 2000. *Translational control of gene expression*. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press.

Takaku H, Mutoh E, Horiuchi H, Ohta A, Takagi M. 2001. Ray38p, a homolog of a purine motif triple-helical DNA-binding protein, Stm1p, is a ribosome-associated protein and dissociated from ribosomes prior to the induction of cycloheximide resistance in *Candida maltosa*. *Biochem Biophys Res Commun 284*:194–202.

Tenenbaum SA, Carson CC, Lager PJ, Keene JD. 2000. Identifying mRNA subsets in messenger ribonucleoprotein complexes by using cDNA arrays. *Proc Natl Acad Sci USA 97*:14085–14090.

Tollervey D, Lehtonen H, Jansen R, Kern H, Hurt EC. 1993. Temperature-sensitive mutations demonstrate roles for yeast fibrillarin in pre-rRNA processing, pre-rRNA methylation, and ribosome assembly. *Cell 72*:443–457.

van Hoof A, Lennertz P, Parker R. 2000. Three conserved members of the RNase D family have unique and overlapping functions in the processing of 5S, 5.8S, U4, U5, RNase MRP and RNase P RNAs in yeast. *EMBO J 19*:1357–1365.

Velculescu VE, Zhang L, Zhou W, Vogelstein J, Basrai MA, Bassett DE Jr, Hieter P, Vogelstein B, Kinzler KW. 1997. Characterization of the yeast transcriptome. *Cell 88*:243–251.

Warner JR. 1982. The yeast ribosome: Structure, function, and synthesis. In: Strathern JN, Jones EW, Broach JR, eds. *The molecular biology of the yeast Saccharomyces: Metabolism and gene expression*. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press. pp 529–560.

Woolford JL Jr, Warner JR. 1991. The ribosome and its synthesis. In: Broach JR, Pringle JR, Jones EW, eds. *The molecular and cellular biology of the yeast Saccharomyces: Genome dynamics, protein synthesis, and energetics*. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press. pp 587–626.

Zong Q, Schummer M, Hood L, Morris DR. 1999. Messenger RNA translation state: The second dimension of high-throughput expression screening. *Proc Natl Acad Sci USA 96*:10632–10636.