The box H +ACA snoRNAs carry Cbf5p, the putative rRNA pseudouridine synthase

Denis L.J. Lafontaine, Cécile Bousquet-Antonelli,1 Yves Henry,1 Michèle Caizergues-Ferrer,1 and David Tollervey2

Institute of Cell and Molecular Biology, University of Edinburgh, King's Buildings, Edinburgh EH9 3JR, UK; 1Laboratoire de Biologie Moleculaire Eucaryote, Centre National de Recherche Scientifique (CNRS), 31062 Toulouse Cedex, France

Many or all of the sites of pseudouridine (Ψ) formation in eukaryotic rRNA are selected by site-specific base-pairing with members of the box H + ACA class of small nucleolar RNAs (snoRNAs). Database searches previously identified strong homology between the rat nucleolar protein Nap57p, its yeast homolog Cbf5p, and the Escherichia coli Ψ synthase truB/P35. We therefore tested whether Cbf5p is required for synthesis of Ψ in the yeast rRNA. After genetic depletion of Cbf5p, formation of Ψ in the pre-rRNA is dramatically inhibited, resulting in accumulation of the unmodified rRNA. Protein A-tagged Cbf5p coprecipitates all tested members of the box H +ACA snoRNAs but not box C + D snoRNAs or other RNA species. Genetic depletion of Cbf5p leads to depletion of all box H +ACA snoRNAs. These include snR30, which is required for pre-rRNA processing. Depletion of Cbf5p also results in a pre-rRNA processing defect similar to that seen on depletion of snR30. We conclude that Cbf5p is likely to be the rRNA Ψ synthase and is an integral component of the box H +ACA class of snoRNP's, which function to target the enzyme to its site of action.

[Key Words: RNA modification; pre-rRNA processing; ribosome synthesis; yeast]

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The rRNAs of all organisms undergo extensive covalent nucleotide modification. In eukaryotes, the rRNAs are generated by post-transcriptional processing of large pre-rRNA species, and these modified nucleotides are formed in the pre-rRNAs, rather than in the mature rRNAs. The most numerous modifications are methylation of the 2'-hydroxyl residue in the ribose moieties (2'-O-methylation) and isomerization of uracil residues to pseudouridine (Ψ). Formation of Ψ residues is thought to occur through base rotation about the C3-C6 axis after cleavage of the glycosyl bond (Goldwasser and Heinrikson 1966; for review, see Ofengand et al. 1995). Additionally, a few positions are modified at the base level; the best described example being the universally conserved m5Am5A doublet at the 3'-end of the 18S rRNA (Lafontaine et al. 1995). Recent data have shown that, in eukaryotes, the sites of both 2' -methylation (Cavaille et al. 1996; Kiss-László et al. 1996; Nicoloso et al. 1996) and Ψ formation (Ganot et al. 1997a; Ni et al. 1997) in the rRNAs are selected by site-specific base-pairing of small nuclear RNAs (snoRNAs) to the pre-rRNAs (for review, see Maden 1996; Tollervey 1996; Bachellerie and Cavallé 1997; Smith and Stettl 1997). The snoRNAs involved can be separated into two major groups, which are designated box C +D snoRNAs and box H +ACA snoRNAs on the basis of conserved sequence elements (Balakin et al. 1996). In the case of 2'-O-methylation, base-pairing of a member of the box C + D class of snoRNAs across the site of methylation positions a conserved sequence element, box D, at a precise distance of 5 bp from the nucleotide to be modified (Cavaille et al. 1996; Kiss-László et al. 1996; Nicoloso et al. 1996). Presumably, proteins associated with box D use this positional information to select the site of modification. In the case of Ψ formation, a member of the box H +ACA class of snoRNAs base pairs to nucleotides flanking the substrate uracil, leaving the base of the nucleotide free for interaction with the modifying enzyme (Ganot et al. 1997a; Ni et al. 1997).

Both major groups of snoRNAs are associated with specific proteins in small nucleolar ribonucleoprotein (snoRNP) particles. All box C +D snoRNAs are associated with the protein fibrillarin (Nop1p in yeast) (Lischwe 1985; Schimmang et al. 1989; Ganot et al. 1997b; for review, see Maxwell and Fournier 1995), and mutations in Nop1p can globally block 2'-O-methylation of the yeast rRNAs (Tollervey et al. 1993). Similarly, all box H +ACA snoRNAs are associated with Gar1p (Girard et al. 1992; Balakin et al. 1996; Ganot et al. 1997b), and mutations in Gar1p can globally inhibit Ψ formation in the rRNA (Bousquet-Antonelli et al. 1997).
Nop1p and Gar1p are not required for the synthesis or stability of the snoRNAs with which they are associated. Gar1p is, however, required for the stable association of the box H + ACA snoRNAs with the pre-rRNA (Bousquet-Antonelli et al. 1997); this association presumably underlies the requirement for Gar1p in \( \Psi \) formation.

Both classes of snoRNAs include species that probably do not act to select sites of rRNA modification but are required for processing of the pre-rRNA. Genetic deple-
tion of the box C + D snoRNAs U3 (Hughes and Ares 1991) or U14 (Li et al. 1990) or of the box H + ACA snoRNA snR30 (Morrisey and Tollervey 1993), inhibits the early pre-rRNA processing reactions at sites \( A_0 \), \( A_1 \), and \( A_2 \), preventing the synthesis of the 18S rRNA (see Fig. 1). For this reason each of these snoRNAs is essential for cell viability. In contrast, none of the snoRNAs that direct rRNA modification is essential for cell viability, although the absence of the \( \Psi \) guide snoRNA, snR10, leads to some cold sensitivity (Tollervey 1987; Ni et al. 1997).

One of the major unresolved questions concerning these systems of snoRNA-directed modification is the relationship between the snoRNAs and the modifying enzymes. Specifically, are the enzymes free components that recognize the structure created by the snoRNA-pre-rRNA duplexes in much the same way tRNA-modifying enzymes and bacterial rRNA-modifying enzymes recognize their RNA substrates? Or are the enzymes physically associated with the snoRNAs, which act directly to target the enzymes to their sites of action?

In contrast to \( \Psi \) formation in the eukaryotic pre-rRNA, the formation of \( \Psi \) in tRNAs and bacterial rRNAs is not known to involve RNA cofactors. In these cases, multiple \( \Psi \) synthases exist; four tRNA \( \Psi \) synthases have been characterized in Escherichia coli (truA, truB, rsuA, and rluA), each of which modifies with high specificity a single site or a number of sites with very similar structures (Kammen et al. 1988; Nurse et al. 1995; Wrzesinski et al. 1995a,b; Simos et al. 1996). A database search (Koo- 
nin 1996) revealed that each of these enzymes is a member of a distinct, evolutionarily conserved family of \( \Psi \) synthases. E. coli truB/P35, which converts U55 to \( \Psi \)55 in the m5U\( \Psi \)CG loop in most tRNAs (Nurse et al. 1995), is strongly homologous to two yeast proteins, Cbf5p and...
YNL480 (Koonin 1996). Recent data have shown that YNL480 (now designated Fus4p) is the yeast tRNA Ψ(55 synthase (Becker et al. 1997). Yeast Cbf5p was originally characterized as an essential protein that showed in vitro binding to centromeres and microtubules (Jiang et al. 1993). Subsequently, Cbf5p was found to be highly homologous (64% identity, 79% homology) to the rat nucleolar protein Nap57p and to be localized to the yeast nucleolus (Meier and Blobel 1994). This suggested that Cbf5p and Nap57p might be the rRNA Ψ synthases in yeast and mammals, respectively. We have therefore investigated this possibility and report here an analysis of the role of Cbf5p in pre-rRNA processing and formation of Ψ in the rRNA.

Results

Construction of a conditional CBF5 allele

Because CBF5 is an essential gene (Jiang et al. 1993), we first constructed a conditional allele by placing its expression under the control of an inducible GAL10 promoter using the one-step PCR method described previously (Lafontaine and Tollervey 1996) (Fig. 2A). On permissive medium [2% raffinose, 2% sucrose, and 2% galactose (rsg)], the growth rate of the GAL::cbf5 strain is identical to that of the otherwise isogenic parental CBF5 strain (doubling every 3 hr). Under these conditions, the level of the CBF5 mRNA in the GAL::cbf5 strain is approximately fivefold higher than in the CBF5 control strain (Fig. 2C, lane 3). This level is expected for a gene whose transcription is driven by the strong GAL10 promoter. Following transfer of the GAL::cbf5 strain to glucose (glu) medium the CBF5 mRNA was rapidly depleted, no mRNA was detected 8 hr after transfer to glu medium (Fig. 2C), and growth slowed progressively, commencing 20 hr after transfer (Fig. 2B). This slow onset in the growth impairment is characteristic of GAL deletion of components required for ribosome synthesis.

Cbf5p is required for pre-rRNA processing

Northern hybridization (Fig. 3) shows that the levels of the mature 18S and 25S rRNA species are identical in the CBF5 control strain and in the GAL::cbf5 strain grown in permissive medium (0 hr lanes in Fig. 3). Following transfer to glu medium (Fig. 3A, 23- to 46-hr lanes) the mature 18S rRNA is progressively depleted in the GAL::cbf5 strain; at later time points depletion of the 25S rRNA is also observed. Analysis of the pre-rRNAs (Fig. 3B-E) shows that the 35S primary transcript is strongly accumulated, while the 27SA2 and 20S pre-rRNAs are depleted and an aberrant RNA species, the 23S pre-rRNA, is detected. The 25S RNA extends from the 5′ end of the 35S to site A3 (Fig. 1) and is generated by direct cleavage of the 35S pre-rRNA at site A3 in the absence of prior cleavage at sites A0, A1, and A2. These effects are characteristic of mutations that inhibit the early pre-rRNA cleavages at sites A0, A1, and A2 (see Fig. 1) and were observed following depletion of several different snoRNAs, including the box H +ACA snoRAs snR10 (Tollervey 1987) and snR30 (Morrissey and Tollervey 1993), and on depletion of Gar1p (Girard et al. 1992), which is associated with the entire class of box H +ACA snoRAs (Balakin et al. 1996). Depletion of Cbf5p also leads to accumulation of the 27SB pre-rRNA (Fig. 3E), consistent with the reduction in the levels of the 25S rRNA. A shorter time course following transfer to glu medium (Fig. 3F) shows that the level of the 35S pre-rRNA is elevated and 27SA2 is reduced as early as 8 hr (<3 generations) after transfer to glu medium, indicating that these effects rapidly follow the loss of Cbf5p. Analysis of low molecular weight RNA (Fig. 4A) shows that the 7S pre-rRNA is also strongly accumulated following depletion of Cbf5p. This accumulation of the 27SB and 7S pre-rRNAs was not observed on depletion of any characterized snoRNA. In addition, a 5.8S rRNA species intermediate in length between 5.8S5 and 5.8S9 was observed on depletion of Cbf5p (* in Fig. 4B). This has also not been observed previously in snoRNA mutants.

Pre-rRNA processing was further analyzed by primer extension. Analysis of the 5′ external transcribed spacer (ETS) shows an increase in the stop corresponding to the 5′ end of the 35S pre-rRNA (position +1, Fig. 5A) in the GAL::cbf5 strain following transfer to glu medium (23-
to 70-hr lanes), consistent with the 35S accumulation detected by Northern hybridization (Fig. 3B-F); however, this was not accompanied by a loss of the pre-rRNA cleaved at site A0 (Fig. 5B). The primer-extension stop at site A0 is elevated on depletion of Cbf5p. The accumulation of the 35S pre-rRNA and 23S RNA indicates that cleavage at site A0 is at least delayed on depletion of Cbf5p. We interpret this observation as showing that cleavages at sites A1 and A2 are more sensitive to the depletion of Cbf5p than is cleavage at site A0. This phenomenon was observed in strains depleted of snR10, snR30, or Gar1p, but not in strains depleted of U3 (Beltrame et al. 1994).

Primer extension through sites in ITS1 shows the loss of the stop corresponding to cleavage at site A0, the 5’ end of the 27SA2 pre-rRNA, and shows the increase of the stops at sites B1S and B1L, the 5’ ends of both the 27SBs and 27SBL and 7Ss and 7SL pre-rRNAs, respectively (Fig. 6). These observations are in good agreement with the results of Northern hybridization in Figures 3 and 4. The accumulation of the long and short forms of 27SB and 7S, shown by the relative stops at B1S and B1L, are not obviously different (Fig. 6, cf. A with C, which shows a shorter exposure of the same gel). The level of the 27SA3 pre-rRNA, shown by the primer-extension stop at site A0, is elevated on depletion of Cbf5p (Fig. 6B). This elevation was also observed in strains depleted of snR30, but was not seen on depletion of any other snoRNP component tested (Morrissey and Tollervey 1993).

No defects in pre-tRNA processing or accumulation of mature tRNAs were detected by Northern hybridization with probes specific for the intron-containing precursor of tRNA\textsubscript{Tyr\textsubscript{CCA}}, tRNA\textsubscript{Val\textsubscript{UGG}}, tRNA\textsubscript{Glu\textsubscript{A}}\textsubscript{GUU}, and tRNA\textsubscript{Phenylalanine\textsubscript{Pro\textsubscript{CA}}\textsubscript{DGG}} and probes specific for mature tRNA\textsubscript{Tyr\textsubscript{GUA}} and tRNA\textsubscript{Pro\textsubscript{GAA}} (data not shown).

Figure 3. Northern analysis of rRNA and pre-rRNA synthesis in a GAL::cbf5 strain. (A) Probes against mature 25S and 18S rRNA (oligonucleotides a and h); (B) probe against the 5’ region of ITS1 (oligonucleotide b); (C) probe against ITS1 between sites A2 and A3 (oligonucleotide c); (D) probe against the 3’ region of ITS1 (oligonucleotide d); (E) probe against the 5’ region of ITS2 (probe f). (F) Shorter time course following transfer to glu medium, hybridized with oligonucleotide c. The oligonucleotides used are depicted in Fig. 1A. RNA was extracted from the CBF5 and GAL::cbf5 strains following growth on rsg medium (0-hr lanes) and at intervals following transfer to glu medium (8-70-hr lanes) and separated on a 1.2% agarose gel containing formaldehyde.

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Cbf5p is required for formation of C in the pre-rRNA

The effects of depletion of Cbf5p on C formation were assessed by pulse labeling of the newly synthesized pre-rRNA and rRNA with \( ^{32}P \). Cells were labeled following growth in permissive rsg medium or following transfer to glu medium for 24 hr. Labeled RNAs, 35S pre-rRNA, mature 25S rRNA, and bulk tRNA, were gel purified, and the nucleotide composition was analyzed by two-dimensional thin layer chromatography (TLC). C\( \text{p} \) content was determined by comparison with other nucleotides present in the same RNA samples. Figure 7E shows the data expressed as the ratio of incorporation into C\( \text{p} \) compared to Ap; comparison of C\( \text{p} \) to Gp or Cp gave similar results (data not shown). The results presented are from one set of experiments; an independent analysis gave similar data (data not shown). The C\( \text{p}: \)Ap ratio in the 25S rRNA from the Cbf5p-depleted strain is \( \sim \)11\% of the value obtained for the wild-type 25S rRNA. This would correspond to a residual level of \( \sim \)3 C residues per 25S rRNA molecule (the wild-type 25S has 30 C residues) (Ofengand et al. 1995). The C\( \text{p}: \)Ap ratio in the 35S rRNA from the Cbf5p-depleted strain is 16\% of the wild-type value, corresponding to \( \sim \)7 C residues (the wild-type 35S has 43 C residues) (Ofengand et al. 1995). It is not clear whether this corresponds to low residual modification of all sites or whether some sites are preferentially modified. Because the 18S rRNA is not synthesized in the Cbf5p-depleted strain this species cannot be analyzed directly. The reduced modification of the 35S pre-rRNA, however, strongly indicates that formation of C in the region of the pre-rRNA corresponding to the mature 18S rRNA is also inhibited by depletion of Cbf5p.

Figure 4. Northern analysis of rRNA and pre-rRNA synthesis in a GAL::cbf5 strain. (A) Probe against ITS2 (probe f); (B) probe against mature 5.8S rRNA (probe e). The oligonucleotides used are depicted in Fig. 1A. RNA was extracted from the CBF5 and GAL::cbf5 strains following growth on rsg medium (0-hr lanes) and at intervals following transfer to glu medium (8- to 70-hr lanes) and separated on an 8% polyacrylamide gel containing 8 M urea. (*) 5.8S species with intermediate length.

Figure 5. Primer-extension analysis of pre-rRNA processing in a GAL::cbf5 strain. (A) The 5' end of the 35S primary transcript at site +1. (B) Site A\( \text{p} \). RNA was extracted from the CBF5 and GAL::cbf5 strains following growth on rsg medium (0-hr lanes) and at intervals following transfer to glu medium (8- to 70-hr lanes) and analyzed by primer extension with oligonucleotide a (Fig. 1A). A DNA sequence made with the same primer is shown as a size marker. Site +1 lies 730 nucleotides from the primer and the sequence is not useful.

Figure 6. Primer-extension analysis of pre-rRNA processing in a GAL::cbf5 strain. (A) Primer extension through sites B1\( \text{p} \), B1\( \text{L} \), A0, and A\( \text{p} \). (B) Longer exposure of A showing the level of stop at site A\( \text{p} \). (C) Shorter exposure of A showing the level of stop at site B1. RNA was extracted from the CBF5 and GAL::cbf5 strains following growth on rsg medium (0-hr lanes) and at intervals following transfer to glu medium (8- to 70-hr lanes) and analyzed by primer extension using oligonucleotide g (Fig. 1A). A DNA sequence made with the same primer is shown as a size marker.

A snoRNA-associated pseudouridine synthase
As an example of the data, Figure 7(A–D) presents the analysis of the 25S rRNA from the CBF5 and GAL::cbf5 strains. The spot corresponding to Cp can be seen in the CBF5 samples (Fig. 7A,B) and in the sample from the GAL::cbf5 strain grown under permissive conditions (Fig. 7C), but is not readily visible in the sample obtained following depletion of Cbf5p (Fig. 7D).

Surprisingly, the level of Ψp in the GAL::cbf5 strain grown in rsg medium was consistently below the expected level. The Ψp:Ap ratios in the 25S and 35S RNA samples was 62% and 67%, respectively, of the values in the corresponding wild-type samples. Northern hybridization indicates that the level of CBF5 mRNA under permissive conditions is elevated compared to the wild type (Fig. 2C). We speculate that this elevation leads to some excess in Cbf5p synthesis, which leads in turn to a form of squelching, in which excess free protein blocks the interaction of other components with the complex, interfering with its function.

Ψ levels in the tRNA fraction are also mildly reduced by depletion of Cbf5p; the Ψp:Ap ratio for the GAL::cbf5 strain was 85% of the wild-type ratio in rsg medium and 71% of the wild-type ratio in glu medium. E. coli truB synthesizes Ψ55 in most tRNAs contributing approximately to ~40%–50% of total Ψ in bulk tRNA (H. Grosjean, pers. comm.), but in yeast, this activity is attributable to Pus4p, another homolog of truB (Koonin 1996; Becker et al. 1997). It seems probable that the reduced Ψp:Ap ratio is an indirect consequence of the impaired growth of the Cbf5p-depleted strain. It is, however, notable that a number of the box H + ACA snoRNAs can be drawn in the consensus structure to act as Ψ guides but do not appear to have target sites in the rRNA (Ganot et al. 1997a). The tRNA fraction represents bulk tRNA and we cannot exclude the possibility that some tRNA(s) or other small RNAs present in this fraction are specifically undermodified on depletion of Cbf5p.

We conclude that, in contrast to E. coli truB, Cbf5p is required for Ψ formation in the pre-rRNA but does not synthesize Ψ55 in the tRNAs.

**Figure 7.** Ψ formation in a GAL::cbf5 strain. Two-dimensional TLC analysis of 32P-labeled 25S rRNA digested with RNAse T2. (A) RNA extracted from the CBF5 strain following growth in rsg medium. (B) RNA extracted from the CBF5 strain 24 hr after transfer to glu medium. (C) RNA extracted from the GAL::cbf5 strain following growth in rsg medium. (D) RNA extracted from the GAL::cbf5 strain 24 hr after transfer to glu medium. Spots corresponding to Ap, Cp, Gp, Up, and Ψp are indicated. (E) Nucleotides separated by two-dimensional TLC were quantitated by PhosphorImager scanning. The ratio between incorporation into Ψp and Ap in 35S pre-rRNA, 25S rRNA, and bulk tRNA is shown following growth in rsg medium, and 24 hr after transfer to glu medium. The Ψp:Ap ratio in tRNA (right) is shown on a different scale from the 35S and 25S RNA samples (left) because of the greater representation of Ψp in tRNA compared to rRNA. (Open bars) CBF5/rsg; (light gray bars) CBF5/glu; (dark gray bars) GAL::cbf5 rsg; (solid bars) GAL::cbf5 glu.

Cbf5p is a component of the box H +ACA class of snoRNPs

To test for a physical association between Cbf5p and the box H +ACA snoRNAs, a Cbf5p–protein A carboxyl fusion was constructed and integrated at the CBF5 locus under the control of its own promoter (see Materials and Methods). In the resulting strain, Cbf5p–protein A is the only source of Cbf5p activity in the cell. This strain had a wild-type growth rate (data not shown), showing the Cbf5p–protein A fusion to be fully functional.

Immunoprecipitation of Cbf5p–protein A with IgG–agarose beads resulted in the coprecipitation of all tested box H +ACA snoRNAs (snR3, snR10, snR11, snR30, snR31, snR33, snR37, and snR42) but did not detectably coprecipitate box C + D snoRNAs (U3, U14, and snR190), RNAse MRP (Fig. 8) or the U5 snRNA (data not shown). The immunoprecipitations were performed on two independent Cbf5p–protein A strains (YDL524-18 and YDL524-19) at 150 mM and 500 mM Kacetate. Co-precipitation of the box H +ACA snoRNAs with a protein–A fusion to the snoRNPs Nop1p (fibrillarin) is observed at 150 mM salt but is lost at the higher salt concentration (Ganot et al. 1997b). In contrast, copre-
cipitation of the H + ACA snoRNAs with Cbf5p was observed at both salt concentrations. No precipitation of any RNA was seen with an otherwise isogenic CBF5 strain expressing only nontagged Cbf5p (Fig. 8, lanes 1–3). The efficiency of coprecipitation of the box H + ACA snoRNAs with Cbf5p–protein A ranges from 30% to 70%, similar to the efficiency with which the box C + D snoRNAs are coprecipitated with a Nop1p–protein A fusion (data not shown).

The levels of the snoRNAs were assessed during depletion of Cbf5p (Fig. 9A,B). Following growth of the GAL::cbf5 strain on rsg medium, the levels of all tested snoRNAs were the same as in the CBF5 control strain. In contrast, all tested box H + ACA snoRNAs, snR3, snR10, snR11, snR31, snR33, snR37, snR42 (Fig. 9A), and snR30 (Fig. 9B) were strongly depleted following transfer of the GAL::cbf5 strain to glu medium. The levels of the box C + D snoRNAs, U3, snR190 (Fig. 9A), and U14 (Fig. 9B) were unaffected, as were the levels of the RNAse MRP RNA (Fig. 9A) and the U5 snRNA (data not shown). Analysis of earlier time points during depletion of Cbf5p shows that the major drop in the level of snR30 occurs between 8 and 16 hr of depletion of Cbf5p (data not shown), in agreement with the onset of the inhibition of processing.

Gar1p, like Cbf5p, is associated with all known members of the family of box H + ACA snoRNAs (Girard et al. 1992). Moreover, a yeast two-hybrid screen has shown that Gar1p interacts physically with Cbf5p (Y. Henry, M. Fromont, P. Legrain, and M. Caizergues-Ferrer, unpubl.). After transfer of the GAL::cbf5 strain to glu medium, the level of Gar1p also falls dramatically (Fig. 9C).

Figure 8. The box H + ACA snoRNAs are associated with Cbf5p–protein A (CBF5–ProtA). Immunoprecipitations were performed at two salts concentrations [150 and 500 mM Kacetate (KAc)] on two CBF5–ProtA strains (YDL524-18 and YDL524-19) and at 150 mM Kacetate on the wild-type isogenic control (CBF5). RNA was extracted from equivalent amounts of total (T), supernatant (S), and pellet (P) fractions and separated on an 8% polyacrylamide gel containing 8 M urea. Probes used for the hybridizations are described in Materials and Methods.

Figure 9. Box H + ACA snoRNP components are codepleted in a GAL::cbf5 strain. H + ACA snoRNAs (A,B) and Gar1p (C) are codepleted with Cbf5p. Probes used for the hybridizations are described in Materials and Methods. RNA was extracted from the CBF5 and GAL::cbf5 strains following growth on rsg medium (0-hr lanes) and at intervals following transfer to glu medium (8- to 70-hr lanes) and separated on an 8% polyacrylamide gel containing 8 M urea. The anti-Gar1p antibody used was described by Girard et al. (1992) and cross-reacts weakly with Nop1p.
We conclude that Cbf5p is a core component of the box H + ACA snoRNPs that is required for the stability of both the RNA and protein components of the snoRNPs.

**Discussion**

We report here a detailed functional analysis of Cbf5p, an essential nucleolar protein (Jiang et al. 1993) and putative $\Psi$ synthase (Koonin 1996). We found that genetic depletion of Cbf5p inhibits both pre-rRNA processing and formation of $\Psi$ in the pre-RNA. Expression of a Cbf5p-protein A fusion protein allowed the co-precipitation of all tested members of the large class of box H + ACA snoRNAs, most of which function as guides for the site-specific formation of $\Psi$ residues in the pre-rRNA (Ganot et al. 1997a; Ni et al. 1997). Members of the other major class of snoRNAs, the box C + D snoRNAs, were not detectably co-precipitated with Cbf5p-protein A nor were other small RNA species tested (U5 and MRP RNA). Moreover, the depletion of Cbf5p resulted in the codepletion of all tested box H + ACA snoRNAs but did not affect the levels of the box C + D snoRNAs or other small RNA species. We conclude that Cbf5p is an integral component of the box H + ACA class of snoRNPs.

Protein components of other small RNP s are required for the stability of the RNA components of the particles; these include the spliceosomal snRNAs (see Cooper et al. 1995 and references therein) and the RNA components of signal recognition particle (SRP; Brown et al. 1994), RNase P and RNase MRP (Lygerou et al. 1994; Lafontaine et al. 1995, and references therein) and the RNA component of the ribonucleoprotein particles. We conclude that Cbf5p is an integral component of the box H + ACA class of snoRNPs.

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lation is not strongly affected by depletion of Cbf5p, making it unlikely that Cbf5p is the eukaryotic tRNA \( \Psi \)55 synthase. In fact, Pus4p, another yeast homolog of tRNA \( \psi \)U (Koonin 1996), is the tRNA \( \Psi \)55 synthase (Becker et al. 1997). We propose that Pus4p and Cbf5p arose in early eukaryotes by gene duplication followed by divergence of function.

**Materials and methods**

Construction of the GAL::cbf5 and CBF5::Prot.A strains

Standard Saccharomyces cerevisiae growth and handling techniques were employed. The transformation procedure was described by Gietz et al. (1992). The wild-type strains used in this study were FY1679-28C and YDL401 (Lafontaine and Tollervey 1996). The GAL::cbf5 strain was created in the YDL401 background by use of a one-step PCR strategy (Lafontaine and Tollervey 1996). The oligonucleotides used for the amplification with plasmid pTL26 were oligonucleotide 1, 5'-TTTCCAAAT-GATGAGATGTTAGGAAAAAATTAATGATCTC-TTGCCCTCCTCTGAT-3' and oligonucleotide 2, 5'-CCT-TAAATAGGAATACTCCCCCAGATTGTATATCGG-5TCCCTCAGATTTGGAATTTTC-3'. Transformants were screened for glucose sensitivity by PCR on yeast colonies and by Southern blot analysis. All the RNA analysis experiments were done in duplicate on two independently isolated GAL::cbf5 strains (YDL521-1 and YDL521-3). The analysis of \( \Psi \) content of rRNAs was made on strain YDL521-1. The CBF5::Prot.A strains expressing Cbf5-protein A were constructed in strain FY1679-28C by use of the same strategy. The oligonucleotides used for the amplification with pTL54 were oligonucleotide 3, 5'-GAAAGCCTGTTAAGTTCCAAAAATATGGCAA-AAAATCTAAGAAATCTAAGAAGGCGTGAGAACCAACATT-TC-3' and oligonucleotide 4, 5'-TACAAGCTGGTGATAAA-GAAAATTCTAGTTTAAATACACCTGAGATCGTC-3'. Transformants were screened by PCR on yeast colonies and by Western blot analysis (using PAP antibody, Sigma). Two independently isolated CBF5::Prot.A strains (YDL524-18 and YDL524-19) were used for the immunoprecipitation experiment presented in Figure 8.

**GAL::cbf5 time course, RNA extraction, Northern hybridization, and primer extension**

For depletion of Cbf5p, cells growing exponentially in permissive conditions (rsg) at 30°C were harvested by centrifugation, washed, and resuspended in 2% glucose minimal medium. The cells were grown in the exponential phase of growth, cells were diluted with prewarmed medium and constantly maintained in exponential phase. RNA extraction, Northern hybridization, and primer extension were as described by Lafontaine et al. (1995). Standard 1.2% agarose/formaldehyde and 8% acrylamide gels were used to analyze the process of the high and low molecular weight rRNAs species, respectively (Tollervey 1987). Ten percent acrylamide gels were used to analyze the rRNA processing. Nine micrograms of total RNA was used for the Northern analysis presented in Figures 2, 3, 5 and 6, whereas 4.5 \( \mu \)g was used for the Northern analysis presented in Figures 4 and 9. Oligonucleotides used for pre-rRNA hybridization were oligonucleotides a, b, c, d, g described previously by Lafontaine et al. (1995) as oligonucleotides d, g, h, i, k, l, respectively, and oligonucleotide f described previously as oligonucleotide b by Mitchell et al. (1996). Oligonucleotides anti-U3, U14, MRP, snR10, and snR190 were as described previously (Girard et al. 1992, Dichtl and Tollervey 1997). Oligonucleotides anti-mature tRNA\( ^{\text{P}} \) and tRNA\( ^{\text{G}} \) and anti-intronic tRNA\( ^{\text{P}} \) and tRNA\( ^{\text{G}} \) were synthesized by D. L. J. L. (Promega). All the RNA analysis experiments were done in duplicate on two independently isolated GAL::cbf5 strains (YDL521-1 and YDL521-3). The analysis of \( \Psi \) content of rRNAs was made on strain YDL521-1. The CBF5::Prot.A strains expressing Cbf5-protein A were constructed in strain FY1679-28C by use of the same strategy. The oligonucleotides used for the amplification with pTL54 were oligonucleotide 3, 5'-GAAAGCCTGTTAAGTTCCAAAAATATGGCAA-AAAATCTAAGAAATCTAAGAAGGCGTGAGAACCAACATT-TC-3' and oligonucleotide 4, 5'-TACAAGCTGGTGATAAA-GAAAATTCTAGTTTAAATACACCTGAGATCGTC-3'. Transformants were screened by PCR on yeast colonies and by Western blot analysis (using PAP antibody, Sigma). Two independently isolated CBF5::Prot.A strains (YDL524-18 and YDL524-19) were used for the immunoprecipitation experiment presented in Figure 8.

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**Analysis of \( \Psi \) levels**

To determine the \( \Psi \) content in rRNAs and trRNAs, strain YDL521-1 was pregrown at 30°C in rich medium containing 2% raffinose, 2% sucrose, and 2% galactose (YP-RSG). The culture was split in two, washed, and resuspended in either rich glucose medium (YPD) or YP-RSG at an OD\( _{600} \) of 0.03. Both cultures were incubated for 6 hr at 30°C before being washed and transferred to similar medium without PO\(_4\) (following the recipe described by Warner (1991)). After a further incubation of 18 hr, 50 ml from each culture was labeled for 15 min with 9 mCi of \( ^{32} \)P orthophosphate (9000 Ci/m mole). Total RNA was extracted and analyzed by electrophoresis on a 1.2% agarose/formaldehyde gel. 35S pre-rRNA, 25S rRNA, and total tRNAs were purified by electrophoresis, digested with RNase T2 (in 50 mM NNa acetate at pH 5.5 at 37°C), and analyzed by two-dimensional gel filtration with TLC as described by Filipowicz and Shatkin (1983). The procedure was used essentially as described by Bousquet-Antonelli et al. (1997).

**Immunoprecipitation of Cbf5p-protein A**

Yeast whole-cell extracts were prepared according to Séraphin and Rosbash (1989). Lysates were made in buffer A (20 mM Tris HCl at pH 8.0, 5 mM MgCl\(_2\), 1 mM DTT, 0.2% Triton X-100, 0.5 mM PMSF, and 150 or 500 mM Kacetate), and supernatants were cleared by centrifugation (56,000 rpm at 4°C for 20 min). Immunoprecipitation experiments were performed as described previously (Garot et al. 1997b). Lysates equivalent to 37.5 OD\( _{600} \) of cells were incubated on a rotating wheel for 2 hr at 4°C with 100 \( \mu \)l of IgG-agarose beads (Sigma A2909), and pre-washed in buffer A in a total volume of 400 \( \mu \)l. Pellets were washed four times for 20 min in 1 ml of buffer A. Each gel lane (T, S, and P) was loaded with RNA from a fraction of the preparation equivalent to 10 OD\( _{600} \) of cells.

**Western blotting**

Total protein extracts corresponding to \( 10^6 \) cells were loaded in each lane. Affinity-purified anti-Gar1p antibodies were used at 1:200 dilution as described by Girard et al. (1992). The anti-Gar1p antibodies weakly cross-react with Nop1p.

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