Cwc23, an Essential J Protein Critical for Pre-mRNA Splicing with a Dispensable J Domain

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Received 26 June 2009/Returned for modification 30 July 2009/Accepted 7 October 2009

J proteins are structurally diverse, obligatory cochaperones of Hsp70s, each with a highly conserved J domain that plays a critical role in the stimulation of Hsp70’s ATPase activity. The essential protein, Cwc23, is one of 13 J proteins found in the cytosol and/or nucleus of Saccharomyces cerevisiae. We report that a partial loss-of-function CWC23 mutant has severe, global defects in pre-mRNA splicing. This mutation leads to accumulation of the excised, lariat form of the intron, as well as unspliced pre-mRNA, suggesting a role for Cwc23 in spliceosome disassembly. Such a role is further supported by the observation that this mutation results in reduced interaction between Cwc23 and Ntr1 (SPP382), a known component of the disassembly pathway. However, Cwc23 is a very atypical J protein. Its J domain, although functional, is dispensable for both cell viability and pre-mRNA splicing. Nevertheless, strong genetic interactions were uncovered between point mutations encoding alterations in Cwc23’s J domain and either Ntr1 or Prp43, a DExD/H-box helicase essential for spliceosome disassembly. These genetic interactions suggest that Hsp70-based chaperone machinery does play a role in the disassembly process. Cwc23 provides a unique example of a J protein; its partnership with Hsp70 plays an auxiliary, rather than a central, role in its essential cellular function.

Hsp70-based machineries constitute a key component of the cell’s chaperone network, playing a central role in many processes, including de novo protein folding, protein translocation across membranes, and remodeling of protein complexes (6, 13). By their ability to bind to short, exposed, hydrophobic stretches of polypeptide, Hsp70s serve as the core of this protein folding machinery. However, Hsp70s cannot function alone. J proteins (often referred to as Hsp40s) are their obligate partners, serving to stimulate Hsp70’s ATPase activity and thereby stabilizing interaction with client proteins (19). J proteins are very diverse but, by definition, contain an ~70-amino-acid “J domain” that interacts directly with the Hsp70 ATPase domain (12, 17). It is well established that the J domain is critical for function of the Hsp70-based chaperone machinery, since single amino acid alterations in its highly conserved HPD motif disrupt function, both in vitro and in vivo, without affecting domain structure (9, 14). The Saccharomyces cerevisiae genome encodes 22 J proteins. Of these, 13 are found in the cytosol and/or nucleus. One, Cwc23, is the focus of this report. Deletion of CWC23 causes inviability in some strain backgrounds, although adaptation or suppression allows slow growth in others (31, 34). The growth defect of cwc23Δ cells cannot be rescued by overexpression of any of the other 12 J proteins (31), indicating that Cwc23 carries out a specialized cellular function. Cwc23 has been linked to pre-mRNA splicing via both genome-wide and spliceosomal component-directed physical interaction studies (7, 25).

Pre-mRNA splicing is a highly precise and stepwise process whereby noncoding introns are removed from nascent transcripts. The splicing reaction is catalyzed by the spliceosome, a large ribonucleoprotein (RNP) complex composed of five small nuclear RNAs and at least 100 different proteins (5, 24, 38). The widely held model of the splicing pathway posits that the spliceosome is not a monolithic, stable complex but rather a series of complexes that must be assembled de novo for each splicing event and subsequently disassembled upon completion. Both the assembly and the disassembly steps of pre-mRNA splicing require a series of macromolecular rearrangements involving changes in RNA-RNA, RNA-protein, and protein-protein interactions. A positive “two-hybrid” interaction between Cwc23 and Ntr1, an essential protein required for efficient spliceosomal disassembly, was recently reported (26). As part of the “NTR complex,” Ntr1 recruits the DExD/H-box ATPase Prp43, which is critical for disassembly, to the spliceosome (4, 35). The interaction surface between Prp43 and Ntr1 involves a region of Ntr1 termed the G patch, a motif found in many proteins and known to be involved in both protein-protein and protein-RNA interactions (1). Given the links between Cwc23 and RNA splicing, we further investigated whether Cwc23 plays a role in this process. Indeed, a partial loss-of-function mutation in CWC23 causes profound global effects on splicing, demonstrating a role of Cwc23 in this process. However, the J domain of Cwc23 is not normally required for either cell viability or pre-mRNA splicing. However, when the interaction between Ntr1 and Prp43 is compromised, Cwc23’s J domain becomes essential, indicating a role for it,
and thus Hsp70-based chaperone machinery, in pre-mRNA splicing.

MATERIALS AND METHODS

Construction of plasmids. A DNA fragment containing 758 bp upstream and 545 bp downstream of start and stop codons of CWC23 was PCR amplified from genomic DNA and cloned in pRS316 (URA3 CEN), pRS314 (TRP CEN) and pRS313 (HIS3 CEN) vectors as a BamHI/SacII fragment. To obtain approxi-
mate vectors (23). Jjj1-J domain (amino acids 1 to 128) was PCR amplified from pRS313-Cwc23 plasmid and cloned in the pRS314 (obtained as described above) with ntr1A carrying wild type NTRI mutants, were made by crossing cwc23-wt cells expressing Cwc23 and Cwc23_His with a HIS3 CEN-based plasmid (pRS313), followed by tetrad dissection to observe the haploid strain.

ntr1A and ppr43A strains were obtained from Beate Schwer (33). Y2244, Y2245, and Y2246, used to assess synthetic growth defects with NTRI mutants, were made by crossing cwc23-6 cells expressing wt Cwc23 or Cwc23_225 from a HIS3 CEN-based plasmid (pRS313), followed by tetrad dissection to observe the haploid strain.

Genetic interactions between NTRI and CWC23 mutants were investigated by transforming pRS413-based plasmids (HIS3 CEN) with wt or G-patch mutant NTRI genes (encoding the alterations L66A, Y74A, or L80A, which were described previously [33]) into Y2244, Y2245, and Y2246. To investigate whether the expression of a J domain fragment could complement the synthetic growth defect between J domain mutants of CWC23 and G-patch NTRI mutants in trans, J domain-encoding fragments of CWC23 (CWC23_6 [CEN ADH]) or CWC23-J (2µm GDP) or another cytosolic J protein gene J11 [J11_1225 (2µm GDP)] were transformed into Y2244, Y2245, and Y2246. The Y2178 strain (cwc23-ade2 [pRS316-Cwc23]) was constructed by swapping the KanMX cassette in the heterozygous diploid cwc23/KanMX strain with the NotI-linearized ade2 disruption cassette plasmid (37). The resulting strain was transformed with the pRS316-Cwc23 diploid and sporulated, and tetrads were dissected to yield Y2178. To test a synthetic genetic interaction with PRP43, yeast strains Y2251 and Y2253 were constructed by crossing Y2178 with ppr43A cells harboring either pRS413-Prp43 or pRS314-Prp43 plasmids (pRS314-Prp43). The construction relies on the having the deletion alleles of both CWC23 and PRP43 were obtained by tetrad dissection. Finally, Y2251 and Y2253 were transformed with pRS313 (HIS3 CEN) plasmids expressing wt Cwc23, Cwc23_225, or Cwc23_1165 (20). Transformants were selected on dropout media, and synthetic genetic interactions between CWC23 and PRP43 mutants were scored after plating cells on 5-FOA medium. The effect of expression of a J domain containing fragment in trans was investigated by transforming pRS413 (CEN ADH) Cwc23-J (2µm GDP), or J11_1225 (2µm GDP) into Y2251 and Y2253 expressing Cwc23_225. Strains Y2305, Y2306, Y2307, Y2308, Y2309, and Y2310 (see Table 1) were made to study the genetic interaction between mutations in CWC23 and other splicingosomal genes. Homozygous diploid strains from the yeast knockout collection (40) for ntr1A, ntr1B, ntr1C, ntr1D, ntr1E, ntr1F, ntr1G, and ntr1H were sporulated. Haploid obtained by tetrad dissection were mated with Y2178. Double deletions of CWC23 and one of the six genes, obtained by tetrad dissection, were transformed with pRS314 or pRS413 harboring wt Cwc23 or Cwc23_225.

Protein expression and purification. His-tagged Saa1 and Sb1 were purified as described previously (15, 28), Cwc23_225-His6 was expressed from pET3a plasmid in E.coli(DE3) cells (22). Cells were induced with 0.2 mM IPTG (isopropyl-β-D-thiogalactopyranoside) at 20°C for 8 h. The cell pellet was resuspended and disrupted using the Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a Ni-NTA agarose column (Novagen). The supernatant was loaded onto a N

TABLE 1. Yeast strains generated in this study

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<th>Strain</th>
<th>Description</th>
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resuspended in 400 μl of TES buffer (10 mM Tris [pH 7.5], 10 mM EDTA, 0.5% sodium dodecyl sulfate [SDS]) and 400 μl of acidic phenol-chloroform-isooamyl alcohol (25:24:1 [pH 4.2]). The cells were lysed by adding 400-μl equivalents of 0.5-mm glass beads, followed by incubation at 65°C for 1 h with intermittent vortexing. The tubes were incubated on ice for 5 min and then centrifuged at 16,000 × g at 4°C. The upper aqueous phase containing the total RNA was precipitated by addition of 1/10 volume of sodium acetate (pH 5.2) and 2.5 volumes of chilled ethanol. Total RNA was spun down for 10 min at 16,000 × g at 4°C. Finally, the RNA pellet was washed with 70% ethanol, air dried, and dissolved in 50 μl of RNase-free distilled water. For use with a full-length actin intron probe, 20 μg of total RNA was resolved on a denaturing morpholinepropanesulfonic acid-formaldehyde 1% agarose gel and transferred by capillarity to a nylon membrane (GE Healthcare). For use with actin intron probe, 20 μg of RNA was resolved on a denaturing morpholinepropanesulfonic acid-formaldehyde 1% agarose gel. Radiolabeled PCR fragment corresponding to the full-length or 4CTT intron labeling system (Promega, Madison, WI). Hybridization was carried out in ULTRATAHyb solution (Ambion) at 42°C, overnight. After the washings, the blots were visualized by using a PhosphorImager.

To monitor pre-mRNA splicing defects on a global scale, splicing-sensitive whole genome microarrays were used. Cultures were grown as previously described (29). Total RNA was isolated as described previously, but for each microarray, cDNA was prepared from 20 μg of total RNA in a 20-μl reaction mixture containing 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM MgCl2, 10 mM dithiothreitol, 0.5 mM ATP, 0.5 mM CTP, 0.5 mM GTP, 0.5 mM TTP, 0.01 mM 5- (3-aminoallyl)-dUTP, 12.5 μg of dNS primer, and 5 μg of M-MLV RT. Labeled cDNA samples were hybridized on custom designed Agilent 8x15K microarrays. These microarrays contain probes targeting over 6,000 yeast genes. For intron-containing genes, the microarrays also contain probes that target regions of the intron, as well as the junction between the intron and exons (29). Microarray design details can be found at NCBI’s Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo/) under accession number GPL8154. Samples were hybridized according to manufacturer’s protocols at 60°C for 17 h. Microarrays were washed for one minute in 6× SSPE (0.9 M NaCl, 60 mM NaH2PO4, 6 mM EDTA), 0.005× Sarkosyl, and then briefly washed in 0.006× SSPE-0.005× Sarkosyl prior to scanning. Images were obtained by using an Axon 4000B scanner, and data were extracted from the images by using Genepix 6.0 software. Raw data were processed by using Biocomputator to implement the Loess normalization function. After normalization, replicate values were averaged to determine the behavior of each feature on the array. Each experiment was performed as a dye-flipped replicate, with the composite behavior being presented in the figures and text. Both raw and processed data are available from GEO.

**RESULTS**

Cwc23’s C terminus, but not its N-terminal J domain, is essential for cell viability. The N-terminal 80-amino-acid segment of *S. cerevisiae* Cwc23 (Fig. 1A), as well as orthologs identified in other fungal species and in higher eukaryotes (see Fig. S1 in the supplemental material), are highly similar in sequence to known J domains. To determine whether the J domain of Cwc23 is essential for its in vivo function, a mutation encoding a histidine-to-glutamic-acid substitution in the invariant HPD motif was made. This particular mutation was selected because it has been demonstrated to severely affect the ability of several J proteins to stimulate the ATPase activity of their partner Hsp70 and consequently their in vivo function (9). Surprisingly, not only was the cwc23H50Q strain viable (Fig. 1B, panels 1 and 2), it grew indistinguishably from wild-type (wt) (Fig. 1B, panels 3 to 5). To address the concern that the H50Q mutation might not completely abolish J domain function, we constructed cwc23ΔJ, with a deletion of the 80 codons of the N-terminal J domain. Remarkably, cwc23ΔJ cells also grew indistinguishably from wt cells (Fig. 1B), establishing that the J domain region is not required for Cwc23’s essential function.

The dispensability of the J domain region of Cwc23 raises the question of whether it is actually a functional J domain. To address this question, we carried out two experiments. First, we used our previous observation that Cwc23, when expressed from the strong GPD promoter, substantially rescued the severe growth defects of cells lacking Ydj1, the most abundant cytosolic/nuclear J protein (31). However, cwc23ΔJΔJ was completely ineffective in rescuing the growth defect of ydj1Δ cells (Fig. 1C), even though it was expressed at levels similar to that of wt Cwc23 (Fig. 1C, right panel). Second, we tested the effect of the H50Q alteration on the ability of Cwc23 to stimulate the ATPase activity of Hsp70. Since this was the first time Cwc23 had been purified, we first tested whether Cwc23 was competent to stimulate the ATPase activity of either of the two classes of cytosolic/nuclear Hsp70s, Ssa and Ssb. Ssa1 and Ssb1 were loaded with [32P]ATP, and the ability of a 225-amino-acid fragment of Cwc23 to stimulate the basal ATPase activities was monitored. Although little effect on Ssb1’s ATPase activity was observed (Fig. 1D, right), the ATPase activity of Ssa1 was stimulated ~7-fold when present in a stoichiometric amount (Fig. 1D, left). This level of stimulation was similar to that of Ydj1, an established J protein partner of Ssa1 (15). The H50Q alteration virtually eliminated this stimulatory ability (Fig. 1D, left). These results support the idea that Cwc23 is a functional J protein, which, like Ydj1 and many other cytosolic J proteins, can partner with Ssa. Nevertheless, inactivation of the J domain does not result in a loss of Cwc23’s essential cellular function.

**Truncation of Cwc23’s C terminus, but not its J domain, causes global defects in pre-mRNA splicing.** Since Cwc23 was found physically associated with the spliceosome, we sought to determine whether Cwc23 is indeed involved in pre-mRNA splicing. Earlier, we reported CWC23 to be an essential gene, since viable colonies could not be obtained using the standard selection on 5-FOA containing medium for mutants whose viability is maintained by a wt gene in a *URA3*-based plasmid (31) (Fig. 1B). However, as previously reported (34), dissection of a cwc23Δ heterozygous diploid strain occasionally yielded
cwc23Δ microcolonies (Fig. 2A, left panel). Total RNA from primary cultures of the cwc23Δ microcolonies and from wt cells was used for hybridization analysis using radiolabeled full-length actin (ACT1) genomic DNA probe. Consistent with a role for Cwc23 in splicing of actin pre-mRNA, two bands were observed in the cwc23Δ sample: one at the position of the mature mRNA found in the wt sample and the other at the position expected for the larger unspliced pre-mRNA species (Fig. 2A, right panel).

Because the haploid cwc23Δ strains commonly accumulated suppressing mutations that could complicate analysis of Cwc23 function, we chose to continue our investigation by searching for partial loss-of-function mutants of CWC23 by truncating the 3′ end of the gene. Although cwc23Δ was inviable (data not shown), cwc231-225, which encodes a protein lacking the C-terminal 58 amino acids, was viable, growing more poorly than wt cells between 23 and 37°C but not forming colonies at 18°C (Fig. 2B). We noted that cells expressing 5- to 10-fold higher levels of Cwc231-225 grew no better than cells expressing nearly normal levels of the mutant protein, supporting our conclusion that Cwc231-225 is not simply a hypomorphic allele but rather is functionally defective (Fig. 2C).

To determine whether pre-mRNA splicing was globally affected when Cwc23 function was compromised, whole-genome splicing microarrays were used. For each intron-containing gene a minimum of three primers, targeting three regions of each pre-mRNA, were present on the microarray: the intron to probe pre-mRNA levels, the exon-exon junction to probe mature mRNA levels, and an exonic region to assess changes in total mRNA levels. By simultaneously considering the pre-mRNA, mature mRNA, and total RNA levels in mutant relative to wt cells, differences in splicing efficiency can be assessed.

As seen in Fig. 3A, significant levels of unspliced pre-mRNA were detected for most intron-containing genes in cells expressing cwc23Δ whether grown at the permissive temperature of 30°C or after a shift to the nonpermissive temperature of 16°C for 30 min. When we consider both the number of transcripts affected and the magnitude of pre-mRNA accumu-
ation, the splicing defects seen in the cwc23Δ,225 mutant are similar to those seen in a strain containing a temperature-sensitive allele of the essential spliceosomal protein Prp43, prp43-Y402A (33) (Fig. 3A). Although no determination can be made regarding the mechanistic role of a protein based solely on the identity of the pre-mRNAs whose splicing is impacted in an experiment such as this (29), these data nevertheless make it clear that Cwc23 plays a prominent, global role in pre-mRNA splicing based on both the widespread defect and the level of pre-mRNA accumulation seen in the cwc23Δ,225 strain.

Cwc23 interacts with Ntr1, an essential spliceosome disassembly factor (4, 35), suggesting that it might also be important for the disassembly process. A hallmark of mutants in this pathway is that the excised lariat introns, which are normally rapidly degraded, become significantly stabilized (2). The accumulation of these lariat-bound complexes sequesters essential spliceosomal complexes, indirectly leading to a global defect in pre-mRNA splicing. To directly test this idea, we probed RNA isolated from cwc23Δ,225 cells with an intron-specific probe, as well as the more standard probe encompassing the full-length actin gene (ACT1). Bands were visualized utilizing a phosphorimager (top panel). As a loading control, the membrane was stained with ethidium bromide to visualize rRNA (bottom panel).

FIG. 3. cwc23Δ,225 is defective in pre-mRNA splicing, but cwc23Δ,1 is not. (A) Global analyses of pre-mRNA splicing. For each of 301 intron-containing genes, the behaviors of the total mRNA, pre-mRNA, and mature mRNA were determined (indicated as T, P, and M, respectively, above each lane; see the diagram at top). Each horizontal line describes the behavior of a single intron-containing gene. Ratio values were calculated for each of the strain comparisons. The data are presented as false-colored representations of the log2 value for each feature. For the cwc23Δ,225 experiments, samples were first collected from both mutant and wt strains while growing at 30°C. An additional sample was collected after both strains had been shifted to 16°C for 30 min. For the prp43Y402A experiment, both mutant and wt strains were grown at 30°C then shifted to 37°C for 30 min prior to sample collection. For the Cwc23Δ,1 experiment, samples were collected from both mutant and wt strains growing at 30°C. (B) cwc23Δ,225 accumulates actin lariat-introns. Equal amounts of total RNA isolated from wt and cwc23Δ,225 cells expressing either Cwc23 (WT) or Cwc23Δ,225 (225) were resolved on denaturing agarose gels, transferred to nylon membrane, and probed with radiolabeled DNA encompassing the full-length actin gene (ACT1). Bands were visualized utilizing a phosphorimager (top panel). As a loading control, the membrane was stained with methylene blue to visualize rRNA (bottom panel).
ing the entire actin gene. cwc23Δ225 cells had high levels of both actin pre-mRNA and intron lariat compared to wt cells (Fig. 3B), indicating a critical involvement of Cwc23 in the splicing disassembly pathway.

Having obtained evidence that Cwc23 plays a role in disassembly of the spliceosome, we addressed whether the J domain was important for splicing. We observed virtually no pre-mRNA splicing defects in the cwc23Δ strain using microarray analysis (Fig. 3A). In addition, the level of the intron lariat in cwc23Δ cells was indistinguishable from that present in wt cells (Fig. 3B). Together, our results confirm that although the C terminus of Cwc23 is required for both cell viability and efficient pre-mRNA splicing, the J domain is dispensable for both.

No compensation by other J proteins in the absence of Cwc23’s J domain. Since the J domain is critical for the function of all yeast J proteins tested thus far, we wanted to determine whether the lack of an observable effect upon deletion of Cwc23’s J domain was attributable to compensation, in trans, by other J proteins. Besides Cwc23, six other J proteins (Apj1, Xdj1, Caij, Sis1, Jji1, and Ydj1) are known to be at least partially localized to the nucleus or involved in nuclear function (www.yeastgenome.org). Thus, we constructed a set of double mutants, each having cwc23Δ and a complete deletion of one of the six J protein genes listed above. Four of the double mutant strains (the apj1Δ cwc23Δ, xdj1Δ cwc23Δ, caij1Δ cwc23Δ, and jji1Δ cwc23Δ strains) expressing cwc23Δ grew indistinguishably from the single J protein gene deletions. In addition, no defects in the splicing of actin pre-mRNA were observed (data not shown). In the case of cells lacking Ydj1, a very subtle but reproducible synthetic growth defect was observed at 18°C (see Fig. S2A in the supplemental material). However, accumulation of actin pre-mRNA was not detected at 23°C or after a shift to 18, 37, or 42°C (see Fig. S2B in the supplemental material). We conclude that the slight synthetic growth defect at 18°C is not related to pre-mRNA splicing. Rather, we think that Cwc23, at its normal low levels, is slightly compensating for the absence of Ydj1, a finding consistent with the robust compensation observed when Cwc23 is expressed at higher levels (Fig. 1C). Since Sis1 is essential, we exploited the fact that levels of Sis1 can be expressed at ca. 10% of normal levels by placing Sis1 under the control of the Tet repressible promoter to test for a genetic interaction between SIS1 and cwc23Δ (3). Cells with lowered levels of Sis1 and either wt Cwc23 or Cwc23Δ grew indistinguishably. Likewise, no defect in the splicing of actin pre-mRNA was detected (data not shown).

As a complementary approach, we queried our microarray data to determine whether cytosolic HSP70s and other J protein genes might be upregulated in CWC23 mutant strains (8, 9, 39). We plotted the geometric mean intensity versus the log ratio value for each of the ~6,000 unique mRNA probes included on our microarray analyses of cwc23Δ225 and cwc23Δ strains compared to a wt strain (see Fig. S2C in the supplemental material). CWC23 mRNA was significantly increased in cwc23Δ225, presumably because it is expressed from the ADH promoter. Even though it is under the control of its endogenous promoter, a modest increase in Cwc23Δ mRNA was observed, perhaps because it is expressed from a plasmid. Strikingly, none of the other 21 J protein genes showed any significant difference in expression compared to the wt strain. Likewise, none of the Ssa or Ssb Hsp70 genes showed any significant change in expression. In sum, we obtained no evidence in either our genetic or our biochemical analyses that any other J domain is functionally substituting in trans when Cwc23’s J domain is absent or nonfunctional. Rather, our data support the idea that under typical laboratory conditions the J domain of Cwc23, and thus Hsp70 machinery function, is dispensable.

Cwc23’s J domain is critical when interaction between Cwc23 and Ntr1 is compromised. Since the Hsp70/J protein chaperone machinery is known to modulate protein-protein interactions, we wanted to determine whether Cwc23’s J domain is important when the function of a protein with which Cwc23 interacts, Ntr1 (26), is compromised. First, we carried out a yeast two-hybrid experiment to exclude the possibility that the J domain of Cwc23 is important for this interaction. Full-length CWC23 and fragments encoding amino acids 1 to 83 (J domain), 1 to 225, 81 to 283 (Cwc23Δ), and 226 to 283 (the C-terminal 58 amino acids) were cloned into a GAL4 activation domain plasmid, and the fusion proteins were coexpressed with a fusion of the GAL4 DNA-binding domain and Ntr1. Since the HIS3 gene was under the control of GAL4 in the tester strain, growth in the absence of histidine is dependent on interaction between Cwc23 and Ntr1. As expected from previous work (26), the full-length Cwc23 fusion allowed robust cell growth (Fig. 4A). Cells expressing the Cwc23Δ fusion grew as well as those expressing full-length protein, while those expressing a fusion of the N-terminal 81 amino acids did not indicate that the J domain is not important for interaction with Ntr1. On the other hand, cells expressing the Cwc231-225 fusion grew extremely poorly in the absence of histidine (Fig. 4A), indicating the importance of the C-terminal 58 amino acids of Cwc23 for interaction with Ntr1. However, a fusion of the C-terminal 58 amino acids did not support growth. These results are consistent with the idea that the C-terminal 58 amino acids of Cwc23 is important, but not sufficient, for interaction with Ntr1, and that the J domain does not play a role in the interaction.

Since the absence of the J domain did not compromise the interaction between Cwc23 and Ntr1, we proceeded to investigate whether mutations in NTR1 have synthetic genetic interactions with CWC23 J domain mutations. We tested three NTR1 point mutations, L68A, Y74A, and L80A, each of which alters the G patch, causing significant defects in interaction with Prp43 in vitro but no obvious defect in vivo (33, 35). We used the plasmid shuffling technique, plating strains with different combinations of NTR1 and CWC23 alleles, as well as a wt NTR1 gene on a URA3-based plasmid. Cells were plated on 5-FOA-containing plates to select for those having lost the URA3-based plasmid and thus the wt NTR1 gene it contained. As expected, the control strains expressing either the wt NTR1 or CWC23 genes grew well on the 5-FOA plates. However, we were unable to recover yeast strains expressing any of the Ntr1 variants in combination with Cwc23Δ (Fig. 4B). We reasoned that this lack of function could be the result of indirect effects on protein conformation, rather than loss of J domain function. Therefore, we combined the H-to-Q substitution mutation in CWC23 described above that renders J domains nonfunctional with G-patch NTR1 mutations. No double mutants containing both cwc23H50Q and ntr1 mutants were recovered.
on 5-FOA plates, suggesting that cells cannot tolerate defects in both the J domain of Cwc23 and the G patch of Ntr1.

Since we demonstrated that the C terminus, but not the J domain, is important for Cwc23’s interaction with Ntr1, we performed the analogous intragenic synthetic genetic interaction test, combining the N-terminal and C-terminal truncations, generating cwc23Δ81-225, Cwc23Δ81-225 was stably expressed (Fig. 4D). However, no viable cwc23Δ81-225 cells were obtained (Fig. 4C). Consistent with this result, cwc23Δ1-225 H50Q was also unable to rescue the viability of a cwc23Δ strain (Fig. 4C). We conclude that J domain function becomes critical when the function of the C-terminal region, which is important for interaction with Ntr1, is compromised.

Specificity of synthetic genetic interaction of CWC23 J domain mutations. Both circumstances in which Cwc23’s J domain was found to be important involved Ntr1: (i) when Cwc23’s interaction with Ntr1 was compromised by the alteration of Cwc23 itself and (ii) when the Ntr1-Prp43 interaction was compromised by the alteration of Ntr1. We pursued the idea that J domain function was important when interaction among the components of the NTR complex was compromised by testing other synthetic genetic interactions. First, we tested a PRP43 mutation, prp43Y402A, an allele of PRP43 known to affect interaction with Ntr1 (33). Again, we used the plasmid shuffling technique, plating strains on 5-FOA-containing plates. As expected, prp43Y402A cells expressing full-length Cwc23 grew indistinguishably from wt cells. However, yeast strains expressing prp43Y402A and cwc23Δ or cwc23H50Q could not be recovered at 18 and 23°C. Double mutants containing prp43Y402A and either cwc23Δ or cwc23H50Q were recovered at 30°C but grew slowly at that temperature (Fig. 5A and data not shown).

To more broadly explore the relationship between Cwc23 and splicing, we next looked for synthetic genetic interactions with components of the spliceosomal machinery that are known to function at steps other than disassembly. We examined interactions with deletions of six nonessential components, including the early-acting U1 component MUD1, the commitment complex factor MUD2, the U2-associated components LEA1 and MSL1, and finally ISY1 and NTC20, which are components of the NTC (for Prp nineteen complex) that is added during spliceosomal activation (5). Notably, the NTR (for nineteen-complex related) components Ntr1 and Ntr2 have been shown to weakly interact with the NTC, suggesting that they could interact with the spliceosome well prior to the disassembly step (35). Nevertheless, none of the genes we tested showed synthetic growth defects with cwc23Δ (see Fig. S3 in the supplemental material), indicating that the severe synthetic growth defects observed with the NTR1 and PRP43 mutations are specific.

The J domain and C-terminal regions of Cwc23 cannot function in trans. The results described above suggest the possibility that Cwc23 carries out two independent functions: the C-terminal region being critical for an interaction with Ntr1, and the N-terminal J domain for an interaction with Hsp70. We therefore examined, again using the 5-FOA selection technique, whether the expression of Cwc23Δ1-225 could suppress the synthetic genetic defects seen in double mutant containing prp43Y402A and either cwc23H50Q or cwc23Δ. The prp43Y402A mutation was chosen because the synthetic growth defects with
was revealed to be a J protein with unusual, if not unique, characteristics. Although it plays a critical role in pre-mRNA splicing, its J domain is not normally required for this function. Unlike the situation with many J proteins, the J domain plays only an auxiliary role; its involvement in splicing is revealed when the function of other proteins (i.e., Ntr1 or Prp43) involved in spicosomal disassembly are compromised.

**Cwc23's role in pre-mRNA splicing: disassembly of the spliceosome.** Several lines of evidence point to an essential role for Cwc23 in the pre-mRNA splicing pathway. First, a partial loss-of-function CWC23 mutant affects both cell fitness and global pre-mRNA splicing. Second, this mutation, a truncation of the codons encoding the 58 C-terminal amino acids, affects Cwc23's physical interaction with Ntr1, a known essential splicing factor (35). More specifically, available data point to a critical role for Cwc23 in the spliceosome disassembly step of the pathway. CWC23 mutants accumulate a product of the splicing reaction, the lariat-intron, which is known to be stabilized upon failure to disassemble the spliceosome (2). Indeed, extensive evidence accumulated over a decade supports a role of Prp43 in catalyzing the final step of splicing, the dissociation of the lariat-intron, and the disassembly of the spliceosome (38). Thus, the synthetic genetic interactions between CWC23 mutations and NTR1 or PRP43 mutations, but not mutations in genes involved in other steps in the pathway, also serve to place Cwc23 at the disassembly step.

**Cwc23: an essential J protein with a nonessential J domain.** The most surprising result of the present study is the lack of a phenotype upon deletion of the J domain of Cwc23; there is no obvious defect in either cell fitness or pre-mRNA splicing. To our knowledge, Cwc23 is the only example of an essential J protein with a nonessential J domain. Usually, alteration of the J domain leads to the same phenotypic effect as deletion of the entire protein. Indeed, in some cases much of a J protein can be deleted with little or no affect, as long as the J domain itself is left intact (18, 41). An extreme example of this is provided by Ydj1, a 409-amino-acid J protein with a well-characterized client protein-binding domain. Although a complete deletion of Ydj1 has severe effects on cell growth, expression of the J domain alone, at the level that Ydj1 is normally present, permits quite robust growth (31). On the other hand, when dramatic effects of mutations outside the J domain have been found, the consequences are typically no more severe than those that only affect J domain mutation. For example, deletion of the region necessary for binding of the J protein Zuo1 to the ribosome results in the same phenotype as disruption of only the J domain (43).

To our knowledge, only two examples in which the J domain of a protein appears to be of less biological importance than other domains have been reported previously: PS8PKR and SP16. Neither case is as striking as that of Cwc23. In the case of PS8PKR, its J domain-independent function appears to be in a different cellular compartment from its J domain-dependent function. In the cytosol, where it is present in low abundance, it acts as an inhibitor of interferon-induced protein kinase (PKR), a J domain-independent activity important for productive infection by influenza virus (42). However, PS8PKR is predominantly found in the endoplasmic reticulum lumen, where it plays an important role as a bona fide J protein cochaperone of Hsp70 (27). SP16 plays a role in flagellar stroke movement...
in Chlamydomonas. A fragment lacking the J domain appears to function as well as full-length protein in regulation of flagellar beating (44), although its exact function in this process is not known. The functionality of the J domain of RSP16 has yet to be demonstrated. RSP16 does have the defining HPD motif, but its orthologs from human, zebrafish, mouse, and mosquito do not (44).

**Function of Cwc23’s J domain.** Both our in vitro and in vivo results establish that *S. cerevisiae* Cwc23 has a functional J domain. It has the capacity to stimulate the weak ATPase activity of the Hsp70, Ssa1, and substantially rescue the severe growth defect of ydj1Δ cells. Both abilities are eliminated by the same single amino acid alteration in the J domain. However, the J domain of Cwc23 is clearly dispensable for cell viability and efficient pre-mRNA splicing. Nevertheless, the severe synthetic genetic interactions between mutations that alter the J domain of Cwc23 in ways known to disrupt functional interaction with Hsp70 and NTR1 or PRP43 mutations that affect the Ntr1:Prp43 interaction suggests that the J domain function of Cwc23 becomes critical when the interaction between Ntr1 and Prp43 is compromised. We suspect that the J domain is important under some environmental condition that we did not reproduce in the laboratory.

The questionable functionality of the J domain of RSP16 orthologs in higher eukaryotes raises the issue of the conservation of Cwc23 as a J protein. However, unlike RSP16 orthologs in higher eukaryotes raises the issue of the conservation of J domain function. Nevertheless, the J domain of Cwc23 is clearly dispensable for cell viability and efficient pre-mRNA splicing. Currently, it is absent from the fungal proteins, is in keeping with this line of logic.

What is the relationship between the role of Cwc23’s J domain, and thus Hsp70, and that of the C-terminal region of Cwc23? Are their functions totally independent or at least partially inter-related? Although we cannot answer these questions with certainty, the results reported here provide some insight. The function of the two domains cannot be completely independent, since the J domain cannot carry out its roles when expressed as an independent polypeptide. Interaction of Cwc23 with Ntr1 may serve to tether the J domain to a particular location, enormously increasing its local concentration, and efficiently allowing recruitment of Hsp70. However, on the other hand, the C-terminal domain must be playing a role beyond simply tethering the J domain since this domain is essential and Cwc23’s J domain is not.

Recent biochemical results indicate that the interaction between Prp43 and Ntr1 is critical in the disassembly step, with Ntr1 not only tethering Prp43 to the spliceosome but also able to activate its helicase activity (4, 33, 36). An involvement of Cwc23 in modulating the interaction between Prp43 and the NTR complex, increasing the efficiency of spliceosome disassembly, is an intriguing possibility. Participation in the remodeling of protein complexes is a known role for Hsp70-J protein systems. Regardless of the exact role of chaperone system in spliceosome disassembly, Cwc23 may provide an extreme example of an “underappreciated class” of J proteins whose biological role is defined more by their non-J domain regions than by their J domains, that is, their traditional Hsp70-related functions. Understanding how such J proteins evolved may afford important insight into the diversity of J protein function and how chaperone systems may be recruited to fine-tune protein complex remodeling.

**ACKNOWLEDGMENTS**

We thank David Brow (University of Wisconsin-Madison) and Beate Schwer (Weill Cornell Medical College) for yeast strains, plasmids, and helpful discussions. We also thank members of the Craig lab for critical comments on this work.

This study was supported by National Institutes of Health Grant GM31107 (E.A.C.).

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