Reverse Genetic Analysis of the Yeast RSC Chromatin Remodeler Reveals a Role for RSC3 and SNF5 Homolog 1 in Ploidy Maintenance

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The yeast “remodels the structure of chromatin” (RSC) complex is a multi-subunit “switching deficient/sucrose non-fermenting” type ATP-dependent nucleosome remodeler, with human counterparts that are well-established tumor suppressors. Using temperature-inducible degron fusions of all the essential RSC subunits, we set out to map RSC requirement as a function of the mitotic cell cycle. We found that RSC executes essential functions during G1, G2, and mitosis. Remarkably, we observed a doubling of chromosome complements when degron alleles of the RSC subunit SFH1, the yeast hSNF5 tumor suppressor ortholog, and RSC3 were combined. The requirement for simultaneous deregulation of SFH1 and RSC3 to induce these ploidy shifts was eliminated by knockout of the S-phase cyclin CLB5 and by transient depletion of replication origin licensing factor Cdc6p. Further, combination of the degron alleles of SFH1 and RSC3, with deletion alleles of each of the nine Cdc28/Cdk1-associated cyclins, revealed a strong and specific genetic interaction between the S-phase cyclin genes CLB5 and RSC3, indicating a role for Rsc3p in proper S-phase regulation. Taken together, our results implicate RSC in regulation of the G1/S-phase transition and establish a hitherto unanticipated role for RSC-mediated chromatin remodeling in ploidy maintenance.

Introduction

Maintenance of ploidy is crucial for sexual reproduction in eukaryotes because the ploidy changes that take place during gametogenesis require two identical chromosome complements. Polyploid plant, insect, amphibian, and mammalian species have been documented, and various forms of somatic polyploidy have been described, including mammalian hematocytes, megakaryocytes, and trophoblasts, insect oocyte nurse cells, and plant endosperm [1–3]. At the cellular level, polyploidy usually represents a highly differentiated state, with increased cell size and elevated metabolic activity. To become polyploid, cells enter a process called endocycling. This usually commences by aborting the mitotic cycle anywhere between G2 (endoreduplication) and cytokinesis (endomitosis), followed by replication [2–4]. Depending on the timing of mitotic exit, cells have multiple chromosome sets contained within a single nucleus or they become multinucleate.

Factors known to drive the switch between mitotic cycling and endocycling include S-phase cyclin-Cdk complexes and their regulators [3,5], as well as the replication origin licensing factors Cdc6, Cdt1, and geminin [6–9]. Such specialized cell-cycle transitions can involve switching between expression of protein isoforms, as reported for cyclin D variants in mammalian trophoblasts [10], or they can be restricted to a variation in oscillation of gene expression, as observed for cyclin E in Drosophila nurse nuclei [3]. Finally, mutations in multiple components of the yeast spindle pole body (Msp1p, Msp2p, Mob1p, Cdc31p, Ndc1p, and Kar1p), the fungal centrosome, have been reported to result in numerical chromosome doubling events in yeast [11–15].

In order to remodel chromosomes, eukaryotes have evolved multi-subunit protein complexes that can alter chromatin structure covalently, by modifying nucleosomes [16,17], or mechanically, via ATP-dependent chromatin remodeling (SNF2-type ATPases) [18,19]. Within the latter class, the SWI2/SNF2 enzymes are represented in yeast by the Sth1p and Swi2p/Snf2p ATPases that reside in the related multi-subunit complexes “remodels the structure of chromatin” (RSC) [20] and mating type “switching deficient/sucrose non-fermenting” (SWI/SNF) [21,22], respectively. RSC and SWI/SNF complexes are structurally related, sharing three subunits and harboring five paralogs [23,24]. Despite their extensive structural homology, dysfunction of various essential RSC components cannot be compensated for by over-expression of SWI/SNF paralogs, arguing that protein motifs that mediate complex assembly and function differ [20,25]. Furthermore, genetic evidence indicates that SWI/SNF and RSC differ fundamentally with respect to interaction with chromatin since histone and SPT6 mutations that suppress snf2A mutants actually enhance conditional sth1Δspt6Δ mutant phenotypes [26].


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Abbreviations: CFU, colony-forming unit; HU, hydroxyurea; MBF, MluI cell cycle box-binding factor; ORF, open reading frame; RSC, remodels the structure of chromatin; SWI/SNF, mating type switching deficient/sucrose non-fermenting

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Author Summary

Some molecules responsible for altering the 3-D organization of chromosomes work as complexes of more than ten different proteins, and many are conserved in fungi, plants, and animals. Two such complexes are called “remodels the structure of chromatin” (RSC) in yeast and “switching deficient/sucrose non-fermenting” (SWI/SNF) in man. SWI/SNF is known to inhibit the advent of multiple types of human cancers. Since cancer is a disease whereby cells unduly divide, we sought to define when in the yeast cell division cycle RSC executes essential functions. Using a generic method to induce inactivation of essential proteins in otherwise healthy yeast cells, we found that the RSC complex is important before chromosome replication as well as before chromosome segregation. Interestingly, combining two of the mutations we had generated caused doubling of the entire chromosome complement of yeast. As it is known that such multiplication of the cellular chromosome complements results in an increased malleability of the genetic patrimony, which itself is known to underlie some of the aggressive traits of human cancers, our discovery suggests new models as to why SWI/SNF is such a potent tumor suppressor, and this may in turn provide valuable new inroads for cancer treatment.

To date, genetic and molecular analyses have implicated RSC in a variety of biological processes including chromosome cohesion and transmission, DNA repair, and transcriptional regulation [27–35]. In addition, RSC interacts with a PKC pathway that impinges on cell polarity through Bim1p, a microtubule-associating protein that ensures spindle pole body asymmetry through Kar9p [36,37].

To address fundamental questions with respect to RSC function, we analyzed generic degron alleles of essential RSC subunits. Here, we report that RSC executes essential functions in G1, G2, and mitosis. Strikingly, integral ploidy segregation. Interestingly, combining two of the mutations we had generated caused doubling of the entire chromosome complement of yeast. As it is known that such multiplication of the cellular chromosome complements results in an increased malleability of the genetic patrimony, which itself is known to underlie some of the aggressive traits of human cancers, our discovery suggests new models as to why SWI/SNF is such a potent tumor suppressor, and this may in turn provide valuable new inroads for cancer treatment.

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Results

Generation of Conditional Alleles of All Essential RSC Complex–Specific Subunits

In order to investigate the role of RSC in cellular physiology, we utilized an inducible protein degradation system based on fusion of an N-terminal heat-inducible ubiquitin ligase-target peptide (“degron”) [40] to the open reading frames (ORFs) of all essential RSC-specific subunits. This included replacement of the endogenous promoters by the Pcoa1 promoter, resulting in Cu2+-driven transcription of the rsc3 alleles. The system also included integration of the Pcoa1-10 promoter at the UBR1 locus, which encodes the N-end rule E3 ligase Ubr1p, that recognizes the N-terminal arginine residue of the degron fusions [41]. This permits suppression of degron fusion degradation by growing cells in glucose media, which represses the Pcoa1-10 promoter, and allows priming of degron-fusion degradation by pre-growing cells in galactose media at 25 °C. Thus, this system permits heat shock–induced, polyubiquitin-mediated degradation of existing cellular protein fusions [41].

Cells expressing degron alleles of the essential RSC subunits (rsc3td, rsc4td, rsc6td, rsc9td, rsc18td, sfh1td) as sole source of that subunit grew at rates comparable to wild-type strains when cultured in glucose at 25 °C, indicating that the degron fusions were functional (unpublished data). Upon induction of ubiquitin ligase Ub1p expression at 25 °C by galactose, rsc3td strains (but none of the other RSC degron strains) arrested growth, and colony formation was strongly diminished (Figure 1A and 1C). This indicates that Rsc3p is exquisitely sensitive amongst RSC subunits to the presence of the N-terminal degron.

Following incubation of rsc3td strains in galactose at 37 °C, growth arrest ensued for all subunits within 3–4 h (Figure 1B). Western blot analysis indicated that degron fusions were depleted to nondetectable levels within 2 h (Figure S1 and

![Figure 1](https://example.com/figure1.png)

**Figure 1. Conditional Depletion of RSC Subunits Terminally Arrests Cells at Multiple Stages of the Cell Cycle**

(A) Characterization of yeast strains bearing degron alleles of RSC subunits. Strains were cultured in galactose media at 25 °C (left panel, top lanes) or 37 °C (left panel, bottom lanes) to deplete degron fusions of RSC subunits for 3, 6, and 9 h (only 9 h shown), and a 10-fold serial dilution was spotted onto rich medium and incubated for 3 d at 25 °C (left panel; see Materials and Methods). In parallel, aliquots were taken following depletion and analyzed for DNA content by flow cytometry (right panel). For a more complete set of strains, see Figure S2.

(B) Growth curves under nonpermissive conditions of several strains used in (A). Wild type; ΔΔ, sft1td; Δ, sft1td; Δ, rsc3td; Δ, rsc4td; Δ, rsc6td; Δ, rsc9td; Δ, rsc18td; Δ, sfh1td; Δ, rsc3td; Δ, rsc4td; Δ, rsc6td; Δ, rsc9td; Δ, rsc18td; Δ, sfh1td; Δ. (C) Cells were shifted from YEP-glucose medium supplemented with 0.1 mM CuSO4 at 25 °C to YEP-galactose supplemented with 0.1 mM CuSO4 at 25 °C, and 10-fold dilutions were spotted after 0 or 16 h onto glucose containing plates with 0.1 mM CuSO4 and incubated at 25 °C. All strains displayed in this figure contain the Pcoa1-UBR1 allele.

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unpublished data) and Sth1pTAP level also decreased (Figure S1), indicating impaired complex integrity. Flow cytometry analysis of cellular DNA content revealed G2/M cell-cycle arrests in rsc6\textsuperscript{td}, rsc8\textsuperscript{td}, and sth1\textsuperscript{td} strains (Figures 1A and S2). sth1\textsuperscript{td} strains gave variable results, usually yielding almost exclusively G2/M cells, though occasionally significant levels of G1-blocked cells were observed. In contrast, both G1- and G2M-arrested cells were invariably observed in rsc8\textsuperscript{td}, rsc5\textsuperscript{td}, and rsc4\textsuperscript{td} strains. Importantly, every combination of RSC degrons that was tested induced both G1 and G2M arrests (Figures 1A and S2).

Irreversible lethals effects, observed as a decrease in colony-forming units (CFUs) upon seed-out onto 2% glucose plates and incubation at 25 °C, were more pronounced and occurred earlier in the 37 °C time course in rsc8\textsuperscript{td} and rsc5\textsuperscript{td} strains, as well as in strains harboring multiple RSC degron fusions (Figure 1A). In the extreme case of the rsc6\textsuperscript{td}, rsc8\textsuperscript{td}, sth1\textsuperscript{td} triple degron strain, less than 1% CFUs remained after 3 h of heat shock (Figure 1A), while equivalent fractions of pre- (Figure 1C) and post-replicative (Figure 2C) cells were observed.

Altogether, these data suggest that the cell-cycle phase of arrest correlates with the kinetics of RSC complex inactivation, with G2M cells being more sensitive to RSC inactivation than G1 cells since G2/M cells accumulate when RSC function is least impaired, as assayed by cell survival.

**RSC Is Essential in the G1 Phase of the Cell Cycle**

As no essential role has previously been described for RSC during G1, we wished to determine whether the G1 arrest we observed upon RSC depletion (Figures 1A and S2) resulted from functional failure in the course of the preceding cell cycle or whether this reflected a genuine essential function for RSC during G1. To this end, the triple rsc6\textsuperscript{td}, rsc8\textsuperscript{td}, sth1\textsuperscript{td} degron combination, which conveyed >99% lethality within 3 h of heat shock (Figure 1A), was employed to deplete RSC from asynchronously cycling cells (Figure 2). Cells were grown overnight in galactose at 25 °C and then blocked in G1 by exposure to α-pheromone (~5 h; boost at ~2.5 h). Release into the cell cycle was achieved by removal of pheromone (0 h). Aliquots of synchronized cells were then taken at 30-min intervals and incubated for 3-h periods at 37 °C so as to deplete RSC from cells traversing consecutive stages of the cell cycle synchronously. After 3 h at 37 °C, cellular DNA content was determined and cells were seeded-out onto permissive plates to determine viability levels by colony formation (Figure 2). RSC inactivation in synchronized cells proved lethal for >95% of the cells in every case (Figure 2), and RSC inactivation resulted in homogeneous G1 and G2M arrests, depending on the time when heat shock was applied (Figure 2).

We conclude that RSC executes essential functions in G1 in addition to its essential roles in G2/M. As we did not observe cells arrested in the process of DNA replication (corresponding to the 0.5 h to 3.5 h time point), our experiments suggest that RSC activity is not required per se for chromosome replication. However, we cannot exclude the possibility that a small portion of the genome failed to be replicated upon RSC depletion (Figure 2, 0.5 h to 3.5 h time point).

**sfh1\textsuperscript{td} and rsc3\textsuperscript{td} Together Induce Single Rounds of Ploidy Doublings**

The above analyses indicated that RSC performs crucial functions during mitosis, G1, and G2, and they implicate RSC in proper cell-cycle progression. This perception was further strengthened in the process of generating yeast strains harboring combinations of degron alleles of essential RSC subunits. Whereas most diploid strains heterozygous for two or three degron alleles produced >80% viable spores, diploid strains heterozygous for sfh1\textsuperscript{td} and rsc3\textsuperscript{td} and homozygous for Pgal::UBR1 yielded less than 10% viable spores (Table S1). This dominant meiotic-lethal phenotype was not due to aberrant ploidy of the parental strains, as both haploid rsc3\textsuperscript{td} and sfh1\textsuperscript{td} strains displayed the expected haploid DNA contents (Figure 1A). Furthermore, the sfh1\textsuperscript{td} and rsc3\textsuperscript{td} strains were able to individually mate with other haploid rsc3\textsuperscript{td} strains to produce diploids that produced >80% viable spores with the expected segregation frequencies of heterozygous markers (Table S1).

We tested the involvement of the Pgal::UBR1 allele by mating a UBR1, sfh1\textsuperscript{td} strain to a UBR1, rsc3\textsuperscript{td} strain. These diploids were fertile (64% viable progeny); however, none of the surviving progeny harbored both the rsc3\textsuperscript{td} and the sfh1\textsuperscript{td} degron alleles (Table 1). This demonstrates that the dominant meiotic-lethal phenotype displayed by double heterozygous rsc3\textsuperscript{td}/RSC3, sfh1\textsuperscript{td}/SFH1, Pgal::UBR1/Pgal::UBR1 diploids was due to repression of UBR1 expression. This suggests that RSC and
UBr1p, or physiological Ubr1p substrates [42], are part of genetic pathways that are redundant to some extent or that form one large pathway in meiosis.

Interestingly, the dominant meiotic-lethal phenotype of diploids homozygous for \( P_{gal}::UBR1 \) and heterozygous for \( rsc3^{td} \) and \( sfh1^{td} \) could be rescued by inclusion of a single copy of \( rsc9^{td} \), but not by inclusion of \( sfh1^{td}, rsc6^{td}, rsc8^{td}, or rsc9^{td} \) alleles. (unpublished data). Remarkably, we observed that every single descendant spore of the triple heterozygous diploid DNA content, regardless of the presence of the \( rsc9^{td} \) allele (>50 tetrads analyzed). The DNA profile of one \( sfh1^{td}, rsc3^{td} \) nonparental di-type tetrad is shown in Figure 3A. Both progeny that inherited the \( rsc3^{td} \) and the \( sfh1^{td} \) alleles have 2C + 4C DNA contents, while the other two spores display the 1C + 2C DNA content expected for haploid yeast. The endodiploid \( sfh1^{td}, rsc3^{td} \) strains responded to mating pheromone (unpublished data) and could mate to produce tetraploid strains (4C8C, Figure 3B). The ploidy shift took place after meiotic segregation of the chromosomes because inheritance of all the heterologous chromosomal loci obeyed the Mendelian 2:2:2:1 frequency.

In order to test whether endodiploid strains could be generated independently of passage through meiosis, we performed endogenous locus replacement experiments in haploid cells. When \( UBR1, rsc3^{td} \) strains were transformed with vectors to convert the wild-type \( SFH1 \) allele to \( sfh1^{td} \), 10% of the resulting colonies were haploid, 80% were diploid, and 10% also harbored tetraploid cells (n = 48, Figure 3C and Table 2). Thus, the endodecay induced by the \( rsc3^{td} \) and \( sfh1^{td} \) alleles could also occur independently of meiosis. Transformation of \( UBR1, sfh1^{td} \) haploid strains with the \( rsc3^{td} \) locus conversion construct yielded fewer endodiploid strains (4C8C, Figure 3C). Inset: Light scatter plots indicating cell sizes.

**Table 1: Synthetic Lethality between \( rsc3^{td} \) and \( sfh1^{td} \)**

<table>
<thead>
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<th>Frequency</th>
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<td>Observed</td>
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<td>Expected if not Sl</td>
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UBr1p, \( sfh1^{td} \), and \( UBR1, rsc3^{td} \) strains of opposing mating type were mated, and resulting diploid strains were induced to sporulate. Spores from 38 ascis were analyzed for colony formation and segregation of \( sfh1^{td} \) and \( rsc3^{td} \) alleles, as well as several auxotrophic markers. Sl, synthetic lethal. doi:10.1371/journal.pgen.0030092.t003

Figure 3. Post-Meiotic and Mitotic Ploidy Doubling of \( sfh1^{td}, rsc3^{td} \) Cells

(A) FACS analysis of the DNA content of the four spores of a single representative tetrad derived from a \( SFH1/sfh1^{td}, RSC3/rsc3^{td}, RSC9/rsc9^{td}, P_{gal}::UBR1/P_{gal}::UBR1 \) diploid. The genotypes of the spores are \( SFH1, RSC3, RSC9, P_{gal}::UBR1 \) (blue), \( SFH1, RSC3, rsc9^{td}, P_{gal}::UBR1 \) (red), \( sfh1^{td}, rsc3^{td}, RSC9, P_{gal}::UBR1 \) (green), \( sfh1^{td}, rsc3^{td}, rsc9^{td}, P_{gal}::UBR1 \) (black). Inset: Light scatter plots indicating cell sizes.

(B) Tetraploid strain (blue) derived from mating of two endodiploids (black). For comparison, a haploid was included (red).

(C) FACS analysis of clones generated by transformation of a \( rsc3^{td} \) strain with a \( sfh1^{td} \) allele. Haploid clones are indicated in red, endodiploids in gray, and tetraploids in blue.

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RSC Genetically Interacts with the Cyclin-Dependent Kinase Cdc28p/Cdk1p

In budding yeast, cell-cycle progression is orchestrated by a single cyclin-dependent kinase, Cdc28p/Cdk1p [43]. As we found RSC to be crucial for passage through multiple stages of the cell cycle, we wished to assess functional interactions between RSC and Cdc28p/Cdk1p. To this end, we employed a \( cdc28^{td} \) degron allele [40]. Upon Ubr1p overexpression, the \( cdc28^{td} \) allele led to a severe decrease in CFUs. This phenotype was exacerbated by inclusion of the \( sfh1^{td} \) allele (Figure 4), arguing that hypomorphic alleles of RSC and Cdc28p/Cdk1p genetically interact. This notion was further substantiated by the observation that \( sfh1^{td} \) cells overexpressing \( Saccharomyces cerevisiae WEE1 \) (\( SWE1 \)), a tyrosine kinase that controls mitosis entry by inhibition of Cdc28p/Cdk1p activity [43,44], were ploidy shifts only took place once or twice strongly suggests that a third biological parameter is involved, and that this parameter was triggered in both the endogenous locus conversion and the meiotic segregation experiments.

In order to test whether endodiploid strains could be generated independently of passage through meiosis, we performed endogenous locus replacement experiments in haploid cells. When \( UBR1, rsc3^{td} \) strains were transformed with vectors to convert the wild-type \( SFH1 \) allele to \( sfh1^{td} \), 10% of the resulting colonies were haploid, 80% were diploid, and 10% also harbored tetraploid cells (n = 48, Figure 3C and Table 2). Thus, the endodecay induced by the \( rsc3^{td} \) and \( sfh1^{td} \) alleles could also occur independently of meiosis. Transformation of \( UBR1, sfh1^{td} \) haploid strains with the \( rsc3^{td} \) locus conversion construct yielded fewer endodiploid strains (4C8C, Figure 3C). Inset: Light scatter plots indicating cell sizes.

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Table 2: Ploidy Alterations by Endogenous Locus Conversion

<table>
<thead>
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<tr>
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Wild-type (WT), sfh1td, or rsc3td strains were transformed with endogenous locus conversion constructs for sfh1td or rsc3td and selected for integration of the respective alleles. Resulting transformants were analyzed for DNA content by flow cytometry (see Figure 3) and results are shown as percentage of colonies analyzed (n = 48). Experiments were performed using cells expressing endogenous levels of UBR1 (UBR1), or cells repressing UBR1 expression (Pgal::UBR1) as indicated.

doi:10.1371/journal.pgen.0030092.t002

...also exquisitely sensitive to overexpression of Ubr1p at 25 °C (Figure 4). Together, these synthetic lethal effects demonstrate that the RSC catalytic ATPase subunit Sth1p genetically interacts with the cyclin-dependent kinase pathway.

Specific Genetic Interaction between the rsc3td Allele and the CLB5 S-Phase Cyclin

Our results suggest that a specific cell-cycle process is impaired in cells that harbor both the sfh1td and rsc3td degron alleles, and that this could relate to a specific cyclin-dependent kinase pathway. In order to map this process, we mated Pgal::UBR1, rsc3td and Pgal::UBR1, sfh1td strains to a panel of deletion strains that lacked any one of the nine Cdk1p/Cdc28p associated cyclins and assessed spore viability on glucose plates. This analysis did not reveal significant genetic interactions between sfh1td and any of the cyclin deletions (Figure 5A). In the case of the rsc3td allele, however, a significant loss of spore viability was observed upon combination with the cdc53Δ allele. As a matter of fact, we did not recover a single UBR1 clone that harbored both the cdc53Δ and the rsc3td alleles, indicating that the latter alleles form a lethal combination, and that lethality was suppressed by repression of Ubr1p levels (using the Pgal::UBR1 allele; Figure 5B). Other UBR1, cyclin deletion, rsc3td double mutants were recovered with the expected frequency, demonstrating a specific interaction between cdc53Δ and rsc3td. We conclude that the rsc3td allele impairs a cell-cycle process that also relies on Clb5p. As this cyclin is known to control late S-phase progression [43,45,46], this suggests that an important S-phase event is disrupted by the rsc3td allele.

The Rereplication Control Machinery Antagonizes rsc3td-Mediated Ploidy Shifts

Endocycling of eukaryotic cells (e.g., mammalian hepatocytes and megakaryocytes) commonly relies on alternative regulation of genes essential for replication control, such as G1/S cyclins, Cdc6, geminin, and Cdt1 [3,6,7,9]. We therefore assessed the role of the yeast origin licensing factor Cdc6p in ploidy shifts induced by rsc3td and sfh1td. As Cdc6p is an essential protein, we attenuated its cellular levels using a strain expressing CDC6 solely from a methionine repressible promoter [49]. Cells were incubated in the presence of 2 mM methionine for 45 min to repress CDC6 transcription, and then they were made competent for transformation. These cells were transformed with control constructs, or with endogenous locus conversion constructs for the sfh1td or rsc3td alleles. Clones were then selected at 25 °C on glucose

![Figure 4: Synthetic Sickness Phenotype of sfh1td, cdc28td, and sfh1td, Pgal::SWE1 Double Mutants](image-url)
plates lacking methionine so as to restore CDC6 transcription. Control cells that had not been depleted of Cdc6p yielded exclusively haploid clones upon conversion of the RSC3 or SFH1 loci to the corresponding degron alleles (Figure 6). In contrast, ploidy shifts were efficiently induced in cells depleted of Cdc6p upon conversion of the RSC3 locus to rsc3Δ, but not upon conversion of the SFH1 locus to sfh1Δ (n = 60; 60% and 0%, respectively, Figure 6). Thus, temporary depletion of Cdc6p appears to phenocopy the sfh1Δ allele but not the rsc3Δ allele.

Next, we turned to the cyclin Clb5p. Besides a role in spindle pole body maturation and duplication [50,51], Clb5p plays a dual role in replication regulation as it is required for proper timing of S-phase initiation, as well as to prevent reinitiation of replication forks that have already fired [52]. Furthermore, deregulation of CLB5 levels has been associated with the occurrence of endoreduplication [52]. Wild type and clb5Δ strains were transformed with the same constructs as above. In this experimental setup, and contrary to meiotic segregation, UBR1, rsc3Δ, clb5Δ mutants could be recovered. Analysis of the resultant rsc3Δ clones (n = 72) showed efficient ploidy doubling in the clb5Δ background (74%; Figure 6) in contrast to control constructs. Conversion of SFH1 to sfh1Δ in the clb5Δ background could also produce endodiploid clones, though at a much lower frequency (1%; Figure 6). Taken together, this indicates that the cellular replication inhibition pathway that depends on CLB5 and CDC6 [18,52] antagonizes the effects of the degron alleles of RSC3 and SFH1.

RSC and Transcriptional Activity of the CLB5 Locus

Previous observations indicate that RSC is recruited to the CLB5 promoter [27], and CLB5 induction was observed in microarray experiments using a rsc3 allele [53]. To further assess the role for RSC in regulation of CLB5 expression, we impaired S-phase progression by exposure to hydroxyurea (HU), an inhibitor of deoxyribonucleotide synthesis. HU treatment activates the S-phase checkpoint that signals through Rad53p and phosphorylation of various targets, including Sth1p, thus culminating in inhibition of S-phase progression [54–56]. Following exposure to HU for 3 h we monitored association of RSC with a number of loci by Sth1pTAP chromatin immunoprecipitation (Figure 7A), and we assessed expression of CLB5 and TPS3 (Figure 7B). HU treatment resulted in up to 3-fold increased association of Sth1p with the CLB5 promoter (Figure 7A), concomitant with repression of CLB5 expression (Figure 7B), much as reported for HTA1 (Figure 7A, [27]). The increased association of RSC complexes with the CLB5 and HTA1 promoters upon HU treatment was specific, as no such effects were observed at TPS3, FUR4, CEN4, at an ORF-free chromosomal element on Chromosome I (ORF-FREE) or in the CLB5 ORF (CLB5-ORF, Figure 7A and 7B). Taken together, these results correlate increased binding of RSC to the CLB5 promoter with inactivation of this locus upon HU treatment (Figure 7A and 7B) and further implicate RSC in transcriptional control of CLB5 expression.

Discussion

The RSC ATP-dependent nucleosome remodeling complex [20] encompasses 17 subunits, and the mutually exclusive paralogs Rsc1p and Rsc2p define two RSC isoforms [57]. The Rsc3p/Rsc30p heterodimer [20,53] preferentially associates with the Rsc1p-bearing RSC isoform (Campsteijn et al., unpublished data). Here, we analyzed RSC requirement
Figure 6. Implication of Replication Control in RSC-Induced Ploidy Shifts

(A) \(P_{\text{met}}:\text{CDC6, cdc6}^{\Delta}\) cells (and wild-type cells, unpublished data) were cultured in the absence (0 min) or presence (45 min) of 2 mM methionine to repress CDC6 expression, and cells were made competent for transformation. After transformation with the indicated constructs (left panel), cells were seeded on plates lacking methionine to induce CDC6 expression. DNA content of resulting transformants is shown (n = 60, cumulative of three independent experiments). Haploid clones are depicted in red, endodiploids in blue, and number of endodiploids is shown as an inset.

(B) Wild-type and \(\text{clb5}^{\Delta}\) cells were transformed with the constructs as indicated (left panel). DNA content of resulting colonies is shown (n = 72). The color scheme is the same as in (A). These data represent the cumulative results of three independent experiments.

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during the course of the cell cycle using conditional degradation alleles (N-degrons) of all essential RSC-specific subunits. We find that RSC controls cell-cycle progression at multiple stages of the cell cycle and uncovered a strong genetic interaction between RSC and cyclin-dependent kinase 1 (Figure 4).

RSC Functions in G2/M

We temporally dissected the mitotic requirement for RSC by depleting RSC subunits from cells harboring G2 or mitosis checkpoint mutations (Figure S3). In keeping with a role for RSC in G2 and mitotic prophase, RSC degron alleles synergized with overexpression of the G2/M transition regulator \(\text{SWE1}^{[43,44]}\), and the same RSC alleles were partially epistatic to a degron allele of the spindle checkpoint factor \(\text{CDC20}^{[58]}\) (Figure S3). On the other hand, a degron allele of the mitotic exit network kinase \(\text{CDC15}^{[59]}\) weakly suppressed the lethal effects of those same RSC subunit degron alleles (Figure S3). Collectively, these results indicate that RSC activity is central to achieving a proper mitosis and that RSC appears to be somewhat more important before the metaphase/anaphase transition than afterward (Figure S3). While these results are consistent with published reports, it remains to be seen whether the essential role of RSC in G2 and in mitosis relates to a role for RSC in gene expression \([27,28,35,53]\), in higher order chromatid structure \([32-34,60,61]\), or both.

RSC Functions in G1

Several lines of evidence provided here argue that RSC functionally intersects with regulation of the G1/S-phase transition. First, cells deprived of RSC arrest in G1 (Figures 1 and 2). Second, we and others \([27]\) find that RSC associates with several \(\text{Mlu}1\) cell cycle box-binding factor (MBF) targets including the \(\text{HTA1/HTB1}\) and \(\text{CLB5}\) promoters (Figure 7, unpublished data). Both \(\text{HTA1/HTB1}\) and \(\text{CLB5}\) are expressed during the G1/S transition and association of RSC correlates with transcriptional inactivity of these loci (Figure 7, \([27]\)). Third, we discovered that the \(\text{rsc}^{3\Delta}\) allele is synthetic lethal with a deletion allele of the cyclin \(\text{CLB5}\) when combined via meiotic segregation (Figure 5). When these two alleles were combined by endogenous locus conversion through DNA transformation, surviving clones could be recovered, however, and the resulting \(\text{clb5}^{\Delta}, \text{rsc}^{3\Delta}\) strains underwent integral ploidy increases (Figure 6). This was also the case when the replication origin licensing factor Cdc6p was transiently depleted (Figure 6). As these genes are crucial for G1/S-phase transition, this very strongly suggests that RSC plays an important role in ploidy maintenance when this stage of the cell cycle is perturbed.

Consistent with this notion, RSC has been reported to interact physically with Swi6p \([62]\), a component of the central heterodimeric G1/S transcription regulators MBF (with Mbp1p) and SBF (with Swi4p), which are considered to be the functional analogs of mammalian E2Fs \([63]\). Finally,
rsc1 cells were shown to display a large cell phenotype that is indicative of impaired cell-cycle entry as has been observed in cln3, beh2, swe4, and swi6 strains [64].

**RSC Has a Facultative Role in Ploidy Maintenance**

The endocyte phenotype we observe in sfh1Δ, rsc3Δ double mutants underscores the important role of RSC in proper cell-cycle progression. The endocycles occur under conditions when the degron fusions were least affected since the levels of the degron-activating ubiquitin ligase Ubr1p were repressed by glucose and since the yeast were kept at 25 °C to keep the DHFRΔ degron fragment folded (Figure 3A) [40,41]. The ploidy shifts must therefore arise from rather subtle deregulation of RSC. It is known that a fraction of the degron-activating ubiquitin ligase Ubr1p was kept the DHFRts degron fragment folded (Figure 3A) [40,41]. Typically, recovery ranged between 0.1%–0.3% of input for the CLB5 promoter. The DNA profiles of cells upon harvesting are shown as an inset. Values are the average of three independent experiments using an STH1Δ allele and standard deviations are indicated.

**B** RSC functions as a repressor of CLB5 expression. Expression levels of the RSC targets CLBS and TPS3 were assessed using quantitative PCR in HU-treated cells and untreated cells. Data are normalized to total RNA concentrations, as well as to the expression levels of these genes in untreated cells and represent the average of three independent experiments. doi:10.1371/journal.pgen.0030092.g007

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**Role of the Pgal::UBR1 Allele in Ploidy Shifts**

It is known that Ubr1p participates in cohesin degradation in mitosis [42]. However, our results indicate that the effects of the Pgal::UBR1 allele in our experiments were largely mediated through Ubr1p’s role in polyubiquitylation of the N-terminal degron fusions we studied. For instance, repressing Ubr1p levels suppressed rather than enhanced the occurrence of ploidy shifts in rsc3Δ, sfh1Δ strains (Table 2). Furthermore, repressing Ubr1p expression through Pgal::UBR1 suppressed rather than enhanced the synthetic lethal interaction between rsc3Δ and clb5A (Figure 5B). However, since the dominant meiotic-lethal phenotype displayed by double heterozygous rsc3Δ/Δ, sfh1ΔΔ, Pgal::UBR1Δ/Δ diploids was due to repression of UBR1 expression (Table 1), our results do suggest that RSC and Ubr1p are part of genetic pathways that are redundant to some extent or that form one large pathway in meiosis.

**Conclusion**

Our experiments indicate that the rsc3Δ and sfh1Δ degron alleles interfere in synergistic ways with cell-cycle progression resulting in environmentally conditioned ploidy shifts. These results formally implicate RSC in ploidy maintenance. The RSC complex has previously been implicated in multiple
molecular processes, including regulation of chromatin cohesion [32], DNA damage response [29–31], nucleocytoplasmic transport [28, 71], and transcription control [27, 28, 35, 53, 72]. Furthermore, and underscores the complexity of RSC function, viable RSC subunit deletion strains have been identified that display long (npl6Δ, hlx1Δ, and ldb7Δ) or short (rsctΔ) telomeres, hinting toward ambivalent roles for RSC in maintenance of telomere length [73, 74], a process that occurs in late S-phase [75]. In light of the pleiotropic physiological functions of RSC, further dissecting RSC-mediated ploidy control will require a detailed understanding of the roles and modes of regulation of individual RSC subunits, as well as understanding the functional interplay of the various processes that rely on RSC.

The functions we ascribe here to RSC, namely ploidy maintenance and control of G1/S-phase transition, appear conserved for human RSC-like complexes [76–81]. Interestingly, it has been shown that mutant forms of the human ortholog of SFR11, the tumor suppressor INI1/SMN5 [38, 39, 82, 83], can induce the appearance of tetraploid cells [76, 81]. Thus, an ancient RSC-dependent ploidy doubling inhibition mechanism may have been recruited in the course of animal evolution to avert incipient cancer.

Materials and Methods

Yeast strains, plasmids, and culturing. With the exception of the S288c mbp1Δ strain (Figure S5) and the S288c cyclin deletion strains (Figure 5), all the yeast used here were descendants of W303 strains. Deegrons were introduced in diploid yeast (YN106) by end-in-homologous recombination of plasmids at the endogenous loci (Table S1). All details are available on request. Verification of the integration events was based on PCR analysis and western blot detection of the modified gene products. For sporulation, diploids were grown overnight on YEP-10% glucose agar plates and then grown overnight in 5 ml of the appropriate SD-glucose amino acid dropout medium containing 40 μg/ml adenine, 0.1 mM CuSO4, and incubated at 25 °C or 37 °C. All the indicated times, 5 μl of cells and 5- or 10-fold serial dilutions were spotted onto YEP plates supplemented with 2% glucose, 40 μg/ml adenine, and 1 mM CuSO4. The plates were incubated at 25 °C and pictures were taken after 2-4 d. For DNA damage experiments (Figure 7), cells were cultured in nonselective medium at 30 °C to an optical density of 0.6, followed by exposure to 150 mM HU for 4-5 h at 65 °C, and DNA was purified by phenol extraction done for 4-5 h at 65 °C, and DNA was purified by phenol extraction.

Flow cytometry analysis. Cells were grown in nonselective medium overnight, pelleted, and collected into 70% ethanol and kept at least 2 h at 20 °C. Subsequently, cells were suspended into 50 mM sodium citrate, sonicated briefly, treated for 2 h with 0.2 mg/ml RNase A at 37 °C, and DNA was stained with 1 μM Sytox dye (Molecular Probes, http://www.probes.invitrogen.com). DNA content was quantified at FL1 on a Becton-Dickinson (http://www.bd.com) Calibur fluorescence activated cell sorter.

Chromatin immunoprecipitation, RNA extraction, and quantitative PCR. Chromatin was prepared as described [84] with several modifications. Cells (20–40 ml) were treated with 1% formaldehyde for 15–20 min at room temperature under constant rotation. Glycine was added to a final concentration of 330 mM and incubation continued for an additional 5–10 min. Cells were gently washed three times with 2% [w/v] cold PBS. The remaining cell pellet was resuspended in lysis buffer (FA-lysis buffer complemented with 1% Triton X-100 and 1 mM DTT) and lysis was performed using glass beads (2-h vortexing on a vortexgenie 2, Scientific Industries, http://www.scientificindustries.com). The obtained lysate was sonicated on ice (four 20-s cycles, with 45 s intervals) and centrifuged for 15 min at 13,000 rpm in a Beckman 56446 rotor. The supernatant (lysate) was used for IP.

DNA content was quantified at http://www.bio-rad.com/MvIQ Single Color Real-Time PCR Detection System using a 2× IQ SYBR Green Supermix. For CHIP, 1/50 of the immunoprecipitated material was used and abundance of immunoprecipitated fragments was compared to 1% input. For cDNA, 1/25 of total cDNA was used and values were normalized as indicated.

Supporting Information

Figure S1. Depletion of Rsc8ptd Compromises RSC Integrity

A rsctΔ STH1Δ mutant strain (YN438) was grown overnight in YP-Gal medium containing 0.1 mM CuSO4 at 25 °C and was subsequently shifted to YP-Gal medium at 37 °C to induce degradation of Rsc8ptd. Aliquots were harvested at the indicated time points and equal amounts of whole cell extracts were analyzed by western blot. Rsc8ptd was visualized using anti-HA mouse antibody and ShlpΔAP using peroxidase-conjugated anti-peroxidase rabbit antibody (Sigma-Aldrich).

Found at doi:10.1371/journal.pgen.0030092.sg001 (786 KB PDF).

Figure S2. Simultaneous Depletion of Multiple RSC Degrons Invariably Yields G1 and G2/M Arrests

Indicated strains were incubated under nonpermissive conditions for 4 h after which DNA content was determined by FACS analysis. To assess colony-forming potential, strains were incubated for 2, 6, or 12 h under nonpermissive conditions, after which 5-fold serial dilutions of the cultures were spotted on YP-glucose plates containing 0.1 mM CuSO4, followed by incubation at 25 °C and photography (inset).

Found at doi:10.1371/journal.pgen.0030092.sg002 (555 KB PDF).

Figure S3. RSC Requirement after Replication

(A–C) Strains harboring the indicated rscΔ alleles and/or the conditional cell division cycle alleles for CDC3, CDC20, or SWE1 were cultured as described (Materials and Methods), followed by shifting to YP-Gal medium containing 0.1 mM CuSO4, and incubated at 37 °C in galactose medium lacking CuSO4. Aliquots of these cultures were seeded upon YP-Gal medium containing 0.1 mM CuSO4 and incubated at 37 °C in glucose medium. DNA content was measured by FACS analysis.

Found at doi:10.1371/journal.pgen.0030092.sg003 (3.7 MB PDF).

Figure S4. ShlpΔAP Association with RSC Depends on Ubr1p Levels

RSC was purified using an STH1ΔAP allele from wild-type (YN400) or sfh1Δ (YN453) strains following overnight culturing at 25 °C in the presence of CuSO4 in glucose (Glu) or galactose (Gal) media to repress or overexpress Ubr1p, respectively. Equal amounts of RSC were loaded in each lane. The position of ShlpΔAP (empty arrowhead) is indicated. All strains used in this figure contain the Pcα-UBR1 allele. Note that loss of Shlp1ΔAP did not perceptibly affect complex integrity.

Found at doi:10.1371/journal.pgen.0030092.sg004 (532 KB PDF).

Figure S5. Implication of Mbp1p in RSC-Mediated Ploidy Shifts

S288c mbp1Δ3 cells were transformed with the rscΔ4 endogenous locus conversion construct. The DNA content of cells from one clone is shown. Note the presence of 4C and 8C cells, indicative of continuous endopolyploidyization.

Found at doi:10.1371/journal.pgen.0030092.sg005 (69 KB PDF).

Table S1. Fertility of Diploids Generated by Mating of Various rscΔ Strains

Diploids generated by mating the indicated haploids were considered fertile (+) when over 80% of spores were able to form haploid colonies. Less than 10% of spores from a sfh1Δ, rscΔ4 diploid were able to form colonies (−). Not all combinations were generated, as indicated by NT (not tested).
Table S2. Yeast Strains Employed by Campstean et al.

Notes: (i) All the yeast strains we generated are descendants of the W303-derived YN2 and YN18 strains and all harbor ADE2 and the trpl–1, ura3–1, his3–11,15, and leu2–3,112 alleles; (ii) All the deletron alleles were first introduced into the YN16 diploid strain and haploid strains were obtained by sporulation; (iii) Lysine auxotrophy was not systematically verified. When a strain is Lys+ it harbors the Δlys2–αWXD50N allele [85].

References


