Cohesin is a protein complex that forms a tripartite ring controlling sister chromatid cohesion, chromosome segregation and organization, DNA replication, and gene expression. Sister chromatid cohesion is established by the protein acetyltransferase Eco1, which acetylates two conserved lysine residues on the cohesin subunit Smc3 and thereby ensures correct chromatid separation in yeast (Saccharomyces cerevisiae) and other eukaryotes. However, the consequence of Eco1-catalyzed cohesin acetylation is unknown, and the exact nature of the cohesive state of chromatids remains controversial.

Here, we show that self-interactions of the cohesin subunits Scc1/Rad21 and Scc3 occur in a DNA replication–coupled manner in both yeast and human cells. Using cross-linking MS-based and in vivo disulfide cross-linking analyses of purified cohesin, we show that a subpopulation of cohesin may exist as dimers. Importantly, upon temperature-sensitive and auxin-induced degron-mediated Eco1 depletion, the cohesin-cohesin interactions became significantly compromised, whereas deleting either the deacetylase Hos1 or the Eco1 antagonist Wpl1/Rad61 increased cohesin dimer levels by ~20%. These results indicate that cohesin dimerizes in the S phase and monomerizes in mitosis, processes that are controlled by Eco1, Wpl1, and Hos1 in the sister chromatid cohesion-dissolution cycle. These findings suggest that cohesin dimerization is controlled by the cohesion cycle and support the notion that a double-ring cohesin model operates in sister chromatid cohesion.

Results

Self-interactions of cohesin subunits in yeast cells

Self-interactions of cohesin subunits have not been detected in yeast (9). In human cells, contradictory observations have been reported (20, 39). To clarify this, we first performed immunoprecipitation (IP) experiments using a similar dual-epitope tag strategy. An ectopic copy of SCC1 (pRS-SCC1, Table 1) under the control of its native promoter was introduced into a haploid yeast strain. The two SCC1 alleles were labeled with a pair of orthogonal epitopes (GFP/FLAG or EPEA/FLAG), which have been well-demonstrated to be orthogonal to each other.

The acetyltransferase Eco1 elicits cohesin dimerization during S phase

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Cohesin is a DNA-associated protein complex that forms a tripartite ring controlling sister chromatid cohesion, chromosome segregation and organization, DNA replication, and gene expression. Sister chromatid cohesion is established by the protein acetyltransferase Eco1, which acetylates two conserved lysine residues on the cohesin subunit Smc3 and thereby ensures correct chromatid separation in yeast (Saccharomyces cerevisiae) and other eukaryotes. However, the consequence of Eco1-catalyzed cohesin acetylation is unknown, and the exact nature of the cohesive state of chromatids remains controversial.

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other in this and previous studies (Fig. 1) (40, 41). When the epitopes were inserted at the C termini of both copies (Sccl-HA-EPEA/Sccl-5FLAG), after EPEA-IP, no Sccl-Sccl interaction was virtually detectable (data not shown), in agreement with a previous study from Nasmyth’s group (9) in yeast. Epitope tagging may occasionally cause unexpected interference in the structure and function of proteins, which turns out to be true for many cohesin subunits (20, 42). To test this possibility, we switched 5FLAG from the C terminus to the N terminus in this and previous studies (Fig. 1) (40, 41). When the self-interaction was apparent as well (Fig. 1B, lane 6), indicating that the intermolecular interaction was due to inappropriate epitope tagging and/or other experimental conditions. We then asked which subunit mediates cohesin self-interaction (Fig. 1A, lane 6). Because EPEA can only be applied at the C terminus, we then labeled both Sccl copies at their N termini with another orthogonal epitope pair, GFP/FLAG. A similar intermolecular interaction was observed in GBP-IP (Fig. 1B, lane 6). These results are consistent with the observations in human cells (20), indicating that the self-interaction of Sccl might be conserved.

The discrepancy could be explained if Sccl self-interaction is interrupted by C-terminal tagging. However, it is also possible that self-interaction might be artificially caused by overexpression of cohesin subunits (22). To test the latter possibility, we next labeled two endogenous Sccl alleles with the same pair of orthogonal epitope tags (i.e. GFP/FLAG) at their genomic loci in the diploid yeast cells. Under the physiological protein levels, the cellular cohesins often contained other components like Pds5 and Wpl1. However, the cohesin species detected and sedimented much faster than 669 kDa, peaking around fraction 13. These data corroborate the existence of higher-order cohesin complexes in vivo.

Next, we omitted the GST tag, which may cause artificial dimerization. The cohesin complexes at the endogenous level were isolated through 5FLAG-Sccl or 5FLAG-Sccl. Silver staining showed that the cohesin complex is purified to a nearly homogeneous level (Fig. 2B). Besides all four cohesin subunits, the cellular cohesins often contained other components like Pds5, as validated by LC-MS. To determine how cohesin interacts with itself, we then performed cross-linking MS (CXMS) of the purified cohesin complexes. The representative cross-linked amino acids mapped to Sccl are shown in Fig. 2 (lane 5), indicating that the intermolecular interaction of Sccl is mediated by other proteins in eukaryotic cells. However, when we repeated the pulldown experiments using purified Sccl proteins, His6-Sccl bound with GST-Sccl (Fig. 1G, lane 4), suggesting a direct physical association.

**Isolation and cross-linking analysis of the cohesin complexes**

To further address the two different cohesion models, it is critical to test whether cohesin subunits can self-associate in the context of the cohesin complex. For this purpose, we next purified the native cohesin complexes from yeast cells containing two copies of Sccl with small (5FLAG) and large (GST) epitopes, respectively. This allowed the simultaneous detection of the two Sccl copies in a single gel by probing with anti-Sccl antibodies. The lysates were first subjected to anti-FLAG affinity purification and FLAG peptide elution. The eluates were then run on a 10–30% glycerol sedimentation/velocity gradient. After centrifugation, fractions (0.5 ml each, labeled from top to bottom) were collected. After separation by SDS-PAGE, immunoblots revealed the co-purification of Scmc3 together with Sccl, suggesting successful isolation of the complex rather than an individual Sccl subunit (Fig. 2A). The peak of the purified complex (fractions 6–9) contained few GST-Sccl (i.e. the second copy of Sccl), sedimenting close to the 669 kDa standard (fraction 8). The theoretical molecular weight of the single-ring four-subunit cohesin complex is 478 kDa. The relatively broad distribution of the cohesin complexes in the glycerol gradient might be due to the co-purification of additional factors like Pds5 and Wpl1. However, the cohesin species containing the second Sccl copy (GST-Sccl) were clearly detected and sedimented much faster than 669 kDa, peaking around fraction 13. These data corroborate the existence of higher-order cohesin complexes in vivo.
that the pairs of cross-linked residues apart from each other in the available three-dimensional structure of Scc3 fragment likely represent the intermolecular interface. To test this, we then substituted these putative pairs by cysteine substitution for the VivosX (in vivo disulfide crosslinking) assay (44). If the two amino acids replaced by cysteine were close enough, a disulfide bond would be introduced by the permeable thiol-specific oxidizing agent 4,4′-dipyridyl disulfide (4-DPS). To simplify the screening and detection, we expressed two Scc3 alleles with a pair of tags (5FLAG-Scc3/13MYC-Scc3) in yeast cells. In WT, Scc3 (either 5FLAG-Scc3 or 13MYC-Scc3) migrated as a monomer (\( \sim 200 \) kDa) with or without 4-DPS treatment in nonreducing SDS-PAGE (Fig. 2, top, lanes 1, 2, 7, and 8). Among all mutated amino acid pairs, a portion of the Scc3-Scc3 cross-linking adducts was only detectable in the Scc3-K99C/Scc3-K1057C pair after 4-DPS treat-
ment (Fig. 2D, compare lanes 3 and 4 and lanes 9 and 10). They migrated more slowly than 300 kDa, close to the expected molecular weight of dimeric Scc3 (~287 kDa). Importantly, the same band was able to be probed by both anti-FLAG (Fig. 2D, top, lane 4) and anti-MYC (Fig. 2D, top, lane 10), confirming that it is a dimeric Scc3 complex. Moreover, the band was abolished in the reducing gel (Fig. 2D, bottom), further validating that it is formed by disulfide cross-linking of the introduced cysteine pair. Altogether, these results suggest the existence of the Scc3 dimer in vivo, consistent with the direct Scc3-Scc3 association in vitro. Intriguingly, the distal location of Lys-99 and Lys-1057 at the unstructured N and C termini of Scc3 also implicates that the twin Scc3 molecules might bind each other in an antiparallel manner to mediate a double-ring form of the cohesin complex.

**Replication-coupled Smc3-Smc3 interaction in human cells**

Because the cohesin status is cell cycle–regulated (45), we wanted to know whether cohesin dimerization is similarly controlled. To test this, we applied a proximity ligation assay (PLA) to visualize the cohesin-cohesin interaction in human cells (46). 5FLAG-Smc3 and 13MYC-Smc3 were introduced into HeLa cells. Cells were grown and arrested in G1 (0 h) by double thymidine block, before release into the fresh medium containing...
EdU for 2, 4, 6, 8, or 10 h. Two Smc3 copies were probed by mouse anti-FLAG and rabbit anti-MYC antibodies, respectively. If two Smc3 proteins are in proximity, their secondary antibodies conjugated to DNA oligonucleotides will bring together another pair of oligonucleotides, which is subsequently ligated and circulated by DNA ligase. The circulated DNA was amplified by rolling circle amplification and finally detected by fluorescence in situ hybridization. In the G1 phase, few fluorescence signals were observed (Fig. 3A), excluding the possible false positives presumably due to the high sensitivity of the PLA method and/or Smc3 overexpression. After G1 release, PLA signals appeared in 2 h and peaked around 6 h (Fig. 3, A and B). These results corroborate the cohesin-cohesin interaction originally discovered by Pati’s group in human cells (20). More importantly, these data also demonstrate that cohesin dimerization does not occur in the G1 phase and is regulated in a cell cycle–dependent manner in human cells. Intriguingly, quantification of both PLA and EdU signals revealed a rough
correlation between them ($r = 0.738$). Although PLA signals appeared a little behind EdU during the early S phase (0–4 h), both of them reached the peak at the same time (6 h), followed by a similar decline (Fig. 3C). Because EdU incorporation is an indicator of genome replication progress, it strongly argues that cohesin-cohesin interaction occurs in a DNA replication–coupled manner. The time lag of PLA signals compared with EdU levels during the early replication stage is not surprising, given that cohesin distributes in an average 67-kb distance along the chromosome in HeLa cells (47).

**Intermolecular cohesin interaction is cell cycle–regulated**

To further elucidate how cohesin dimerization is regulated, we investigated it in the synchronized yeast cells. For this purpose, a strain carrying FLAG-Scc1 and GFP-Scc1 was grown at 30 °C and arrested in G1 by α-factor (0 min). After release into S phase, cells were collected at different time points. Then we carried out GBP-IP of whole-cell extracts. Although Scc1 is expressed in G1 (Fig. 4A, lane 3, input (IN)), few Scc1 proteins co-precipitated with themselves (Fig. 4A, top panel). If we normalized the precipitated GFP-Scc1 (second panel), the co-precipitated 5FLAG–Scc1 gradually increased and peaked around 45 min (S phase), followed by a decline in M phase (Fig. 4, A (first panel) and B). The relative Scc1–Scc1 interaction was quantified as the 5FLAG-Scc1/GFP-Scc1 ratio in the precipitates, which clearly fluctuated with the cell cycle (Fig. 4C). Consistent with the results above in human cells, these data suggest that cohesin dimerization occurs exclusively in S phase in a cell cycle–regulated fashion.

Notably, there was increased Scc1 expression during S phase (Fig. 4A). To test whether cohesin dimerization in the S phase is due to the increased Scc1 protein level, we overexpressed both GFP-Scc1 and 5FLAG–Scc1 by strong promoters. This resulted in a very high level of both versions of Scc1 in G1 (Fig. 4D, lane 2, bottom). However, the Scc1–Scc1 interaction remained very weak at that time and augmented in S phase (Fig. 4D, top), similar to that in WT (Fig. 4A, top). Meanwhile, the amounts of Smc3 in the precipitates were not significantly changed (Fig. 4D, third panel), indicating a constant Scc1–Smc3 interaction throughout the cell cycle. These data suggest that cell cycle–regulated cohesin dimerization is not merely due to the fluctuation of the Scc1 protein level.

**Cohesin dimerization shares common factors with sister chromatid cohesion**

The above results suggest a similar cell cycle–regulated pattern between cohesin-cohesin interaction and sister chromatid cohesion. Notably, both of them occur concomitantly with DNA replication. These facts prompted us to speculate on a functional relationship between the two critical events. To test this notion, we carried out five sets of experiments.

First, given that sister chromatid cohesion occurs on chromatin, we asked how cohesin-cohesin interaction is controlled spatially. To address this question, we prepared native chromatin-bound fraction (Chr) and nonchromatin-bound fraction (supernatant (SN)) before FLAG-IPs. Cohesin existed in both fractions (Fig. 4E, lanes 3 and 4). However, the intermolecular interaction of Scc1 was detectable exclusively in the Chr fraction (Fig. 4E, compare lanes 7 and 8). This suggests that cohesin is dimerized in the context of chromatin as well.

Second, we examined whether the vital cohesion establishment factor, Eco1, is required for the cohesin-cohesin interaction. Because Eco1 is essential for cell viability, we combined both temperature-sensitive (td) and auxin-induced (aid) degrons to deplete cellular Eco1 protein. The Ubr1 and Tir1 ubiquitin E3 ligases were induced by galactose. The td and aid degrons were turned on by switching from 25 to 37 °C and adding indole-3-acetic acid (IAA), respectively. These led to cell death (Fig. 4F) and abolished S phase Smc3 acetylation (Fig. 4H, bottom, lanes 7–10), indicating effective Eco1 depletion. However, the first S phase progression right after Eco1 depletion was only subtly affected (Fig. 4G). Meanwhile, we monitored the intermolecular cohesin interaction during the cell cycle through EPEA-IP and immunoblotting in the Chr. In WT, the cohesin-cohesin interaction displayed a cell-cycle pattern (Fig. 4, H and J) as shown in Fig. 4C, but relatively slow, which is in accord with the slower cell-cycle progression under this condition (Fig. 4G). When Eco1 was depleted, co-precipitated 5FLAG–Scc1 was largely decreased (Fig. 4, H and J), whereas the chromatin-associated Scc1 levels of both versions were not much affected (Fig. 4H, bottom). Meanwhile, Scc1–Smc3 interaction was not affected either. These data suggest that Eco1 is required for cohesin dimerization, but not for chromatin association of single rings. Third, Smc3 acetylation is erased by deacetylase Hos1 in ana-phase and recycled in the subsequent cell cycle, so we examined the change of cohesin-cohesin interaction in the absence of Hos1. In the GFP-Scc1/p5FLAG–Scc1 dual-tagged haploid background, WT or mutant cells were cultured and arrested in G2 by nocodazole. Although the amounts of both GFP–Scc1 and 5FLAG–Scc1 were nearly equal in WT and mutant cells (Fig. 5A, lanes 5 and 6), the hos1Δ cells showed a significant augment of Scc1–Scc1 interaction (Fig. 5A, compare lanes 11 and 12). Similar results were obtained from the diploid cells in which two endogenous Scc1 copies carry the same pair of orthogonal epitopes (Fig. 5B, compare lanes 8–10). These results suggest that Hos1 either partially relieves cohesin-cohesin interaction in the M phase or prevents precocious cohesin-cohesin interaction before the S phase.

Fourth, prior to Eco1-dependent cohesion establishment, cohesin remains dynamic on chromatin due to the destabilized activity of Wpl1. The essential function of ECO1 can be bypassed by WPL1 deletion (33, 34), so we next compared the cohesin-cohesin interaction in the presence or absence of Wpl1. The experiments were basically conducted as described for hos1Δ. When WPL1 was deleted, cohesin oligomerization increased prominently in both G1 (Fig. 5A, compare lanes 11 and 13) and S (Fig. 5A, compare lanes 9 and 10). Consistently, in asynchronized diploid cells, a dramatic increase was observed in the absence of Wpl1 as well (Fig. 5D, compare lanes 6–8). These data indicate that Wpl1 prevents the cohesin-cohesin interaction, correlating with a loose and dynamic association of cohesin with chromatin in G1.

Fifth, based on the ratio of GFP–Scc1/5FLAG–Scc1 in the cell extracts and precipitates, we estimated the percentage of cohesin dimers at the endogenous protein levels in diploid cells.
Figure 4. Cohesin-cohesin interaction is regulated by Eco1 during the cell cycle. A, the GFP-SCC1/pSFLAG-SCC1 cells were grown, synchronized in G1, by α-factor (0 min), and released into S phase at 25 °C for the indicated time. The cell lysates were subjected to GBP-IP and IB against anti-FLAG and anti-GFP antibodies. B, a representative cell cycle profile analyzed by flow cytometry of the samples used in A. C, quantification of the relative intermolecular interaction of cohesin during the cell cycle. The densities of the FLAG-Scc1 and GFP-Scc1 bands in the precipitates were quantified. The ratio of FLAG-Scc1/GFP-Scc1 was calculated to indicate the relative cohesin-cohesin interaction in each sample. The maximum percentage among all samples was normalized to 100%. To ensure that the signals were within the linear range, immunoblots with appropriate exposure were quantified by Quantity One (Bio-Rad). Data shown are the mean ± S.D. (error bars) of three biological replicates. D, both GFP-SCC1 and 5FLAG-SCC1 under control of the GAL1 promoter were overexpressed in α-factor–arrested cells by galactose. All other experimental conditions were the same as described in A. E, the exponentially grown GFP-SCC1/p5FLAG-SCC1 cells were collected and fractionated into native Chr and nonchromatin-bound SN as described under “Experimental procedures.” Both SN and Chr fractions were subjected to FLAG-IP and IB using anti-Scc1 antibodies and anti-FLAG antibodies. 5FLAG-Scc1 cannot be well-detected in INPUT fraction using anti-Scc1 antibodies. Bottom, 5FLAG-Scc1 detected by anti-FLAG antibodies. F, efficient depletion of Eco1 via combined td and aid degrons leads to cell death. The growth of WT (ECO1) and Eco1 depletion strains (td-Eco1-aid) was examined by spotting on the medium with or without IAA at either 25 or 37 °C. G, Eco1 depletion causes only subtle changes in the cell-cycle progression. Shown are representative cell-cycle profiles of WT and Eco1 depletion strains used in H. After release from G1 arrest, cells were collected at the indicated time at 37 °C and analyzed by flow cytometry. H, Eco1 depletion interferes with cohesin-cohesin interaction on chromatin. Synchronized cells were prepared as in G. Native Chr was prepared as described under “Experimental procedures.” ScC1–3HA-EPEA was then precipitated via a C-tag affinity matrix and probed with the indicated antibodies. I, the relative cohesin-cohesin interaction in the presence or absence of Eco1 was quantified as described in C. Data shown are the mean ± S.D. of three biological replicates. *, p < 0.05; **, p < 0.01.
The measured cellular levels of GFP-Scc1 and 5FLAG-Scc1 were nearly identical (Fig. 5E). Through serial dilutions of the precipitates, we quantified the band densities of GFP-Scc1 and 5FLAG-Scc1 probed by anti-Scc1 antibodies in the same gel. The percentage of cohesin dimers was roughly estimated through the following formula,

\[
\text{Dimer} \% = \frac{3 \times \text{B5FLAG-Scc1 in IP} \times \text{dilution}}{\text{(B5FLAG-Scc1 in IP} \times \text{dilution))} \times 100\% \quad \text{(Eq. 1)}
\]

In asynchronized WT cells, \(~20\%\) of cohesins could be detected in the dimeric state (Fig. 5E). Intriguingly, \(~20\sim30\%\) of Smc3 is acetylated in budding yeast in a previous report (35).

Using a similar method, Cattoglio et al. (43) recently reported that cohesin dimers occupy at least \(~8\%\) of mouse embryonic stem cells. When WPL1 was deleted, cohesin dimers increased up to \(40\%\) in yeast (Fig. 5F). This result suggests that Wpl1, the anti-establishment factor of cohesion, acts as a negative regulator in cohesin dimerization as well. Taken together, all of these lines of evidence suggest that cohesin dimerization is cell cycle–regulated as the sister chromatid cohesion/dissolution cycle by the same mechanisms (i.e. Wpl1/Eco1/Hos1).

**Discussion**

Here, we show that cohesin is dimerized in S phase and monomerized again in mitosis and G1, which is controlled by the same regulators (Eco1, Wpl1, and Hos1) as the sister chromatid cohesion/dissolution cycle. Besides this biochemical evidence described here and literature (20, 43), genetic interactions also support cohesin-cohesin interactions (19). Both yeast cohesin and prokaryotic SMC condensin have been proposed to act as dimers in extruding DNA loops (48, 49).
EDITORS’ PICK: Two-ring cohesin

Table 2

<table>
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<tr>
<th>Strain</th>
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<tr>
<td>BY7471</td>
<td>MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0</td>
<td>In stock</td>
</tr>
<tr>
<td>BY7472</td>
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<td>YSD03</td>
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<td>This study (Fig. 3, E–H)</td>
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Notably, through bifluorescent complementation assays, Zhang et al. (20) also showed a similar antiparallel orientation of Scc1-Scc1 in human cells, generally in agreement with the results shown in this study. The only difference lies in the number of Scc3 subunits in the cohesin dimer. According to a very recent study from the Peters group, the stoichiometry of the four cohesin subunits remains 1:1:1:1 (monomer) or 2:2:2:2 (dimer) throughout the cell cycle in human (47). Therefore, the discrepancy might be due to the different experimental procedures/conditions.

Although the exact interface of such a cohesin handcuff remains to be solved, we speculate that it might be mediated via self-association of Scc3 rather than Scc1 for at least two reasons. First, both pulldown and VivosX data show a direct physical association of two Scc3 molecules. Second, lack of Scc3 or Eco1 causes a defect in sister chromatid cohesion but not in cohesin binding to DNA, whereas Scc1 is indispensable for both (29, 30, 50). Besides the canonical single-ring structure, dimerization may provide an additional mechanism for cohesin to execute various functions in sister chromatid cohesion, DNA repair, chromatin loop extrusion, and high-order chromatin organization (21). It will also be very interesting to investigate how Eco1-catalyzed acetylation and Wpl1 regulate the structural/conformational change of cohesin in the future.

Experimental procedures

Strain and plasmid construction

Strains and plasmids used in this study are listed in Tables 1 and 2, respectively.

Preparation of antibodies

To raise polyclonal antibodies specific to Scc1 and Smc3, purified Scc1N (amino acids 1–333) and Smc3 hinge domain were used to immunize rabbits. Polyclonal antibodies were affinity-purified. Scc1 and Smc3 beads were prepared by immortalizing purified Scc1N and Smc3 proteins to NHS-activated agarose beads as recommended by the manufacturer (GE Healthcare).

Cell synchronization and flow cytometry analysis

Cells were grown to logarithmic phase, and 7.5 μg/ml α-factor was added for cell synchronization in G1 phase. After washing twice, G1-arrested cells were released in fresh medium and continued growth for the indicated time. Cells were collected and fixed with 70% ethanol and then processed for flow cytometry using a BECKMAN Cytoflex-S flow cytometer.

Conditional depletion of cellular Eco1 protein

The efficient depletion of endogenous Eco1 protein was achieved through a two-degron strategy. td and aid degrons were added to the N and C terminus of Eco1, respectively. The corresponding two ubiquitin ligases (E3), UBR1 and OsTIR1, were integrated into the genomic UBR1 locus under control of the galactose-inducible Gal1-10 promoter. Cells were first grown at 25 °C in rich medium containing 0.1 mM Cu2+ supplemented with 2% raffinose before transferring to 2% galactose to induce the expression of two E3s. Two degrons were turned on by adding 1 mM IAA (for aid) and switching to 37 °C (for td) for 2 h. The protein level of Eco1-MYC was measured by immunoblotting (IB) with anti-MYC and anti-Smc3ac antibodies.

Whole-cell extracts (WCE) and IB

WCE of 100 OD600 units of asynchronous or synchronized cells were prepared by glass bead beating (Mini-Beadbeater-16, Biospec) in lysis buffer (50 mM HEPES/KOH, pH 7.4, 150 mM NaCl, 1 mM EDTA, 10% glycerol, 1 mM DTT, 1 mM PMSF, protease inhibitor tablets (EDTA-free; Roche Applied Science)). Protein samples were separated by SDS-PAGE and immunoblotted with the antibodies specifically indicated in each figure. Antibodies used in this study are as follows: mouse anti-FLAG M2-specific mAb (1:1000; Sigma), rabbit polyclonal anti-GFP (1:500; GeneScript), mouse anti-HA M2-specific mAb (1:1000; Sigma), rabbit anti-ubr1::PGal1-UBR1-PGAP-OsTIR1-9MYC-Ura3 (p315-SFLAG-Scc1::LEU2 p313-ECO1::His3). Horseradish peroxidase–conjugated anti-rabbit or anti-mouse IgG was used as the secondary antibody (1:10,000; Sigma).
Monoclonal GBP agarose, monoclonal anti-EPEA agarose (Thermo Fisher), and monoclonal anti-FLAG M2 affinity gel (Sigma–Aldrich) were used for IP. IP was performed using strains co-expressing the tagged versions of each protein as indicated in each figure. After three washes, the proteins specifically associated with beads were boiled and analyzed by SDS-PAGE and IB using the indicated antibodies.

**Glycerol gradient centrifugation**

The native protein complexes in the peptide eluates after FLAG-IPs were concentrated and applied to the top of a 10–30% glycerol gradient in EBX-3 buffer (50 mM HEPES/KOH, pH 7.5, 150 mM KCl, 2.5 mM MgOAc, 0.1 mM ZnOAc, 2 mM NaF, 0.5 mM spermidine, 20 mM glycerophosphate, 1 mM ATP, 1 mM DTT, 1 mM PMSF, protease inhibitor tablets (EDTA-free; Roche Applied Science)). The gradients were centrifuged in a P55ST2 swinging bucket rotor (Hitachi CP100NX ultracentrifuge) at 120,000 × g for 9 h using slow deceleration. After centrifugation, the fractions were collected from the top of the gradient and subjected to SDS-PAGE and immunoblots. Aldlase (158 kDa) and thyroglobulin (669 kDa) were used as size markers.

**CXMS**

5FLAG-Scc3 was prepared by FLAG-IP of yeast WCE and FLAG peptide elution. About 15 μg of purified Scc3 in a volume of 15 μl was cross-linked through incubation with the lysine cross-linker disuccinimidyl suberate (DSS) at a final concentration of 0.5 mM for 1 h at room temperature. The final concentration of 20 mM NH₄HCO₃ was added to quench the reaction. The cross-linked proteins were precipitated with ice-cold acetone of 4–5-fold volume at −20°C overnight, resuspended in 8 μl urea, 100 mM Tris, pH 8.5. After trypsin digestion, the LC-MS/MS analysis was performed on an Easy-nLC 1000 UHPLC (Thermo Fisher Scientific) coupled to a Q Exactive HF Orbitrap mass spectrometer (Thermo Fisher Scientific). Peptides were loaded on a precolumn (75-μm inner diameter, 4 cm long, packed with ODS-AQ 12 nm–10 mm beads from YMC Co., Ltd.) and separated on an analytical column (75-μm inner diameter, 13 cm long, packed with ReproSil-Pur C18-AQ 1.9-μm 120-Å resin from Dr. Maisch GmbH) using a linear gradient of 0–35% buffer B (100% acetonitrile and 0.1% formic acid) at a flow rate of 250 nl/min over 73 min. The top 20 most intense precursor ions from each full scan (resolution 60,000) were isolated for HCD MS2 (resolution 15,000; NCE 27) with a 15% and 5% cross-linked peptides with the cutoffs of false discovery rate of 0.001.

**Disulfide cross-linking to capture site-specific protein-protein interactions in vivo**

The Scc3-Scc3 interaction was captured by a disulfide cross-linking method in yeast cells (44). The indicated pairs of amino acid residues in Scc3 were substituted by cysteine. WT or mutant cells were cultured in 5 ml of CSM medium (without cysteine) at 30 °C to OD₆₀₀ of 0.5 before the addition of 180 μM 4-DPS (Sigma–Aldrich). The cultures were resuspended for 20 min and then quenched with 20% TCA. The cells were pelleted and washed with 20% TCA before homogenization in the presence of 400 μl of 20% TCA and ~450 μl of glass beads using Mini-Beadbeater-16 (Biospec). N-Ethyl maleimide was added to prevent any free thiol groups from cross-linking after cell lysis. Proteins were extracted and separated by nonreducing and reducing SDS-PAGE for immunoblots against the indicated antibodies as described previously (44).

**PLA**

The PLA was performed as described previously (51). Briefly, HeLa cells were fixed with 4% paraformaldehyde (Sigma–Aldrich) in PBS for 15 min, permeabilized with 0.1% Triton X-100 (Sigma) for 5 min, and blocked for 1 h with a blocking solution (250 μg/ml BSA, 2.5 μg/ml sonicated salmon sperm DNA, 5 mM EDTA, 0.05% Tween 20 in PBS). Cells were washed with PBS and incubated in two primary antibodies. The primary antibodies used were as follows: mouse monoclonal anti-FLAG (1:100; Sigma) and rabbit polyclonal anti-MYC (1:100; 16286-1-AP, Proteintech). After washing with PBS, samples were incubated with secondary antibodies conjugated with PLA probes for 1 h at 37°C. After washing with PBS, samples were incubated with ligation-ligase solution for 30 min at 37°C. Then the samples were washed with PBS and continued with amplification-polymerase solution incubation for 90 min at 37°C. The detection mix was added, followed by incubation for 30 min at 37°C. Then the slide was kept in the dark. After washing three times for 5 min each with PBS, slides were mounted using Duolink in situ Mounting Medium with 4,6-diamidino-2-phenylindole. Pictures were taken using a fluorescent microscope (Leica DMI8).

**Native chromatin fractionation**

Native chromatin fractionation was performed as described (40, 52) with minor modifications. Yeast cells of 200 OD₆₀₀ units were spheroplasted by 75 units/ml lyticase. Crude extracts were prepared by Triton X-100 treatment and fractionated via sucrose cushion in 500 μl of EBX-3 buffer (50 mM HEPES/KOH, pH 7.4, 150 mM NaCl, 2.5 mM MgCl₂, 0.1 mM ZnOAc, 5 mM NaF, 1 mM NaVO₄, 10 mM β-glycerophosphate, 1 mM ATP, 1 mM DTT, 1 mM PMSF, protease inhibitor tablets (EDTA-free; Roche Applied Science). The supernatant contained non-chromatin-bound proteins. Chromatin-bound proteins in the pellet were released by incubation in EBX-3 buffer containing 500 units/ml of benzonase (Sigma) for 60 min at 4°C.

**In vitro pulldown assay**

An approximately 10 pm concentration of each protein was mixed with GSH Sepharose 4B (GE Healthcare Life Sciences) in 100 μl of binding buffer (50 mM HEPES-NaOH, pH 7.6, 150 mM NaCl, 10% glycerol, 1 mM EDTA, 1 mM PMSF, 1 μg/μl BSA, and 0.1% Triton X-100) and incubated for 1 h at 4°C. The beads were washed at least three times prior to Western blotting.
**EDITORS’ PICK: Two-ring cohesin**

### Statistical analyses

Statistical analyses were performed using GraphPad Prism software. The data are presented as the mean ± S.D. Student’s t test was employed to determine the statistical significance of the differences. A value of p < 0.05 was regarded as statistically significant.

### Data availability

All data are contained within the article.

### References