

**TITLE: Genome-wide mapping of the cohesin complex in the yeast *Saccharomyces cerevisiae***

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## SUMMARY

**Background:** In eukaryotic cells, cohesin holds sister chromatids together until they separate into daughter cells during mitosis.

**Methodology/Principle Findings:** We have used chromatin immunoprecipitation coupled with microarray analysis (ChIP chip) to produce a genome-wide description of cohesin binding to meiotic and mitotic chromosomes of *S. cerevisiae*. The identification of cohesin binding peaks in ChIP chip data was facilitated by a novel automated algorithm, PeakFinder.

**Conclusions/Significance:** Cohesin sites are highly conserved in meiosis and mitosis, suggesting that chromosomes share a common underlying structure during different developmental programs. A negative correlation between cohesin sites and meiotic recombination sites suggests meiotic exchange is spatially regulated to promote exchange between homologs rather than sister chromatids. On chromosome arms cohesin associated regions occur with a semi-periodic spacing of 11 kb that correlate with AT content. The number of sites correlates with chromosome size. Cohesin binding to neighboring sites is not cooperative. Cohesin sites are strongly biased towards regions between convergent transcription units. Transcript elongation into a cohesin binding site inhibits cohesin binding. Thus transcription and cohesion are apparently incompatible processes. This genome-wide view of mitotic and meiotic cohesin binding provides an important framework for the exploration of cohesins and cohesion in other genomes.

## INTRODUCTION

Sister chromatid cohesion ensures that daughter cells inherit complete copies of their genome. Cohesion in eukaryotic cells is mediated by a multisubunit protein complex called cohesin. Cohesin consists of four proteins: Smc1, Smc3, Scc1/Mcd1, which is called kleisin and is the target of the protease separase, and Scc3. These proteins have recently been proposed to form a ring structure that encircles sister chromatids (Gruber et al., 2003). Alternately, the ring may act as a snap (Milutinovich and Koshland, 2003). Cohesion is established during replication and maintained until metaphase in mitosis (Uhlmann and Nasmyth, 1998). All members of the cohesin complex are essential in *S. cerevisiae* since mutation results in the precocious dissociation of sister chromatids.

Cohesion serves at least two roles in the cell with respect to accurate genome transmission. Firstly, cohesion proximal to the centromere facilitates biorientation of chromosomes with respect to the spindle and it prevents splitting of chromosomes while other chromosomes biorient (Tanaka et al., 2000). Secondly, cohesion along chromosome arms is suggested to be essential for proper chromosome condensation in yeast. In meiosis, cohesin at most arm sites disappears prior to the first nuclear division. The meiotic cohesin complex contains Rec8 instead of Scc1/Mcd1 (Klein et al., 1999). Cohesion is maintained distal to crossovers between homologs, which links them and facilitates their bi-orientation on the meiotic I spindle. Cohesin is also maintained at pericentric regions which is essential for biorientation of chromosomes at the spindle for the second nuclear division (Buonomo et al., 2000).

We are interested in understanding the *cis* determinants of cohesin binding. Cohesin associated regions have been identified in yeast using chromatin immunoprecipitation. In these studies cohesin association with chromatin was followed at low resolution along the entire length of chromosome III (3 Kb intervals) or high resolution (300 bp intervals) at limited regions on chromosome III, V, and XII (Blat and Kleckner, 1999; Laloraya et al., 2000; Megee et al., 1999; Tanaka et al., 1999). These

studies showed associations of cohesin with specific regions of chromosomes; one of the regions of intense association is centromeres. In addition to the enrichment of cohesin in the pericentric region of Chromosome III, Blat and Kleckner found a spacing of cohesin associated regions of 13 kb along the arms of chromosome III (Blat and Kleckner, 1999). A similar spacing was observed in a limited region of chromosome XII (Laloraya et al., 2000). These studies also noted a correlation of cohesins with elevated AT content. The average size of the mapped sites was 0.8-1 kb (Laloraya et al., 2000). Based on three sites mapped to high resolution, cohesins were proposed to associate with the boundaries of transcriptionally-silent regions (Laloraya et al., 2000).

Despite these insights into *cis* determinants of cohesion, many aspects of the cohesin-DNA interaction remain obscure. The high resolution studies sampled very little of the genome while the low resolution analysis of chromosome III does not answer questions about the position of cohesin relative to smaller-scale genome features, such as transcription units. Furthermore, chromosome III is the sex chromosome of budding yeast and like the case in many organisms, it has unusual properties including large domains of repressed recombination, silent mating type loci, and different patterns of replication. Some discrepancies between high and low resolution studies have emerged including, for example, whether cohesins are found at telomeres.

One approach to better understand *cis* determinants of cohesin binding is to analyze them by a genomic approach. To obtain a genome-wide picture of cohesin binding to *S. cerevisiae* chromosomes at 1-2 kb resolution, we used a combination of chromatin immunoprecipitation and microarray methods, often referred to as ChIP chip technology. To identify peaks of cohesin binding we developed an automated algorithm for locating peaks in ChIP data. We used a similar approach to map all the cohesins on an “ectopic chromosome”, a yeast artificial chromosome containing a 334 Kb insert from human chromosome VII. The advantage of this comprehensive approach is that it allows us to compile information from a large number of sites, which greatly facilitates the assessment of cohesin distribution, and the significance of correlations with many local properties of the genome such as base composition and coding content. Furthermore it allows us to evaluate whether cohesin binding is influenced by strain background, transcription, or developmental programs like meiosis. We used this genomic

information to manipulate individual cohesin sites to begin to test the predictions arising from genomic correlations.

## RESULTS

### *Determining sites at which cohesin interacts with the yeast genome*

We used the genome-wide approach of ChIP chip to identify and evaluate *cis* determinants of cohesin sites. We began the study using Mcd1-18Myc as the protein target in the W303a strain background. Cells were arrested in metaphase by a temperature sensitive mutation in *CDC16*, a subunit of the anaphase promoting complex required to degrade Pds1p, a negative regulator of anaphase (Cohen-Fix and Koshland, 1997; Yamamoto et al., 1996). We were interested in determining potential correlations between cohesin binding and genome features such as base composition, transcriptional state, and known *cis* determinants of chromosome transmission. Earlier studies have used simple ratio “thresholds” to define binding sites in ChIP chip data (Iyer et al., 2001; Lieb et al., 2001; Wyrick et al., 2001). A single genome-wide threshold would not work well for our data because 1) peak height is high at pericentric regions and diminishes towards the end of chromosomes, and a threshold would have the effect of skewing all the binding sites towards the centromere-proximal regions, 2) binding sites in ChIP chip data are frequently defined by several array elements, complicating the identification of *cis* determinants and 3) much of the analysis has to be done manually. In this study, we used a more comprehensive, automated approach, implemented in the PeakFinder program, which discerns and filters the peaks from a variable local background and maps the tip of the peak to a single array element.

We validated our methods by comparing the results to previously collected data. Laloraya et al., 2000, discovered nine sites in the arms of chromosome III and XII using ChIP followed by semi-quantitative PCR. All of those sites could be identified as peaks in the microarray data using PeakFinder (for Chromosome III see Figure 1A). Blat and Kleckner, 1999, had mapped cohesin sites to 3-kb resolution on chromosome III. Although the number of identified peaks is increased in our data (23 vs. 33), the increase can largely be accounted for by higher resolution mapping and better peak identification. Qualitatively the results are comparable, including that 1) the peak height at cen III is the highest for the chromosome, 2) the height of the peaks declines towards the ends of the

chromosome and 3) peaks correlate with AT content (Figure 2). Therefore, our methods confirm and extend results of previous studies.

To demonstrate the internal consistency and reproducibility of our data, we compared peaks of cohesin for Mcd1-18Myc in W303a (Figure 1A), Scc1/Mcd1-6HA in A364a (Figure 1B), and Smc3-6Myc in A364a (Figure 1C). The agreement between the location of cohesin peaks in different strain backgrounds is good (correlation coefficient=0.76 for Mcd1/Scc1 ChIP in strains A364a and W303a) and is excellent when different members of the cohesin complex are used as baits in the same genetic background (correlation coefficient=0.96 for Mcd1/Scc1 and Smc3 ChIP in strain A364a). The lower correlation coefficient for strain backgrounds as compared to protein complex members likely reflects real sequence differences between strains that contribute to the peak profile.

#### *Genomic distribution of cohesin*

The levels of cohesin on all the chromosomes are similar and follow a very similar pattern: large regions of intense binding in the pericentric domain and less intense, shorter sites distributed in a semi-periodic manner throughout the arms. We evaluated whether cohesin was associated with *cis* determinants of chromosome transmission including centromeres, telomeres, and origins of replication. Cohesin shows an intense, large (30-50 kb) dense region of binding in pericentric domains (Figure 2). Although it has been proposed that telomeres do not associate with cohesin (Blat and Kleckner, 1999), we found 9 of the 32 telomeres to be associated with cohesin. However, the height of the peaks associated with telomeres and subtelomeric regions is lower than at internal regions, which may reflect either lower affinity or occupancy of cohesin at these regions (Figure 3A). On chromosome III, where replication origins have been functionally mapped (Poloumienko et al., 2001), we note an association of cohesion peak tips and shoulders with origins (Figure 1A, only high firing origins are indicated). While the significance of the limited association of cohesin with telomeres and origins is unclear at this time, cohesin enrichment proximal to all centromeres clearly supports previous studies implicating a requirement for the coupled function of cohesion and the centromere in chromosome segregation.

While some cohesin is associated with known *cis* determinants of chromosome transmission, the vast majority of sites are not. The number of cohesin peaks per chromosome shows an excellent correlation to chromosome length ( $R^2=0.96$ , Figure 3B). The mean distance between sites was 10.9 kb, with a standard deviation of 6.7 kb (Figure 3C). There are 50 regions of the genome with large gaps between neighboring peaks (24 kb or greater, i.e. the mean plus 2 standard deviations or more); these are randomly scattered throughout the arms of the larger chromosomes, however, the four smallest chromosomes do not have any such gaps. The spacing of peaks is conserved for the most part in pericentric regions, with an additional “baseline” level of binding. Cohesin distribution therefore appears to be nonrandom with a tendency for even distribution. This pattern suggests arm sites perform a critical function for chromosome transmission.

#### *Cohesin binding is biased towards AT rich sequences*

Cohesin peaks were strongly associated with AT rich regions as can be seen from the comparison of the distribution of the AT percentage for the genome features on the array (Figure 4A, grey bars) and for the 1,095 features associated with cohesin peaks (Figure 4A, red bars). We found that 810 of the 1,095 array elements defined as cohesin sites have AT content above the yeast median of 62.6% ( $p<0.0001$ ). Cohesin peaks are significantly associated with intergenic regions, with 765 out of 1,095, or 70%, of all peaks located in such regions ( $p<0.0001$ ) even though intergenic regions make up only 27% of the genome length. Since intergenic regions in *S. cerevisiae* are more AT rich than ORFs, we asked if the AT bias could be explained by the bias towards intergenic sequences by comparing the AT content of all intergenic regions with the AT content of intergenic regions associated with cohesin (598 out of 765 above median,  $p<0.0001$ , Figure 4B). The peaks observed at ORFs are also higher in AT content than ORFs on average ( $p=0.0005$ ). Thus, AT content, while not the sole determinant, is an important factor for cohesin association.

We observed local oscillations of AT content in a 5 kb sliding window, which corresponded to cohesin peaks in chromosome arms (Figure 2), thus extending to the whole genome the observation for chromosome III (Blat and Kleckner, 1999). Furthermore, all 16 pericentric regions have local peaks of AT content (Figure 2).

Interestingly, the sequence elements associated with cohesin in the pericentric domain contain nearly equal numbers of ORF and intergenic sequences, as might be expected if binding is mainly directed by the centromere and base composition and disregards other genomic features such as transcription units (Weber et al., cosubmitted).

#### *Distribution of cohesin on a YAC*

The semi-regular spacing of cohesin and the correlation with local oscillations of base composition suggested that AT content and/or a measuring mechanism might control cohesin distribution. In order to test this possibility, we employed a non-essential ectopic chromosome. We used ChIP followed by quantitative PCR to map cohesin sites in a YAC containing 334 kb of human DNA from chromosome VII. The pericentric region on the right end of the YAC shows a broad (~35 kb) intense association with cohesin. This is similar to the cohesin association with endogenous pericentric regions. However, the spacing of cohesin does not have the same periodic nature as on endogenous chromosomes. For example, the leftmost 83 kb of the YAC contains only one peak of cohesin resulting in two large gaps for cohesin of 38 and 45 kb (Figure 5A). These two gaps are larger than any of the gaps found on the small endogenous yeast chromosomes. The human DNA fragment does not contain oscillations of AT content similar to those observed in the yeast genome, nor does the pattern of cohesin association appear to reflect base composition in this context. Thus, the difference in the distribution of cohesin sites in the arms of the YAC supports the idea that sequence contributes to cohesin distribution in yeast and evolution has selected for an even distribution on endogenous chromosomes.

To further test the contribution of sequence to cohesin binding, we took advantage of the fact that none of the human sequences were essential for yeast survival. We replaced the region from 156-162 kb, which contains a cohesin binding site, with the gene encoding for geneticin resistance and saw that this region was no longer associated with cohesin (Figure 5B). Neighboring regions are unaffected and *de novo* cohesin binding is not observed. This suggested that some property of the sequence, rather than its precise location or context, was responsible for cohesin binding.

### *Transcription and cohesin*

Inspection of the intergenic regions associated with cohesin revealed a tight association with intergenic regions in which transcription is converging, and additionally, an extreme bias against association with intergenic regions in which transcription is diverging. Among the cohesin associated intergenic regions that could be assigned to a category, 86% were in intergenic regions with converging transcription, 12% were in intergenic regions with surrounding unidirectional transcription, and only 2% were in intergenic regions that are between divergent transcription. These regions are represented in the genome in approximately a 1:2:1 ratio, respectively, making this result highly statistically significant ( $p < 0.0001$ ). In fact, 39% of the convergent intergenic regions in the genome have peaks of cohesin binding and nearly half of all cohesin sites are in convergent intergenic regions. These percentages approach the predictive power of consensus sequences for identifying binding sites of their cognate transcription factor (Chu et al., 1998; Lieb et al., 2001). Convergent intergenic regions have high AT content compared to the genome at large; the bias of the intergenic sequences associated with cohesin can be partly explained by the AT bias of convergent intergenic regions (Figure 4C).

865 of the 1,095 sites can be explained by one or more of the following factors: 1) within 25 kb of a centromere, 2) above average AT content or 3) intergenic region with converging transcription. This leaves 230 sites unexplained. Of these, 43 are intergenic. Most of these are simply difficult to assign to a transcriptional category. Interestingly, of the 230 “unexplained” sequences, 187 are in ORFs, which is more than half of all the ORFs associated with cohesin. These ORFs are not enriched for any characteristics with regard to function, dubiousness, transcription level, or essentiality. They do not have significantly lower peak height, which might otherwise indicate that these are false peaks. This means that while proximity to a centromere, AT content, or converging transcription can explain nearly all (over 94%) of the cohesins in intergenic regions, the *cis* determinants that make ORFs good cohesin sites (about 17% of total cohesin sites) are difficult to ascertain.

Attempts to identify a genome-wide linear consensus binding site for cohesin using BioProspector (Liu et al., 2002), MobyDick (Bussemaker et al., 2000), AlignACE

(Hughes et al., 2000), and MEME (Bailey and Elkan, 1994) did not return a sequence with predictive value. However, when we took the group of “unexplained” ORF sequences and looked for a common motif using BioProspector, we identified two repetitive sequences that were strongly enriched relative to the genome: (CAR)<sub>5</sub> ( $p=10^{-65}$ ) and (GAN)<sub>10</sub> ( $p=10^{-76}$ ). The p values reflect the significance of these sequences as calculated based on a Monte Carlo simulation for the yeast genome. These sequences were rare in intergenic regions in yeast. These sequences were not present in the YAC. Further experiments will be required to determine if these repeats are targeted by cohesin. Interestingly, human cohesin has been localized in Alu repeats (Hakimi et al., 2002), suggesting that repetitive DNA may be prone to a particular structure or chromatin configuration preferred by cohesin, or may accumulate in regions that are bound by cohesin.

#### *The mechanism of the negative association between transcription and cohesin binding*

The bias towards intergenic regions being associated with cohesin suggested a general incompatibility between transcription and cohesin association. In addition, it has been shown that transcription can disrupt centromeric cohesin and results in chromosome missegregation and cell death (Tanaka et al., 1999). Cohesin at arm sites at the HMR locus, the right telomere of chromosome III, and the *RDN1* array was noted to be at the boundaries of silent chromatin (Laloraya et al., 2000).

We analyzed whether changing the transcriptional program could change the association of cohesin with a locus. We grew cultures with either 2% glucose or 2% galactose as the carbon source and arrested them in metaphase using nocodazole. The main difference between metaphase arrest in the presence of nocodazole and in ts-*cdc16* is that cohesin binding at pericentric regions is increased in the former case (unpublished observation). We carried out ChIP chip analysis in parallel with monitoring gene expression in the same cells using ORF arrays. Of the regions where gene expression changed 5-fold or more, only two regions were associated with cohesin. One peak of cohesin binding in glucose was associated with the promoter of the *GAL2* gene (Figure 6A), which was induced 42-fold in galactose. This had a dramatic effect on the local profile of cohesin binding (Figure 6B). The promoter region of *GAL2* becomes a

“valley” of cohesin binding and the single peak observed in glucose is split into two peaks, in effect adding a new peak to the region. The second region is an uncharacterized ORF, YDL218W, whose expression is induced 11-fold in the presence of glucose compared to galactose. This ORF is associated with cohesin in the presence of galactose, but this association is reduced when glucose is present (data not shown). The peaks surrounding both regions were unaffected. These results demonstrate that high levels of transcription are incompatible with cohesin binding. It also supports the results observed with the human DNA that neighboring cohesin sites behave independently.

There are a number of mechanisms that could account for the incompatibility between transcription and cohesin binding. Transcription of a region during G1 may prevent new association of cohesin, or transcription may displace cohesin in G2. We explored the mechanistic link between transcription and cohesin association at the previously characterized cohesin sites CARC1 and CARL2 (Laloraya et al., 2000). 0.8 kb of CARC1 and 1.4 kb of CARL2 were moved next to a galactose-inducible promoter (pGAL1-10) on a plasmid. Strains containing one of these two plasmids were grown with 2% raffinose as the carbon source, arrested in G1 with alpha factor, and then released from G1 in the presence of nocodazole, producing a metaphase arrest. Galactose was added to half the culture. One hour after the addition of galactose, cultures were fixed with formaldehyde and processed for ChIP. Semi-quantitative PCR was used to monitor the distribution of cohesin. With the appropriate use of primers, cohesin association with CARC1 and CARL2 on the plasmid and the endogenous locus could be distinguished. Galactose-induced transcription had no effect on association of cohesin with the endogenous loci (data not shown) but disrupted cohesin associated with the 5' end of both CARC1 and CARL2 on the plasmid (Figure 7A). This result demonstrates that transcription during G2 can displace cohesin.

The displacement of cohesin may be due to a competition between RNA pol II and cohesin for DNA or transcript elongation may remove cohesin. We tested if the incompatibility was dependent on transcript elongation. A culture was arrested with nocodazole and galactose-responsive transcription was induced by the addition of galactose, as described above. Thiolutin was added to half of this culture immediately prior to the addition of galactose. Thiolutin inhibits transcript elongation but presumably

does not inhibit the binding of RNA pol II (Parker et al., 1991). The effect as monitored at CARL2 was dependent upon elongation since the addition of thiolutin prevented the displacement of cohesin (Figure 7B). This result demonstrates that the binding of RNA pol II *per se* does not affect cohesin binding, but transcript elongation can displace cohesin within the G2 portion of a single cell cycle.

### *Meiotic cohesin*

The transcriptional program of a cell changes under different conditions, such as the developmental program of sporulation. We used ChIP chip to analyze the location of the meiosis-specific cohesin complex (Klein et al., 1999; Watanabe and Nurse, 1999) using Rec8-3HA as the ChIP target in the SK1 strain background, which is a rapidly and synchronously sporulating strain. We did not know if the pattern of sites would be similar to the mitotic complex since no information on the *cis* determinants of this complex has been reported. In general, the pattern of cohesin in meiotic and mitotic cells is very similar (correlation coefficient=0.77 across SK1 genome comparing Rec8 to Mcd1, for coordinates 295-345 kb and 440-460 kb on ChrXII see Figure 8, data for all chromosomes provided as supplemental material). Pericentric regions contain broad, intense regions of cohesin association and there are nonrandomly spaced cohesin sites in the arms.

The most notable difference between meiotic and mitotic cohesin is at the ribosomal DNA (rDNA) locus and the surrounding region. (Nocodazole arrest does not affect cohesin binding in the rDNA in A364a or W303a.) The rDNA is encoded in an approximately 1-2 Mb region on the right arm of Chromosome XII consisting of 100-200 tandem copies of a 9.1 kb repeat. The region to the left of the first repeat has been shown to contain a cohesin binding site at *PCD1* (Laloraya et al., 2000) that is pronounced in mitosis but diminished for meiotic cohesin (Figure 8A). The transcription of this gene is induced early in meiosis, which may explain why cohesin binding to this site is diminished (Chu et al., 1998). There is another peak of cohesin binding that localizes to the left border of the rDNA repeat (Laloraya et al., 2000) that is absent for meiotic cohesin (Figure 8A). Although information regarding the transcription of rDNA in meiosis is unavailable, genes involved in the processing of the 35S transcript, such as

*ROK1*, *RRS1*, and *EBP2* (Wade et al., 2001), are down-regulated 5-15 fold by 0.5 hours in meiosis, and ribosomal protein genes are also down-regulated an average of 5-fold (Chu et al., 1998), suggesting that significantly reduced transcription may alleviate the transcriptional boundary status of this region and could explain the difference in cohesin. These two major differences between the patterns of mitotic and meiotic cohesin suggest that the meiotic complex is influenced by transcription in a similar manner to the mitotic complex.

We compared the location of meiotic cohesin to the location of the double-strand breaks (DSBs) that initiate meiotic recombination (Gerton et al., 2000). We found a negative correlation (correlation coefficient=-0.26); DSBs tend to occur in regions where meiotic cohesin is absent, and meiotic cohesin tends to be located in regions that contain low levels of DSBs (Figure 8B). Interestingly, the rDNA contains a DSB hotspot and is not bound by meiotic cohesin but is associated with the mitotic complex (Figure 8A). Cohesin has been shown to be required for the formation of the axial elements that become the lateral elements of the proteinaceous structure known as the synaptonemal complex (SC) (Klein et al., 1999). The SC organizes meiotic chromosomes and aids interhomolog recombination. In fact, meiotic cohesin has been shown to be required for meiotic recombination (Klein et al., 1999). This result suggests that recombination can recognize chromosome structure/organization provided by cohesin and avoids sites of sister-sister proximity.

## Discussion

We have used ChIP chip to map the genome-wide pattern of cohesin association under several different growth conditions (metaphase arrest by ts-*cdc16* or nocodazole, galactose or glucose as a carbon source, induction of meiosis) and in three different yeast strain backgrounds (W303a, SK1, A364a) to 1-2 kb resolution. Using an algorithm that assesses cohesion binding by comparison of signal to variable local background, we find that the majority of cohesin binding sites are remarkably constant under these different circumstances. Distribution of cohesins throughout the genome appears to depend on a combination of base composition, sequence, and transcriptional activity. We find evidence for three types of cohesin sites in the genome: 1) cohesin associated with the centromere and pericentric domain, 2) cohesin associated with intergenic regions in chromosome arms and 3) cohesin associated with ORFs in chromosome arms. The association of cohesin with these three types of sites is subject to different genomic parameters. Cohesin at centromeres and pericentric regions is spread over a broad domain with an elevated “baseline” level and is not affected by the natural transcriptional and coding status. Much of the cohesin in chromosome arms is located in transcriptionally converging intergenic regions. ORFs in chromosome arms where cohesin is found are enriched for repetitive sequences. This suggests that there may be three mechanisms to load cohesin, consistent with what has been proposed for cohesin in meiotic chromosomes for *S. pombe* (Kitajima et al., 2003). A unifying feature of all three types of sites is high AT content.

Pericentric regions contain the most intense and broadest levels of cohesin in the genome (for a more complete analysis of pericentric cohesin see Weber et al). This finding is consistent with a model in which a centromere contains determinants of two opposing processes: 1) pulling the chromosomes apart, via the assembled kinetochore attached to a microtubule, and 2) keeping chromosomes together, via pericentric cohesion. The intensity and breadth of cohesin binding at pericentric regions is similar for all chromosomes, implying microtubules pull all chromosomes with comparable force, regardless of their length. On the other hand, the number of binding sites per chromosome is proportional to its length. This result implies that arm cohesion is not a direct measure of the force exerted by spindle microtubules, and may serve a different

function, for instance, to achieve similar levels of condensation. The model in budding yeast that cohesin can participate in genome maintenance in two ways, namely condensation via arm cohesin and biorientation via pericentric cohesin, is intriguing in light of the recent finding that cohesin complexes with different subunits are found on arms and pericentric regions on meiotic chromosomes in *S. pombe* and apparently serve different functions (Kitajima et al., 2003).

Cohesin cannot stay bound to DNA in the face of active transcript elongation based on three independent cohesin sites (promoter of *GAL2*, *CARC1*, *CARL2*). If cohesin and transcript elongation were incompatible, then we would also expect to find sites biased towards intergenic regions, which we do. However, we find a strong bias towards intergenic regions with converging transcription, and a bias against intergenic regions with surrounding unidirectional transcription or diverging transcription, suggesting that intergenic regions with converging transcription may have especially low transcription. These regions may have evolved particularly strong transcriptional stops since they are quite short on average and the cell may need to avoid transcription from one side extending to the other to prevent the synthesis of antisense RNA. The protection of sequence elements important for the replication and segregation of eukaryotic chromosomes from transcription may be a general necessity for their proper function *in vivo*. For instance, transcription through an ARS (Snyder et al., 1988) or a centromere (Hill and Bloom, 1987) disrupts their function.

The observed antagonistic relationship between transcription and cohesin binding in chromosome arms can be explained in two ways. Firstly, transcript elongation may be directly responsible for displacing cohesin. In this type of model, cohesin loading/binding is random and transcription (and possibly other DNA metabolic processes) “pushes” cohesin into place or strips cohesin from inappropriate locations in each cell cycle. Secondly, transcript elongation may be indirectly responsible for localizing cohesins, for example by accumulation of “nonpermissive” chromatin in transcribed regions and “permissive” chromatin in nontranscribed regions. This type of genome-wide demarcation of transcription units has been shown to occur in *S. cerevisiae* (Nagy et al., 2003) and may depend on histone variants. The preferential location of cohesin in heterochromatin in *S. pombe* also supports the idea of chromatin

modification/structure as the basis for cohesin localization (Bernard et al., 2001; Nonaka et al., 2002). The possibility also exists that cohesin itself may influence transcriptional status and act as a transcriptional boundary (Hagstrom and Meyer, 2003).

Despite the subunit difference between the meiotic and mitotic cohesin complex, we find that the association of cohesin with DNA in meiotic cells is similar to that in mitotic cells and that the constitutive peaks of meiotic cohesin binding are negatively correlated with DSB sites. Our findings are consistent with the proposed model that cohesins are at meiotic chromosome cores and recombination occurs in chromatin loops where the actual site of recombination is transiently located at the axis (Blat et al., 2002). If, in fact, meiotic cohesin defines the axial cores and loops of chromosomes, this has interesting implications for meiosis. First, conservation of cohesin location in homologs would result in a characteristic loop pattern that could act as a type of molecular bar code, perhaps facilitating initial pairing and/or alignment of homologs by loop size. There is evidence that the chromosome structure needed for interhomolog contacts can be provided in part by meiotic cohesin (Pelttari et al., 2001). Moreover, in *S. pombe*, SC is largely absent (Kohli and Bahler, 1994), suggesting that this organism can accomplish meiotic chromosome organization using only the structure provided by the cohesin-containing chromosomal core. Our results suggest that the recombination machinery can sense chromosome organization provided by cohesin and takes advantage of this to orchestrate DSB formation to occur distal to sites of high sister proximity.

The differences in binding of meiotic and mitotic cohesin on Chromosome XII may mean that the location of the meiotic complex is also transcriptionally motivated. Hence, meiotic recombination in a given organism may be somewhat dependent on the spacing of cohesin as established in premeiotic S phase, which is in turn responsive to transcription. Interestingly, the genome-wide distribution of DSBs is positively correlated with regions of high GC content, divergent promoters, and transcription factor binding. This raises the possibility that to a large extent, the location of proteins involved in meiotic recombination and chromosome organization (e.g. Spo11, Rec8) is dictated by a combination of base composition and transcriptional state.

Genome-wide studies of protein-DNA complexes afford a richer understanding of the role of these complexes in the biology of an organism and its genome. As more of

these maps are developed, our understanding of the *cis* determinants of genome transmission, and ultimately chromosome segregation, will be enriched. In the process of analyzing the first genome-wide map of cohesin in any organism, we developed PeakFinder, a program able to sensitively identify binding sites of protein-DNA complexes in their local genomic environment, and potentially useful for future ChIP chip studies. While budding yeast appears to have largely opted for placement of cohesin in AT rich, transcriptionally inactive regions, other organisms with much longer and more complicated transcriptional units, different base composition properties, or different levels of condensation may have opted for different strategies for the placement of cohesin, which may in turn affect the stability of those genomes. The genome-wide analysis of cohesin in *S. cerevisiae* will serve as a useful framework upon which to explore attributes of cohesin localization in higher eukaryotes.

## MATERIAL AND METHODS

### *ChIP methods*

ChIPs were performed as previously described (Laloraya et al., 2000; Meluh and Koshland, 1997). Quantitative PCR analysis was performed as previously described (Laloraya et al., 2000).

### *Cell culturing*

For the meiotic timecourse, cultures were grown in YPA, then transferred to SPM. Timepoints were removed for ChIP at 4, 6, 8, 10, and 12 hours post-transfer to SPM. Nocodazole-mediated arrest was accomplished by adding nocodazole to a final concentration of 15 µg/ml to the media. All cultures were grown at 30°C. Shifting cultures to 37°C in prewarmed media induced metaphase arrest in *cdc16-ts* cells.

### *DNA amplification, labeling, and hybridization*

Preparation of Cy5 and Cy3 labeled DNA, hybridization, and analysis were performed as previously described (Bohlander et al., 1992; Gerton et al., 2000). The microarrays used in this study contained each ORF and each intergenic region in the yeast genome as individual spots (Iyer et al., 2001). For each experimental condition, a minimum of two independent immunoprecipitations was performed. DNA from the immunoprecipitation was labeled with Cy5 and competitively hybridized with total genomic DNA labeled with Cy3. Hybridizations with fluor reversal were also performed for DNA from at least one of the immunoprecipitations for each condition. At least three arrays were analyzed per experimental condition, and the median values were used to represent the dataset. The meiotic experiments were done in the SK1 strain background and although two independent timecourses were performed, the results from a single representative timecourse were used for analysis. The resolution of these genome-wide maps is limited by 1) the shear size of the DNA fragments (mean of 1 kb) and 2) the size of the elements on our microarrays (mean of 0.9 kb). We do not expect these fragment size distributions to introduce a significant bias in our mapping effort since the previously estimated size of a cohesin binding region at an arm site is 0.8-1.0 kb (Laloraya et al., 2000).

The arrays were scanned using an Axon 4000B scanner and quantitated using GenePix 4.0. Results were stored in the AMAD database. Data was normalized and then filtered in the following way: intensity was required to be  $\geq 200$ , flagged spots were not used, and spots were required to have a correlation coefficient of  $\geq 0.5$ . For analysis purposes, any feature with less than two measurements was excluded (with the exception of the meiotic timecourse). Data were analyzed in Microsoft Excel or in PeakFinder, a program that we developed specifically for finding peaks in ChIP data (details and program available at <http://>). Briefly, PeakFinder takes the fluorescence ratios and samples them at the indicated interval of bps. The  $\log_2$  of the data is then smoothed. The first derivative of the smoothed line is used to identify peaks, and the corresponding peak is then located in the raw data since the nature of the smoothing algorithm dampens the peak height. PeakFinder allows filtering of peaks based on the parameters of the peak. The specific conditions used to identify cohesin peaks analyzed in the *cdc16-ts* dataset were 1) sampling  $\log_2$  transformed ratios at 100 bp intervals, 2) smoothing over 8 rounds using a 9 point Gaussian-weighted moving average, 3) filtering of peaks with a left and right rise of less than 0.1 and a height less than 0.4 ( $\log_2$  space). These conditions identified all peaks mapped to high resolution on chromosome III and XII (Laloraya et al., 2000). PeakFinder is unable to identify one-sided peaks; therefore telomeres were manually inspected for cohesin binding.

### YAC

PCR primers were designed to amplify 150-300 bp sequences, at one kilobase intervals along the entire length of the 1572 YAC (Green et al., 1995). Nucleotides 1-3683 contain the vector sequences from pYAC4 including the telomere and *URA3*. Nucleotides 326702 to 332707 contain vector sequences from pYAC4 including the centromere, *TRP1* and *ARS1*. The YAC was introduced into the strain 1377 A1 4B and two independent cultures were grown to exponential phase and nocodazole was added. After 3 hours growth at 23°C, more than 90% of cells were arrested in metaphase. Cultures were processed for ChIP as described previously.

*Thiolutin*

0.8 kb from CARC1 and 1.4 kb from CARL2 were cloned into pUNI and then recombined with pYCE to form pCM34 and pCM38. This places the pGAL(1-10) promoter immediately adjacent to cohesin associated regions. pCM34 and pCM38 were introduced into 1377-4A1 4B by transformation. Strains with pCM34 and pCM38 were initially grown in complete media lacking uracil with raffinose as a carbon source. This medium selects for retention of the plasmids and prevents transcription from the Gal-inducible promoter. These cultures were diluted ~100 fold in YEP raffinose and grown to  $7 \times 10^6$ /ml. Cultures were arrested in G1 with alpha factor, released from G1 in the presence of nocodazole and grown for 3 hours to generate an M phase arrest. Cultures were split in two and one half received galactose to a final concentration of 4%. One hour after addition of galactose, cultures were fixed and processed for ChIP. Experiments with thiolutin were performed as described above except thiolutin was added to a final concentration of 3 $\mu$ g/ml just prior to galactose addition. Primers were generated that amplified 5' and 3' regions of CARC1 and CARL2 in the endogenous locus and on pCM34 and pCM38. Reduction in cohesin binding was expressed as the ratio of the amount of cohesin bound to the 5' or 3' ends of the CAR on the plasmids with the 5' or 3' regions of the CAR in the genome.

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Author contributions. PCM, JLG, and DEK conceived and designed the experiments and wrote the paper. PCM, JLG, DEK, CM, EU, and HGY performed the experiments. JLD contributed reagents/materials/analysis tools. JLD, EFG, JLG, PCM, and DEK analyzed the data. EFG wrote PeakFinder.

## FIGURE LEGENDS

Figure 1. Interactions between cohesin and chromosome III in *S. cerevisiae*. The centromere is indicated with a black circle, the smoothed data is indicated with a green line. 50 kb intervals are indicated by vertical grey lines. A) Data generated from a *cdc16*-arrest ChIP for Mcd1-18Myc in W303a. The midpoint of each feature is used to represent the  $\log_2$  of the median red:green ratio (left y axis) with a black line, high firing replication origins are indicated with black triangles, and previously mapped CARC2, CARC1, CARC3, CARC4, CARC5, CARC6 (Laloraya et al., 2000) correspond to peaks 9, 10, 29, 30, 31, 32, respectively. Peaks are located and numbered by PeakFinder (with the exception of telomeres) using the parameters described in the Material and Methods. B) Smoothed data from *cdc16*-arrest ChIP for Mcd1/Scc1-6HA in A364a. C) Smoothed data from *cdc16*-arrest ChIP for Smc3-6Myc in A364a.

Figure 2. Visual representation of the interactions between Mcd1-18Myc and the *S. cerevisiae* genome in W303a. For each of the 16 chromosomes the centromere is indicated with a black circle, the smoothed data (based on the  $\log_2$  of the ratio) is indicated with a green line (left y axis), and the %GC is indicated by a red line (right y axis). Vertical grey bars mark 50 kb intervals. Peaks are located and numbered by PeakFinder (with the exception of telomeres) using the parameters described in the Material and Methods. For Chromosome XII, peaks 41 and 42 correspond to the previously described peaks CARL1 and CARL2 (Laloraya et al., 2000).

Figure 3. Features of peaks. A) A 5-point moving average of the distance in kb from the telomere (x axis) is plotted as a function of a 5 point moving average of the  $\log_2$  value for the associated peaks (y axis). B) Chromosome length (x axis) is plotted as a function of the number of cohesin peaks (y axis). A line was fitted using the least squares method and  $R^2=0.96$ . C) The distance between peaks in kb was binned; the average distance between peaks is 10.9 kb and the median is 9.3 kb.

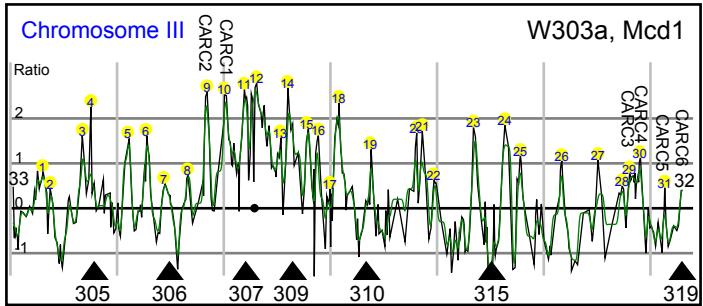
Figure 4. Peaks and AT content. A) The AT content for each array element was calculated and binned in 1% intervals (grey bars, left y axis). The AT content for each array element that is a cohesin peak was also binned (red bars, right y axis). B) The AT content for each intergenic array element was binned in 1% intervals (grey bars, left y axis). The AT content for each intergenic array element that is a cohesin peak was also binned (red bars, right y axis). C) The AT content for each convergent intergenic array element was binned (grey bars, left y axis) and the AT content for each convergent intergenic array element that is a cohesin peak was also binned (red bars, right y axis).

Figure 5. Cohesin sites were mapped using ChIP followed by semi-quantitative PCR with primers at 1 kb intervals in a YAC containing human DNA. A) Cohesin binding for the entire YAC is shown. B) Cohesin binding in the region spanning 135-180 kb is shown for the wildtype YAC (black diamonds) and for the YAC containing a replacement of the sequences at 156-162 kb with the gene encoding geneticin resistance (grey squares).

Figure 6. Transcription affects the cohesin peak at the promoter of *GAL2*. SGD coordinates 260-320 kb (x axis) and a gene map are depicted for chromosome XII. The strain 1827-22D (isogenic to the strain in Figure 1 except *CDC16*) was grown with either 2% glucose (A) or 2% galactose at the carbon source (B). Cultures were arrested with nocodazole and ChIP chip was performed. The smoothed data (as the  $\log_2$  of the ratio) is depicted in green, the peaks found by PeakFinder are indicated with black dots, and the region corresponding to the *GAL2* promoter is indicated with a grey bar. Transcription of *GAL2* is upregulated 42-fold in (B).

Figure 7. Effect of transcript elongation on cohesin associated with CARC1 and CARL2 located on a plasmid next to a galactose inducible promoter. A) The fold reduction in cohesin binding in the presence (+) or absence (-) of galactose-induced transcription is depicted as a function of the 5' or 3' end of the locus. B) The fold reduction in cohesin binding at CARL2 during galactose-induced transcription in the presence (+) or absence (-) of thiolutin, an inhibitor of transcript elongation.

Figure 8. Meiotic cohesin. DSB data is shown in red, Rec8 data in black and Mcd1 data in grey. A) Ratios for meiotic cohesin are compared to mitotic cohesin in SK1 for kbps 440-461 on chromosome XII. For the mitotic culture, cells were arrested with nocodazole. For meiotic cells, timepoints were collected every two hours from hour 4-12 after transfer to SPM. The median ratio value was used to represent the data. The gene structure for this locus is shown below the graph with genes encoded by the Watson strand labeled on top and genes encoded by the Crick strand labeled on the bottom. B) Ratios for meiotic cohesin are compared to mitotic cohesin and DSBs for kbps 295-345 on Chromosome XII.

**A****B****C**