Whole-proteome genetic analysis of dependencies in assembly of a vertebrate kinetochore

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Kinetochores orchestrate mitotic chromosome segregation. Here, we use quantitative mass spectrometry of mitotic chromosomes isolated from a comprehensive set of chicken DT40 mutants to examine the dependencies of 93 confirmed and putative kinetochore proteins for stable association with chromosomes. Clustering and network analysis reveal both known and unexpected aspects of coordinated behavior for members of kinetochore protein complexes. Surprisingly, CENP-T depends on CENP-N for chromosome localization. The Ndc80 complex exhibits robust correlations with all other complexes in a “core” kinetochore network. Ndc80 associated with CENP-T interacts with a cohort of Rod, zw10, and zwilch (RZZ)–interacting proteins that includes Spindly, Mad1, and CENP-E. This complex may coordinate microtubule binding with checkpoint signaling. Ndc80 associated with CENP-C forms the KMN (Knl1, Mis12, Ndc80) network and may be the microtubule-binding “workhorse” of the kinetochore. Our data also suggest that CENP-O and CENP-R may regulate the size of the inner kinetochore without influencing the assembly of the outer kinetochore.

Introduction

Genetic and biochemical analyses have led to identification of ~100 proteins that localize at centromeres and kinetochores (Takahashi et al., 1994; Obuse et al., 2004; Foltz et al., 2006; Okada et al., 2006; Ohta et al., 2011; Perpelescu and Fukagawa, 2011; Higgins, 2013; Tanaka, 2013). A group of 16 proteins known as the CCAN (constitutive centromere-associated network) comprises the inner, chromatin-proximal portion of the kinetochore (Cheeseman and Desai, 2008; Westhorpe and Straight, 2013; Fukagawa and Earnshaw, 2014). CCAN components remain associated with centromeres across the cell cycle and are a foundation for outer kinetochore assembly during mitosis. The CCAN is composed of discrete subcomplexes (De Wulf et al., 2003; Foltz et al., 2006; Okada et al., 2006; Hori et al., 2008b; Nishino et al., 2012). The precise interactions among CCAN proteins and complexes in chromosomes are being studied in many laboratories, and several models have been proposed (DeLuca and Musacchio, 2012; Fachinetti et al., 2013; Cheeseman, 2014; Fukagawa and Earnshaw, 2014; Westhorpe and Straight, 2015; Kim and Yu, 2015).

The mid and outer kinetochore are also characterized by the presence of protein complexes, including CENP-O/-P/-Q/-R/-U (throughout, we will use this shorthand when listing multiple CCAN proteins, e.g., CENP-O, CENP-P, and CENP-Q), Ndc80, Mis12, Rod, zw10, and zwilch (RZZ), and the Nup107/160 nucleoporin complexes. The Ndc80 and Mis12 complexes, together with the protein KNL-1, form the KMN network, which is a major site of microtubule binding in the outer kinetochore (Cheeseman et al., 2006).

Some of these complexes have been isolated and characterized structurally. In addition to several CENP-A nucleosome-related structures (Sekulic et al., 2010; Tachiwana et al., 2011; Kato et al., 2013), structures have also been reported for the dimerization domain of CENP-C (Cohen et al., 2008), a bonsai form of the Ndc80 complex (Ciferri et al., 2008), as well as several of the protein domains involved in that complex (Wei et al., 2006, 2007), the CENP-T-W-S-X complex (Nishino et al., 2012), the Knl1/Mis12 complex (Petrovic et al., 2014), the Iml3/Chl4 heterodimer (Hinshaw and Harrison, 2013), and the Ska complex (Jeyaprakash et al., 2012). However, functional analysis of these complexes is complicated, because in chromosomes, they form an insoluble network. Thus, studies of the functions and dependencies of the proteins in their “native environment” (e.g., in situ in mitotic chromosomes) are crucial.

Here, we combined quantitative proteomics using stable isotope labeling by amino acids (SILAC) technology (Ong et
al., 2002) with DT40 genetics to map a vertebrate kinetochore by monitoring the behavior of the entire mitotic chromosome proteome after the depletion of defined components. We previously showed that this approach can track the behavior of individual protein complexes in the presence of hundreds or thousands of other proteins (Ohta et al., 2010).

Our studies define dependency pathways for the stable association of a number of protein complexes with mitotic chromosomes. Several unexpected relationships were found. The data suggest that the organization of kinetochore proteins into functional complexes may be more complicated than suggested by previous studies.

**Results**

**Strategy and overview**

Analysis of the proteome of DT40 mitotic chromosomes by mass spectrometry (Ohta et al., 2010) enabled us to both make a list of proteins that associate with mitotic chromosomes and also unearth specific protein–protein interactions within and between protein complexes (Ohta et al., 2010; Samejima et al., 2012). Here, we used similar unbiased whole-proteome quantification to define dependency relationships for kinetochore protein assembly.

Several caveats should be kept in mind when comparing our data with other studies. First, because chromosome isolation requires a very high mitotic index (>80%), cultures must be healthy enough to continue to cycle. Therefore, most of our experiments with conditional knockout (KO) cells (with the exception of null alleles of nonessential genes) were performed before the target protein was completely lost. Second, in order to obtain a mitotic index of >80%, cultures were blocked for 12 h with nocodazole. This may induce some alterations in the kinetochore, but all of our experiments compare wild-type and mutant chromosomes subjected to an identical treatment. Third, our analysis detected changes in the entire proteome of mitotic chromosomes, not only at kinetochores. This is potentially significant, as despite the apparent specificity of antibody staining, a recent study reported that ~70% of CENP-A is located at noncentromeric sites in RPE-1 cells (Bodor et al., 2014). The ratio of centromeric to noncentromeric binding is not known for other kinetochore proteins.

We isolated mitotic chromosomes from 11 DT40 mutant cell lines for whole-proteome analysis. Eight of those lines are conditional knockouts where the target gene is disrupted and cell lines for whole-proteome analysis. Eight of those lines contribute to a list of proteins that associate with mitotic chromosomes and also unearth specific protein–protein interactions within and between protein complexes (Ohta et al., 2010; Samejima et al., 2012). Here, we used similar unbiased whole-proteome quantification to define dependency relationships for kinetochore protein assembly.

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We isolated mitotic chromosomes from 11 DT40 mutant cell lines for whole-proteome analysis. Eight of those lines are conditional knockouts where the target gene is disrupted and cells are kept alive by a rescuing cDNA that is silenced by adding conditional knockouts where the target gene is disrupted and cell lines for whole-proteome analysis. Eight of those lines contribute to a list of proteins that associate with mitotic chromosomes and also unearth specific protein–protein interactions within and between protein complexes (Ohta et al., 2010; Samejima et al., 2012). Here, we used similar unbiased whole-proteome quantification to define dependency relationships for kinetochore protein assembly.

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We isolated mitotic chromosomes from 11 DT40 mutant cell lines for whole-proteome analysis. Eight of those lines are conditional knockouts where the target gene is disrupted and cells are kept alive by a rescuing cDNA that is silenced by adding doxycycline (CENP-C, CENP-H, CENP-I, CENP-K, CENP-M, CENP-N, HUURP, and mis18a; we refer to these cells as GEN ENAMEOFF). Three lines are null strains in which the nonessential genes encoding CENP-O, CENP-R, or CENP-S were deleted (referred to as GEN ENAMEOFF). Mutant and wild-type chromosomes were labeled with stable isotopes in vivo (SILAC; Ong et al., 2002). The relative abundance of proteins in the two proteomes was calculated from ratios of heavy and light peptides derived from the wild type and mutant, respectively (expressed as the H/L ratio). 1,500 to 2,200 proteins were quantified in each experiment.

In a control experiment where inversely labeled wild-type chromosomes were compared with one another, ~80% of the proteins had a H/L ratio between 0.66 (≈2−0.6) and 1.32 (≈2+4) (Fig. S1 A). Typically, >50% of proteins quantified in mutant chromosomes had a H/L ratio in this range. After silencing or loss of a CCAN protein, the target protein and a subset of other kinetochore proteins were typically among the most depleted proteins, whereas the remaining kinetochore proteins showed relatively little change in their abundance (Fig. S1 D). The pattern of effects on other kinetochore proteins varied for different target proteins.

Proteins known to form protein complexes exhibited coordinated behavior and were reproducibly grouped together in the same clusters (Fig. 1 and Table S1). This included components of the Ndc80, Mis12, RZZ, chromosome passenger complex (CPC), anaphase-promoting complex/cyclosome, Nup107/Nup160 nucleoporin, dynein, and dynactin complexes (Fig. 1). Meta-analysis of variations in the kinetochore proteome performed by combining results from the different genetic perturbations also allowed us to identify novel cohorts of kinetochore proteins. We define a “cohort” as a group of proteins that exhibit coordinated behavior in response to diverse genetic perturbations but have not been independently shown to form a protein complex.

Hierarchical clustering analysis of the H/L ratios across all experiments identified two clusters of proteins that appeared to correspond to contaminants and hitchhikers (red lines at left in Fig. 1). Hitchhikers were defined in Ohta et al. (2010) as cytoplasmic proteins that bind to mitotic chromosomes after nuclear envelope breakdown but do not have a role in mitotic chromosome structure or function. These and other proteins whose variation correlated with the tissue culture medium in which cells were grown were excluded from our statistical analysis as explained in Materials and methods.

A subset of CCAN proteins is depleted from CENP-OFF and CENP-HOFF chromosomes

As a first approach to determining the effects of disrupting the CCAN on kinetochore composition, we determined the proteome of chromosomes isolated from CENP-OFF or CENP-HOFF cells. CENP-I and CENP-H are closely interacting CCAN members (Nishihashi et al., 2002; Okada et al., 2006; Basilico et al., 2014).

In a typical experiment with CENP-OFF chromosomes, 1,504 proteins were quantified. Depletion of CENP-I was efficient, with ~12% of the wild-type level remaining on mutant chromosomes (H/L ratio = 8.09). CENP-H/K/-L/-N/-T were also significantly depleted, with <16% of wild-type levels remaining (Fig. 2 A and B; and Fig. S1 D). In contrast, CENP-A and CENP-C were little affected, with >72% remaining on the chromosomes.

A scatterplot of the H/L ratios of 1,421 proteins from two replicate experiments shows that these observations were reproducible (Fig. 2 B). In these plots of H/L ratios in experiment i versus H/L ratios in experiment ii, good correlation is shown when points cluster along a tight diagonal line. This plot reveals that CENP-H/K/-L/-N/-T are the proteins most affected by CENP-I depletion, with H/L ratios nearly as large as CENP-I (Fig. 2 B). These proteins form a discrete cluster separate from the rest of the population, suggesting that they comprise one or more protein complexes that are not stably associated with CENP-FOFF chromosomes. CENP-S/X were also significantly depleted from these chromosomes, and they formed a distinct cluster.
CENP-O/-P/-Q/-R/-U were somewhat less depleted and exhibited a tight cluster of H/L ratios (Fig. 2 B, inset). Outer kinetochore proteins, including members of the Ndc80 complex, clustered with similar H/L ratios, and members of the RZZ and Mis12 complexes were also among the top 5% most reduced proteins (above and to the right of the two orthogonal blue lines).

Similar results were obtained after CENP-H depletion. Fig. 2 C shows a scatterplot of the H/L ratio for 1,515 proteins from two replicate experiments with CENP-H OFF chromosomes.

In summary, depletion of CENP-I or CENP-H from mitotic chromosomes caused a reproducible downstream pattern of depletion of both inner and outer kinetochore proteins from isolated mitotic chromosomes.
Figure 2. Behavior of CENP-H,-I,-K,-M,-N,-L,-T in CENP-I and CENP-H KOs. (A) Histograms show the distribution of $\log_2(H/L \text{ ratio})$ of all proteins quantified, ribosomal proteins, and centromere proteins. CCAN proteins (red) are shown as stacked columns. Proteins with a positive score (rightwards on the abscissa) were depleted from CENP-I OFF chromosomes. A blue line designates the top 5%. Those with a negative score (leftward on the abscissa) are accumulated in CENP-I OFF chromosomes. (B) CENP-I OFF: H/L ratios of centromere proteins (blue), CCAN proteins (red), and others (gray) from two replicate experiments are plotted against one another on a log scale in this scatterplot. The blue lines designate the top 5% most depleted proteins. Proteins that decreased in the CENP-I OFF chromosomes map to the top right, and those that increased map to the bottom left. Enlarged plot of the areas boxed in left panel is shown in the blue box on the right. CCAN proteins (red) are designated with the prefix “CENP-” removed. Members of the Ndc80 complex are in blue, whereas members of the Mis12 complex and KNL1 are in green. (C) CENP-H OFF: H/L ratios from two replicate experiments are plotted against one another. Abbreviations and color-coding are as in B. A magnified plot of the boxed area is shown in a blue box. Note that to appear in scatterplots here and below, proteins must have been identified in both experiments being compared. Very small proteins that give rise to few peptides, such as CENP-M, CENP-S, and CENP-X, were occasionally not detected and are therefore not shown in some of the plots. wt, wild type.
effect on the behavior of centromere proteins, in particular CCAN proteins (Figs. 3 C and S2).

A similar correlation was obtained for comparisons involving CENP-K\(^{OFF}\) and CENP-M\(^{OFF}\). In all, proteomes of chromosomes from CENP-H\(^{OFF}/\)P\(^{OFF}/\)K\(^{OFF}/\)M\(^{OFF}\) cells form one closely correlated group (top left yellow box in Fig. 3 C), consistent with them comprising a protein complex (Basilico et al., 2014). Similarly, proteomes of chromosomes from CENP-O\(^{KO}\) and CENP-R\(^{KO}\) form a distinct group (Fig. 3 C, bottom right yellow box).

Importantly, these correlations were diminished when cross-comparisons were made between proteomes of chromosomes depleted of proteins associated with different kinetochore subcomplexes (Figs. 3 B and S2). For example, proteome comparisons between chromosomes isolated from CENP-C\(^{OFF}\), CENP-P\(^{OFF}\), CENP-H\(^{OFF}/\)P\(^{OFF}/\)K\(^{OFF}/\)M\(^{OFF}\)/N\(^{OFF}\), and CENP-O\(^{KO}/\)R\(^{KO}\) cells showed a significantly reduced correlation. This indicates that these four groups of proteins affect the overall chromosomal association of centromere proteins in different ways.

CENP-T behaves coordinately with CENP-N and CENP-L

CENP-N was originally identified as a CCAN member (Foltz et al., 2006; Izuta et al., 2006; Okada et al., 2006) that associates with CENP-A nucleosomes (Carroll et al., 2009; Hillwig et al., 2011). CENP-N, CENP-L, and CENP-T were by far the most depleted proteins in CENP-N\(^{OFF}\) chromosomes (Fig. 4 A). CENP-H and CENP-I were also significantly decreased but had H/L ratios in a separate (less depleted) cluster together with members of the CENP-O/-P/-Q/-U complex, the Ndc80 complex, the RZZ complex, Mad1, and CENP-E (Fig. 4 A, inset).

These data suggest that CENP-N might be part of a protein cohort with CENP-L and CENP-T that interacts with CENP-H/-I/-K/-M to form a larger protein assembly in intact mitotic chromosomes. To reiterate, we use the term cohort to describe a group of proteins whose correlated behavior is consistent with them forming a protein complex that has yet to be independently confirmed.

CENP-H/-I/-K/-M and CENP-N/-L had very similar profiles in virtually all experiments, with the exception of CENP-N\(^{OFF}\) cells (Fig. 4 B). (A “profile plot” is an illustrative summary of changes in the abundance of proteins across all experiments [see Materials and methods]. The gray lines plot levels of all 1,409 proteins analyzed in all experiments.) An unexpected result was obtained when comparing the CENP-N\(^{OFF}\) proteome against its CENP-H\(^{OFF}\) or CENP-P\(^{OFF}\) counterparts. Despite CENP-N being part of the CENP-H/-I/-K/-M/-N cluster, when proteomes comprising only CCAN proteins were compared, those derived from CENP-N\(^{OFF}\) chromosomes did not exhibit strong correlations with the others. This is seen as scatter away from the diagonal in Fig. 3 B and a lower correlation in the matrix of Fig. 3 C. This suggests that CENP-N is not always associated with CENP-H/-I/-K/-M.

The profile plots for CENP-N and CENP-L are nearly identical, consistent with studies that these proteins form a heterodimeric complex when they are loaded on chromosomes (Carroll et al., 2009; Hinshaw and Harrison, 2013). Both proteins were significantly depleted from chromosomes isolated from CENP-H\(^{OFF}/\)P\(^{OFF}/\)K\(^{OFF}/\)M\(^{OFF}/\)N\(^{OFF}\) cells. Their reduction was, however, more modest in chromosomes from other CCAN mutant cells, i.e., CENP-C\(^{OFF}/\)S\(^{IKO}/\)R\(^{IKO}\) (Fig. 4 B).

Unexpectedly, the profile plot for CENP-T was strikingly similar to CENP-N and CENP-L except in CENP-S\(^{KO}\) experiments (Fig. 4 B). CENP-T was one of the most depleted proteins in chromosomes from CENP-H\(^{OFF}/\)P\(^{OFF}/\)K\(^{OFF}/\)M\(^{OFF}/\)N\(^{OFF}\) cells (Fig. 4, B and C). This suggests a strong dependency of CENP-T on CENP-H/-I/-K/-M/-L, particularly on CENP-N and CENP-L. Although CENP-T on its own has a DNA binding activity in vitro (Hori et al., 2008a), its centromere association may also require CENP-H/-I/-K/-M/-N. Indeed a reduction of CENP-T levels in CENP-H\(^{OFF}\) cells was reported previously (Hori et al., 2008a). CENP-T and CENP-W make a DNA binding complex with their histone fold domains (Hori et al., 2008a), and both proteins show essentially identical profiles in these experiments (Fig. 4 C).
CENP-S and CENP-X may function in part independently of CENP-T

In addition to a CENP-T/-W dimer, a CENP-T/-W/-S/-X tetramer has also been reported at centromeres (Nishino et al., 2012). The profile plot of CENP-S, however, did not always follow that of CENP-T in isolated mitotic chromosomes (Fig. 4 C). For instance, CENP-S was less affected than CENP-T by depletion of CENP-H/-I/-N, suggesting that CENP-S/-X may participate in another complex. Indeed, CENP-S/-X also associates with FANCM (Singh et al., 2010; Yan et al., 2010).

For comparison, protein profiles for known complexes, such as the four core histones, the cohesin complex and CPC appear as single lines (Fig. S3).

Because CENP-S is dispensable for growth in DT40 cells, we could obtain a complete KO cell line (Amano et al., 2009). CENP-S peptides were not detected on the chromosomes from CENP-S KO cells. This results in an H/L SILAC ratio of zero or infinite value, and the H/L ratios for individual CENP-S peptides were sometimes dealt with as missing values by the Andromeda search engine (i.e., disregarded in calculating the H/L ratio for a given protein). We therefore reviewed the data manually, and the MS1 spectrum of one representative peptide (AAV HYTTGCLCQDVADKGVFLSK, charge +4) was identified with heavy-labeled species (i.e., from wild-type cells; Fig. 5 A, orange boxes). We observed no trace of the corresponding light-labeled peptide, confirming the absence of CENP-S from CENP-S KO chromosomes.

By far, the most strongly affected protein in CENP-S KO chromosomes was its binding partner, CENP-X (Amano et al., 2009), with <10% remaining (Fig. 5 B). Inspection of MS1 spectra of a representative CENP-X peptide (QAQAEDDE KVDIEHVEK, charge +4) confirmed that this peptide was virtually absent (data not shown). After CENP-X, the next most depleted centromere proteins were CENP-T and CENP-W, but their depletion was much less extreme. Thus CENP-S KO chromosomes still retain some functional CENP-T/-W dimer. This may explain the viability of CENP-S KO cells.

CENP-N,-L were not reduced as much as CENP-T/-W on CENP-S KO chromosomes (Figs. 4 B and 5 B). Rather, the H/L ratio of CENP-N and CENP-L fell in the same cluster as CENP-H/-I/-K/-M and close to CENP-P/-Q/-R/-U (Fig. 5 B). This suggests that CENP-N and CENP-L are upstream of CENP-T for localization on chromosomes.

Interestingly, outer kinetochore components, including the KMN, RZZ, and Ska complexes plus CENP-E and Mad1, were more depleted than CCAN components on chromosomes lacking CENP-S (Fig. 5 B). Indeed, CENP-T can recruit the Ndc80 complex to chromosomes (Hori et al., 2013; Nishino et al., 2013).

CENP-C is required for association of the KMN network with chromosomes

CENP-C links the centromeric chromatin with the outer kinetochore. The C-terminal and central regions of CENP-C interact with CENP-A nucleosomes (Kato et al., 2013), the N terminus binds to Mis12 in the KMN network (Carroll et al., 2010; Przewloka et al., 2011; Screpanti et al., 2011), and the PEST region binds CENP-H/-I/-K/-M (Klare et al., 2015). Profile plots showed only modest changes in CENP-C abundance after depletion of other CCAN proteins (Fig. 6 A). Notably, significant...
CENP-C depletion caused a reduction in Mis12 complex proteins and KNL1 to an extent similar to that of the Ndc80 complex (Fig. 6 B). This stoichiometric codepletion is consistent with a direct interaction between CENP-C and the Mis12 complex (Przewloka et al., 2011; Screpanti et al., 2011) and contrasts with depletion of CENP-H/-I/-K/-M/-N, where Ndc80 levels fell with much less effect on the Mis12 complex (Fig. 6 C).

Proteins engaged in a protein complex should show coordinated behavior (i.e., low variance in their SILAC ratios) in our experiments. The variance of the SILAC ratios for the Ndc80 and Mis12 subcomplexes and KNL1 was small in chromosomes from mis18ΔOFF, CENP-COFF/SKO/ΔOΔO/ΔRΔΔ cells (Fig. 6 D). This suggests that components of the KMN network holocomplex behaved together as a single entity in those mutants. In contrast, the variance between the subcomplexes was significantly larger in chromosomes from CENP-IPOFF/PΩF/KOFF/MOFF/NOFF cells. This suggests that not all Ndc80, Mis12, and KNL1 behave as a single holocomplex. Importantly, the Ndc80 and Mis12 complexes, respectively, were apparently intact in chromosomes from those cells because the variance within each subcomplex remained small. Assembly of the KMN network may be defective in chromosomes from CENP-HPOFF/PPOFF/KOFF/MOFF/ΔOFF cells, and this might explain the results of an earlier study (Amaro et al., 2010). Alternatively, a subpopulation of the Ndc80 complex may not be engaged in the KMN network.

The RZZ complex is involved in silencing of spindle checkpoint signaling (Karess, 2005). Spindly bridges RZZ and dynein (Griffis et al., 2007). Profile plots of Ndc80 and RZZ look very similar to each other in most mutant chromosomes (Fig. 6 E). However, RZZ was much less depleted than the Ndc80 complex in CENP-COFF chromosomes, forming a separate cluster in scatterplots of CENP-COFF experiments (note the relative locations of the orange and blue boxes in Fig. 6 B). The reduction of chromosome-associated RZZ complex may be linked to effects on the Ndc80 complex in chromosomes depleted of CENP-H/-I/-K/-M/-N, but this does not occur in CENP-COFF chromosomes (Fig. 6 E).

Partial CENP-A depletion has little effect on CENP-C levels
Available CENP-A conditional KO cells do not die when CENP-A transcription is silenced, suggesting that they have acquired additional mutations (Régnier et al., 2005). We therefore adopted other strategies to deplete centromeres of CENP-A. HJURP is a chaperone that is required for CENP-A loading onto centromeres (Dunleavy et al., 2009; Foltz et al., 2009). We silenced HJURP expression by exposure of KO cells (Perpelescu et al., 2015) to doxycycline for 84 h. This lowered chromosomal levels of HJURP by at least 80%. After this treatment, CENP-A was the most depleted centromere protein, with 18–28% remaining on the chromosomes (Fig. 7 A).
CENP-N/-L/-T/-S were the next most depleted centromere proteins after CENP-A, in \textit{HJURP}^{OFF} chromosomes. KIF2C (MCAK), Mis18α, and Mis18β accumulated on chromosomes from \textit{HJURP}^{OFF} cells (Fig. 7 A). Mis18BP1/KNL2 was essentially unaffected (Fig. 7, A and C).

Mis18α works together with Mis18β and Mis18BP1 in telophase to prime sites for CENP-A recruitment on chromosomes (Fujita et al., 2007). Mis18α and Mis18β were the most depleted proteins when Mis18α transcription was silenced (Fig. 7 B). Mis18BP1 was also significantly depleted, though much less so than Mis18α or Mis18β. Profile plots of the three proteins imply that Mis18BP1 may not associate with Mis18α and Mis18β in chromosomes isolated from nocodazole-treated cells (Fig. 7 C). After Mis18α and Mis18β, CENP-A was the most depleted centromere protein in \textit{mis18α}^{OFF} chromosomes (Fig. 7 B). CENP-N/-L/-T/-W also showed a significant decrease, with CENP-H/-I/-K being less affected. Interestingly, chromosomal levels of CENP-C were little affected by the reduction of CENP-A in \textit{HJURP}^{OFF} or \textit{mis18α}^{OFF} chromosomes despite the fact that CENP-C has been reported to interact with CENP-A (Carroll et al., 2010).

Taken together, reduction in the amount of CENP-A coincided well with the reduction of CENP-N/-L/-T/-W. This observation is reminiscent of the results of CENP-N depletion, where CENP-N/-L/T were the most affected proteins.

**Accumulation of CCAN proteins on CENP-O^{KO} chromosomes**

CENP-O^{KO} and CENP-R^{KO} cells are viable (Okada et al., 2006). CENP-O forms a complex with CENP-P/-Q/-U and CENP-R (Hori et al., 2008b), and these proteins were significantly depleted from \textit{CENP-O}^{KO} chromosomes (Fig. 8, A and C). CENP-O/-P/-Q/-U were depleted to a somewhat lesser extent from \textit{CENP-R}^{KO} chromosomes (H/L ratio \(\sim 2\); Fig. 8, C and D). The tight cluster suggests that CENP-O/-P/-Q/-U were lost as a single entity in the absence of CENP-R (though their depletion...
was less severe than seen with loss of CENP-O). Interestingly, CENP-H/-I/-K/-N/-L/-T/-S accumulated on chromosomes isolated from CENP-OKO and CENP-RKO cells (Fig. 8, B and D). This could reflect an enlargement of the inner kinetochore, as cells adapt to continued growth without CENP-O/-P/-Q/-R/-U, either as a direct effect or possibly by modulating the expression or stability of other proteins. Importantly, this accumulation of CCAN proteins was not accompanied by an increase in KMN and RZZ complex components. Thus, increasing the content of CCAN proteins does not necessarily increase the size of the outer kinetochore.

Clustering and correlation networks within the kinetochore

The fact that proteins in the same complex consistently show very similar H/L ratios across experiments allowed us to perform clustering analysis and map a correlation network of kinetochore proteins (Fig. 9). The clusters seen in Fig. 9 A confirm previous descriptions of CCAN complexes, e.g., CENP-H/-I/-K, CENP-S/-X, CENP-O/-P/-Q/-R/-U, as well as the Mis12, Ndc80, and Ska complexes in the outer kinetochore. They also reveal the existence of two previously undescribed protein cohorts: CENP-N/-L/-T in the inner kinetochore and Rod/Zw10/Zwilch/Spindly/CENP-E/Mad1 in the outer kinetochore.

The similarity of H/L ratio profiles between pairs of proteins was gauged by Pearson correlation coefficient (Fig. S4). The correlation between every pair of proteins in the chromosomes was summarized as a matrix shown in Fig. 9 B, with a blowup in Fig. S5. A profile of these correlations against the rest of the proteome was used for hierarchical clustering analysis so that proteins with strong correlations are grouped together. One cluster that was enriched for kinetochore proteins was scrutinized in detail (Fig. 9 B). The Mis12 complex, KNL1, and the Ndc80 complex together comprised a single correlation cluster (yellow). This is the KMN network (Cheeseman and Desai, 2008). The Ndc80 complex also formed part of a second cluster together with CENP-N/-L/-T. Interestingly, CENP-N/-L/-T and CENP-H/-I/-K were grouped separately.

In both clustering analysis of H/L ratios and the correlation meta-analysis, CENP-E and Mad1 made a single cluster with the RZZ complex (Fig. 9, A and B). Correlation analysis revealed a link of this RZZ supercohort with CENP-N/-I/-T
This RZZ cohort also showed a good correlation with the Ndc80 complex, suggesting a significant interaction. On the other hand, the RZZ cohort did not exhibit a high correlation with the Mis12 complex, suggesting that RZZ assembly on chromosomes is linked with Ndc80CENP-T rather than with Ndc80CENP-C.

Discussion

This analysis differs from previous studies of kinetochore assembly in that it exclusively concerns untagged endogenous proteins in situ in native mitotic chromosomes. The results were not constrained by requiring antibodies that may exhibit varying affinities or accessibilities to their target epitopes, tags that might impair protein function in subtle ways, or the need to find experimental conditions where the proteins are soluble.

Dependencies on CENP-A and CENP-C

Neither CENP-A nor CENP-C depends on any other CCAN protein for association with mitotic chromosomes. Depletion of CENP-A and CENP-C was not accompanied by reduction of other proteins to the same extent as themselves, even though CENP-A depletion decreased the chromosomal accumulation of CENP-N/L/T and, to a lesser extent, CENP-H/I/J/K/O/P/Q/R/U. Thus, CENP-A and CENP-C do not have protein cohorts as defined by this analysis. This is not the case for most kinetochore components. In the case of the depletion of CENP-H, CENP-I, CENP-K, CENP-M, and CENP-N and loss of CENP-O and CENP-S, one or more other proteins were reduced as much...
as the target protein. Our work supports the view that CENP-A is a marker for the site of kinetochore assembly rather than a structural foundation for the kinetochore (Prendergast et al., 2011).

CENP-N binds to CENP-A (Carroll et al., 2009), and in our experiments, chromosomal association of CENP-N/-L depended on CENP-A. CENP-T/W/S/-X has been reported to bind to DNA independently of CENP-A (Hori et al., 2008a). The unexpected dependency that we observe for CENP-T/-W on CENP-N/-L may favor accumulation of CENP-T/-W near CENP-A nucleosomes. Consistent with this, CENP-N and CENP-T coprecipitated from chromatin extracts as part of the CENP-A associated complex (Foltz et al., 2006) and map at a similar radial position by superresolution microscopy (Suzuki et al., 2014).

CENP-C depletion also had a relatively minor effect on assembly of the inner kinetochore in these experiments. This was surprising in light of the recent study that CENP-C interacts in vitro with a complex of CENP-H/-I/-K/-M (Basilico et al., 2014; Klare et al., 2015) and previous work showing that CENP-C is required for kinetochore localization of CENP-N/-L in yeast (Tanaka et al., 2009; Hinshaw and Harrison, 2013). One possibility is that our depletion of CENP-C (14% remaining on chromosomes) was insufficient to phenocopy the effects seen in previous studies. Alternatively, contributions with other components may also promote the centromere localization of CENP-H/-I/-K/-M in DT40 cells.

CENP-C depletion severely disrupted outer kinetochore assembly. Levels of the entire KMN network were severely reduced on CENP-C–depleted chromosomes. This fits with the view of CENP-C as an essential link between the inner and outer kinetochore (Przewloka et al., 2011; Screpanti et al., 2011).

A dependency correlation network for the chicken kinetochore

A network constructed from the correlation matrix based on SILAC ratios for all proteins provides a graphic demonstration of relationships between kinetochore proteins and integrates the diverse experiments reported here (Fig. 10 A). Importantly, no novel proteins clustered among the CCAN members, suggesting that all members of this group of proteins are now known.

The correlation analysis splits “core” CCAN components into the CENP-H/-I/-K/-M complex and CENP-N/-L/-T/-W...
The Ndc80 complex as a hub of kinetochore dependencies

Remarkably the Ndc80 complex appears to be a “hub” of the kinetochore dependency network. This complex provides a physical link between kinetochores and dynamic spindle microtubules and has roles in microtubule capture, monitoring the state of microtubule binding (Alushin et al., 2010, 2012), error correction (Cheeseman et al., 2006; DeLuca et al., 2006), and subsequent transport of chromosomes into daughter cells upon anaphase onset (Tooley and Stukenberg, 2011). Ndc80 is the only complex that shows robust correlations with all other cohorts and complexes diagrammed here (Fig. 10 A). For example, behavior of the CENP-N/-L/-T/-W cohort does not correlate with the Mis12 complex, and CENP-H/-I/-K/-M complex behavior does not correlate with either the Mis12 or RZZ complexes. The Ndc80 complex also shows robust interactions with the Ska complex, which was not included in Fig. 10 A because its interactions as deduced from correlation analysis are surprisingly complex.

We noted from analysis of the variance across all experiments that the Ndc80 complex does not always covary with the other components of the KMN network (the Mis12 complex and Knl1). Indeed, two different types of Ndc80 supercomplex had previously been suggested (Gascoigne et al., 2011; Schleiffer et al., 2012; Nishino et al., 2013). We will refer to these as Ndc80^{CENP-C} and Ndc80^{CENP-T}. The spatial distribution of CENP-C and CENP-T on centromeres is different (Ribeiro et al., 2010), and it was suggested from reconstitution experiments that those supercomplexes might have distinct functions (Hori et al., 2013). In Ndc80^{CENP-C}, CENP-C binds to the Mis12 complex and Knl1, thereby forming the KMN network. In Ndc80^{CENP-T}, Spc24 and Spc25 bind CENP-T directly upon phosphorylation of the CENP-T N-terminus (Nishino et al., 2013). The Mis12 complex competes with CENP-T for this binding site. Thus, Ndc80^{CENP-T} does not associate with Mis12 and Knl1 and therefore does not form a KMN network.

Our data suggest that Ndc80^{CENP-C} and Ndc80^{CENP-T} may serve different functions in the kinetochore (Fig. 10 B). Ndc80^{CENP-C} exhibits dependency relationships consistent with interactions with the KMN network. It may therefore function primarily in microtubule binding, although a role in the spindle checkpoint has also been suggested (Kim and Yu, 2015). It was previously suggested that the RZZ complex might associate with the KMN network (Varma et al., 2013); however, our dependency analysis suggests a closer functional association between Ndc80^{CENP-T} and the expanded RZZ cohort. We do not see dependency interactions between the RZZ cohort and Mis12 components.

The RZZ cohort revealed by our analysis consists of RZZ components plus Spindly, CENP-E, and Mad1. These proteins exhibit such tight correlations with one another that they are likely to form a physical complex in chromosomes. We propose terming this the RZZ–MES (Rod, Zw10, Zwilch, Mad1, CENP-E, Spindly) supercomplex. This complex has not been observed in solution and may only form when its constituents are associated with chromosomes. RZZ is involved in recruiting Mad1/Mad2 to kinetochores (Karess, 2005), and Mad1 in turn recruits CENP-E (Akeria et al., 2015). CENP-E is required to convert kinetochore–microtubule interactions from lateral to end-on (Shrestha and Draviam, 2013). Thus, Ndc80^{CENP-T} may cooperate with the RZZ–MES to coordinate end-on microtubule attachments with spindle checkpoint signaling. It will be interesting in future experiments to determine whether Mps1 kinase preferentially associates with Ndc80^{CENP-T} (Hiruma et al., 2015; Ji et al., 2015).

Perspectives

This study of the entire mitotic chromosome proteome in a comprehensive set of inner kinetochore mutants has led to the elucidation of a network of protein dependencies throughout the kinetochore. This network divides the CCAN into four...
subcomplexes that appear to be relatively independent of one another for localization to mitotic chromosomes (Fig. 10). Perhaps surprisingly, we identified close functional links between CENP-N/-L and CENP-T/-W consistent with them acting as a complex in the kinetochore. Our data also suggest that the RZZ complex may actually be part of a larger RZZ–MES supercomplex that coordinates microtubule attachments with checkpoint signaling in the outer kinetochore. This analysis will hopefully stimulate future biochemical and cell biology experiments to explore the novel relationships identified here.

Materials and methods

Cell culture and medium

The chicken lymphoma B cell line DT40 was grown in RPMI1640 medium supplemented with 10% FBS and 1% penicillin/streptomycin.

For SILAC, wild type (clone18), CENP-\( ^\text{KO} \), and CENP-\( ^\text{KO} \) were grown with 10% dialyzed FBS (mol wt cutoff, 10,000). Other cell lines were grown with complete FBS. For SILAC labeling of lysine and arginine, 100 µg/ml \( ^{13}\text{C},^{15}\text{N} \)-labelled lysine and arginine were added to the medium with dialyzed FBS.

1 µg/ml doxycycline was used to silence the rescuing cDNA expression of conditional KO cell lines. We refer to such doxycycline-treated cells as \( \text{GENENAME}^{\text{OFF}} \) (e.g., as \( \text{CENP-C}^{\text{OFF}} \)).

Cell lines

Details of the following KO cell lines are described in the original publications: \( \text{CENP-C}^{\text{ON/OFF}} \) (Kwon et al., 2007), \( \text{CENP-H}^{\text{ON/OFF}} \) (Fukagawa et al., 2001), \( \text{CENP}^{\text{FROSE}} \) (Nishihashi et al., 2002), \( \text{CENP}^{\text{FROSE}}, \text{CENP-M}^{\text{FROSE}} \), and \( \text{CENP-O}^{\text{FROSE}} \) (Okada et al., 2006), \( \text{CENP}^{\text{KROSE}} \) (Ribeiro et al., 2010), \( \text{CENP-K^{ROSE}} \) (Hori et al., 2008b), \( \text{CENP}^{\text{KROSE}} \) (Amano et al., 2009), and \( \text{HIURP}^{\text{KROSE}} \) and \( \text{Mis18}^{\text{KROSE}} \) (Perpelescu et al., 2015).

Cell lines designated \( \text{GENENAME}^{\text{ON/OFF}} \) are conditional KOs where all or a portion of an essential gene has been removed and cells are kept alive by a cDNA whose expression can be silenced by addition of doxycycline. Nonessential genes were absolute KOs, designated \( \text{GENENAME}^{\text{KO}} \). Expression of exogenous “rescue” cDNAs encoding CENP-C/-H/-M/-N or Mis18α were turned off by treatment with doxycycline for 48 h before harvest of cells. \( \text{CENP-P}^{\text{ON/OFF}} \) and \( \text{CENP-K}^{\text{ON/OFF}} \) cells were incubated with doxycycline for 36 h. \( \text{HIURP}^{\text{KROSE}} \) and \( \text{Mis18}^{\text{KROSE}} \) cells were treated with doxycycline for 84 h.

In all cases, cells were incubated with nocodazole for the last 12 h before harvest.

Preparation of mitotic chromosomes

DT40 cells were incubated with 0.5 µg/ml nocodazole for 12–13 h before harvest. The length of incubation in doxycycline was calibrated such that a minimum mitotic index of >75% was achieved. Longer incubations resulted in increased apoptosis and a decreased mitotic index as cultures became less healthy. Mitotic chromosomes were isolated in the polyamine-EDTA buffer system (Lewis and Laemmli, 1982). The protocol was optimized for chicken DT40 cells with some modifications. A maximum of two missed cleavages was allowed. Carbamidomethylation of cysteine was set as a fixed modification. Oxidation of methionine and acetylation of the N terminus were set as variable modifications. Peptide and protein identifications were filtered to 7. A maximum of two missed cleavages was allowed. Carbamidomethylation of cysteine was set as a fixed modification. Oxidation of methionine and acetylation of the N terminus were set as variable modifications. Peptide and protein identifications were filtered to 1% false discovery rate.
Processing of data
The combined data from 38 experiments contained 2,760 protein IDs. To minimize noise, we removed protein entries that occurred in <25 experiments. 1,667 proteins remained after this filtering process (Table S1). Unprocessed data were used to draw scatter plots and histograms. In cases where discrepancies in protein H/L ratio were found in the replicates, we inspected the MS1 data manually. Where MS1 peaks suffered from interference because of coeluting signals, the corresponding peptide H/L ratio was removed from the analysis. Centromere proteins affected by this data curation were CENP-M, CENP-R, CENP-U, CENP-W, CENP-X, APC4, and APC5.

Filtering out contaminant proteins
To compare the proteomes of mutant and wild-type chromosomes, it was necessary to differentially label cells with stable isotopes (SILAC) in order to distinguish the chromosomal proteins of mutant and wild-type cells from one another. The metabolic labeling with heavy amino acids used for SILAC requires growth of the cells in medium with dialyzed FBS. Unfortunately, many DT-40 conditional KO cell lines do not grow in medium with dialyzed FBS. We have been unable, despite repeated efforts, to determine the explanation, and we thus grew most mutant cell lines in medium with complete FBS.

To test whether the proteome of isolated mitotic chromosomes changed when cells were cultured in conventional medium or medium with dialyzed FBS, we determined the proteome of wild-type mitotic chromosomes isolated from cells grown under the two sets of conditions. The histogram in Fig. S1 A shows the distribution of log2(H/L ratios) for the 1,667 proteins quantified in this experiment. The distribution was unimodal but skewed to the left. Multiplex analysis identified a second minor peak, comprising ~15% of the total and centered at 2−0.855 = 0.55 (Fig. S1, A and C).

Cluster analysis with our complete dataset identified three subgroups whose H/L ratios fluctuated in a manner different from the rest (Fig. 1). The first subgroup contained CCAN proteins. The second subgroup is highlighted as purple trees at the top of Fig. 1. They were probably contaminants, many of which were not identified in wild-type mitotic chromosomes. They may be derived from interphase or apoptotic cells. The third group, also highlighted as purple trees, clustered at the bottom of Fig. 1. This group contained proteins that accumulated on chromosomes from cells grown with FBS relative to those grown in dialyzed FBS. The distribution of their H/L ratios coincides with the second minor peak (Fig. S1, B and E). These proteins were almost exclusively identified as cytoplasmic in our previous analysis (Fig. S1 F; Ohta et al., 2010). Because the proteins of the second minor peak were predominantly cytoplasmic, we filtered this set of 259 proteins from our subsequent analyses. This filtration was important, as it decreased random scatter in our data and allowed us to more accurately determine the variance of bona fide chromosomal proteins.

Profile plots
A profile plot is an illustrative summary of changes in the abundance of proteins across experiments (Fig. 4 B). The H/L ratio of a protein in one experiment is plotted along a vertical line, in this case with positive H/L ratios below the x axis so that descending lines reflect decreasing values of the protein in question. Members of the same protein complex typically follow a very similar pattern. The superimposed box plots with whiskers provide a convenient criterion to assess the significance of changes in the abundance or H/L ratio of each protein. The interquartile box contains 50% of all H/L ratios measured in each experiment, with the whiskers encompassing more than 95% of all the total ratios (assuming a normal distribution of values).

Online supplemental material
Fig. S1 shows for several representative experiments the distribution of total proteins and centromere proteins as well as showing the distribution of contaminating proteins that were removed from our statistical analysis. Fig. S2 demonstrates a step-by-step correlation analysis between a pair of experiments with a good correlation (CENP-H OFF vs. CENP-P OFF) and a pair of experiments with a poor correlation (CENP-H OFF vs. CENP-N OFF). Fig. S3 shows profile plots for the CPC, core histones, and the cohesin complexes. Fig. S4 is a step-by-step correlation analysis between the RZZ component Rod and the Mis12 component Nsl1 (poor correlation) and CENP-T (good correlation). Fig. S5 is a blowup of Fig. 9 B, with the positions of several key complexes indicated. Table S1 lists the H/L ratios of all proteins in every experiment. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201508072/DC1.

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