Human chromokinesin KIF4A functions in chromosome condensation and segregation

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Accurate chromosome alignment at metaphase and subsequent segregation of condensed chromosomes is a complex process involving elaborate and only partially characterized molecular machinery. Although several spindle associated molecular motors have been shown to be essential for mitotic function, only a few chromosome arm–associated motors have been described. Here, we show that human chromokinesin human HKIF4A (HKIF4A) is an essential chromosome-associated molecular motor involved in faithful chromosome segregation. HKIF4A localizes in the nucleoplasm during interphase and on condensed chromosome arms during mitosis. It accumulates in the midzone from late anaphase and localizes to the cytokinetic ring during cytokinesis. RNA interference–mediated depletion of HKIF4A in human cells results in defective prometaphase organization, chromosome mis-alignment at metaphase, spindle defects, and chromosome mis-segregation. HKIF4A interacts with the condensin I and II complexes and HKIF4A depletion results in chromosome hypercondensation, suggesting that HKIF4A is required for maintaining normal chromosome architecture. Our results provide functional evidence that human KIF4A is a novel component of the chromosome condensation and segregation machinery functioning in multiple steps of mitotic division.

Introduction

Faithful segregation of the genome involves an elaborate macromolecular machine in which the mitotic spindle plays a central role. Defects in components that control spindle organization and function often lead to chromosome mis-segregation, aneuploidy, and cellular abnormalities (Pihan and Doxsey, 1999; Jallepalli and Lengauer, 2001). The dynamic nature of the spindle apparatus is believed to be maintained both by the dynamic instability of microtubules (MT) as well as several force producing MT motors (Scholey et al., 2003). Poleward and away from the pole forces balance each other during metaphase congression and are responsible for chromosome motility toward the poles (Marshall, 2002). Polar ejection forces may be generated either by dynamic MTs or by plus-end–directed motor including the chromokinesins, which associate with chromosome arms (McIntosh et al., 2002). Chromokinesins represent a family of chromosome arm-binding kinesins consisting of two distinct types of members: chromokinesins/KIF4 and the Kid homologues (Sekine et al., 1994; Vernos et al., 1995; Wang and Adler, 1995; Williams et al., 1995; Tokai et al., 1996; Yan and Wang, 1997; Antonio et al., 2000; Funabiki and Murray, 2000). Both types of chromokinesins are nuclear during interphase and localize on condensed chromosome arms during mitosis. In humans, two KIF4 members exist: HKIF4A and HKIF4B (Ha et al., 2000). Human KIF4A (HKIF4A) is a 140-kD protein that contains several conserved structural motifs including a kinesin-like motor domain, a long coiled-coil region, a nuclear localization signal, a DNA-binding motif and a cysteine-rich Zn fingerlike motif. The protein has been shown to interact with BRCA2-associated factor 35 and the DNA methyltransferase DNMT3B (Lee and Kim, 2003; Geiman et al., 2004). Although HKIF4A associates with chromosomes during mitosis, no information as to the function of the protein is available (Lee et al., 2001). Here, we show by RNA interference (RNAi) that HKIF4A is a novel multifunctional component of the chromosome condensation and segregation machinery.

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Abbreviations used in this paper: HKIF4A, human KIF4A; MT, microtubule; RNAi, RNA interference.

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Results and discussion

To gain insight into HKIF4A function, we raised a mouse mAb specific against the extreme COOH-terminal domain of human chromokinesin HKIF4A (Fig. 1A; see Materials and methods). In Western blots of MRC-5 cell extracts, the HKIF4A antibody detected a single band of 140 kD (Fig. 1A). In subcellular fractionation of nonsynchronized cells, the protein was highly enriched in the nuclear extract and only trace amounts were detected in the cytoplasmic fraction (Fig. 1A). During mitosis HKIF4A associates along the entire arms of condensed chromosomes (Fig. 1B). In addition to the chromosomal localization, the protein accumulates in the mid-zone from anaphase A to cytokinesis (Fig. 1B). From anaphase B to cytokinesis HKIF4A is present in the mid-body as two distinct rings connecting the MTs from the two half spindles (Fig. 1B, inset). In late cytokinesis, until the two daughter cells pinch off, the protein persists in the center of the mid-body (Fig. 1B). Costaining of HKIF4A with tubulin shows partial colocalization at the spindle poles and at the central spindle (Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200401142/DC1).

HKIF4A is essential for prometaphase organization and metaphase alignment

To determine the in vivo function of HKIF4A, we depleted the protein from MRC-5 cells by RNA interference. The cellular level of HKIF4A decreased by almost 90% of its initial amount after two consecutive transfections 24 h apart (Fig. 2A). HKIF4A RNAi did not affect cellular tubulin or lamin A/C levels (Fig. 2A) and RNAi against lamin A/C did not affect HKIF4A levels (not depicted). HKIF4A depletion resulted in an accumulation of mitotic cells. Although the mitotic index was 0.11 ± 0.06 in mock-transfected control cells, it was 0.2 ± 0.01 in HKIF4A-depleted cells 48 h after transfection (P < 0.05). HKIF4A-depleted mitotic cells showed pronounced defects in various stages of mitosis (Fig. 2A).
65% of prometaphase cells lacked the typical doughnut shape arrangement of chromosomes, chromosomes were frequently misaligned, and anaphase separation was often incomplete (Fig. 2 B). Similar observations were made upon microinjection of anti-HKIF4A antibody into prometaphase cells (Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200401142.DC1). Quantitation of the distinct mitotic stages of RNAi-transfected cells (Fig. 2 C) indicated that 48 h after transfection the fraction of prometaphase and metaphase cells was dramatically higher (50 ± 5.7%) than in mock-treated cells (29 ± 1.3%). The severity of the observed mitotic defects appeared roughly correlated with the level of HKIF4A depletion (not depicted).

**Depletion of chromokinesin HKIF4A causes mitotic spindle defects, anaphase bridges, and aneuploidy**

To determine the role of HKIF4A in mitotic spindle function, we analyzed MTs and chromosomes from mock-transfected and HKIF4A-depleted MRC-5 cells 48 h after transfection with RNAi (Fig. 3). Compared with mock-transfected cells, immunofluorescence microscopy showed dramatic mitotic spindle defects (Fig. 3 A). MT organization of both prometaphase and metaphase spindles was abnormal and was accompanied by chromosome alignment defects (Fig. 3 A, arrow). In a number of cases spindle poles appeared less focused, and in extreme cases chromosomes scattered out of the spindle axis and the spindle completely lost its integrity (Fig. 3 A, solid arrowheads). In addition to prometaphase and metaphase defects, HKIF4A depletion also caused defective cytokinesis (Fig. 3 A). Cells lacking HKIF4A frequently exhibited lagging chromosomes in anaphase and after anaphase, and although the cells started to constrict, the cleavage furrow did not ingress completely (Fig. 3 A, forked arrow). Almost 50% of anaphase cells exhibited lagging chromosomes or chromatin bridges. Some anaphase bridges were observed to persist into telophase, resulting in formation of a large nucleus, binucleate cells, and multiple micronuclei (not depicted).

Amongst all prometaphase cells, 66% of RNAi-treated cells showed disorganized prometaphase figures compared with 11% of control cells (Fig. 3 B). Similarly, 63% of RNAi-treated metaphase cells showed mis-aligned metaphases compared with 14% control cells. In depleted cells, defective spindles were observed in 78% of cells (n = 220; Fig. 3 C). 40 ± 4.2% of spindles were disorganized, 27 ± 5.3% of spindles were defocused, and 11 ± 3.8% of spindles were multipolar (Fig. 3 C).

To determine whether these mis-segregation and cytokinesis defects resulted in aneuploidy of daughter cells, metaphase chromosome spreads from mock or HKIF4A RNAi-depleted
cells were prepared. 80% of spreads of HKIF4A-depleted cells were aneuploid. 53% of HKIF4A-depleted cells had lost one or more chromosomes and 25% of cells had gained one or more chromosomes (Fig. 3 D). Less than 1% of aneuploid spreads were found in control cells.

**HKIF4A is required for maintaining normal metaphase chromosome morphology**

Because HKIF4A is localized all along the condensed chromosome arms, we examined the consequences of HKIF4A depletion on the structural integrity of mitotic chromosomes. Metaphase chromosome spreads from mock-transfected or HKIF4A RNAi-transfected cells were prepared after 2 h of colcemid block and stained with DAPI (Fig. 4). RNAi-mediated depletion of HKIF4A induced significant hypercondensation and chromosomes from HKIF4A-depleted cells were dramatically shorter than chromosomes from mock-transfected cells (Fig. 4 A). The average length of control chromosomes was 4.88 \( \mu \text{m} \) with a range between 1.5 and 10 \( \mu \text{m} \), reflecting the variable sizes of human chromosomes. The width of the chromosomes was on average 0.68 \( \mu \text{m} \) with a range of 0.5–0.8 \( \mu \text{m} \) (Fig. 4 B). In contrast, chromosomes from depleted cells were on average 3-\( \mu \text{m} \) long and 1.2-\( \mu \text{m} \) wide, with a range of 1.1–5.5 \( \mu \text{m} \) in length and 0.8–1.5 \( \mu \text{m} \) in width (Fig. 5 B). These differences were statistically significant at the P < 0.001 level. To rule out that the observed hypercondensation of chromosomes was caused by artifacts of chromosome spread preparation, and more importantly, to exclude the possibility that hypercondensation was caused by prolonged presence of chromosomes in mitosis, we analyzed chromosomes in intact cells. We followed progression of mitosis from nuclear envelope breakdown to telophase in single living HeLa cells stably expressing histone H2B-GFP that are either mock-transfected or RNAi-transfected (Fig. 4 C). In the majority of cells in the RNAi-treated population, chromosomes were more condensed compared with mock-transfected cells even before breakdown of the nuclear envelope in early prophase.
To ask whether HKIF4A depletion leads to hypercondensation of chromosomes via the condensation machinery, we tested whether HKIF4A physically interacts in vivo with condensin. Two distinct condensin complexes, condensin I and II, which share the SMC subunits hCAP-C and -E, but differ in their non-SMC components, hCAP-D, -G, and -H, have been described previously (Ono et al., 2003). Immunoprecipitation with anti-HKIF4A antibody from nuclear extract of nonsynchronized MRC-5 or HeLa cells or from mitotic HeLa extracts specifically pulled down hCAP-E, -G, and -G2 (Fig. 5 A; see Fig. S3 for controls). The physical association of HKIF4A with both condensin complexes I and II was corroborated by immunofluorescence microscopy of chromosomes in intact mitotic cells (Fig. 5, B–D). HKIF4A partially colocalized with hCAP-E, -G, and -G2 along the length of the chromosomes in what appeared as overlapping punctate regions, possibly indicating that only a subpopulation of HKIF4A interacts with condensin subunits (Fig. 5, B–D).

If HKIF4A indeed functionally interacts with the condensin complex, one might predict that loss of HKIF4A affects condensin distribution. To test this prediction, we localized hCAP-E in HKIF4A-depleted MRC-5 cells. RNAi targeted against HKIF4A did not affect the overall protein level of condensin hCAP-E in extracts of nonsynchronized or mitotic cells (Fig. 5 E). The distribution of hCAP-E, -G, and -G2 on chromosomes was altered in HKIF4A-depleted intact dividing cells (Fig. 5 F). HKIF4A-depleted chromosomes lacked the axial localization of hCAP-E, -G, and -G2, partially relocalized and appeared diffusely distributed over the condensed mitotic chromatin mass. These data support an interaction between HKIF4A and the condensin complex.

Although HKIF4 has previously been localized to mitotic chromosomes (Lee et al., 2001) our results extend these observations by demonstrating a functional role for HKIF4A in chromosome segregation, cytokinesis, and structural integrity of chromosomes.

A role of HKIF4A as a molecular motor is suggested by its close homology with the other KIF4 kinesin family members mouse KIF4 (Sekine et al., 1994), *Xenopus* Xklp1 (Vernos et al., 1995), and *Drosophila* KLP3A (Williams et al., 1995). In this function, it may contribute to generating an away from the pole force and cooperate with other plus- and minus-end–directed motors to create the force balance required for spindle bipolarity and chromosome alignment at
Figure 5. HKIF4A interacts with components of condensin I and II. (A) Western blot of anti-HKIF4A pull-down from nuclear or mitotic extract. hCAP-E, -G, and -G2 physically associate with HKIF4A. Protein G beads without antibody or mouse IgG were used as controls. Input loading was one fifth of total. (B–D) Colocalization of HKIF4A with condensin I and II complex. HKIF4A (green) partially colocalized with condensin components hCAP-E, hCAP-G, and hCAP-G2 (red) in punctate regions along the length of the chromosome arms. Far right panels show higher magnifications of individual chromosomes from corresponding merged panels. Bar, 5 μm. (E) Western blot of cell extracts from mock- and HKIF4A RNAi-transfected MRC-5 nonsynchronized and mitotic cells with hCAP-E antibody showed that the condensin level remained unchanged after depletion of HKIF4A. (F) Loss of chromokinesin HKIF4A results in condensin components failing to localize along the chromosome axis in a defined pattern. hCAP-E, G, and G2 (green) were diffusely distributed over the condensed mitotic chromatin mass (DNA, blue). Bar, 5 μm.
metaphase (Goshima and Vale, 2003; Kwon et al., 2004; Bringmann et al., 2004). This interpretation is consistent with our observations because in the majority of HKIF4A-depleted cells, chromosomes were scattered along the length of the spindle, and a large number of aberrant spindle structures were generated. Furthermore, localization of HKIF4A on the cytokinetic mid-body is reminiscent of its Drosophila homologue KLP3A in cytokinesis during Drosophila male meiosis (Williams et al., 1995, 1997). Our observation that chromosome segregation is not completely blocked but continues at a low level until at least three cycles suggests that HKIF4A is redundant with the other chromokinesin Kid (Levesque and Compton, 2001) and kinetochore-associated plus-end motors (Yen and Schara, 1996; Kapoor and Compton, 2002). Consistent with redundancy amongst these motors, KLP3A has been shown to be dispensable in Drosophila (Goshima and Vale, 2003; Kwon et al., 2004).

Apart from its possible role as a molecular motor, our observations suggest that HKIF4A might also have an additional, and possibly complementary, function as a critical component in chromosome condensation. We find that HKIF4A interacts with both condensin I and II complexes and the depletion of the protein in vivo leads to hypercondensation of chromosomes. Similar to condensin I and II complexes, topoisomerase II and some condensin subunits, HKIF4A localizes in an alternating, punctate pattern along the metaphase chromosome axis (Maeshima and Laemmli, 2003; Ono et al., 2003). Depletion of HKIF4A from chromosomes appeared to partially delocalize condensin subunits from the chromosome axis, which is consistent with their physical interaction. We speculate that HKIF4A might function as a molecular linker and/or spacer between chromosome condensation proteins and DNA to contribute to higher order organization of metaphase chromosomes. Its depletion might thus be expected to result in a collapse of the chromosome fiber, giving rise to the observed hypercondensation phenotype. HKIF4A may, together with condensin and other nonhistone proteins, form the structural framework of the metaphase chromosome (Earnshaw and Laemmli, 1983; Hudson et al., 2003; Swedlow and Hirano, 2003; Gassmann et al., 2004; Strick et al., 2004). Consistent with such a role of HKIF4A, we find multiple defects both in chromosome structure and mitotic spindle organization. Similar phenotypes including formation of anaphase bridges in chromosome structure and mitotic spindle organization.


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