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Agostinho, Ana; Manneberg, Otto; van Schendel, Robin; Hernández-Hernández, Abrahan; Kouznetsova, Anna; Blom, Hans; Brismar, Hjalmar; Höög, Christer

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High density of REC8 constrains sister-chromatid axes and prevents illegitimate synaptonemal complex formation

Ana Agostinho1*, Otto Manneberg2, Robin van Schendel3, Abrahan Hernández-Hernández1, Anna Kouznetsova1, Hans Blom2, Hjalmar Brismar2 and Christer Höög1

1 Department of Cell and Molecular Biology, Karolinska Institutet, Berzelius väg 35, 171 77 Stockholm, Sweden
2 Science for Life Laboratory, Dept of Applied Physics, Royal Institute of Technology, PO Box 1031, 17121, Solna, Sweden
3 Department of Human Genetics, Leiden University Medical Center, PO Box 9600, 2300 RC, Leiden, The Netherlands

*Corresponding Author
Ana Agostinho
Department of Cell and Molecular Biology
Karolinska Institutet
Berzelius väg 35
171 77 Stockholm, Sweden
Tel: +46852487386
Fax: +468323672
E-mail: ana.agostinho@ki.se

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Abstract

During meiosis, cohesin complexes mediate sister-chromatid cohesion (SCC), synaptonemal complex (SC) assembly and synapsis. Here, using super-resolution microscopy, we image sister-chromatid axes in mouse meiocytes that have normal or reduced levels of cohesin complexes, assessing the relationship between localization of cohesin complexes, SCC and SC formation. We show that REC8 foci are separated from each other by a distance smaller than 15% of the total chromosome axis length in wild-type meiocytes. Reduced levels of cohesin complexes result in a local separation of sister-chromatid axial elements (LSAE), as well as illegitimate SC formation at these sites. REC8, but not RAD21 or RAD21L-cohesin complexes flank sites of LSAE, whereas RAD21 and RAD21L appear predominantly along the separated sister-chromatid axes. Based on these observations and a quantitative distribution analysis of REC8 along sister-chromatid axes, we propose that the high density of randomly distributed REC8 cohesin complexes promotes SCC and prevents illegitimate SC formation.

Keywords: cohesin/ meiosis/ super-resolution microscopy/ synaptonemal complex/ sister-chromatid cohesion
Introduction

Sister-chromatid cohesion (SCC) ensures that chromosomes are correctly segregated in mitotic and meiotic cells [1]. SCC is established during DNA replication by cohesin complexes. These multi-subunit protein complexes form ring-like structures that hold the newly replicated sister-chromatids together from S-phase until anaphase.

During meiosis, cohesion along chromosome arms is lost prior to anaphase I to allow the segregation of homologous chromosomes (homologs), whereas centromeric cohesion is released prior to anaphase II to allow segregation of sister-chromatids. In vertebrates, the mitotic cohesin complex is composed of four core components: two structural maintenance of chromosomes (SMC) proteins, SMC1α and SMC3, the α-kleisin RAD21 and one of two stromal antigen (SA) proteins SA1 or SA2 (also called STAG1 and STAG2). Several meiosis specific components have been identified in mammals, including: SMC1β, α-kleisins REC8 and RAD21L and SA protein SA3/STAG3 [2-10].

Meiotic cohesin complexes contribute to the assembly of the synaptonemal complex (SC), a meiosis-specific structure that facilitates crossover recombination by tethering two homologs. The SC has a characteristic tripartite ladder-like structure; approximately 100 nm wide [11,12], where transverse filaments connect a central element to the lateral elements (LEs) (AEs are referred to as LEs upon synapsis) of each homolog. Several SC proteins have been identified in mammals: AE proteins SYCP2 and SYCP3, transverse filament protein SYCP1 and central element proteins SYCE1, SYCE2, SYCE3 and TEX12 [13-19].

AEs assemble along the axis of sister chromatids at the leptotene stage of meiosis I [20], possibly as two separate parallel structures that are tightly associated [21]. Synapsis (tethering two homologs) then commences at the zygotene stage of meiosis I, when the AEs of the two homologs become progressively juxtaposed. SC formation is complete at the pachytene stage of meiosis I, concomitant with the completion of reciprocal crossover events (for review see [22]).

SMC1β is first detected on sister chromatids at the leptotene stage of meiosis I, and remains at centromeres of chromosomes until the anaphase stage of meiosis II [2,10,23]. Smc1β−/− spermatocytes have been shown to have impaired SCC, incomplete synapsis and
to display shortened AEs with extensions of chromatin loops, suggesting a structural role for SMC1β in meiotic chromosome axis organization [23,24]. Premature loss of chromosome arm and centromeric cohesion at the first meiotic division in Smc1β−/− oocytes, leads to high levels of chromosome missegregation, resulting in sterility [23].

Three different α-kleisins have been shown to be expressed in mammalian meiotic cells. REC8 is detected on chromosomes prior to DNA replication at the pre-leptotene stage of meiosis I and remains bound at centromeres until the anaphase stage of meiosis II. Rec8−/− mice retain SCC at the centromeres but exhibit loss of SCC along chromosome arms [25,26]. SC formation occurs illegitimately between sister-chromatids in Rec8−/− mice [25,26], suggesting an active role of REC8 in directing SC formation to take place between homologs, and thus the existence of a cohesin-based regulatory mechanism for SC assembly and synapsis.

RAD21L appears on chromosomes after DNA replication and declines after the pachytene stage of meiosis I [4,5]. Rad21L−/− spermatocytes retain SCC but display impaired synapsis, where SCs form predominantly between non-homologous chromosomes [27,28].

RAD21 is detected at chromosomes at the pachytene stage of and remains bound to centromeres at the metaphase stage of meiosis I. Contradictory results regarding the expression of RAD21 prior to the pachytene stage of meiosis I have been reported [4,5,8,29,30], and the absence of a meiotic mutant with selective abrogation of RAD21 has prevented a direct study of the contribution of this α-kleisin to meiotic SCC. Based on the studies of Rec8−/− mice, however, it has been proposed that REC8, and not RAD21, is responsible for the canonical cohesion function (i.e., holding sister-chromatids together) in meiotic cells [4,5,28].

Finally, STAG3 is detected uniformly on chromosomes from the leptotene stage to the diplotene stage of meiosis I. STAG3 is required for stabilization of REC8 cohesin complexes and their association with the meiotic chromosome axes [31-33]. Accordingly, hypomorphic Stag3 mutant mice with a severe loss of STAG3 expression display a limited amount of REC8 and a phenotype similar to that of Rec8−/− mice, including impaired meiotic recombination and aberrant SC formation, predominantly between the shortened AEs of sister-chromatids [31].
Here, we have employed super-resolution microscopy to study the role of different mammalian meiotic cohesin-core components in SCC establishment/maintenance and SC formation. We detected local separation of sister-chromatid axial elements (LSAE) in univalent chromosomes of hypomorphic Stag3 mutant and Smc1β−/− spermatocytes, accompanied by illegitimate SC formation at these sites. Sites of LSAE were flanked by REC8, but not, RAD21 or RAD21L cohesin complexes. We propose, based on a quantitative distribution analysis of REC8 foci along sister-chromatid axes, that local separation of sister-chromatid AEs is prevented by a high density of randomly distributed, yet closely juxtaposed, REC8-containing cohesin complexes.
Results

Separation of sister-chromatid axes revealed by super-resolution microscopy

In cells at the pachytene stage of meiosis I, a distance of approximately 100 nm separates paired AEs. This distance is smaller than the diffraction limit of conventional light microscopes (approximately 250 nm), therefore, in order to study axis organization in genetic backgrounds with different levels of REC8-mediated cohesion, nuclear spreads were analysed with super-resolution Structured Illumination Microscopy (SIM). Wild-type, Rec8−/− and homozygous Stag3TgTn(sb-cHS4, Tyr)2312Cove (a hypomorphic allele referred hereafter as Stag3 mutant [31]) mutant spermatocytes were immunostained with antibodies against AE protein SYCP3, and an anti-centromere antibody (ACA). In wild-type pachytene cells, the two sister-chromatids of each homolog are tightly associated and were here detected in a single AE (Fig 1A), whereas the AEs of synapsed homologs (bivalents) were detected as two parallel SYCP3-labeled structures with associated telocentric centromeres (Fig 1A). In Rec8−/− spermatocytes, where the sister-chromatids of univalents have lost their tight association provided by REC8-mediated cohesion, two separate AEs are observed [25,26]. Univalents could thus be visualized in Rec8−/− spermatocytes harboring two discernible SYCP3-labeled sister-chromatid AEs (referred hereafter for simplification, as sister-AEs) with associated centromeres (Fig 1A).

REC8 levels are strongly reduced in Stag3 mutant mice [31]. Consistently, and similarly to Rec8−/− spermatocytes, SYCP3-labeled axes detected in Stag3 mutant spermatocytes at a zygotene-like stage, displayed two separated sister-AEs (Fig 1B, magnified view). Consistent with a reduction, but not an abrogation of REC8 expression, sister-chromatids closely associated in a single AE could also be detected (Fig 1B, magnified view). We found that 69% of axes (288/414 axes associated with centromeres, from 11 nuclei) in Stag3 mutant spermatocytes displayed some degree of sister-AE separation, whereas the remaining 31% of sister-chromatids appeared length-wise conjoined in a single AE (126/414 axes, Fig 1B, graph). Sister-chromatids displaying AE separation were subsequently grouped into two classes: those that displayed extensive separation (as shown
in Fig 1B, centre) and those that displayed restricted sites with local separation of AEs (LSAE) along the axes or close to the centromeres (Fig 1C). LSAE was detected in 34% of axes (142/414 axes) whereas extensive separation of AEs was detected on 35% of axes (146/414 axes) (Fig 1C, graph). Despite the occurrence of LSAE close to the centromeres, these were not separated, as shown by the close association of the two ACA foci (Fig 1C).

Given the presence of univalents in Smc1β−/− spermatocytes [23,24], we next investigated the occurrence of LSAEs in this mutant background (Fig 1D). 16% of all univalent axes (65/404 axes, from 10 nuclei) displayed sites of LSAE, whereas extensive separation of AEs was never observed (Fig 1D, graph) in this mutant. The presence of LSAE in Stag3 mutant and Smc1β−/− spermatocytes was separately confirmed using Stimulated Emission Depletion (STED) microscopy (Fig 1E). The chromosomal regions at which LSAE was observed in Stag3 mutant and Smc1β−/− spermatocytes, were further characterized by comparing the inter-axis-distances measured at these sites with the inter-axis distances between the AEs of synapsed wild-type homologs and the inter-axis distances between the sister-AEs of Rec8−/− univalents (Fig 1F and Fig 1H). The median inter-axis distance at sites of LSAE in both Stag3 mutant and Smc1β−/− spermatocytes (150-175 nm), was similar to that of AEs of synapsed wild-type homologs and sister-AEs of Rec8−/− univalents (Fig 1F). No difference in inter-axis distance between at sites of LSAE was detected in Stag3 mutant univalents, irrespectively of where LSAEs were localized along the axis of chromosomes (Fig 1G).

In summary, we found that changes in the levels of STAG3, SMC1β and REC8, to a variable degree contribute to local and extensive separation of sister-AEs.

Illegitimate synapsis takes place at sites of local separation of AEs

Illegitimate SC assembly occurs between the sister-AEs in Rec8−/− spermatocytes [25,26]. In this mutant background, upon synapsis, AE/LEs have been shown to be separated by a distance similar to that of wild-type AE/LEs of synapsed homologs [26]. Since the inter-axis distances measured at the sites of LSAE in Stag3 mutant and Smc1β−/− spermatocytes were comparable to the distances separating the AEs of wild-type and Rec8−/− spermatocytes (Fig...
we analysed whether inter-sister SC formation took place at sites of LSAE in Stag3 mutant and Smc1β−/− spermatocytes. Transverse filament protein SYCP1 was detected within the sites of LSAEs in Stag3 mutant and Smc1β−/− spermatocytes, as well as between the AEs of wild-type chromosomes and the sister-AEs of Rec8−/− univalents (Fig 2A, filled arrowhead and Fig EV1 A). 95% of Stag3 sister-chromatids with LSAE (114/120 affected axes) and 78% of Smc1β−/− sister-chromatids (53/68 affected axes) assembled SCs at these regions (Fig 2A, graphs). Additional SC components such as SYCE1, SYCE2 and TEX12 were also detected within sites of LSAE, in Stag3 mutant and Smc1β−/− spermatocytes (Fig 2B, filled arrowheads and Fig EV1 B).

Quantification of signal distribution within the regions of LSAE in Stag3 mutant spermatocytes further demonstrated the formation of a tripartite SC: two SYCP3 intensity peaks (Fig 2C, empty arrowheads) flanked one peak of TEX12, SYCE2, SYCE1 or TEX12. We note that the C-terminal region of SYCP1 is located within the AEs, explaining the appearance of two small peaks within the SYCP3 signal for this protein (Fig 2C, filled arrowheads). These results show that tripartite SC formation occurs at sites of LSAE in Stag3 mutant and Smc1β−/− spermatocytes.

Sites with local separation of AEs are flanked by the REC8-cohesin subunit

We next accessed the distribution of the individual α-kleisins (REC8, RAD21L and RAD21) in relation to LSAE. Stag3 mutant and Smc1β−/− spermatocytes were immunostained with antibodies against SYCP3, SYCE1 and one of the three α-kleisins: REC8, RAD21L and RAD21. REC8 was detected co-localizing with SYCP3-labeled AEs of wild-type chromosomes throughout meiotic prophase (Fig EV2 A). RAD21L starts to disappear from the chromosome axes during the pachytene stage in wild-type spermatocytes, being only weakly detectable by the diplotene stage (Fig EV2 B). Coinciding with the gradual disappearance of RAD21L, RAD21 was detected from the pachytene to the diplotene stages of meiosis I in wild-type spermatocytes (Fig EV2 C). We found that in Stag3 mutant, as well as in Smc1β−/− spermatocytes, REC8 foci were detected flanking the sites of LSAE (Fig 3A, and Fig EV3 A). A vast majority (81%) of LSAE sites in Stag3 mutant axes (63/78 axes analysed in 13 nuclei).
had closely flanking REC8 foci (Fig 3A, graph and Fig 3D). RAD21L and RAD21 were frequently found overlapping with sister-AEs in Stag3 mutant and Smc1β−/− spermatocytes, but not flanking regions of LSAE (Fig 3B, C, D and Fig EV3 B and C), implying that local presence of RAD21L does not restrict LSAE.

In agreement with these results, the expression of RAD21L and RAD21 in Rec8−/− spermatocytes was not sufficient to prevent extensive separation of AEs (Fig 3B and Fig EV3 D, E [28]). Thus, while all three different α-kleisins associate with the axes, the localization of REC8 flanking LSAE, strongly suggests that only REC8 directly prevents LSAEs during meiosis.

A high density of REC8 prevents LSAEs and illegitimate SC assembly in wild-type spermatocytes

The X and Y sex chromosomes share only a short homology region called the pseudo autosomal region (PAR) (Fig 4A, filled arrowhead) [34,35]. PAR undergoes crossover recombination and synapsis during meiosis, whereas the rest of X and Y-chromosomes remain unsynapsed and in this sense have an organization similar to what is observed in univalent chromosomes. We used this feature of sex chromosomes to analyse the distribution of REC8 along the axes of unsynapsed sister-chromatids in wild-type spermatocytes. We first measured the inter-axis distances along sister-AEs of X-chromosomes, in wild-type spermatocytes (Fig 4B, scheme). We found the AEs to be separated by a median distance of 100 nm, a significantly narrower inter-axis distance than observed at sites of LSAEs in the Stag3 mutant (Fig 4B, graph). In order to identify regions along X-chromosomes at which SC formation is observed, wild-type pachytene spermatocytes were immunostained with antibodies against SYCP3 and SYCE2. SYCE2 was detected abundantly at the PAR but only sporadically between sister-AEs of the X-chromosomes (Fig 4C). Importantly, while short regions of AE separation were observed along the X-chromosomes, SYCE2 was absent from these regions (Fig 4C, empty arrowhead).

To analyse the distribution of REC8 along sister-AEs of X-chromosomes, individual X-chromosomes were computationally straightened and divided into 25 regular intervals. We
detected an average of 16 REC8 foci per X-chromosome (n=225, for 14 X-chromosomes analysed) (Fig 5A). The distribution of REC8 foci between the 25 intervals did not deviate substantially from the average that reflects an evenly spread foci distribution (dotted line), with the exceptions of the PAR and the terminal region of the X-chromosomes (corresponding to the centromeric domain), at which a higher density of REC8 was observed (Fig 5B). Thus, REC8 foci appear randomly distributed along AEs, excluding the terminal regions. We also analysed the frequency distribution of inter-REC8 distances along the sister-AEs of X-chromosomes. We found the majority of REC8 foci (95%) to be separated by a relative short distance: less than ~15% of the chromosome axis length (Fig 5C, grey area in histogram).

The typical small distances between adjacent REC8 foci could result from an active mechanism, such as genetic interference which ensures an even spacing of recombination events along the axis of chromosomes [36], or be due to a random distribution of a high number of REC8 foci per chromosome. To distinguish between these two possibilities, we first estimated the strength of interference among REC8 foci by fitting the frequency distribution of inter-focus distances to the gamma distribution. The result is a best-fit probability density curve of which the shape parameter (ν) is a relative indicator of interference strength (the higher the value of ν, the stronger the interference and the more evenly distributed the foci are [36]). The theoretical interference level of randomly distributed foci is equal to 1, nevertheless inter-focus distances smaller than 1.4% of the chromosomes length can not be detected due to the resolution limit of our method. Thus, we simulated random foci distributions using this value as a constraint (see methods section for details), and compared the level of interference obtained for randomly simulated foci distributions (ν') with that obtained for the experimental inter-REC8 distances (ν). The low level of interference detected (ν=2.9) (Fig 5D) and the similarity between ν=2.9 (s.e. 0.27) and ν'=2.4 (s.e. 0.02) (Fig EV4 A and B) suggests that active mechanisms, such as genetic interference, play a minor role in REC8 positioning.

Secondly, the observed median distance between REC8 foci along the sister-AEs of X-chromosomes was plotted against computationally generated predictions for even distributed foci (indicative of active redistribution of REC8) or randomly distributed foci (Fig 5E) (see methods section for details). The observed median distance between REC8 foci of
5% of the chromosome axis length intersects the random distribution curve given the average of 16 foci per chromosome (Fig 5E). We obtained the same trend when plotting the median distances between foci subdivided in three categories based on the number of REC8 foci per chromosome: 11-14, 15-18 and 19-22 foci. Together the two analyses indicate that the seemingly uniform distribution of REC8 foci is likely due to a relative high number of foci per chromosome and not a result of an active mechanism that insures an even or clustered distribution.

The high density of REC8 foci along wild-type X-chromosomes (Fig 5) and the correlation between the occurrence of LSAEs and REC8 deficiency (Fig 1 and 3) implies that relative large distances between REC8 foci may lead to the occurrence of LSAEs. We tested this prediction by measuring the distance between flanking REC8 foci at sites of LSAEs in Stag3 mutant spermatocytes. Indeed, we found in this mutant background, a median distance of 28% of the chromosome axis length between flanking REC8 foci, significantly larger than that observed for the wild-type X-chromosomes (Fig 5F).

In agreement with our hypothesis, illegitimate SC formation does not take place in wild-type REC8-proficient zygotene spermatocytes: neither between the indistinguishable/tightly associated sister-AEs of synapsing chromosomes (Fig 6A, filled arrowheads) nor along yet-unsynaped chromosomes (Fig 6B). Accordingly, we found a high density of REC8 foci along the yet-unsynapsed chromosomes (average of 23 foci per chromosome, Fig 6C) and a median distance between REC8 foci of 4% of the chromosome axis length, which is similar to wild-type X-chromosomes yet significantly smaller than the distances at LSAEs in Stag3 mutant axes. Importantly, in contrast to REC8 foci flanking sites of LSAEs we found nearly all foci in wild-type spermatocytes to be separated by distances smaller than 15% of the chromosomes axis length (Fig 6E).

In summary, our results support a model where random positioning of a high density of REC8 foci along the chromosome axes ensures that nearly all REC8 cohesin complexes become separated by a distance of less than 15% of the chromosome axis length, sufficient for preventing the separation of sister-AEs and illegitimate SC assembly.
In this study we have analysed the individual role of the different α-kleisins for meiotic SCC and synapsis, in genetic backgrounds with different levels of cohesin function. We show that Stag3 mutant and Smc1b−/− spermatocytes display univalent axes interrupted by axial “openings” revealing the local appearance of two sister-AEs, referred to as local separation of AEs (LSAEs), accompanied by illegitimate SC assembly at sites of LSAEs. We also show that remaining REC8 in Stag3 mutant spermatocytes is detected along single AEs, in most cases directly flanking sites of LSAEs, and that once the distance between REC8 foci increases to more than 15% of the chromosome axis length, LSAEs is observed. Based on these results, we propose that LSAE observed in Stag3 mutant and Smc1b−/−, represents local loss of REC8-mediated sister-chromatid arm cohesion.

In budding yeast, chromatin immunoprecipitation techniques (i.e Chip-chip and ChIP-seq) have detected cohesins predominantly enriched at the centromere and intergenic regions, and distributed in a non-random manner, approximately every 10kb along chromosome arms [37-41]. By directly quantifying and analysing the distribution of REC8 along unsynapsed sister-AEs of X-chromosomes and autosomes, as well as at sites of LSAE in Stag3 mutant spermatocytes, we provide evidence that maintaining a high density of REC8 foci along the chromosome axes prevents the separation of sister-AEs and illegitimate SC assembly. Importantly, our analysis did not provide evidence to support the existence of an active regulatory mechanism governing the positioning of REC8 along the axes. Instead, a high density of REC8 foci, randomly distributed and separated by a minimum distance of 15% of a chromosome axis length, could be sufficient to maintain SCC. It is tempting to speculate that a dynamic, or flexible, behaviour for cohesin association with chromosomes could be in place in order to maintain SCC. In fact, in mouse and human cells, a large fraction of cohesin-binding sites on chromosomes overlap with those of the transcriptional insulator CCCTC-binding factor (CTCF) [42,43], whereas only a minor fraction of cohesin is detected with the cohesin loader subunit Scc2. Thus, cohesin could reposition from its initial binding sites on chromosomes, sliding along chromatin, while remaining topologically bound to chromosomes [44,45].
What is the interplay between REC8-mediated cohesion and inter-homologue SC assembly? The identification of sites of LSAEs that were flanked by REC8 foci allowed us to further elucidate this fundamental question. All SC components analysed (SYCP1, SYCE1, SYCE2 and TEX12) were detected within the sites of LSAE along sister-AEs. Furthermore, the inter-axis distances at sites of LSAEs was similar to that measured in Rec8-null cells, indicating that inter-sister SC assembly also takes place in these sites of LSAEs.

Given the deleterious consequences of loss of SCC and aberrant SC assembly between sister-chromatids for meiotic progression and animal fertility, meiocytes need to ensure sufficient REC8 cohesin complexes along chromosome axes, possibly by controlling REC8 expression, stabilization [31] and loading [46]. By comparing the levels of REC8 cohesin in oocytes of young versus aged mice, as well as the effect of REC8 depletion in naturally aged mice, it has been proposed that increased reproductive aging correlates with depletion of cohesin from chromosome arms and centromeres, leading to erroneous bi-orientation in meiosis I and aneuploidy in eggs [47,48]. Thus, it could be of interest to further investigate whether REC8 would be subject to an age-dependent change in density/distribution along sister-AEs.

It has been suggested, based on the appearance of RAD21 staining of chromosomes in Rec8/Rad21L DKO, that RAD21 could mediate canonical SCC in meiotic cells [49]. However, a separate study of Rec8/Rad21L DKO mice did not detect SMC3 or RAD21 associated with the axial aggregates in the DKO, and also observed an increased distance between sister-FISH signals, arguing that any residual cohesion in the Rec8/Rad21L DKO would be mediated by a cohesin-independent linkage, such as DNA catenation [28]. Furthermore, the SC assembled between sister-AEs in Rec8 mutant spermatocytes spans 100 nm [26], making it hard to envision the two sister-chromatids in this situation being entrapped by RAD21-containing cohesin rings having an approximate diameter of 45 nm [50-52]. We show here that RAD21 localizes along both sister-AEs at sites of LSAE, further suggesting that REC8 but not RAD21-containing cohesin complexes, prevent separation of sister-AEs.

In addition to REC8 and RAD21, STAG3 is known to associate with RAD21L [3-5], thus, a residual level of RAD21L in Stag3 mutant mice could promote SCC. We found however RAD21L foci, along both sister-AEs at sites of LSAE and illegitimate SC formation,
showing that RAD21L is highly unlikely to maintain canonical SCC. In agreement with this result, RAD21L has been suggested to have a prominent role in DSB-independent homolog association and pairing [28], not SCC.

In summary, our data strongly argues that REC8-containing cohesin complexes provide canonical SCC, not RAD21 or RAD21L, at the prophase stage of meiosis I in spermatocytes. A high density of randomly distributed REC8 cohesin complexes along the axes of sister-chromatids prevents illegitimate inter-sister SC assembly, by keeping axes at a distance that is too narrow to allow the assembly of the SC components.
Materials and methods

Mice

Stag3, Smc1β−/− and Rec8−/− mice have been previously described [23,25,31]. All mice were used in accordance with regulations provided by the Stockholms Norra animal ethics committee of Karolinska Institutet.

Immunostaining and antibodies

For preparation of spermatocyte spreads, a drying-down technique [53] was applied, with minor changes. In brief: single tubuli from decapsulated testes were dissected in PBS and allowed to swell in hypotonic buffer (1M Tris HCL pH 8.2; 1M Sucrose; 1M Na-citrate; 0.5M EDTA; 0.1M DTT; 0.2M PMSF; 50x EDTA-free protease-inhibitor) for 30-90mins, cells were then washed out of seminiferous tubules by thorough resuspension in 100mM sucrose solution, and fixed in 1% paraformaldehyde coated slides. Incubation of primary antibodies was done at room temperature overnight. The following primary antibodies were used: guinea pig anti-SMC1β, and anti-C-terminal SYCP1 antibodies [54]; guinea pig anti-SYCE1, anti-SYCE2, and anti-TEX12 antibodies [14]; rabbit anti-RAD21L and anti-REC8 antibodies [4]; mouse anti-SYCP3 (sc-74569) from Santa Cruz Biotechnology; rabbit anti-RAD21 (ab154769) from Abcam; rabbit anti-SMC1α (LS-C91803) from LifeSpan BioSciences; human anti-centromere antibody (ACA, 15-234-0001) from Antibodies Inc. The secondary antibodies used were: Alexa-488 goat anti-mouse; Alexa-555 goat anti-rabbit and goat anti-guinea pig; Alexa-647 goat anti-human (Molecular Probes Inc.). For STED microscopy secondary antibodies used were: Alexa-594 goat anti-mouse (Molecular Probes Inc.); STAR 635P goat anti-rabbit (Abberior). Prolong Gold antifade reagent without DAPI was used as mounting medium (P36930, Life Technologies). Samples were excluded if fixation or immuno-labeling were not satisfactory. Cell nuclei with compromised integrity due to preparation were also excluded. Whenever possible biological triplicates are shown.
Super-resolution fluorescence microscopy

SIM imaging was performed on a Carl Zeiss Elyra PS.1 microscope equipped with 405-, 488-, 561- and 642-nm excitation lasers. The objective used was a Plan-Achromate 100x/1.46 oil DIC M27. Emission was collected sequentially through appropriate dichroic mirrors and bandpass filters set at 495-575 nm for 488 nm excitation, 570-650 nm for 561 nm excitation, and above 655 nm for 642 nm excitation. SIM processing was done with the included ZEN software with selection of automatic settings for evaluation of the raw data (i.e. theoretical PSF, selection of noise filter setting, frequency weighting, baseline settings etc.) [55]. The optimal grid size was automatically assigned to each wavelength by the Zeiss Zen software, and the grid was rotated 5 times at 5 phases for each image. After evaluation, the SIM images were checked for possible artifacts (e.g. honey comb patterns of intensity in the image) so appropriate selections of evaluation settings were applied. Calibration on 40 nm beads generated a lateral precision of approximately 80 nm +-5nm at 488 nm excitation. Images were processed with an integrated ELYRA S system software (Zen 2011 SP2 Black).

To confirm SIM generated images super-resolution STED imaging was also applied. STED imaging was performed on a Leica SP5 TiSa STED system equipped with pulsed diode lasers (PDL 800-B, PiqoQuant) for excitation at 532 nm and 640 nm and tunable near-infrared pulsed depletion laser (MaiTai, Spectra Physics). A 100X/1.4 NA chromatically red-shifted oil immersion objective lens (HCX PL APO STED, Leica Microsystems) was used for STED imaging. Fluorescence signals were passed through a 0.8-0.9 Airy unit pinhole, a dichroic mirror and separate bandpass filters (582/75 and 685/40 from Semrock) placed in front of two avalanche photodiodes. Image frames (1024x1024) were acquired sequentially line-by-line at scan speed of 600 lines per second with a pixel size of 25 nm. Images were deconvolved and processed with Huygens software (Scientific Volume Imaging).

Quantitative analysis of REC8 along chromosomes

Intensity profiles of REC8 along the X-chromosomes, asynapsed autosomes in wild-type and asynapsed chromosomes in Stag3 mutant spermatocytes were initially measured in two
ways: a) by manually tracing the chromosome axes, labelled by SYCP3 antibody, in FIJI [56] and by an in-house constructed algorithm that automatically traced the chromosome axes and then calculated the intensity profile as maxima of seven pixel wide cross sections perpendicular to the trace. The results were found to be equally valid for peak analysis, yet the manual method handled better chromosome intersections and loops and was thus was used for the data collection. All further analysis was done in MATLAB (MathWorks, Natick, MA, USA). The distances were measured as the percentage of the chromosomal axis length. The intensity data was filtered by subtracting the mean, smoothing by a 3-point moving average and finally offsetting and normalizing to the range [0,1]. A 1000-point spline interpolation was then calculated for the intensity profile and used for further analysis. The Matlab Signal Processing toolbox was used to extract the locations of all peaks of a minimum height 0.1, minimum prominence 0.04 and with a minimum peak-to-peak distance of 0.15 μm. These values were arrived at heuristically. Maxima in the raw image caused by non-chromosomal or unspecific binding were excluded based on location.

The strength of the putative REC8 foci interference was measured by fitting the frequency distribution of the inter-focus distances to the gamma distribution. The simulation of the random foci distribution was performed by random cast of 16 foci (a median number of REC8 foci, found on X-chromosome) to a chromosomal axis, repeated 100,000 times, and subsequent exclusion of the axes where inter-focus distances turned to be less than the resolution limit, i.e. 1.4% of the chromosome axis length. Importantly, the interference-related parameter $\nu$ of the simulated frequency distribution of the inter-focus distances was equal to 1.04 before the filtering, which corresponds to the random distribution [36] and corroborates the validity of the chosen method of simulation.

The generation of random and even foci distributions along the chromosomal axes was performed in silico. The even distribution is calculated as $d = (n-1)^{-1}$, where $n$ denotes the number of foci and $d$ the distance between foci. The random distribution was determined by randomly placing $n$ foci on a chromosome. For each random placement the median distance between all foci was calculated as a fraction of the chromosome axis length and this was repeated 10,000 times for each $10 \leq n \leq 20$. The random distribution represents the average of the median of 10,000 random placements.
Statistics

The statistical analysis was performed with the help of GraphPad Prism 6 software (GraphPad Software, Inc). $P$ values reported in Figure legends are two-tailed probabilities calculated by Mann–Whitney two-sided non-parametric test. The non-parametric tests were used as the data distributions did not pass the D'Agostino & Pearson omnibus normality test with $\alpha=0.05\%$. 
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Author contributions

AA designed, performed and analyzed the experiments/data; OM and RS did the computational analysis and mathematic modeling for foci distribution; AH provided the initial hypothesis; AK performed statistical analysis; HB and HB provided access and technical support with super-resolution microscopy; AA and CH wrote the manuscript.
Conflict of Interest

The authors declare they do not have any conflict of interest.
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Figure Legends

Figure 1. Visualization of sister-chromatid axes and sites of local separation of axial elements with super-resolution microscopy.

A) Representative nuclear spreads of wild-type pachytene and Rec8<sup>−/−</sup> pachytene-like spermatocytes. Nuclear spreads were immunostained for SYCP3 and ACA. Magnified views are indicated by dashed areas. Schematic representation on magnified chromosomes represents tightly associated sister-AEs (separated for easier representation) in paired wild-type homologs, and the appearance of two distinguishable/separated sister-AEs once REC8-mediated cohesion is lost in Rec8<sup>−/−</sup> univalents. Bars, 10 μm in spreads and 1 μm on insets.

B) Representative nuclear spread of zygotene-like Stag3 mutant spermatocytes. Nuclear spreads were immunostained for SYCP3 and ACA. Magnified views are indicated by dashed areas. Schematic representation on magnified univalents represents: separation of sister-AEs (centre) and close association of sister-AEs (right). Bellow: graph showing the percentages of axes with: separation of AEs (dark grey area) and closely associated AEs (light grey area). 414 axes analysed, from 11 nuclei. Bars, 10 μm in spreads and 1 μm on insets.

C) Magnified views of zygotene-like Stag3 mutant univalents with LSAEs. Nuclear spreads were immunostained for SYCP3 and ACA. Schematic representation indicates sites of LSAEs. Bellow: graph showing the percentages of axes with: LSAEs (red area), extensive separation of AEs (dark grey area) and closely associated AEs (light grey area). 414 axes analysed, from 11 nuclei. Bars, 1 μm.

D) Representative nuclear spread of zygotene-like Smc1β<sup>−/−</sup> spermatocytes. Nuclear spreads were immunostained for SYCP3 and ACA. Magnified views are indicated by dashed areas. Schematic representation on magnified univalents represents sites of LSAEs. Bellow: graph showing the percentages of axes with: LSAEs (red area), extensive separation of AEs (dark
grey area) and closely associated AEs (light grey area). 404 axes analysed, from 10 nuclei. Bars, 10 μm in spreads and 1 μm on insets.

E) STED images of representative zygotene-like Stag3 mutant and Smc1β−/− univalents displaying LSAEs. Nuclear spreads were immunostained for SYCP3. Bars, 1μm.

F) Graph indicating the inter-axis distances measured in wild-type pachytene bivalents; pachytene-like Rec8−/− and zygotene-like Stag3 mutant and Smc1β−/− univalents. Each measurement in wild-type and Rec8−/− corresponds to the median of 3 distances measured along one homolog (n=60). Each measurement in Stag3 mutant and Smc1β−/− mutant axes correspond to 1 distance measured at sites of local separation of AEs (n=40 and n=20, respectively). Horizontal lines indicate median.

G) Graph indicating the inter-axis distances measured at terminally and centrally located sites of LSAEs in zygotene-like Stag3 mutant univalents. Each measurement corresponds to 1 distance measured at terminally (n=20) and centrally (n=20) located sites of local separation of axial elements. Horizontal lines indicate median.

H) Schematic representation of the axis architecture observed in the different backgrounds analysed: close association of sister-AEs rendering a single AE per homolog (wild-type), separation of sister-AEs, with appearance of two individual sister-AEs (Rec8−/−), and LSAEs rendering local “axial openings” with two individual sister-AEs (Stag3 mutant and Smc1β−/−). Centromeres are shown in red. For easier comparison of distance between axes, a red bar of equal length was added to each chromosome drawing.

Figure 2. Inter-sister SC formation takes place within sites of local separation of axial elements.

A) Representative wild-type pachytene bivalents; pachytene-like Rec8−/−, zygotene-like Stag3 mutant and Smc1β−/− univalents. Nuclear spreads were immunostained for SYCP1, SYCP3
and ACA. Filled arrowheads indicate sites of LSAEs with detectable SYCP1. Bars, 1 μm.

Bellow: graphs showing the percentages of sites of LSAEs with detectable SC assembly along sister-AEs of Stag3 mutant and Smc1β−/− univalents (n=120 and n=68, respectively).

B) Representative zygotene-like Stag3 mutant univalents. Nuclear spreads were immunostained for SYCP3, ACA and: SYCE1, SYCE2 and TEX12. Filled arrowheads indicate SC assembly between sites of LSAEs. Bars, 1 μm.

C) Quantification of signal distribution within sites of LSAEs, in Stag3 mutant spermatocytes. Signal distribution measured for SYCP3 and: SYCP1, SYCE1, SYCE2 and TEX12. Empty arrowheads indicate signal intensity peaks that correspond to each of the two sister-chromatid axes, filled arrowheads indicate SYCP1 peaks.

**Figure 3. Localization of α-kleisins REC8, RAD21L and RAD21 in relation to sites with local separation of axial elements.**

A) Representative zygotene-like Stag3 mutant and Smc1β−/− univalents. Nuclear spreads were immunostained for SYCP3, SYCE1 and REC8. Bellow: graph showing the percentages of Stag3 mutant axes with sites of LSAEs with and without flanking REC8 foci. 78 axes with LSAEs were analysed. Bars, 1 μm.

B) Representative pachytene-like Rec8−/−, zygotene-like Stag3 mutant and Smc1β−/− univalents. Nuclear spreads were immunostained for SYCP3, SYCE1 and RAD21L. Bars, 1 μm.

C) Representative zygotene-like Stag3 mutant and Smc1β−/− univalents. Nuclear spreads were immunostained for SYCP3, SYCE1 and RAD21. Bars, 1 μm.

D) Schematic representation of univalents axes (black lines) with sites of LSAEs, and relative distribution of REC8 (green), RAD21L grey) and RAD21 (grey).
Figure 4. Narrow inter-axis distance prevents illegitimate SC formation along sister-chromatids of wild-type X-chromosomes.

A) Representative wild-type pachytene sex chromosomes. Nuclear spreads of pachytene spermatocytes were immunostained for SYCP3. Filled arrowheads indicate the PAR. Dashed area indicated in centre panel corresponds to the magnified view on the right panel. Bars, 10 μm in spreads and 1 μm on insets.

B) Graph indicating the inter-axis distances measured at sites of local separation of axial elements in zygotene-like Stag3 mutant univalents and along pachytene wild-type X-chromosomes. Each measurement in the X-chromosomes corresponds to the median of 3 distances (according to the scheme in figure) (n=54). Each measurement in Stag3 mutant corresponds to 1 distance measured at sites with local separation of axial elements (n=40). Horizontal lines indicate median. p < 0.0001, obtained with two-tailed Mann-Whitney test.

Bellow: schematic representation of the XY pair: sister-AEs are coloured in black and grey for easier visualization. Filled arrowhead indicates PAR. Purple bars in scheme indicate regions where inter-axis distances are measured.

C) Representative pachytene wild-type sex chromosomes. Nuclear spreads of pachytene spermatocytes were immunostained for SYCP3 and SYCE2. Dashed area indicated in centre panel corresponds to the magnified view on the right panel. Empty arrowhead indicates two discernable sister-AEs without SYCE2. Bars, 10 μm in spreads and 1 μm on insets.

Figure 5. Analysis of REC8 distribution along the sister-chromatid axes of wild-type X-chromosomes.

A) Analysis of REC8 distribution in representative pachytene wild-type sex chromosomes. Nuclear spreads of pachytene spermatocytes were immunostained for SYCP3 and REC8. Bars, 10 μm in spreads and 1 μm on insets. Magnified XY pair is indicated by dashed area.
Scatterplot showing the number of REC8 foci per X-chromosome. 225 foci identified in 14 X-chromosomes. Horizontal line indicates the mean, error bars indicate s.d. 3.02.

B) Top: representative computationally straightened pachytene wild-type X-chromosomes. Nuclear spreads were immunostained for SYCP3 and REC8. Chromosomes were aligned at the PAR, and subdivided into 25 regular intervals. Bar, 1 μm. Bellow: histogram showing the distribution of the percentages of REC8 foci (n=225) among 25 regular intervals along 14 X-chromosomes. Dotted line indicates mean.

C) Histogram showing the relative frequency of inter-REC8 distances along X-chromosomes. 211 inter-REC8 distances from 14 X-chromosomes. Grey area represents 15% of the chromosome axis length. The respective cumulative distribution function is shown.

D) Histogram showing the best fit of the observed inter-REC8 distances to the gamma distribution. Green curve indicates the best fit of the observed inter-REC8 distances. $v$ indicates the value for which the best fit was obtained, with estimated standard error 0.27.

E) Graph comparing the median distance of REC8 foci with computationally predicted even and random distributions. Median distances between foci subdivided in three categories (11-14, 15-18 and 19-22 REC8 foci per chromosome). Purple asterisk indicates the median distance of all REC8 foci.

F) Scatterplot comparing inter-REC8 distances along on X-chromosomes with the distances between flanking REC8 foci at sites of LSAEs in the Stag3 mutant. 211 inter-REC8 distances measured along X-chromosomes and 10 distances measured between flanking REC8 foci in Stag3 mutant. Grey area represents 15% of the chromosome axis length. Horizontal lines indicate the median. $p < 0.0001$, obtained with two-tailed Mann-Whitney test.

Figure 6. Analysis of REC8 distribution along the sister-chromatid axes of wild-type autosomes.
A) Representative yet-unsynapsed autosome from wild-type zygote spermatocytes. Nuclear spreads were immunostained for SYCP3 and SYCE2. Magnified autosome is indicated by dashed area. Filled arrowheads indicate yet-unsynapsed axes regions. Bars, 10 μm in spreads and 1 μm on insets.

B) Representative unsynapsed autosome from wild-type zygote spermatocytes. Nuclear spreads were immunostained for SYCP3, REC8 and ACA. Magnified autosome is indicated by dashed area. Bars, 10 μm in spreads and 1 μm on insets.

C) Scatterplot comparing the average number of REC8 foci along zygote autosomes and X-chromosomes. Number of REC8 foci were quantified along 15 zygote autosomes and 14 X-chromosomes. Each dot represents the number of REC8 foci on each chromosome. Total number of foci identified: zygote autosomes (343), X-chromosomes (225). Horizontal lines indicate the mean, error bars indicate s.d.: 7.42 and 3.02 for zygote autosomes and X-chromosomes, respectively. $p = 0.0060$, obtained with two-tailed Mann-Whitney test.

D) Histogram showing the relative frequency of inter-REC8 distances along yet-unsynapsed zygote autosomes. 294 inter-REC8 distances analyzed in 14 chromosomes. Grey area represents 15% of the chromosome axis length. The respective cumulative distribution function is shown.

E) Scatterplot comparing the measured inter-REC8 distances on yet-unsynapsed zygote autosomes, X-chromosomes and sites of LSAEs in Stag3 mutant. Number of inter-REC8 distances for yet-unsynapsed zygote autosomes, X-chromosomes and sites of local separation of axial elements in Stag3 mutant, $n=294$, $n=211$ and $n=10$, respectively. Horizontal lines indicate the median. $p < 0.0001$, obtained with two-tailed Mann-Whitney test.
Expanded View Figure Legends

Figure EV1. Chromosomal localization of SC components in wild-type and mutant spermatocytes with reduced cohesin function.

A) Representative whole nuclei of wild-type pachytene; pachytene-like Rec8\textsuperscript{-/-} and zygotene-like Stag3 mutant and Smc1β\textsuperscript{-/-} spermatocytes. Nuclear spreads were immunostained for SYCP1, SYCP3 and ACA. Filled arrowheads indicate the bivalent and univalents shown on Fig 2A. Bars, 10 μm.

B) Representative whole nuclei of zygotene-like Stag3 mutant spermatocytes. Nuclear spreads were immunostained for SYCP3, ACA and each of the following SC components: SYCE1, SYCE2 and TEX12. Filled arrowheads indicate the univalents shown on Fig 2B. Bars, 10 μm.

Figure EV2. Chromosomal localization of meiotic α-kleisins during prophase I.

A) Representative nuclear spreads of wild-type spermatocytes. Nuclear spreads from leptotene to diplotene stages of meiotic prophase were immunostained for REC8 and SYCP3. Bars, 10 μm.

B) Representative nuclear spreads of wild-type spermatocytes. Nuclear spreads from leptotene to diplotene stages of meiotic prophase were immunostained for RAD21L and SYCP3. Bars, 10 μm.

C) Representative nuclear spreads of wild-type spermatocytes. Nuclear spreads from leptotene to diplotene stages of meiotic prophase were immunostained for RAD21 and SYCP3. Bars, 10 μm.

Figure EV3. Chromosomal localization of α-kleisins in relation to sites of local
separation of axial elements and SC formation, in mutant spermatocytes with reduced cohesin function.

A) Representative whole nuclei of zygotene-like Stag3 mutant and Smc1β−/− spermatocytes. Nuclear spreads were immunostained for REC8, SYCE1 and SYCP3. Filled arrowheads indicate the Stag3 mutant and Smc1β−/− univalents shown on Fig 3A. Bars, 10 μm.

B) Representative whole nuclei of zygotene-like Stag3 mutant and Smc1β−/− spermatocytes. Nuclear spreads were immunostained for RAD21L, SYCE1 and SYCP3. Filled arrowheads indicate the Stag3 mutant and Smc1β−/− univalents shown on Fig 3B. Bars, 10 μm.

C) Representative whole nuclei of zygotene-like Stag3 mutant and Smc1β−/− spermatocytes. Nuclear spreads were immunostained for RAD21, SYCE1 and SYCP3. Filled arrowheads indicate the Stag3 mutant and Smc1β−/− univalents shown on Fig 3C. Bars, 10 μm.

D) Representative whole nuclei from early zygotene-like to pachytene-like stages in Rec8−/− spermatocytes. Nuclear spreads were immunostained for RAD21L, SYCE1 and SYCP3. Magnified views on E are represented by dashed areas on nuclear spreads. Filled arrowhead indicates the Rec8−/− univalent shown on Fig 3B. Bars, 10 μm.

E) Magnified views of Rec8−/− univalents shown in D. Magnified univalents from early zygotene-like to pachytene-like stages of meiotic prophase were immunostained for RAD21L, SYCE1 and SYCP3. Bars, and 1 μm.

Figure EV4. Gamma probability distribution modeling of inter-focus distances.

A) Histogram showing the relative frequency of computationally generated inter-focus distances (grey bars) and the best fit of the distances to the gamma distribution (blue curve). ν′ indicates the value for which the best fit was obtained. Estimated standard error 0.02.
B) Graph comparing the best fit of the observed inter-REC8 distances to the gamma distribution (green curve), and the best fit of computationally generated inter-focus distances (dashed curve). \( \nu \) indicates the value for which the best fit was obtained for the inter-REC8 distances, with estimated standard error 0.27. \( \nu' \) indicates the value for which the best fit was obtained for the computationally generated inter-focus distances, with estimated standard error 0.02.
Figure 3. Agostinho et al.
Figure 4. Agostinho et al.
Figure 6. Agostinho et al.
Figure EV1. Agostinho et al.
Fig EV4. Agostinho et al.