Synaptonemal complex components are required for meiotic checkpoint function in *C. elegans*

Tisha Bohr, Guinevere Ashley[†], Evan Eggleston[†], Kyra Firestone and Needhi Bhalla*

Department of Molecular, Cell and Developmental Biology, University of California, Santa Cruz, Santa Cruz, CA 95064

[†]co-second authors

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*corresponding author: nbhalla@ucsc.edu

Department of Molecular, Cell and Developmental Biology

225 Sinsheimer Labs

University of California, Santa Cruz

Santa Cruz, CA 95064

phone: (831) 459-1319

fax: (831) 459-3139

Abstract

Synapsis involves the assembly of a proteinaceous structure, the synaptonemal complex (SC), between paired homologous chromosomes and is essential for proper meiotic chromosome segregation. In *C. elegans*, the synapsis checkpoint selectively removes nuclei with unsynapsed chromosomes by inducing apoptosis. This checkpoint depends on Pairing Centers (PCs), *cis*-acting sites that promote pairing and synapsis. We have hypothesized that the stability of homolog pairing at PCs is monitored by this checkpoint. Here, we report that synaptonemal complex components SYP-3, HTP-3, HIM-3 and HTP-1 are required for a functional synapsis checkpoint. Mutation of these components does not abolish PC function, indicating they are bonafide checkpoint components. These data suggest that, in addition to homolog pairing, SC assembly may be monitored by the synapsis checkpoint.

Introduction

Meiosis is the specialized cell division by which cells undergo one round of DNA duplication and two successive rounds of division to produce haploid gametes from diploid organisms. During sexual reproduction, fertilization restores diploidy to the resulting embryo. In order for meiotic chromosomes to segregate properly in meiosis I and II, homologs pair, synapse and undergo crossover recombination (BHALLA *et al.* 2008). If homologous chromosomes fail to segregate properly, this can produce gametes, such as egg and sperm, with an improper number of chromosomes, termed aneuploidy. Embryos that result from fertilization of aneuploid gametes are generally inviable, but can also exhibit developmental disorders (HASSOLD AND HUNT 2001). Therefore, checkpoint mechanisms monitor early meiotic prophase events to avoid the production of aneuploid gametes (MACQUEEN AND HOCHWAGEN 2011).

Synapsis involves the assembly of a proteinaceous complex, the synaptonemal complex (SC), between paired homologous chromosomes and is essential for crossover recombination (BHALLA AND DERNBURG 2008). In *C. elegans*, the synapsis checkpoint induces apoptosis to

remove nuclei with unsynapsed chromosomes and prevent aneuploid gametes (BHALLA AND DERNBURG 2005) (Figure 1A). The synapsis checkpoint requires Pairing Centers (PCs) (BHALLA AND DERNBURG 2005), *cis*-acting sites near one end of each chromosome. PCs also promote pairing and synapsis (MACQUEEN *et al.* 2005) by recruiting factors, such as the zinc-finger containing proteins ZIM-1, ZIM-2, ZIM-3 and HIM-8 (PHILLIPS *et al.* 2005; PHILLIPS AND DERNBURG 2006), and the conserved polo-like kinase PLK-2 (HARPER *et al.* 2011; LABELLA *et al.* 2011). We have hypothesized that the synapsis checkpoint monitors the stability of pairing at PCs as a proxy for proper synapsis (DESHONG *et al.* 2014; BOHR *et al.* 2015). However, whether the process of synapsis is also monitored by the synapsis checkpoint is currently unknown.

Upon entry into meiosis, axial elements assemble between replicated sister chromatids to support homolog pairing and synapsis. In most species, axial elements consist of HORMA domain proteins (HORMADs) (HOLLINGSWORTH *et al.* 1990; ARAVIND AND KOONIN 1998; CARYL *et al.* 2000; FUKUDA *et al.* 2010; WOJTASZ *et al.* 2009). In *C. elegans*, four HORMAD proteins, HTP-3, HIM-3, HTP-1, and HTP-2, comprise the axial elements of the SC and play overlapping but distinct roles during meiotic prophase (ZETKA *et al.* 1999; COUTEAU *et al.* 2004; COUTEAU AND ZETKA 2005; MARTINEZ-PEREZ AND VILLENEUVE 2005; GOODYER *et al.* 2008). Synapsis is complete when the central element of the SC is assembled between paired axial elements of homologous chromosomes. In *C. elegans*, the central element includes the factors SYP-1, SYP-2, SYP-3 and SYP-4 (MACQUEEN *et al.* 2002; COLAIACOVO *et al.* 2003; SMOLIKOV *et al.* 2007; SMOLIKOV *et al.* 2009). Loss of any one of these proteins produces a similar mutant phenotype: extensive asynapsis of all chromosomes and a delay in meiotic progression (MACQUEEN *et al.* 2002; COLAIACOVO *et al.* 2003; SMOLIKOV *et al.* 2007; SMOLIKOV *et al.* 2009). In *syp-1* mutants, the synapsis checkpoint response induces germline apoptosis (Figure 1A) (BHALLA AND DERNBURG 2005). However, it's unclear whether *syp-2*, *syp-3* or *syp-4* mutants elicit the same checkpoint response as *syp-1* mutants. Genetically ablating the checkpoint response does not affect the meiotic delay associated with asynapsis in *syp-1* mutants (DESHONG *et al.* 2014;

BOHR *et al.* 2015), indicating that these two events are not mechanistically coupled. Recent work has implicated the HORMADs as a primary mediator of this delay (KIM *et al.* 2015).

Here, we report that some SC components are required for the synapsis checkpoint. *syp-2* mutants resemble *syp-1* mutants and elevate apoptosis in response to the synapsis checkpoint. *syp-4* mutants also exhibit elevated apoptosis similar to *syp-1* and *syp-2* mutants. However, the elevation in apoptosis observed in *syp-4* mutants is not dependent on the synapsis checkpoint component PCH-2, suggesting there may be differences in the way the synapsis checkpoint can be regulated. By contrast, *syp-3* mutants do not elicit a synapsis checkpoint response, showing that SYP-3 is required for the synapsis checkpoint. Similarly, *htp-3*, *him-3* and *htp-1* mutants are also defective in the synapsis checkpoint. Finally, loss of SYP-3, HTP-3, HIM-3 or HTP-1 does not abrogate PC function, consistent with these proteins playing a direct role in the checkpoint.

Results and Discussion

SYP-3 is required for the synapsis checkpoint

syp-1 mutants exhibit increased germline apoptosis as a result of the synapsis checkpoint (due to asynapsis) and the DNA damage checkpoint (due to an inability to repair double strand breaks [DSBs]) (Figure 1A) (BHALLA AND DERNBURG 2005). SPO-11 is required for the introduction of meiotic DSBs (DERNBURG *et al.* 1998) and PCH-2 is required for the synapsis checkpoint (BHALLA AND DERNBURG 2005). We've previously shown that loss of SPO-11 or PCH-2 in otherwise wild-type backgrounds does not affect germline apoptosis (BHALLA AND DERNBURG 2005). However, *syp-1;spo-11* and *pch-2;syp-1* double mutants display lower levels of germline apoptosis than *syp-1* single mutants because of loss of the DNA damage or synapsis checkpoint response, respectively. (Figure 1A) (BHALLA AND DERNBURG 2005). Loss of both checkpoints in *pch-2;spo-11;syp-1* triple mutants result in wild-type levels of apoptosis (Figure 1A) (BHALLA AND DERNBURG 2005).

To determine if other *syp* mutants behave similarly we quantified apoptosis in null *syp-2*, *syp-3* and *syp-4* mutants (Figure 1B, C and D). Mutation of *syp-2* elevated germline apoptosis levels similar to those seen in *syp-1* mutants (Figure 1B), suggesting that *syp-2* mutants exhibit both DNA damage and synapsis checkpoint responses. To verify that *syp-2* mutants exhibit a DNA damage checkpoint response, we introduced a mutation of *spo-11* into a *syp-2* background. We observed decreased apoptosis to intermediate levels in *syp-2;spo-11* double mutants (Figure 1B), indicating that *syp-2* mutants exhibit a DNA damage checkpoint response. To determine if *syp-2* mutants exhibit a synapsis checkpoint response we observed apoptosis in *syp-2;pch-2* double mutants which also had intermediate levels of germline apoptosis (Figure 1B). This verifies that *syp-2* mutants elevate germline apoptosis due to the synapsis checkpoint. Furthermore, mutation of both *pch-2* and *spo-11* reduced apoptosis to wild-type levels in a *syp-2* background (Figure 1B). These data indicate that the elevation of apoptosis observed in *syp-2* mutants is in response to both the DNA damage and synapsis checkpoints, similar to *syp-1* mutants (BHALLA AND DERNBURG 2005).

Next we analyzed *syp-4* mutants and found that germline apoptosis was also elevated (Figure 1C) comparable to *syp-1* and *syp-2* mutants (Figure 1B). Moreover, *spo-11;syp-4* double mutants resembled *spo-11;syp-1* and *spo-11;syp-2* double mutants (BHALLA AND DERNBURG 2005) (Figure 1B and C), indicating that *syp-4* mutants have elevated apoptosis due to the DNA damage checkpoint. However, germline apoptosis was unaffected in *syp-4;pch-2* and *syp-4;pch-2;spo-11* mutants compared to *syp-4* and *syp-4;spo-11* mutants, respectively (Figure 1C). From these data we conclude that there is either another unknown meiotic checkpoint that leads to elevated apoptosis in *syp-4* mutants or that the genetic requirements for the synapsis checkpoint in *syp-4* mutants are different than that of *syp-1* and *syp-2* mutants.

We also quantified apoptosis in *syp-3* mutants and observed increased apoptosis compared to wild-type worms but not to levels observed in *syp-1* single mutants (Figure 1D). This suggests that unlike *syp-1, syp-2 and syp-4* mutants, *syp-3* mutants either have a

functional DNA damage or synapsis checkpoint, but not both. To determine which checkpoint was responsible for the elevated apoptosis observed in *syp-3* mutants we first quantified apoptosis in *syp-3;spo-11* double mutants (Figure 1D). Mutation of *spo-11* in a *syp-3* background reduced apoptosis to wild-type levels (Figure 1D), indicating that the elevation in apoptosis observed in *syp-3* mutants is dependent on the DNA damage checkpoint. To ensure that the elevation in apoptosis observed in *syp-3* mutants is due solely to the DNA damage checkpoint and not due to the synapsis checkpoint, we monitored germline apoptosis in *syp-3;pch-2* mutants. Mutation of *pch-2* in the *syp-3* background did not reduce apoptosis (Figure 1D), indicating that the elevation in apoptosis observed in *syp-3* mutants is not dependent on the synapsis checkpoint. Therefore, although chromosomes are unsynapsed in *syp-3* mutants (SMOLIKOV *et al.* 2007), the synapsis checkpoint response is abrogated.

These data suggest that SYP-3 is required for the synapsis checkpoint. To verify this, we quantified apoptosis in *syp-3;syp-1* double mutants (Figure 1D). *syp-3;syp-1* double mutants had intermediate levels of germline apoptosis (Figure 1D), indicating loss of either the DNA damage checkpoint or the synapsis checkpoint but not both. Mutation of *syp-3* in a *pch-2;syp-1* background did not further decrease apoptosis (Figure 1D), confirming that SYP-3 is not required for the DNA damage checkpoint. However, *syp-3;spo-11;syp-1* triple mutants had wild-type levels of apoptosis (Figure 1D), signifying loss of the synapsis checkpoint. Altogether these data show that SYP-3, but not SYP-2 or SYP-4, is required for the synapsis checkpoint.

HORMAD proteins HTP-3, HIM-3 and HTP-1 are required for the synapsis checkpoint

Imaging of meiotic chromosomes by electron microscopy in *C. elegans* suggests that SYP-3 is closely associated with the axial elements of the SC (SCHILD-PRUFERT *et al.* 2011). Because of this, we decided to test whether axial element proteins, specifically HORMADs, are required for the synapsis checkpoint using null mutations of each gene (Figure 2). First, we tested whether HTP-3 and HIM-3 are required for the synapsis checkpoint by monitoring apoptosis in

htp-3 and *him-3* mutants (Figure 2A). *htp-3* and *him-3* mutants produced wild-type levels of apoptosis (Figure 2A), despite their inability to synapse chromosomes (GOODYER *et al.* 2008; ZETKA *et al.* 1999). Thus, these mutants elicit neither a DNA damage checkpoint nor a synapsis checkpoint response. HTP-3 is required for DSB formation in meiosis (GOODYER *et al.* 2008) and HIM-3 is thought to promote inter-homolog recombination by inhibiting inter-sister repair (COUTEAU AND ZETKA 2011; COUTEAU *et al.* 2004; MARTINEZ-PEREZ *et al.* 2008). These phenotypes could explain the inability of these mutants to generate a DNA damage response. To further investigate a possible role for HTP-3 and HIM-3 in the synapsis checkpoint, we introduced mutations of *htp-3* and *him-3* into *syp-1* mutants and quantified apoptosis. *htp-3;syp-1* and *him-3;syp-1* double mutants have wild-type levels of germline apoptosis (Figure 2A), indicating that, even in the *syp-1* background, HTP-3 and HIM-3 are indeed required for the synapsis checkpoint.

We then tested whether HTP-1 and HTP-2 are required for the synapsis checkpoint. *htp-1* single mutants synapse their chromosomes non-homologously (COUTEAU AND ZETKA 2005; MARTINEZ-PEREZ AND VILLENEUVE 2005) and had intermediate levels of apoptosis (Figure 2B). These data suggest that *htp-1* mutants elicit a DNA damage or synapsis checkpoint response but not both. *htp-2* single mutants have no obvious meiotic defects (COUTEAU AND ZETKA 2005) and exhibited wild-type levels of apoptosis (Figure 2B), indicating that *htp-2* mutants do not produce a DNA damage or synapsis checkpoint response. *htp-1* is close to *spo-11* on chromosome IV, making it difficult to create *htp-1 spo-11* double mutants. Therefore, to investigate which checkpoint was responsible for the intermediate levels of apoptosis observed in *htp-1* mutants we instead abrogated the DNA damage checkpoint using a mutation in *cep-1*, the *C. elegans p53* orthologue (DERRY *et al.* 2001; SCHUMACHER *et al.* 2001). Mutation of *cep-1* in the *htp-1* background reduced apoptosis to wild-type levels while mutations of *pch-2* had no effect on germline apoptosis when compared to *htp-1* single mutants (Figure 2B). This indicates that the elevation in apoptosis observed in *htp-1* mutants is dependent on the DNA damage

checkpoint and not the synapsis checkpoint. Furthermore, these data suggest that either non-homologous synapsis does not result in a synapsis checkpoint response or that HTP-1 may be required for the synapsis checkpoint.

To test if HTP-1 is required for the synapsis checkpoint, we took advantage of the partially redundant roles of HTP-1 and HTP-2 during meiotic synapsis. *htp-1 htp-2* double mutants have unsynapsed chromosomes (COUTEAU AND ZETKA 2005; MARTINEZ-PEREZ AND VILLENEUVE 2005), similar to *htp-3* and *him-3* single mutants (GOODYER *et al.* 2008; ZETKA *et al.* 1999), allowing us to evaluate whether unsynapsed chromosomes elicit a synapsis checkpoint response in the absence of HTP-1. Similar to *htp-1* single mutants, *htp-1 htp-2* double mutants exhibited intermediate apoptosis (Figure 2B), showing that abrogation of the synapsis checkpoint in *htp-1* mutants is not the product of non-homologous synapsis and supporting the possibility that HTP-1 is required for the synapsis checkpoint. Moreover, unlike *htp-3* and *him-3* mutants (Figure 2A), *htp-1* and *htp-2* single mutants, as well as *htp-1 htp-2* double mutants, activate germline apoptosis in response to the DNA damage checkpoint (Figure 2B), further supporting the idea that meiotic HORMADS also play distinct roles during meiotic prophase. In addition, these data demonstrate that HTP-1 and HTP-2 do not appear to play redundant roles in the DNA damage checkpoint's induction of germline apoptosis. This is in contrast to the redundant roles they play in regulating meiotic progression when chromosomes are unsynapsed (KIM *et al.* 2015).

To further validate that HTP-1 is required for the synapsis checkpoint we observed apoptosis in *htp-1;syp-1* and *htp-2;syp-1* double mutants (Figure 2C). While mutation in *htp-2* had no effect on apoptosis in the *syp-1* background, we observed reduced apoptosis to intermediate levels in *htp-1;syp-1* double mutants compared to *syp-1* single mutants (Figure 2C), indicating loss of one checkpoint. To verify that the synapsis checkpoint but not the DNA damage checkpoint is abrogated in the *htp-1*;*syp-1* background we observed apoptosis in *htp-1;pch-2*;*syp-1 and htp-1;cep-1;syp-1* triple mutants. Mutation of *cep-1* in the *htp-1;syp-1*

background reduced apoptosis to levels comparable to wild-type worms (Figure 2C) demonstrating that the elevation of apoptosis observed in *htp-1;syp-1* mutants is dependent on the DNA damage checkpoint. In addition, mutation of *pch-2* did not further decrease apoptosis in the *htp-1;syp-1* background (Figure 2C), showing that the elevation of apoptosis observed in *htp-1;syp-1* mutants is not dependent on the synapsis checkpoint. Therefore, the synapsis checkpoint is abrogated in *htp-1;syp-1* mutants. However, while apoptosis in *htp-1;pch-2*;*syp-1* triple mutants was significantly higher than wildtype, *htp-1;pch-2*;*syp-1* triple mutants had reduced levels of apoptosis in comparison to *pch-2;syp-1* double mutants (Figure 2C), suggesting that loss of HTP-1 affects the synapsis checkpoint more severely than loss of PCH-2. Lastly, similar to *htp-1;syp-1* double mutants, *htp-1 htp-2;syp-1* triple mutants exhibited intermediate levels of apoptosis compared to *syp-1* single mutants and wild-type worms (Figure 2C), further verifying that HTP-2 is not redundant with HTP-1 when considering checkpoint activation of apoptosis. Altogether, these data show that HTP-3, HIM-3, and HTP-1, but not HTP-2, are required for the synapsis checkpoint.

HTP-3 and HIM-3 disrupt localization of some but not all PC proteins.

HTP-3, HIM-3 and HTP-1 could be directly required for the synapsis checkpoint or these proteins could be involved in regulating other mechanisms that are required for the synapsis checkpoint. For example, since PCs are required for the synapsis checkpoint (BHALLA AND DERNBURG 2005), we were concerned that *htp-3, him-3* and *htp-1* mutants might have defects in PC function. Since *htp-1* single mutants produce non-homologous synapsis (COUTEAU AND ZETKA 2005; MARTINEZ-PEREZ AND VILLENEUVE 2005) and our analysis of apoptosis indicates that loss of HTP-2 has no effect on synapsis checkpoint signaling (Figures 2C), we performed experiments to address this using *htp-1 htp-2* double mutants, which have unsynapsed chromosomes (COUTEAU AND ZETKA 2005; MARTINEZ-PEREZ AND VILLENEUVE 2005) allowing better comparison with *htp-3* and *him-3* single mutants. We localized ZIM-2, a protein that binds

to and is required for PC function of Chromosome V (PHILLIPS AND DERNBURG 2006), in wild-type worms and *htp-3*, *him-3* and *htp-1 htp-2* mutants in early meiotic prophase nuclei (Figure 3A). In wild-type worms ZIM-2 forms robust patches at the nuclear periphery in these nuclei (Figure 3A) (PHILLIPS AND DERNBURG 2006). We observed ZIM-2 staining in *htp-1 htp-2* double mutants similar to wild-type worms (Figure 3A). However, *htp-3* and *him-3* mutants had less robust ZIM-2 localization compared to wild-type worms (Figure 3A). We saw similar results in *htp-3*, *him-3* and *htp-1 htp-2* mutants when we stained for ZIM-1 and ZIM-3 (data not shown), which bind the PCs of Chromosomes I and IV and Chromosomes II and III, respectively (PHILLIPS AND DERNBURG 2006).

The defect in robustly localizing ZIMs to PCs in *htp-3* and *him-3* mutants (Figure 3A) might explain why these mutants are defective in the synapsis checkpoint. However, a single unsynapsed X chromosome, with an active PC, is sufficient to elicit a checkpoint response (BHALLA AND DERNBURG 2005). Therefore, we also localized the X chromosome PC binding protein, HIM-8 (Figure 3C) (PHILLIPS *et al.* 2005). We observed staining patterns similar to wild-type worms in *htp-3*, *him-3* and *htp-1 htp-2* mutants (Figure 3B). We also determined whether X chromosome PCs were functional in these mutant backgrounds by localizing PLK-2 (Figure 3B), a kinase that is recruited by PCs to promote synapsis and the synapsis checkpoint (HARPER *et al.* 2011; LABELLA *et al.* 2011). In *htp-3*, *him-3* and *htp-1 htp-2* mutants, PLK-2 co-localized with HIM-8 (Figure 3B), indicating X chromosome PCs were active. Altogether, these data argue against the interpretation that mutations in HORMAD proteins abrogate the synapsis checkpoint indirectly due to defects in PC function and support the conclusion that they are involved in the synapsis checkpoint response.

syp-3 mutants have active PCs

Similar to *htp-3*, *him-3* and *htp-1 htp-2* mutants, *syp-3* mutants have unsynapsed chromosomes but fail to elevate germline apoptosis in response to the synapsis checkpoint

(Figure 1D). Unlike *htp-3*, *him-3* and *htp-1 htp-2* mutants, *syp-3* mutants display a delay in meiotic progression (SMOLIKOV *et al.* 2007), likely because HTP-3, HIM-3, HTP-1 and HTP-2 are present to promote this delay (KIM *et al.* 2015). However, this delay in meiotic progression does not depend on PC function (KIM *et al.* 2015), raising the possibility that *syp-3* mutants abrogate the synapsis checkpoint due to defective PCs. To directly test this, we localized PLK-2 in meiotic prophase in *syp-3* mutants and compared them to wild-type worms, *syp-1*, *syp-2* and *syp-4* mutants. Similar to wild-type animals and *syp-1* (HARPER *et al.* 2011; LABELLA *et al.* 2011), *syp-2* and *syp-4* mutants, *syp-3* mutants robustly localized PLK-2 to PCs (Figure 4A). Moreover, unlike wild-type germlines, PLK-2 localization is extended on PCs in *syp-3* mutants, similar to *syp-1*, *syp-2* and *syp-4* mutants (Figure 4A).

We complemented this evaluation of PC function by localizing ZIM-2 and HIM-8 in *syp-3* mutants and compared this to *syp-1*, *syp-2* and *syp-4* mutants. ZIM-2 forms robust patches in meiotic nuclei in *syp-3* mutants, similar to *syp-1, 2 and 4* mutants (Figure 4B). Furthermore, HIM-8 localizes to all meiotic nuclei in *syp-3* mutants and co-localizes with PLK-2 (Figure 4C). These data show that SYP-3 is required for the synapsis checkpoint in a mechanism distinct from regulating PC function.

Altogether, our data show that some SC components, namely SYP-3, HTP-3, HIM-3 and HTP-1, are required for the synapsis checkpoint. Therefore, we suggest that the synapsis checkpoint may monitor some aspects of SC assembly to prevent aneuploid gametes from being produced. Uncovering which specific functions of SYP-3 and the HORMADs are required for the synapsis checkpoint are intriguing questions to be addressed in future studies.

Surprisingly, despite having similar defects in synapsis, we found that not all central element components of the SC are equivalent in the context of checkpoint function. While *syp-2* mutants essentially phenocopy *syp-1* mutants, *syp-4* mutants appear to have a functional synapsis checkpoint that is PCH-2 independent. We favor the interpretation that there may be differences in the genetic requirements for the synapsis checkpoint depending on what the checkpoint is

responding to. Loss of PCH-2 stabilizes pairing in *syp-1* mutants (DESHONG *et al.* 2014), leading us to hypothesize that this stabilization of pairing is what satisfies the synapsis checkpoint in *pch-2;syp-1* and *pch-2;syp-2* double mutants. Therefore, it is possible that this stabilization does not occur in *pch-2;syp-4* mutants, providing an explanation for why PCH-2 is not required for the synapsis checkpoint in *syp-4* mutants. Alternatively, SYP-4 could be playing another role during the synapsis checkpoint. SYP-4 was identified by virtue of its two-hybrid interaction with SYP-3. However, unlike SYP-3, SYP-4 does not show an interaction with either SYP-1 or SYP-2 by two-hybrid (SMOLIKOV *et al.* 2009). While there are a variety of reasons why relevant protein-protein interactions might not be recapitulated by yeast two-hybrid assays, these negative data suggest that SYP-4 could uniquely interact with SYP-3 during synapsis. For example, one scenario consistent with our data is that when SYP-3 is not bound to SYP-4, SYP-3 signals to the synapsis checkpoint and when it is bound to SYP-4, this signal is silenced. Future experiments will address this hypothesis.

Materials and Methods

Genetics and Worm Strains

The wildtype *C. elegans* strain background was Bristol N2 (BRENNER 1974). All experiments were performed on adult hermaphrodites at 20° under standard conditions. Mutations and rearrangements used were as follows:

LG I: *htp-3(tm3655)*, *syp-4 (tm2713)*, *cep-1(gk138)*, *syp-3(ok258)*, *hT2 [bli-4(e937) let-?(q782) qIs48]* (I;III)

LG II: *pch-2(tm1458)*

LG IV: *htp-1(gk174)*, *htp-2(tm2543)*, *him-3(gk149)*, *spo-11(ok79)*, *nT1[unc-?(n754) let-?(m435)] (IV, V)*, *nT1 [qIs51]* (IV, V)

LG V: *syp-2(ok307), syp-1(me17), bcIs39(Pim::ced-1::GFP)*

Quantification of Germline Apoptosis

Scoring of germline apoptosis was performed as previously descried in (BHALLA AND DERNBURG 2005). L4 hermaphrodites were allowed to age for 22 hours at 20°C. Live worms were mounted under coverslips on 1.5% agarose pads containing 0.2mM levamisole. A minimum of twenty-five germlines were analyzed for each genotype by performing live fluorescence microscopy and counting the number of cells fully surrounded by CED-1::GFP. Significance was assessed using a paired t-test. All experiments were performed at least twice.

Antibodies, Immunostaining and Microscopy

Immunostaining was performed on worms 20 to 24 hours post L4 stage. Gonad dissection were carried out in 1X EBT (250 mM HEPES-Cl pH 7.4, 1.18 M NaCl, 480 mM KCl, 20 mM EDTA, 5 mM EGTA) + .1% Tween 20 and 20mM sodium azide. An equal volume of 2% formaldehyde in EBT (final concentration was 1% formaldehyde) was added and allowed to incubate under a coverslip for five minutes. The sample was mounted on HistoBond (75x25x1mm from Lamb) slides and freeze-cracked and incubated in methanol at -20°C for one minute and transferred to PBST. Following several washes of PBST the samples were incubated for 30-min in 1% bovine serum albumin diluted in PBST. A hand-cut paraffin square was used to cover the tissue with 50 µL of antibody solution. Incubation was conducted in a humid chamber overnight at 4°C. Slides were rinsed in PBST, then incubated for 2 hours at room temperature with fluorophore-conjugated secondary antibody at a dilution of 1:500. The samples were then mounted in 13 ul of mounting media (20 M N-propyl gallate (Sigma) and 0.14M Tris in glycerol) with a No. 1 ½ (22mm^2) coverslip and sealed with nail polish.

Primary antibodies were as follows (dilutions are indicated in parentheses): guinea pig anti-ZIM-2 (1:2500; PHILLIPS AND DERNBURG 2006), guinea pig anti-PLK-2 (1:750; HARPER *et al.* 2011) and rat anti-HIM-8 (1:250; PHILLIPS AND DERNBURG 2006) Secondary antibodies were Cy3 anti-rabbit (Jackson Immunochemicals) and Alexa-Fluor 488 anti-guinea pig and anti-rat (Invitrogen).

All images were acquired at room temperature using a DeltaVision Personal DV system (Applied Precision) equipped with a 100X N.A. 1.40 oil-immersion objective (Olympus), resulting in an effective XY pixel spacing of 0.064 or 0.040 μm. Images were captured using a “camera” Three-dimensional image stacks were collected at 0.2-μm Z-spacing and processed by constrained, iterative deconvolution. Imaging, image scaling and analysis were performed using functions in the softWoRx software package. Projections were calculated by a maximum intensity algorithm. Composite images were assembled and some false coloring was performed with Adobe Photoshop.

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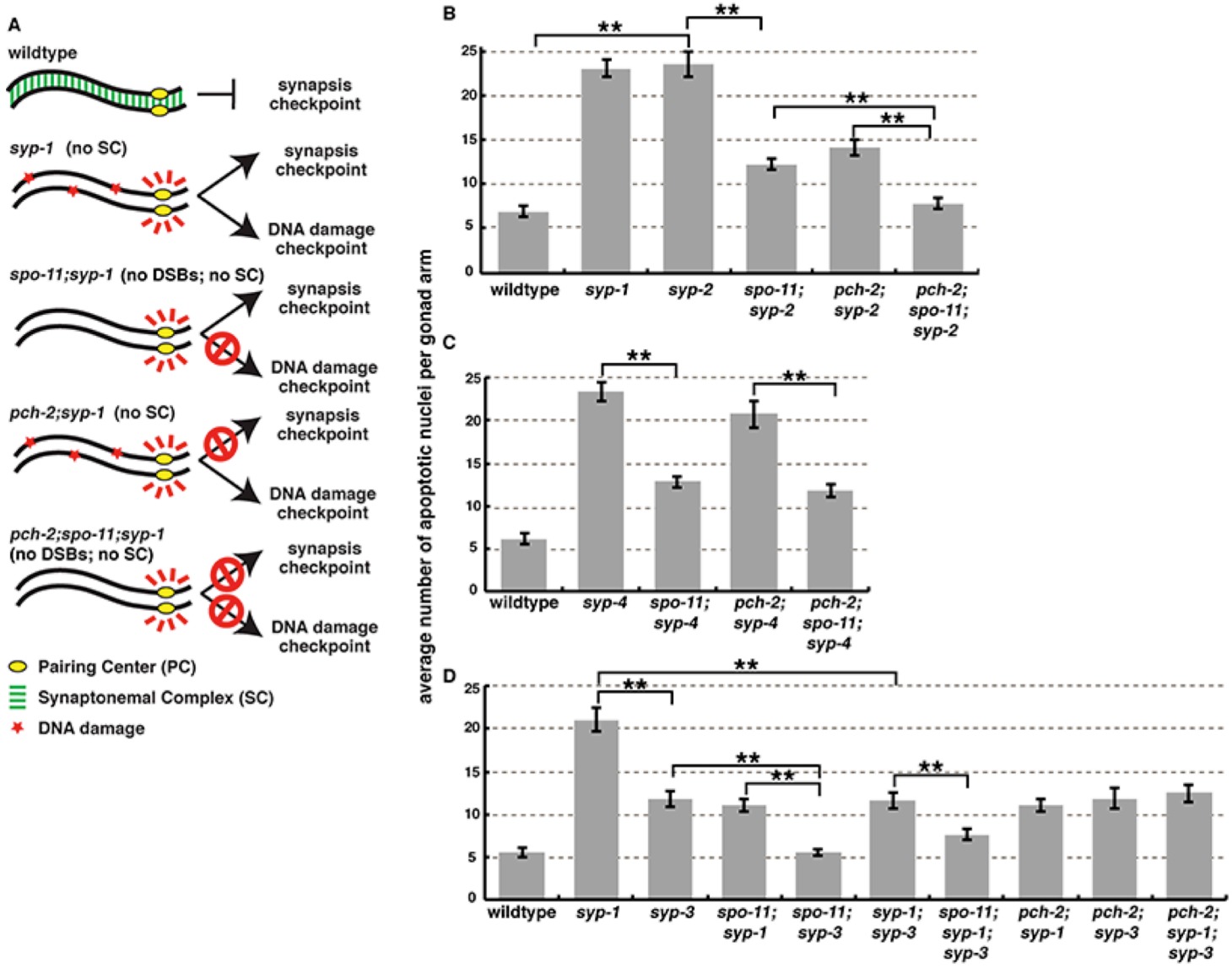

Figure 1. SYP-3 is required for the meiotic synapsis checkpoint. (A) Cartoons depicting meiotic checkpoint activation in *C. elegans*. (B) Elevation of germline apoptosis in *syp-2* mutants is dependent on *spo-11* and *pch-2*. (C) Elevation of germline apoptosis in *syp-4* mutants is dependent on *spo-11* but not on *pch-2*. (D) Elevation of germline apoptosis in *syp-3* mutants is dependent on *spo-11* but not on *pch-2*. Mutation of *syp-3* reduces apoptosis in *syp-1* and *syp-1;spo-11* double mutants but not *syp-1;pch-2* double mutants. Error bars represent ±SEM. A * indicates a p value < 0.01 and a ** indicates a p value < 0.0001 in all graphs.

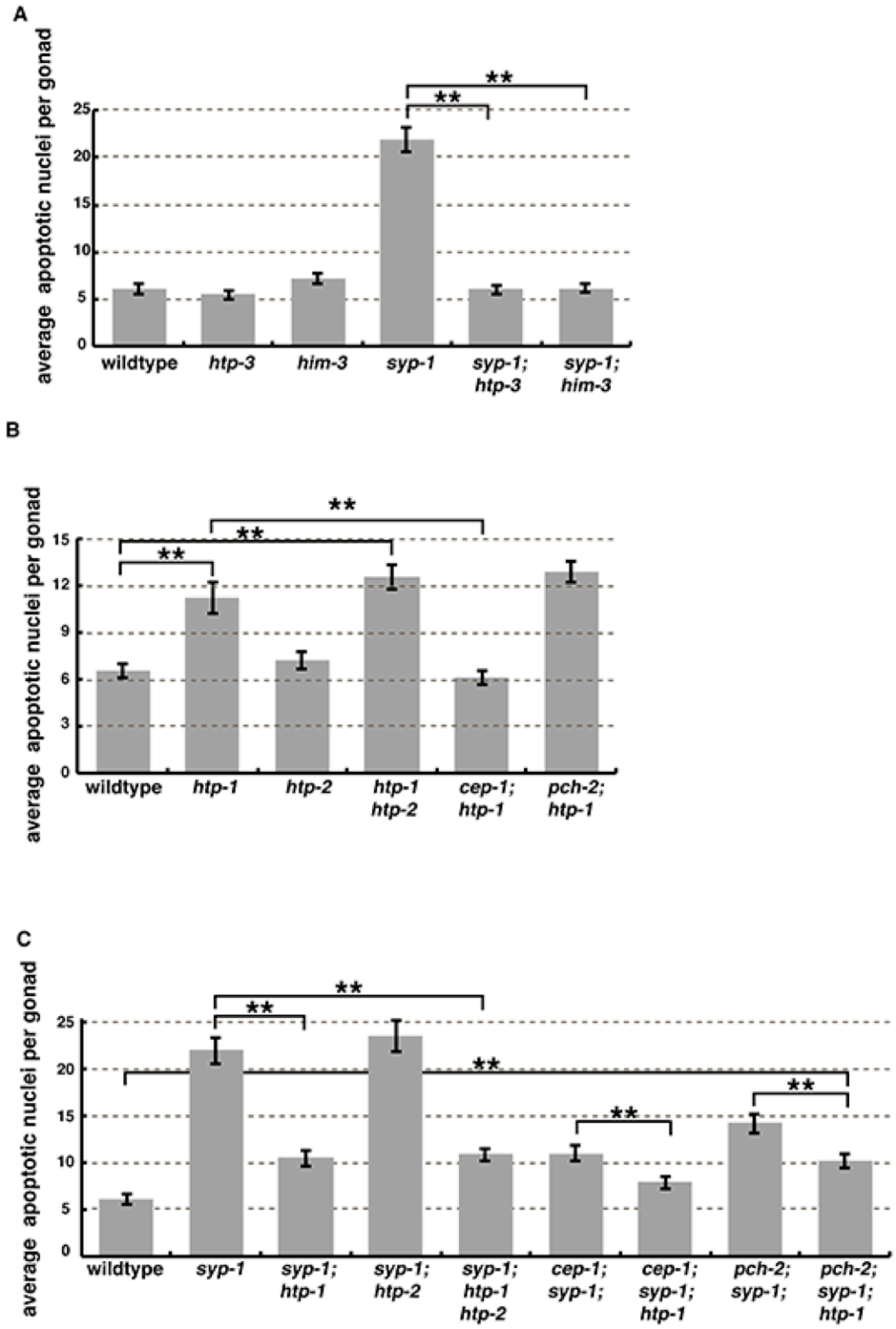

Figure 2. HTP-3, HIM-3 and HTP-1 are required for the synapsis checkpoint. (A) *htp-3 and him-3* mutants have wild-type levels of germline apoptosis and reduce germline apoptosis in *syp-1* mutants. **(B)** The elevation of germline apoptosis in *htp-1* mutants is *cep-1* dependent but not *pch-2* dependent. **(C)** Mutation of *htp*-1 reduces germline apoptosis in *syp-1* single and *cep-1;syp-1* double mutants.

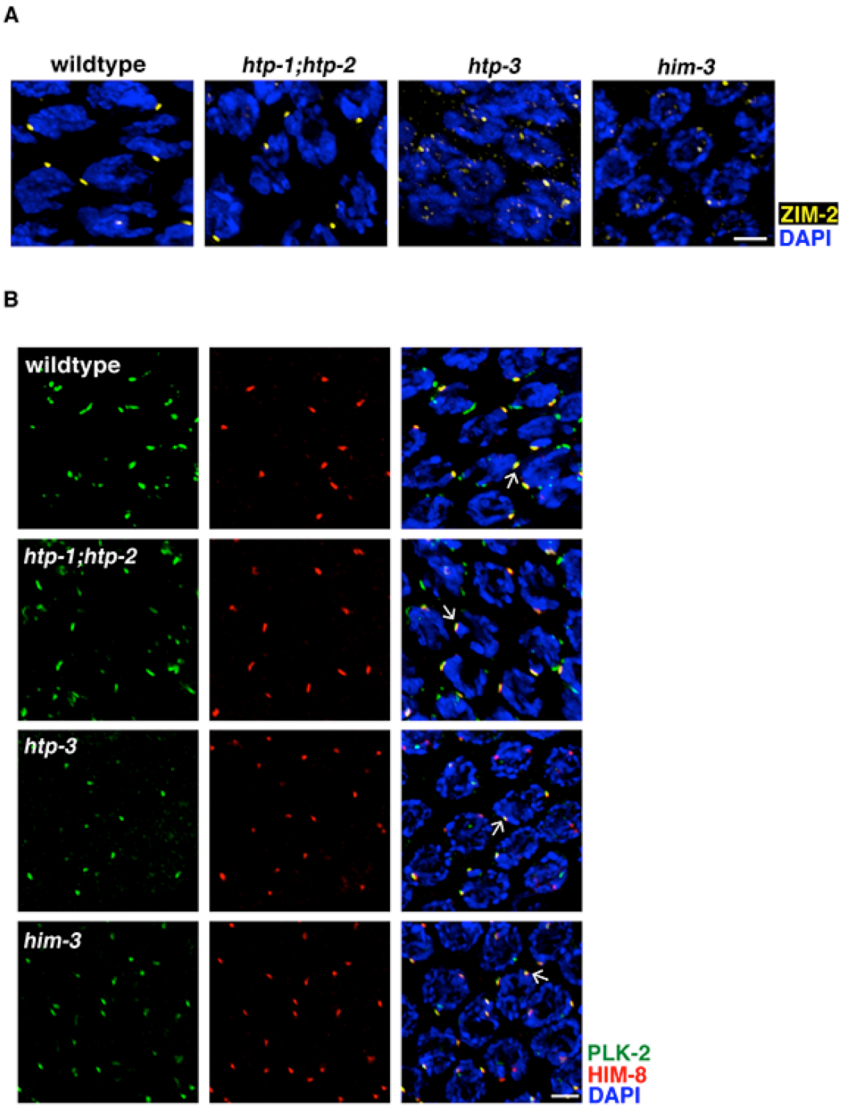

Figure 3: HTP-3 and HIM-3 disrupt localization of some but not all PC proteins. (A) Images of early meiotic prophase nuclei in wild-type worms, *htp-1/2, htp-3,* and*, him-3* mutants stained to visualize ZIM-2 (yellow) and DAPI (blue). **(B)** Images of early meiotic prophase nuclei in wild-type worms, *htp-1/2, htp-3,* and*, him-3* mutants stained to visualize PLK-2 (green), HIM-8 (red) and DAPI (blue). Arrow indicates an example of colocalization of PLK-2 and HIM-8. Scale bar represents 2 μm.

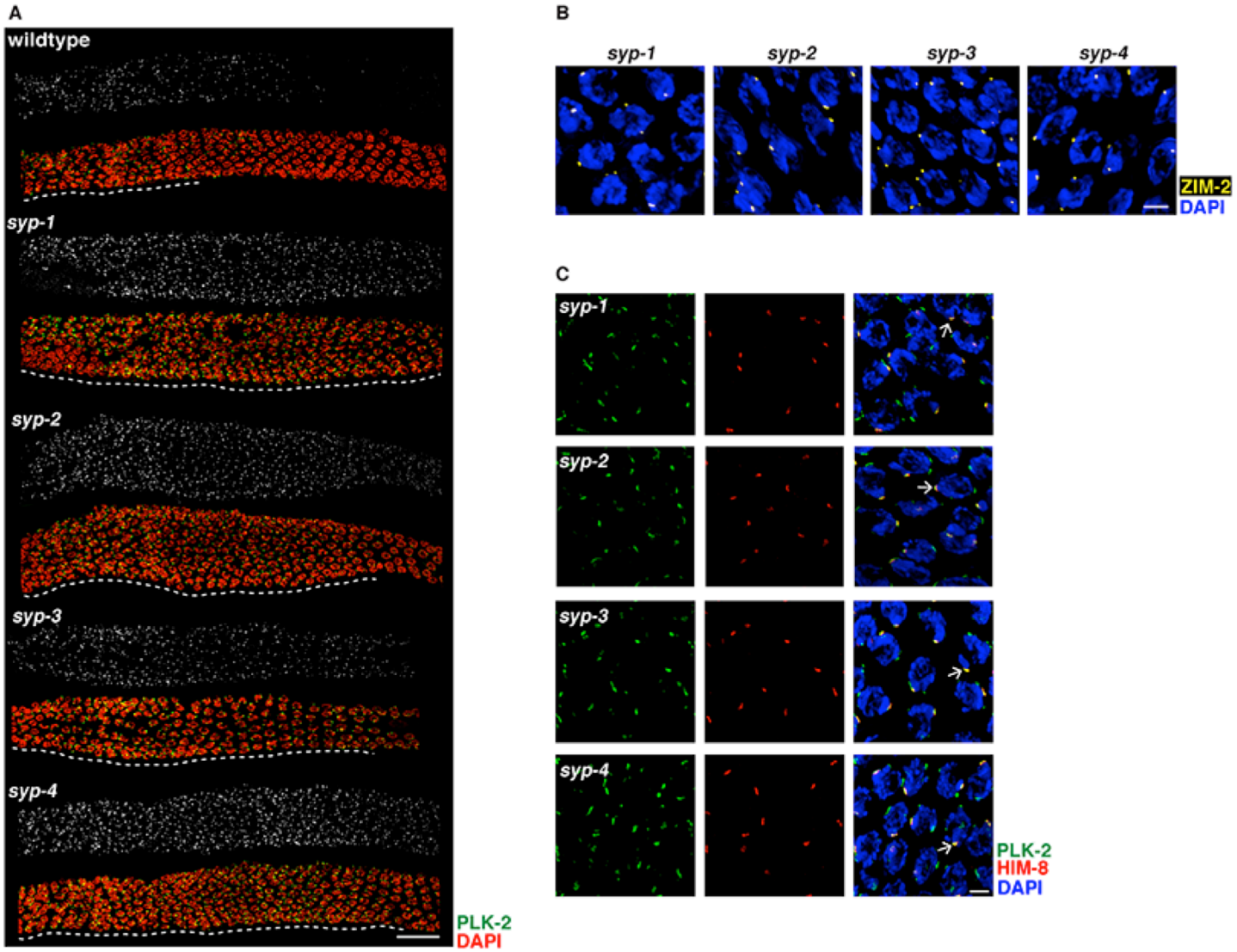

Figure 4: *syp-3* mutants have active PCs. (A) Images of germlines, from entry into meiosis until late meiotic prophase, of wild-type worms, *syp-1*, *syp-2, syp-3*, and *syp-4* mutants stained to visualize PLK-2 (green and grayscale) and DAPI (red). Delay in meiotic progression indicated by white dashed line. Scale bar represents 30 µm. **(B)** Images of early meiotic prophase nuclei in wild-type worms, *syp-1*, *syp-2, syp-3*, and *syp-4* mutants stained to visualize ZIM-2 (yellow) and DAPI (blue). **(C)** Images of early meiotic prophase nuclei in wild-type worms, *syp-1*, *syp-2, syp-3*, and *syp-4* mutants stained to visualize PLK-2 (green), HIM-8 (red) and DAPI (blue). Arrow indicates an example of colocalization of PLK-2 and HIM-8. Scale bar represents 2 µm.