

***Drosophila* FANCM Helicase Prevents Spontaneous Mitotic Crossovers
Generated by the MUS81 and SLX1 Nucleases**

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ABSTRACT

Several helicases function during repair of double-strand breaks (DSBs) and handling of blocked or stalled replication forks to promote pathways that prevent formation of crossovers. Among these are the Bloom syndrome helicase BLM and the Fanconi anemia group M (FANCM) helicase. To better understand functions of these helicases, we compared phenotypes of *Drosophila melanogaster* *Blm* and *Fancm* mutants. As previously reported for BLM, FANCM has roles in responding to several types of DNA damage, in preventing mitotic and meiotic crossovers, and in promoting the synthesis-dependent strand annealing pathway for repair of a double-strand gap. In most assays, the phenotype of *Fancm* mutants is less severe than that of *Blm* mutants, and the phenotype of *Blm Fancm* double mutants is more severe than either single mutant, indicating both overlapping and unique functions. It is thought that mitotic crossovers arise when structure-selective nucleases cleave DNA intermediates that would normally be unwound or disassembled by these helicases. When BLM is absent, three nucleases believed to function as Holliday junction resolvases – MUS81-MMS4, MUS312-SLX1, and GEN – become essential. In contrast, no single resolvase is essential in mutants lacking FANCM, although simultaneous loss of GEN and either of the others is lethal in *Fancm* mutants. Since *Fancm* mutants can tolerate loss of a single resolvase, we were able to show that spontaneous mitotic crossovers that occur when FANCM is missing are dependent on MUS312 and either MUS81 or SLX1.

INTRODUCTION

Helicases are best known as enzymes that separate the strands of duplex nucleic acids, but many DNA repair helicases process more complex structures to direct repair pathways toward specific outcomes (reviewed in Brosh 2013). The Bloom syndrome helicase (BLM) has activities that promote disassembly of D-loops and double-Holliday junction (dHJ) intermediates (Karow *et al.* 2000; Van Brabant *et al.* 2000; Wu and Hickson 2003). These activities prevent formation of crossovers during repair of DNA double-strand breaks (DSBs) (reviewed in Andersen and Sekelsky 2010). Disassembly of a D-loop is a key step in the non-crossover synthesis-dependent strand annealing (SDSA) pathway. *Drosophila* BLM plays an important role in SDSA during gap repair, most likely by promoting D-loop disassembly after repair synthesis (Adams *et al.* 2003; McVey *et al.* 2004b). Likewise, the *Saccharomyces cerevisiae* ortholog, Sgs1, generates non-crossovers during meiotic DSB repair and mitotic gap repair (De Muyt *et al.* 2012; Mitchel *et al.* 2013). If D-loops are not disassembled, repair may proceed to generate a

dHJ intermediate. BLM collaborates with topoisomerase 3 α and other proteins to disassemble dHJs into non-crossover products *in vitro*, a process termed dissolution (Wu and Hickson 2003). Evidence for dHJ dissolution *in vivo* comes from meiotic return-to-growth experiments and mitotic gap repair assays in budding yeast (Dayani *et al.* 2011; Mitchel *et al.* 2013). If a dHJ is not dissolved, it must be resolved by structure-selective endonucleases (resolvases), which may generate reciprocal crossover products.

FANCM helicase also prevents crossing over (reviewed in Whitby 2010). *FANCM* mutations in humans cause Fanconi anemia (FA), a hereditary disorder characterized by developmental abnormalities, bone marrow failure, and cancer predisposition (reviewed in Soulier 2011). Cells from FA patients exhibit heightened sensitivity to agents that cause DNA interstrand crosslinks (ICLs), suggesting a defect in ICL repair (reviewed in Kim and D'andrea 2012). FANCM is thought to function during an early step in the FA repair pathway, perhaps in damage recognition and recruitment of additional FA proteins. FANCM

also has functions outside of the FA pathway. Anti-crossover functions for FANCM and its orthologs have been observed in several contexts. Spontaneous sister chromatid exchange is elevated in mouse embryonic fibroblasts and chicken DT40 cells that lack FANCM (Mosedale *et al.* 2005; Bakker *et al.* 2009). Orthologs in *Saccharomyces cerevisiae* (Mph1) and *Schizosaccharomyces pombe* (Fml1) promote non-crossover outcomes during mitotic DSB repair (Sun *et al.* 2008; Prakash *et al.* 2009; Mazón and Symington 2013; Mitchel *et al.* 2013), and meiotic crossovers are elevated in *Arabidopsis FANCM* mutants and *S. pombe fml* mutants (Crismani *et al.* 2012; Lorenz *et al.* 2012). Like BLM, FANCM and its orthologs can branch migrate HJs and disassemble D-loops (Gari *et al.* 2008; Sun *et al.* 2008; Prakash *et al.* 2009). FANCM is not thought to not be capable of catalyzing dissolution; hence, it has been proposed that the D-loop disassembly activity of Fml1 and Mph1 promotes SDSA, thereby preventing formation of dHJs and resolution of these into crossovers (Sun *et al.* 2008; Prakash *et al.* 2009; Mitchel *et al.* 2013).

Biochemical and genetic studies have identified several likely nuclear HJ resolvases (reviewed in Schwartz and Heyer 2011). Among these, GEN1/Yen1 appears to have the greatest selectivity for HJs, but also has activity on 5' flaps and replication fork-like structures (Ip *et al.* 2008). Genetic studies in vertebrate cells, budding yeast, and *C. elegans* have failed to identify a major function for GEN1 or its orthologs in generating meiotic or mitotic crossovers (Blanco *et al.* 2010; Ho *et al.* 2010; Tay and Wu 2010; Wechsler *et al.* 2011; Agostinho *et al.* 2013; Saito *et al.* 2013). In budding yeast, Yen1 functions are revealed in *mus81 yen1* double mutants, leading to the hypothesis that Yen1 functions as a backup to the Mus81–Mms4 endonuclease (Blanco *et al.* 2010; Ho *et al.* 2010; Tay and Wu 2010; Wechsler *et al.* 2011).

Mus81–Mms4/Eme1 and its orthologs have important roles in generating meiotic and mitotic crossovers in several organisms (Boddy *et al.* 2001; De Los Santos *et al.* 2003; Berchowitz *et al.*

2007; Ho *et al.* 2010; Wechsler *et al.* 2011). Although this enzyme was reported to cut HJs (Boddy *et al.* 2001; Chen *et al.* 2001), studies with recombinant protein found that intact HJs are not a good substrate, but nicked HJs, D-loops, and 3' flaps are (Ehmsen and Heyer 2008). This apparent paradox suggested models in which crossovers are generated by cleavage of a D-loop (Whitby 2005) or a structure with nicked HJs (Osman *et al.* 2003; Schwartz and Heyer 2011). Another solution suggested by recent studies is that Mus81–Mms4/Eme1 functions as an HJ resolvase together with the Slx1 nuclease, with Slx1 making the first nick and Mus81 then cutting the nicked HJ (Castor *et al.* 2013; Garner *et al.* 2013; Wyatt *et al.* 2013). Human SLX1 was previously shown to have HJ resolution activity *in vitro*; this activity is dependent on SLX4, a scaffolding protein that also interacts with MUS81–EME1 (Fekairi *et al.* 2009; Muñoz *et al.* 2009; Svendsen *et al.* 2009). Thus, it is proposed that SLX4 coordinates the activities of SLX1 and MUS81–EME1 to coordinately resolve HJs.

Not surprisingly, helicase and resolvase gene mutations often show genetic interactions. In *S. cerevisiae*, *sgs1* mutations are synthetically lethal with mutations in *mus81* or *mms4*, and with mutations in *slx1* or *slx4*, (Kaliraman *et al.* 2001; Fricke and Brill 2003). Lethality of *sgs1 mus81* mutants is suppressed by mutations that prevent recombination, but lethality of *sgs1 slx1* (or *slx4*) is not, suggesting different causes for the lethality.

The above discussion hints at the inherent functional complexity between BLM, FANCM, and resolvases. We have sought to tease apart some of this complexity through genetic studies in the model metazoan *Drosophila melanogaster*. Mitotic crossovers are highly elevated in *Drosophila Blm* mutants, and these mutants have defects in SDSA and meiotic recombination (Adams *et al.* 2003; McVey *et al.* 2004a; McVey *et al.* 2004b; Kohl *et al.* 2012). *Blm* mutations are synthetically lethal with mutations in *mus81*, *mus312* (encodes the ortholog of Slx4), *Slx1*, or *Gen* (Trowbridge *et al.* 2007; Andersen *et al.* 2009; Andersen *et al.* 2011). As in yeast, different double

mutants have different phenotypes that reveal different functional overlaps.

We describe here characterization of *Drosophila* *Fancm* mutants and comparison to *Blm* mutants. We show that FANCM has roles in preventing both mitotic and meiotic crossovers, independent of its function in the FA pathway, though the mitotic crossover frequency is lower in *Fancm* mutants than in *Blm* mutants. Similarly,

Fancm mutants have a defect in SDSA repair of a gap, but it is significantly less severe than the defect in *Blm* mutants. Unlike *Blm* mutations, *Fancm* mutations are not synthetically lethal with single resolvase gene mutations; however, some combinations of multiple resolvase mutations are lethal to *Fancm* mutants. Finally, we show that spontaneous mitotic crossovers that occur in the absence of FANCM are dependent on MUS312 and either MUS81 or SLX1.

MATERIALS AND METHODS

Drosophila stocks: Fly stocks were maintained at 25°C with standard medium. Mutants were heteroallelic or hemizygous for null alleles (Table 1). Mutations in *Fancm* (CG7922) were found by TILLING (Cooper *et al.* 2008). *Fancm*⁰⁶⁹³ is T-to-C substitution at 3R: 27,905,053 that generates a nonsense mutation (L78ter). In experiments reported here, *Fancm* mutants were *Fancm*⁰⁶⁹³ / *Df(3R)ED6058*. *Fancl*^{LL00701} is an insertion of a *PBac*{*SAstopDsRed*} element into the boundary between the first intron and second exon, between codons 37 and 38 (Schuldiner *et al.* 2008). The stock from the Drosophila Genetic Resource Center (Kyoto) had three *P* elements inserted onto other locations on the same chromosome arm; we removed these by recombination before doing experiments with *Fancl*^{LL00701}. Alleles of other genes are listed in Table 1.

Table 1. Mutations used in this study.

Allele	Type	Reference
<i>Blm</i> ^{N1}	deletion	McVey <i>et al.</i> 2007
<i>Blm</i> ^{D2}	nonsense	Kusano <i>et al.</i> 2001
<i>Gen</i> ⁵⁹⁹⁷	frameshift	Andersen <i>et al.</i> 2011
<i>mei-9</i> ^a	missense	Yıldız <i>et al.</i> 2004
<i>mus312</i> ^{D1}	nonsense	Yıldız <i>et al.</i> 2002
<i>mus312</i> ^{Z1973}	nonsense	Yıldız <i>et al.</i> 2002
<i>mus81</i> ^{Nhe}	frameshift	Trowbridge <i>et al.</i> 2007
<i>slx1</i> ^{F931}	missense	Andersen <i>et al.</i> 2011
<i>spn-A</i> ⁰⁵⁷	missense	Staeva-Vieira <i>et al.</i> 2003
<i>spn-A</i> ^{093A}	nonsense	Staeva-Vieira <i>et al.</i> 2003

Sensitivity assays: Sensitivity to DNA-damaging agents was determined as in Yıldız *et al.* (2002). For HN2 and MMS, 250 µl of an aqueous solution at the indicated concentrations was added to the medium on which larvae were feeding. For IR, vials with larvae were exposed to gamma rays in an irradiator with 145 Ci of ¹³⁷Cs. Adults

were counted daily from day 10 (after parents were first placed in vials) until day 18. Most treatments had at least three technical replicates (treatments on different days), each with ten biological replications (different vials). Vials with fewer than 20 total progeny in either the untreated or treated brood were discarded. Relative survival was calculated for each vial as the ratio between mutant and control flies in the treated vial, normalized to the same ratio in the untreated vial. To estimate absolute survival, we compared the number of control progeny in treated and untreated vials. For low doses, these were 81% (HN2), 82% (MMS), and 89% (IR). This reduced recovery is probably because flies in untreated vials were allowed to mate and lay eggs for three days, whereas flies in treated vials were allowed to lay eggs for only two days. Normalizing to these numbers, the highest doses had 81% (HN2), 56% (MMS), and 47% (IR) absolute survival. Statistical analyses were done in Prism 6 (GraphPad). For treatments that involved more than two genotypes, a Kruskal-Wallis test with a Dunn post-test was done. *P* values reported are corrected for multiple comparisons. Treatments that involved only two genotypes were compared using an unpaired t test.

Mitotic crossover assay: Mitotic crossovers in the male germline were measured as in McVey *et al.* (2007), using the genetic markers *st* and *Sb*. Each vial, each with a single male, was counted as a separate biological replicate. Vials with fewer than 20 progeny were discarded. Statistical analyses were done in Prism 6 (GraphPad). For treatments that involved more than two genotypes, a Kruskal-Wallis test with a Dunn post-test was done. *P* values reported are corrected for multiple comparisons.

Meiotic crossover and non-disjunction assays: To measure meiotic crossovers, virgin females of the genotype *net dpp*^{d-ho} *dp b pr cn* /+; *Fancm*⁰⁶⁹³ /

Df(3R)ED6058 (or wild-type control) were collected and aged 1-4 days, then crossed to *net dpp^{d-ho} dp b pr cn* males. Progeny were counted and scored for each marker from days 10-14 after the cross was set up. To measure non-disjunction of the X chromosome, virgin females were crossed to males carrying *Dp(1;Y)B^S*, a Y chromosome carrying the *B^S* dominant marker. Normal progeny were females with wild-type eyes and males with Bar eyes; non-disjunctive progeny were females with Bar eyes (XXY progeny from XX ova or XY sperm) and males with wild-type eyes (XO progeny from nullo-X ova or nullo-XY sperm).

SDSA assay: The $P\{w^a\}$ assay was done as described previously (McVey *et al.* 2004a), using the *CyO*, $H\{w^+, \Delta 2-3\}$ transposase source. Because *Df(3R)ED6058* has a w^+ allele associated with the deletion, the deletion chromosome was marked with *Sb* and only *Sb+* progeny were scored for eye color. A control was done with *Sb Df(3R)ED6058 / +* males; the results were not different from previous controls that did not have this *Df* chromosome.

Data archiving: Raw data have been deposited into the Carolina Digital Repository with the digital object identifier [10.15139/S3159M](https://doi.org/10.15139/S3159M).

RESULTS

Sensitivity of *Fancm* mutants to DNA damaging agents: To investigate functions of *Drosophila* FANCM that are independent of the FA pathway, we compared phenotypes of *Fancm* mutants to those of *Fancl* mutants, since FANCL is an essential component of the FA pathway but has no other known roles in DNA repair or recombination. Given the central function of the FA pathway in responding to ICLs, we first assayed sensitivity to a crosslinking agent, the nitrogen mustard mechlorethamine (HN2). *Fancl* mutants are hypersensitive to a high dose of HN2 (Fig. 1A), consistent with a previous study that showed hypersensitivity to crosslinking agents after RNAi knockdown of FANCL {Marek, 2006 #2953}. *Fancm* mutants were significantly more sensitive than *Fancl* mutants at this dose and were also hypersensitive to a lower dose of HN2, at which *Fancl* mutants were not hypersensitive.

The greater sensitivity of *Fancm* mutants suggests that FANCM has an FA-independent role in responding to ICLs or to another type of damage induced by HN2. Like most crosslinking agents, HN2 can induce mono-adducts and intra-strand crosslinks in addition to ICLs (Wijen *et al.* 2000). We therefore assayed sensitivity to methyl methanesulfonate (MMS), which generates mono-adducts but not crosslinks (Beranek 1990). *Fancl* mutants were not hypersensitive to MMS at the doses assayed, but *Fancm* mutants showed significant hypersensitivity to a high dose (Fig. 1B). Studies in other model

organisms revealed functions for FANCM orthologs in DSB repair pathways (Sun *et al.* 2008; Prakash *et al.* 2009; Crismani *et al.* 2012; Lorenz *et al.* 2012; Mazón and Symington 2013; Mitchel *et al.* 2013), so we also measured sensitivity to ionizing radiation (IR). *Fancm* mutants were hypersensitive to IR but *Fancl* mutants were not, suggesting an FA-independent role for FANCM in DSB repair (Fig. 1C).

Given the functional similarities between FANCM and BLM, we compared sensitivity between *Fancm* and *Blm* mutants. *Blm* mutants had about the same severity of hypersensitivity to HN2 as *Fancm* mutants, but were significantly more sensitive to MMS and to IR (Fig. 1). *Blm Fancm* double mutants are fully viable in the absence of exogenous damage, but were more sensitive to MMS and HN2 than either single mutant. This suggests the existence of separate FANCM-dependent and BLM-dependent pathways for responding to base adduct damage and possibly to ICLs. Double mutants also appear to be more sensitive to IR than single mutants, but the difference between *Blm* and *Blm Fancm* is not statistically significant. This suggests that FANCM participates in a subset of the BLM-dependent responses to DSBs (*e.g.*, one of multiple branches that converge on or diverge from a BLM-dependent step). Vial-to-vial variation is often large in whole-animal assays such as this, especially at doses where survival is low, and this may have

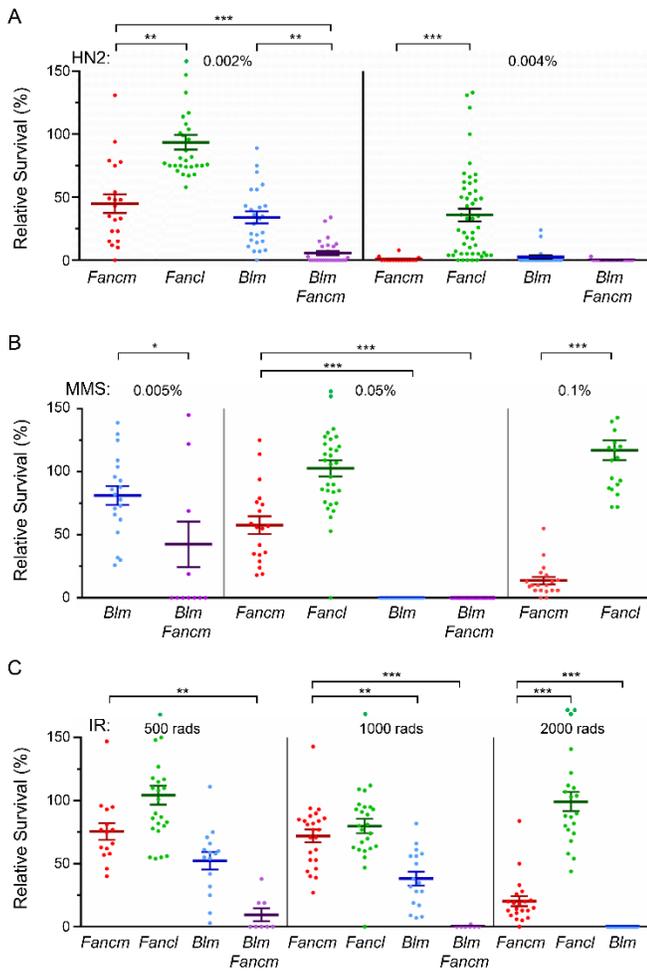


Figure 1. Comparison of sensitivities of *Fancm*, *Fancl*, and *Blm* mutants. Plots show survival of the indicated mutants relative to control flies in the same vial after exposure to (A) the nitrogen mustard mechloramine (HN2), (B) methyl methanesulfonate (MMS), or (C) ionizing radiation (IR). Survival of control flies did not appear to be reduced at the lower doses used here, but the highest doses reduced survival of control flies by approximately 19% (HN2), 46% (MMS), and 53% (IR) (see Materials and Methods). Each dot represents one vial. Heavy bars are means, error bars are standard error of the mean. $n =$ (left to right) HN2: 20, 30, 25, 28 | 16, 49, 20, 23; MMS: 26, 19 | 22, 32, 24, 28 | 19, 20; IR: 15, 25, 15, 8 | 24, 25, 17, 28 | 21, 21, 25. Statistical comparisons were done for *Fancm* compared to each other genotype and *Fancm Blm* double mutants compared to *Blm* single mutants: *, $P < 0.05$; **, $P < 0.01$, ***, $P < 0.001$ (corrected for multiple comparisons; see Materials and Methods); statistically significant comparisons are indicated. Seven of the 625 data points, all from *Fancl* vials, are off the scale and are not shown (values in parentheses): 0.002 HN2 (1.92), 0.05% MMS (1.97), 0.1% MMS (1.84, 1.84, and 1.80), and 500 rads IR (1.92 and 1.76).

prevented us from detecting some real differences. If *Blm Fancm* double mutants are actually more sensitive to IR than *Blm* single mutants, it would suggest that FANCM and BLM contribute to different repair mechanisms, though this would not preclude overlap in the same mechanism.

Meiotic crossovers are elevated in some regions of the genome when FANCM is absent: *S. pombe* Fml1 and *Arabidopsis* FANCM suppress crossovers during meiotic recombination (Crismanni *et al.* 2012; Knoll *et al.* 2012; Lorenz *et al.* 2012), and Fml1 and *S. cerevisiae* Mph1 suppress crossovers in vegetative cells (Sun *et al.* 2008; Prakash *et al.* 2009; Mazón and Symington 2013). We therefore assayed both meiotic and mitotic crossovers in *Drosophila Fancm* mutants. Meiotic crossovers were scored in five adjacent intervals spanning the tip of 2L to the base of 2R, a region comprising about 20% of the genome. The genetic distance across this region increased from 45.0

centiMorgans (cM) in wild-type females to 53.2 cM (118% of wild type) in *Fancm* mutants (Fig. 2A; $P < 0.0001$). The increase is restricted to the two centromere-proximal intervals, each of which has about a three-fold increase in crossovers compared to wild-type (Fig. 2A, 2B). Double-crossovers (DCOs) were also significantly more frequent in *Fancm* mutants: There were 44 DCOs among 2320 progeny (1.9%) from wild-type females, compared to 79 DCOs among 1484 progeny (5.3%) from *Fancm* ($P < 0.0001$). When progeny with multiple crossovers (DCOs and a small number with triple crossovers) are excluded, the crossover rates are not significantly different across the entire region assayed ($P = 0.1061$), but remain significantly elevated in the two proximal intervals ($P < 0.0001$ in each case; no significant differences in other intervals). Thus, in *Fancm*

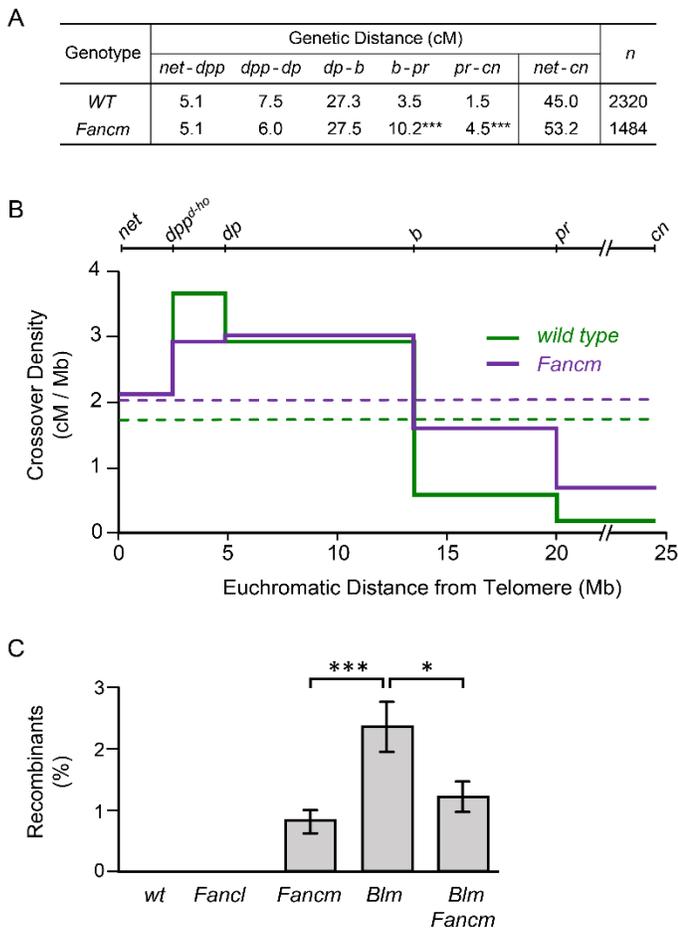


Figure 2. Meiotic and mitotic crossover elevation in *Fancm* mutants. (A) Genetic distances, in centiMorgans (cM), are given for five adjacent intervals on chromosome 2. *** $P < 0.0001$; other intervals were not significantly different ($P = 0.9647, 0.0776, \text{ and } 0.9406$). (B) Meiotic crossover density. Data from (A) were graphed as crossover density, in cM per megabase pair (Mb). The markers used are shown above the graph. Hash marks between *pr* and *cn* indicate the position of the centromere and pericentric heterochromatin (about 16 Mb, not counted in distances shown). Solid lines depict density in each interval; dotted lines are mean density across the entire region. (C) Mitotic crossovers in the male germline. Bars show mean percentage of progeny that were recombinant between *st* and *Sb*. Error bars are standard error of the mean. No crossovers were detected in wild-type (wt) or *Fancl* mutant males. *Fancm*, *Blm*, and *Blm Fancm* were each significantly different from each of these two ($P < 0.01$ for each comparison). The difference between *Fancm* and *Blm Fancm* was not significant ($P > 0.99$). *, $P < 0.0294$; ***, $P < 0.0001$. P values reported have been adjusted for multiple comparisons (see Materials and Methods). $n =$ (left to right) 40, 41, 46, 39, and 30.

mutants meiotic crossovers are elevated, but in only a subset of the genome.

This elevation does not appear to have any negative impact on chromosome segregation. In an assay for meiotic non-disjunction of the X chromosome, we detected one case of non-disjunction among 1698 progeny of wild-type females, and one among 1592 progeny of *Fancm* mutant females ($P = 0.9636$ by chi square).

Meiotic crossovers are elevated in some regions of the genome when FANCM is absent: We assayed spontaneous mitotic crossovers in the male germline because there are no meiotic crossovers in males (Morgan 1912). We scored crossovers between the visible markers *st* and *Sb*, which are separated by more than 36 Mbp (~20% of the genome). Crossovers were not detected among progeny of wild-type males or *Fancl* mutant males, but were significantly elevated in *Fancm* mutant males (Fig. 2C). In the same assay, the crossover frequency in *Blm* mutants is about three-fold

higher than in *Fancm* mutants. The rate in *Blm Fancm* double mutants was not significantly different than in *Fancm* single mutants but was significantly lower than in *Blm* single mutants. A straightforward interpretation of this result is that FANCM functions upstream of BLM in pathway that prevents mitotic crossovers; however, this is likely to be an oversimplification, given the multiple functions of these enzymes and the possibility of partial overlap in function (see Discussion).

FANCM has a modest role in SDSA: Hypersensitivity to IR and elevated mitotic crossovers suggest a role for FANCM in DSB repair, independent of its role in the FA pathway. It has been proposed that *S. pombe* Fml1 and *S. cerevisiae* Mph1 promote SDSA by disassembling D-loops (Sun *et al.* 2008; Prakash *et al.* 2009; Mitchel *et al.* 2013), but this hypothesis has not been tested directly using an assay specific for SDSA. We used a gap repair assay in which products of SDSA can be distinguished from other types of repair (Adams *et al.* 2003; McVey *et al.* 2004a). A gap

is generated by excision of a $P\{w^a\}$ element from the male X chromosome. This element carries the *apricot* allele of the *white* gene (w^a), in which a *copia* retrotransposon is inserted into an intron, resulting in orange eye color instead of the wild-type red color (Fig. 3B). Excision leaves a DSB that is repaired using the sister chromatid as a template. Since the sister still has an intact $P\{w^a\}$ element, this amounts to gap repair. Repair by two-ended SDSA can result in annealing between the long terminal repeats (LTRs) at the ends of *copia*, giving a product with only one LTR instead of an entire *copia*. Progeny that inherit this product have red eyes. This red-eyed class was decreased by ~50% in *Fancm* mutants compared to controls (Fig. 3A), revealing a reduced ability to complete repair by SDSA. In *Blm* mutants, the decrease in SDSA is significantly more severe (Fig. 3A, McVey *et al.* 2007). Other types of repair result in loss of *white* gene function, which we recover as progeny with yellow eyes. In wild-type flies this is almost exclusively aborted SDSA, in which there is templated synthesis from one or both ends of the gap followed by joining through an alternative end-joining pathway (Adams *et al.* 2003; McVey *et al.* 2004a; McVey *et al.* 2004c; Chan *et al.* 2010). Molecular analyses of these repair products shows that synthesis tracts are significantly shorter in *Blm* mutants than in

wild-type flies (Adams *et al.* 2003), but did not reveal any differences between wild type and *Fancm* mutants (Fig. 3B).

Fancm and *Blm* mutants both have elevated spontaneous mitotic crossovers and a decreased ability to complete SDSA repair of a gap, but the defects in *Blm* mutants are more severe in both assays. Since *Fancm* is epistatic to *Blm* for mitotic crossovers and SDSA is thought to be an important pathway in crossover avoidance during DSB repair, we asked whether *Fancm* is epistatic to *Blm* in our SDSA assay. However, we were unable to generate any *Blm Fancm* double mutant males carrying both the $P\{w^a\}$ element and transposase. This appeared to be due to recombination defects, since flies that also lacked the strand exchange protein Rad51 (*spn-A* mutants), and therefore are incapable of initiating recombination, do survive infrequently.

Spontaneous mitotic crossovers in the absence of FANCM require the scaffolding protein MUS312 and either MUS81 or SLX1: To better understand how spontaneous mitotic crossovers in *Fancm* mutants are generated, we asked whether any HJ resolvases are required. We made double mutants between *Fancm* and the genes encoding each of the catalytic subunits of the putative resolvases: *Gen*,

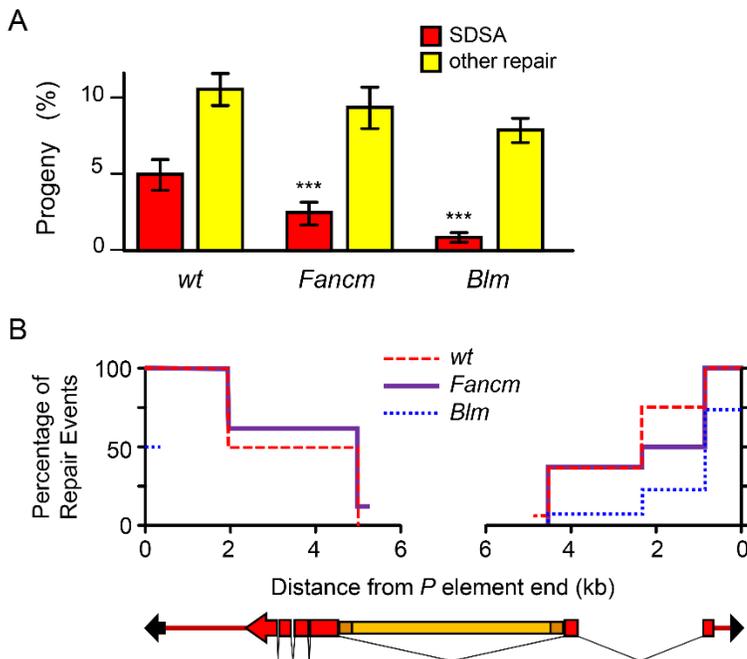


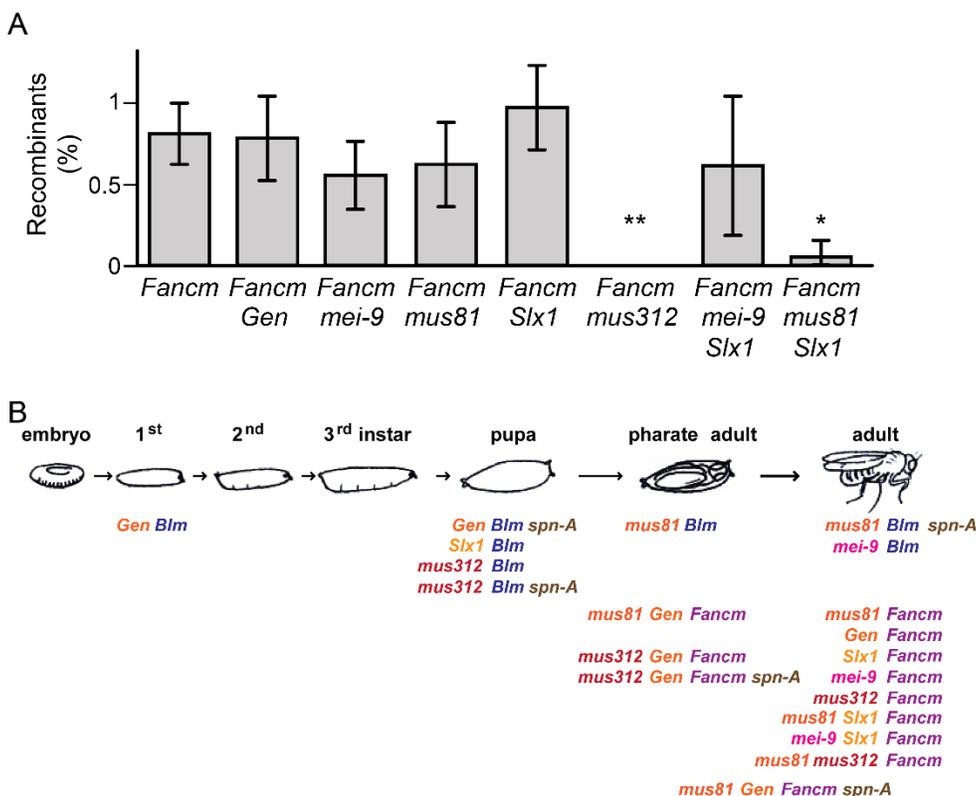
Figure 3. SDSA defects in *Fancm* mutants. (A) Gap repair outcomes. Bars show mean fraction of flies in each repair class: red bars for repair by SDSA, yellow bars for other types of repair (usually aborted SDSA followed by end joining). Of the remaining flies, most came from cells that did not experience an excision event, though a small percentage may also be repair of the entire gap by SDSA. *Blm* data are from McVey *et al.* (2007). Error bars are standard error of the mean. $n = 85$ for *Fancm* and 45 for control. ***, $P < 0.001$ compared to wild type. (B) Kaplan-Meier graph showing the amount of synthesis from each end of the P element in non-SDSA progeny (those with yellow eyes). PCR was done on sons of these progeny to detect synthesis from the left end at 5 bp, 1.7 kb, , and 5.2 kb from the cut site and from the right end at 5 bp, 920 bp, 2.4 kb, and 4.6 kb from the cut site. *Blm* data are from Adams *et al.* (2003); the left end was only analyzed at 5 bp in that study. The drawing at the bottom represents the $P\{w^a\}$ element: black arrows, P element ends; red, *white* gene (boxes, exons; lines, introns); orange, *copia* element (dark, long terminal repeats). $n = 16$ (*Fancm*), 83 (wild type), and 147 (*Blm*).

mus81, *Slx1*, and *mei-9*. There was no significant difference in crossover frequency in any of these double mutants relative to *Fancm* single mutants (Fig. 4A). However, crossovers were completely eliminated in double mutants with *mus312* (Fig. 4A). MUS312 is a scaffolding protein that interacts physically and functionally with both MEI-9 (the *Drosophila* ortholog of Rad1/XPF) and SLX1 (Yıldız *et al.* 2002; Andersen *et al.* 2009), so we considered the possibility that SLX1 and MEI-9 have redundant roles in generating these mitotic crossovers in *Fancm* mutants. This does not appear to be the case, since *mei-9; Slx1 Fancm* triple mutants have the same crossover rate as *Fancm* single mutants and both double mutants (Fig. 4A). Orthologs of MUS312 from vertebrates (SLX4) and *C. elegans* (HIM-18) interact physically with MUS81 (Fekairi *et al.* 2009; Muñoz *et al.* 2009; Svendsen *et al.* 2009; Saito *et al.* 2013). A similar interaction has not been reported for the *Drosophila* proteins, and we failed to detect such an interaction in yeast two-hybrid assays (unpublished data). Nevertheless, we asked whether MUS81 and SLX1 might be acting redundantly to make mitotic crossovers in *Fancm* mutants. Crossovers were nearly absent in *mus81; Slx1 Fancm* triple mutants (Fig. 4A), suggesting that MUS81 and SLX1 indeed act

redundantly to make these crossovers, and that both nucleases require MUS312 for this function.

Simultaneous loss of FANCM and multiple resolvases is lethal: In *Drosophila*, each of the three putative mitotic HJ resolvases (MUS81–MMS4, GEN, and MUS312–SLX1) are each essential when BLM is absent (Trowbridge *et al.* 2007; Andersen *et al.* 2009; Andersen *et al.* 2011). The experiments described above show that none of them are essential when FANCM is absent, and that at least males are fertile (we did not assay female fertility, since several of these resolvases are required for meiotic recombination and their absence causes high levels of non-disjunction and low fecundity). However, synthetic lethality was observed when certain combinations of resolvases were removed (Fig. 4B). As in budding yeast (Blanco *et al.* 2010; Ho *et al.* 2010; Tay and Wu 2010), *Drosophila* MUS81–MMS4 and GEN have a partially redundant or compensatory relationship (Andersen *et al.* 2011). Simultaneous loss of both MUS81–MMS4 and GEN is lethal in *Fancm* mutants (Fig. 4B). The *mus81; Gen Fancm* triple mutants survive to the pharate adult stage, which is the same stage at which *mus81; Blm* double mutants die but much later than lethality of *Gen Blm* double

Figure 4. Phenotypes of *Fancm* mutants lacking one or more resolvases. (A) Mitotic crossovers in *Fancm* mutants lacking various resolvases. Error bars are standard error of the mean. Statistical significance was determined relative to *Fancm* single mutants *, $P = 0.0298$; **, $P = 0.0083$. P values reported have been adjusted for multiple comparisons (see Materials and Methods). $n =$ (left to right) 46, 18, 18, 22, 17, 23, 20, and 22. (B) Lethality and viability of mutants lacking a helicase and one or more resolvases. At the top is a drawing of the developmental life cycle of *Drosophila*. Various genotypes lacking one of the anti-crossover helicases (BLM or FANCM) and one or more of the putative resolvases are listed below the stage at which they die. Those listed below the adult live to adulthood. Life cycle stages and *Blm* mutant results are modified from Andersen *et al.* (2011).



mutants, which only survive until the 2nd instar larval stage. Preventing recombination partially suppresses *mus81*; *Blm* and *Gen Blm* lethality: *mus81*; *Blm spn-A* mutants are semi-viable (about 70% live to adulthood), and *Gen Blm spn-A* mutants survive to the pupal stage (Trowbridge *et al.* 2007; Andersen *et al.* 2011). To ask whether *mus81*; *Gen Fancm* inviability is similarly due to recombination defects, we made

mus81; *Gen Fancm spn-A* quadruple mutants. A few quadruple mutants did survive to adulthood (four, compared to 84 expected), and these had rough eyes and cuticle defects suggestive of high rates of cell death during development. *Gen mus312 Fancm* triple mutants also died as pharate adult pupae; mutating *spn-A* had no apparent effect on this lethality (Fig. 4B).

DISCUSSION

Comparison of *Drosophila Fancm* and *Fancl* mutants for hypersensitivity to DNA damaging agents (Fig. 1) indicates that, as in fungi and plants, *Drosophila* FANCM has functions outside of the FA pathway. Among the agents we tested, *Fancl* mutants were hypersensitive to only the crosslinking agent HN2, consistent with a primary or sole function for FANCL in the FA pathway. *Fancm* mutants were more sensitive to HN2 and, unlike *Fancl* mutants, were hypersensitive to the alkylating agent MMS and to ionizing radiation. Among these FA-independent roles, we focus on functions that may prevent crossovers.

FANCM in meiotic recombination: *Drosophila Fancm* mutants have a significant elevation in both meiotic and mitotic crossovers (Fig. 2). Interestingly, the increase in meiotic crossovers was observed only in the two most proximal intervals, each of which had three-fold more crossovers than wild-type females. Elevated meiotic crossovers have also been reported for *Arabidopsis FANCM* mutants, but in this case the elevation seems to be genome-wide (Crismani *et al.* 2012). The significance and cause of the elevation in *Drosophila* being restricted to only the two proximal intervals is unknown. One of these (*pr-cn*) includes the centromere and pericentric heterochromatin. It seems unlikely that the crossovers we recovered occurred in heterochromatic regions, since these are normally devoid of DSBs (Jang *et al.* 2003), but we did not directly determine whether the crossovers between *pr* and *cn* were in the euchromatic or heterochromatic portion of this interval.

Based on immunolocalization of meiotic recombination proteins, Knoll *et al.* (2012) hypothesized that *Arabidopsis FANCM* suppresses crossovers

produced by MUS81, which is usually responsible for only 10-15% of meiotic crossovers in normal meiosis (Berchowitz *et al.* 2007). In *Drosophila*, most meiotic crossovers are generated by a complex whose catalytic subunit is MEI-9, which is orthologous to XPF/Rad1 (Sekelsky *et al.* 1995). No role in generating meiotic crossovers has been detected for MUS81 (Trowbridge *et al.* 2007), so it will be interesting to determine whether the extra meiotic crossovers in *Fancm* mutants are dependent on MEI-9, MUS81, or another resolvase or combination of resolvases.

FANCM in synthesis-dependent strand annealing: Mitotic crossovers are elevated in the germlines of *Fancm* mutant males (Fig. 2). Previous studies found elevated mitotic crossovers in *S. pombe fml1* mutants and in *S. cerevisiae mph1* mutants (Sun *et al.* 2008; Prakash *et al.* 2009; Mazón and Symington 2013; Mitchel *et al.* 2013). It is important to note that these studies in fungi involved enzymatic induction of DSBs, whereas the crossovers we measured are spontaneous. Our experiments do not provide insight into the sources of these crossovers. FANCM may direct repair of spontaneous lesions toward non-crossover outcomes, or loss of FANCM may cause an increased incidence of some lesions, such as a DSBs, that might be precursors to crossovers.

Mph1 and Fml1 have been proposed to promote DSB repair through the non-crossover SDSA pathway by disrupting D-loops (Sun *et al.* 2008; Prakash *et al.* 2009; Tay *et al.* 2010; Mitchel *et al.* 2013). Hypersensitivity to ionizing radiation and elevated mitotic crossover frequency are consistent with *Drosophila FANCM* having a function in SDSA. In our gap repair assay for SDSA, we

detected a 50% reduction in progeny with the phenotype diagnostic of completed SDSA repair, confirming a role for FANCM in this process (Fig. 3). BLM/Sgs1 also has anti-crossover functions during DSB repair. Although this is usually discussed in terms of the dHJ dissolution function, a function in SDSA is also apparent in the finding that Sgs1 generates meiotic NCOs (De Muyt *et al.* 2012) and that *Drosophila Blm* mutants are severely compromised in the $P\{w^a\}$ gap repair assay for SDSA (Adams *et al.* 2003). Molecular and genetic analysis of gap repair products from *Blm* mutants revealed that synthesis tracts are significantly shorter than in wild-type males, and deletions into flanking DNA sequences are significantly more frequent (Adams *et al.* 2003; McVey *et al.* 2007). It is thought that repair of the large gap in the $P\{w^a\}$ assay requires multiple cycles of strand exchange, synthesis, and D-loop disassembly (McVey *et al.* 2004a). This led to a model in which BLM is required for D-loop disassembly, and in absence of BLM these structures are cut by a structure-selective endonuclease, leading to flanking deletions. This hypothesis raised the question of why there are synthesis tracts at all in *Blm* mutants. We propose BLM-topoisomerase 3 α is essential for disassembling D-loops only after lengthy synthesis, but that FANCM can disassemble shorter D-loops. Although some features of this model are attractive, it does not explain why there is an SDSA defect in *Fancm* mutants. It is also possible that FANCM and BLM both promote SDSA by disassembling D-loops, but that they act at different stages of male germline development.

Resolvases in generating mitotic crossovers in *Fancm* mutants: Spontaneous mitotic crossovers that occur in the absence of FANCM require the MUS312 nuclease scaffold protein and either MUS81 or SLX1 (Fig. 3A). One simple interpretation is that FANCM acts at an early stage to direct repair down a non-crossover pathway (*e.g.*, SDSA). In the absence of FANCM, an HJ-containing intermediate is generated, and it is the resolution of this intermediate by MUS81 or SLX1 that generates a crossover. Recent *in vitro* experiments suggest that vertebrate MUS81 and SLX1

collaborate to resolve HJs, with SLX1 making an initial nick and MUS81 making a second nick, and both being coordinated by the MUS312 ortholog SLX4 (Castor *et al.* 2013; Garner *et al.* 2013; Wyatt *et al.* 2013). Our result is more consistent with MUS81 and SLX1 having redundant functions. If *Drosophila* MUS81 and SLX1 work together to resolve HJs, then it must not be loss of this activity that prevents crossovers when FANCM is absent.

The different phenotypes of *mus81* and *Slx1* mutants indicate that each enzyme has unique functions, but this does not preclude redundant or co-dependent functions (Trowbridge *et al.* 2007; Andersen *et al.* 2009). *S. cerevisiae* and human MUS81–EME1 and SLX4–SLX1 both cut flap and replication fork structures *in vitro* (Fricke and Brill 2003; Ehmsen and Heyer 2008; Wyatt *et al.* 2013). It is possible that, rather than working late on a HJ intermediate, MUS312–MUS81–MMS4 or MUS312–SLX1 can both generate DSBs by cutting aberrant replication fork structures that would normally be processed by FANCM. Some of these DSBs may then be repaired through a pathway that results in a crossover with the homologous chromosome. Given the anti-crossover roles of BLM during DSB repair, however, we might expect a synergistic effect on mitotic crossover frequency in *Blm Fancm* double mutants. Instead, we saw a crossover frequency more similar to that of *Fancm* single mutants. One weakness of this crossover assay is that we cannot detect complete failure of repair, since this would likely result in apoptosis or spermatocyte defects. *Blm Fancm* males did not produce fewer progeny than single-mutant males, but we would not be able to detect reductions of the same magnitude as the mitotic crossover frequency (~2% in *Blm* single mutants).

We also found that *mus81 Gen Fancm* and *Gen mus312 Fancm* mutants are inviable. In the former of these genotypes, inviability may be explained by functional overlap between MUS81–MMS4 and GEN. *S. cerevisiae* Mus81–Mms4 and Yen1 exhibit partial redundancy, with Yen1 appearing to function primarily as a backup to Mus81–Mms4 (Blanco *et al.* 2010; Ho *et al.* 2010; Tay and Wu 2010).

Redundancy has also been observed between *Drosophila* MUS81–MMS4 and GEN, although the relationship appears to be reversed, with *Gen* mutants having more severe phenotypes than *mus81* mutants (Andersen *et al.* 2011). Inviability in *mus81 Gen Fancm* triple mutants is weakly suppressed by preventing recombination. This suggests that either the death of *mus81 Gen Fancm* mutants is only partially due to defects in recombination or that the alternatives to RAD51-mediated recombination are also detrimental.

No functional overlaps have been reported for GEN and MUS312–SLX1 or their orthologs. Triple mutants that lack GEN, MUS312, and FANCM may be inviable because of an accumulation of damage, some resulting from loss of GEN and FANCM and some resulting from loss of MUS312–SLX1 and FANCM. This lethality may also be in part due to loss of both GEN and those MUS81 activities that require MUS312, or some more complex interaction involving all three nucleases.

Concluding remarks: In summary, our analysis shows that *Drosophila Fancm* mutants have similar phenotypes to *Blm* mutants in several assays. These defects are generally less severe in *Fancm* mutants and more severe in *Blm Fancm* double mutants. This suggests that FANCM and BLM have overlapping functions and that these

helicases are partially redundant or either can partially compensate for loss of the other; however, several of the phenotypes we assayed, such as viability after treatment with DNA-damaging agents, viability of flies carrying mutations in multiple genes, and mitotic crossing over, are fairly crude genetic readouts that might have several underlying causes. Thus, more detailed mechanistic studies will be necessary to tease apart the different cellular functions of BLM, FANCM, and the HJ resolvases.

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