Meiotic MCM Proteins Promote and Inhibit Crossovers During Meiotic Recombination

Michaelyn Hartmann,* Kathryn P. Kohl,† Jeff Sekelsky,*§ and Talia Hatkevich*‡

*Curriculum in Genetics and Molecular Biology, †Department of Biology, and §Integrative Program in Biological and Genome Sciences, University of North Carolina, Chapel Hill, North Carolina 27599 and ‡Department of Biology, Winthrop University, Rock Hill, South Carolina 29733

ORCID IDs: 0000-0002-4424-677X (J.S.); 0000-0002-2307-047X (T.H.)

ABSTRACT Crossover formation as a result of meiotic recombination is vital for the proper segregation of homologous chromosomes at the end of meiosis I. In many organisms, crossovers are generated through two crossover pathways: Class I and Class II. To ensure accurate crossover formation, meiosis-specific protein complexes regulate the degree to which each pathway is used. One such complex is the mei-mini-chromosome maintenance (MCM) complex, which contains MCM and MCM-like proteins REC (ortholog of Mcm8), MEI-217, and MEI-218. The mei-MCM complex genetically promotes Class I crossovers and inhibits Class II crossovers in Drosophila, but it is unclear how individual mei-MCM proteins contribute to crossover regulation. In this study, we perform genetic analyses to understand how specific regions and motifs of mei-MCM proteins contribute to crossover regulation. In this study, we perform genetic analyses to understand how specific regions and motifs of mei-MCM proteins contribute to crossover regulation. In this study, we perform genetic analyses to understand how specific regions and motifs of mei-MCM proteins contribute to crossover regulation. In this study, we perform genetic analyses to understand how specific regions and motifs of mei-MCM proteins contribute to crossover formation, and distribution. Our analyses show that the long, disordered N-terminus of MEI-218 is dispensable for crossover formation, and that mutations that disrupt REC’s Walker A and B motifs differentially affect Class I and Class II crossover formation. In recWalker A mutants, Class I crossovers exhibit no change but Class II crossovers are increased. However, in recWalker B mutants, Class I crossovers are severely impaired and Class II crossovers are increased. These results suggest that REC may form multiple complexes that exhibit differential REC-dependent ATP-binding and -hydrolyzing requirements. These results provide genetic insight into the mechanisms through which mei-MCM proteins promote Class I crossovers and inhibit Class II crossovers.

KEYWORDS Drosophila; meiotic recombination; meiosis; crossover; mei-MCM

To reestablish the diploid genome upon sexual fertilization, the genome of progenitor germ cells must be successfully reduced by one-half through meiosis. Accurate reduction of the genome at the end of meiosis I requires crossover formation between homologous chromosomes during meiotic recombination. Meiotic recombination is initiated by the formation of multiple double-strand breaks (DSBs); the majority of meiotic DSBs are repaired as noncrossovers, while a selected subset is repaired as crossovers between homologs [reviewed in Lake and Hawley (2012)].

Two distinct types of meiotic crossovers have been described: Class I and Class II. First defined in budding yeast (de los Santos et al. 2003), Class I and Class II crossovers exist in most sexually reproducing organisms, but the relative proportions of each crossover type vary among organisms (Hollingsworth and Brill 2004). In Drosophila, most—if not all—crossovers are generated through the Class I pathway (Hatkevich et al. 2017), as shown through their dependence on the putative catalytic unit of the Class I meiotic resolvase MEI-9 (Sekelsky et al. 1995; Yildiz et al. 2002) and their display of crossover interference (Hatkevich et al. 2017). Most crossovers in Drosophila are also dependent upon a group of (mini-chromosome maintenance) MCM or MCM-like proteins, called the mei-MCM complex (Baker and Carpenter 1972; Grell 1978; Liu et al. 2000; Kohl et al. 2012).

The mei-MCM complex consists of REC (the Drosophila ortholog of MCM8), MEI-217, and MEI-218. REC appears
to be a bona fide MCM protein, based on conservation of both the N-terminal MCM domain and the C-terminal AAA+ ATPase domain, which includes Walker A and B boxes that bind and hydrolyze ATP (Figure 1A). In contrast, MEI-217 and MEI-218 are highly divergent MCM-like proteins, and together resemble one full MCM protein. MEI-217 is structurally similar to the MCM N-terminal domain, though this similarity is not detected in basic local alignment search tool or conserved domain searches (Kohl et al. 2012). The C-terminus of MEI-218 has a domain related to the AAA+ ATPase domain, but key residues are not conserved, including the Walker A and B motifs, which are critical for binding and hydrolyzing ATP, respectively (Iyer et al. 2004) (Figure 1B). Because key residues in the Walker A and B motifs are not conserved, MEI-218 may not exhibit ATPase activity or it may exhibit partial function. In addition, MEI-218 has a long N-terminal extension that is poorly conserved and is predicted to be disordered. The function of this region is unknown, but gene swap studies suggest that it may contribute to differences in the recombination landscape among Drosophila species (Brand et al. 2018). For further analysis and details regarding the evolution of the mei-MCM complex, see Supplemental Material, Figures S1–S3.

While most crossovers are generated through the Class I pathway in wild-type Drosophila and are mei-MCM-dependent, mutants that lack the Bloom syndrome helicase (Blm) generate only Class II crossovers, based on their independence of MEI-9 and lack of the patterning (e.g., interference) that is associated with Class I crossovers (Hatkevich et al. 2017). Blm is an ATP-dependent 3'–5' helicase that exhibits vital anticrossover functions in both meiotic and somatic DSB repair [reviewed in Hatkevich and Sekelsky (2017)]. Interestingly, mutations in mei-MCM and Blm genes genetically interact. In Blm mutants, crossovers are reduced by 30% but in a Blm rec double mutant, crossovers are significantly increased compared to wild-type (Kohl et al. 2012). This suggests that the mei-MCMs may function to inhibit crossovers within the Class II pathway, in addition to their role in promoting crossovers in the Class I pathway.

While the mei-MCMs function as a complex, little is known about how individual mei-MCMs contribute to Class I and II crossover regulation. Here, we investigate specific features of MEI-218 and REC to better understand how these proteins contribute to meiotic recombination. We find that the N-terminus of MEI-218 is dispensable for crossover formation and general crossover distribution. By mutating key residues in REC's Walker A and B motifs (recKA and recDA, respectively), we find that recKA mutants exhibit no Class I crossover defect, while Class II crossovers are significantly increased. Surprisingly, recDA mutants exhibit a severe decrease in Class I crossovers and a significant increase in Class II crossovers. Our results suggest that the mei-MCMs function in multiple roles and may complex in a variety of configurations to properly regulate crossover formation.

Materials and Methods

Drosophila stocks

Flies were maintained on standard medium at 25°C. Some mutant alleles have been previously described, including mei-9a (Baker and Carpenter 1972; Yildiz et al. 2004),
mei-218\textsuperscript{1} and mei-218\textsuperscript{6} (Baker and Carpenter 1972; McKim et al. 1996), Blm\textsuperscript{N1} and Blm\textsuperscript{D2} (McVey et al. 2007), and rec\textsuperscript{1} and rec\textsuperscript{2} (Grell 1978; Matsubayashi and Yamamoto 2003; Blanton et al. 2005). The maternal-effect lethality in Blm\textsuperscript{N1}/Blm\textsuperscript{D2} mutants was overcome by the upstream activation sequence (UAS)::GAL4 rescue system, as previously described (Kohl et al. 2012).

**Generating mei-218 transgenic alleles**

The transgenes for mei-218\textsuperscript{ΔN} and mei-218\textsuperscript{FL} were constructed by cloning cDNA for mei-218 into P(attBUASpW) (Addgene). Full-length mei-218 included codons 1–1186; the mei-218\textsuperscript{ΔN} transgene included codons 527–1186. Transgens were made by integrating into a pC31 landing site in 2A on the X chromosome.

**Generating rec\textsuperscript{DA} and rec\textsuperscript{DA} mutants**

Annealed oligonucleotides were inserted into BbsI-digested pU6-BbsI-chiRNA plasmid (Addgene) (rec\textsuperscript{SC}: 5′-CTTCGC CGAGAAGGGATAGTAAAC-3′ and rec\textsuperscript{DA}: 5′-CTTGGTTCG AGTGCTACACTCAG-3′). The resulting plasmids were co-injected with repair template plasmid, consisting of synthesized gBlocks (Integrated DNA Technologies) cloned into pBlueScript plasmid (sequences available on request). Injected larvae were raised to adulthood and their male progeny were crossed to TM3/TM6B females (Bloomington Drosophila Stock Center) to generate stocks, after which DNA was extracted for screening through PCR and restriction digest.

**Nondisjunction assay**

X-chromosome nondisjunction (NDJ) was assayed by mating virgin females to y \textit{cv} \textit{vf}/T(1;Y)B\textsuperscript{5} males. Each cross was set up as a single experiment with 20–50 separate vials. The progeny of each vial were counted separately. Viable NDJ progeny are XXY females with Bar eyes, and XO males with Bar\textsuperscript{+} eyes and the phenotypes from y \textit{cv} \textit{vf} chromosome. Total (adjusted) represents the total with inviable exceptional progeny accounted for (XXX and YO). NDJ rates and statistical comparisons were done as in Zeng et al. (2010).

**Crossover distribution assay**

Crossover distribution on chromosome 2L was scored by crossing virgin net \textit{dpp}\textsuperscript{d-ho} dp b pr cn/+ female flies with the mutant background of interest to net \textit{dpp}\textsuperscript{d-ho} dp b pr cn homozygous males. Each cross was set up as a single experiment with ≥ 25 separate vials scored. The first set of vials was flipped after 3 days of mating into vials of a new batch, although these were counted as one experiment. Batch effects for recombination assays have not been observed in repeated studies for multiple genotypes used in this study (Figure S4). These include wild-type (unpublished data, M. Hartmann), Blm (unpublished data, M. Hartmann), rec (Blanton et al. 2005; Kohl et al. 2012), mei-9 (Sekelsky et al. 1995), and mei-9; rec (Blanton et al. 2005). All progeny were scored for parental and recombinant phenotypes. Crossover numbers in flies are shown as cM where cM = (number of crossovers/total number of flies) * 100. $\chi^2$ tests with Bonferroni correction were performed for each interval. For total cM, Fisher’s exact test was used to compare total crossovers to the total number of flies. Crossover distribution is represented as cM/Mb where Mb is length of the interval without transposable elements (TEs), because crossovers rarely occur within TEs (Miller et al. 2016).

**Protein structure and alignment**

Structural domains of proteins were determined by using PHDRE 2. All of the MCM regions identified correspond to the protein data bank identifier (ID) #c2vl6C and the AAA ATPase domains identified correspond to protein data bank ID #d1g8pa. Alignment of the Walker A and Walker B motifs (Kohl et al. 2012) was done using MEGA 5 with the ClustalW program. Idetical and conserved residues are shaded based on groups of amino acids with similar chemical properties.

**Data availability**

All data necessary for confirming the conclusions in this paper are included in this article, and in supplemental figures and tables. Drosophila stocks and plasmids described in this study are available upon request. Figure S1 illustrates the distribution of MSH4, MSH5, MCM8, MCM9, MEI-217, and MEI-218 in Diptera. Figure S2 illustrates the structure of MEI-217 and MEI-218 in Diptera. Figure S3 shows sequence alignments of MEI-218. Figure S4 compares crossover frequencies in different batches of the same genotype. Figure S5 details the cross scheme of the mei-218 transgene experiments. Table S1 includes analysis of genetic interval differences between wild-type and mei-218\textsuperscript{FL}. Table S1 includes analysis of genetic interval differences between mei-218\textsuperscript{FL} and mei-218\textsuperscript{ΔN}. Table S2 includes the complete data set for calculating NDJ of wild-type, rec\textsuperscript{DA}-/rec\textsuperscript{DA}, and rec\textsuperscript{DA}/+ flies. Table S3 includes all data sets for meiotic crossovers for all genotypes discussed. Supplemental material available at Figshare: https://doi.org/10.25386/genetics.8009426.

**Results and Discussion**

The \textit{N}-terminus of MEI-218 is dispensable for crossover formation

MCMDC2 is a distantly related member of the MCM family of proteins in mammals that is unique in that the ATPase domain is predicted to be incapable of binding or hydrolyzing ATP. Orthologs in Dipteran insects are further distinguished by possessing an N-terminal extension of variable length in different species. \textit{D. melanogaster} MEI-218 can be divided into three distinct regions (Figure 1A): an N-terminal tail (residues 1–500), a central acidic region (residues 500–800), and a
C-terminal ATPase-related region (residues 850–1116) (Kohl et al. 2012; Brand et al. 2018). The N-terminal and middle regions are predicted to be disordered (Kohl et al. 2012), and are poorly conserved (Figure S3). Results obtained through gene-swap experiments suggest that the N-terminal tail and central region regulate crossover number and distribution within Drosophila species (Brand et al. 2018).

To genetically examine the function of the N-terminus of MEI-218, we compared the functions of a transgene that expresses a truncated form of MEI-218 that lacks the N-terminal 526 amino acids (mei-218N) to a matched full-length transgene (mei-218FL) (Figure 2A). Due to the relatively high conservation among Drosophila species, the middle region of MEI-218 was retained for this experiment (Figure S3). Using the UAS/GAL4 system (Duffy 2002), we expressed both constructs in mei-218 null mutants using the germline-specific nanos promoter and measured crossovers along five adjacent intervals, which span most of 2L and part of 2R (Figure S4; for simplicity, we refer to this chromosomal region as 2L.)

In wild-type females, the genetic length of 2L is 45.8 cM (Hatkevich et al. 2017) (Figure 2B), whereas mei-218 mutants exhibit a severe decrease in crossovers, with a genetic length of 2.92 cM (Kohl et al. 2012). Expression of mei-218FL in mei-218 mutants (mei-218FL) fully rescues the crossover defect, exhibiting a genetic length of 54.1 cM. Unexpectedly, expression of mei-218 DeltaN in mei-218 mutants (mei-218 DeltaN) restored crossing over to the same level as in mei-218; mei-218FL flies (55.9 cM; not significant, \(P = 0.61\)).

Brand et al. (2018) previously expressed D. mauritiana MEI-217 and MEI-218 in D. melanogaster, and found that crossovers were increased in proximal and distal regions, resulting in an overall change in crossover distribution. We examined crossover distribution in mei-218; mei-218FL and mei-218; mei-218 DeltaN flies (Figure 2C). Overall, distributions were similar, with both genotypes exhibiting strong inhibition of crossovers near the centromere (referred to as the centromere effect; Beadle 1932) and the majority of the crossovers being placed in the medial–distal regions (Figure 2C).

We conclude that the N-terminal tail of MEI-218 is dispensable for both crossover formation and overall distribution on chromosome 2L. This conclusion is supported by the observation that, of 16 sequenced mutations in D. melanogaster mei-218, 14 are nonsense or frameshift, and the only two missense mutations alter residues in the C-terminus (amino acids 845 and 1107) (Collins et al. 2012).

The reasons why the MCM domains have been separated into MEI-217 and MEI-218 polypeptides, and why MEI-218 has an N-terminal extension, are unknown, but this structure has been maintained for >250 MY of Dipteran evolution (Figure S2). Interestingly, the expression of MEI-218 is fairly high in testes (Thurmond et al. 2018), even though males do not experience meiotic recombination. The predominant or exclusive transcript in males does not encode MEI-217 (Thurmond et al. 2018), the seemingly obligate partner for MEI-218 in female meiotic recombination. Males that lack mei-218 are viable, fertile, and do not exhibit elevated NDJ.
The Walker A mutation (recCA) results in the substitution of a conserved lysine residue with alanine; in other AAA+ ATPases, including replicative MCMs, this mutation prevents binding of ATP (Bell and Botchan 2013). The Walker B mutation (recDA) results in the substitution of a conserved aspartic acid with alanine; in MCMs and other AAA+ ATPases, this mutation destroys the ability to coordinate Mg++ for ATP hydrolysis (Bochman et al. 2008).

We assayed crossover frequency along 2L in recKA and recDA mutants (Figure 3B). Surprisingly, recKA ATP-binding mutants exhibit a genetic length of 44.9 cM, which is not significantly different from that of wild-type flies (P = 0.4016), suggesting that ATP binding by REC is not required for crossover formation. Conversely, there is a severe reduction in crossovers in recDA mutants, with a genetic length of 1.6 cM (P < 0.0001), suggesting that REC’s ability to hydrolyze ATP is required for crossover formation.

Because the genetic length of recDA is significantly lower than that of rec null mutants (Figure 3B, P < 0.0001), we hypothesized that recDA is an antimorphic mutation. To test this, we examined crossover levels and X chromosome NDJ in recDA/rec+ (Figure 3, B and C, respectively). The genetic length of 2L in recDA/rec+ is slightly lower than in wild-type flies, but is not significantly different (43.9 and 45.8 cM, respectively; P = 0.35). For X-NDJ, both wild-type flies and rec+/rec+ mutants exhibit rates < 0.5%, while recDA/rec+ mutants exhibit a significant increase to 1.4% NDJ (P < 0.0001). These data support the conclusion that recDA is weakly antimorphic and suggest that recDA results in an inactive mei-MCM complex that is antagonistic to the wild-type complex. In light of these interpretations, we propose that the mei-MCM complex binds to recombination sites independently of REC binding to ATP, and that REC-dependent ATP hydrolysis is required for the removal of the mei-MCM complex from these sites.

The phenotypes of recKA and recDA mutants suggest that REC’s ability to hydrolyze ATP is required for crossover formation, whereas its ATP-binding capability is dispensable. The disparate requirements for REC’s ATP binding and hydrolysis are similar to those of other ATPase-dependent complexes. RAD51 paralogs, which form multiprotein complexes and contain Walker A and B motifs, are proposed to exhibit ATPase activity in trans between adjacent subunits, each of which contributes a Walker A or Walker B motif to the active site (Wu et al. 2004, 2005; Wiese et al. 2006). Because neither MEI-217 nor MEI-218 possess an ATPase domain that harbors conserved key enzymatic residues (Figure 1B) (Kohl et al. 2012), we propose that the ATPase activity of the mei-MCM complex requires REC for ATP hydrolysis and an unknown mei-MCM protein for ATP binding. Alternatively, because REC is highly diverged, its Walker A and B motifs may function noncanonically. Biochemical studies are needed to test these hypotheses, but these may require the identification of the putative missing subunit.

REC ATPase motifs are required for crossover formation

Of the three known mei-MCM subunits, only REC harbors well-conserved Walker A and B motifs, suggesting that REC has ATP-binding and -hydrolysis activity (Kohl et al. 2012). It is unknown whether the mei-MCM complex utilizes REC’s putative ATPase activity for its function in vivo. To test this, we used clustered regularly interspaced short palindromic repeats/Cas9 to introduce mutations into rec that were predicted to disrupt the functions of the Walker A and B motifs (Figure 3A). The Walker A mutation (recCA) results in the substitution of a conserved lysine residue with alanine; in other AAA+ ATPases, including replicative MCMs, this mutation prevents binding of ATP (Bell and Botchan 2013). The Walker B mutation (recDA) results in the substitution of a conserved aspartic acid with alanine; in MCMs and other AAA+ ATPases, this mutation destroys the ability to coordinate Mg++ for ATP hydrolysis (Bochman et al. 2008).

For these hypotheses, but these may require the identification of the putative missing subunit.
REC-dependent ATP hydrolysis is required for MEI-9-dependent crossovers

To gain insight into the crossover pathways that are used in recKS and recAD mutants, we examined whether these crossovers require the Class I endonuclease/resolvase. In Drosophila, the catalytic subunit of the putative Class I mei-9 endonuclease is MEI-9 (Sekelsky et al. 1995; Yildiz et al. 2002; Hatkevich et al. 2017). The 2L genetic length within a mei-9 mutant is 2.75 cM (Figure 4), demonstrating that ≥90% of crossovers are dependent upon MEI-9. However, the genetic length in mei-9; rec mutants is not significantly different from that of rec null single mutants (4.11 vs. 4.66 cM, P = 0.64), suggesting that, in the absence of REC, the resulting crossovers are likely independent of MEI-9. Similarly, it has been shown previously that mei-218 mei-9 double mutants do not have reduced crossovers compared to mei-218 single mutants (Sekelsky et al. 1995), indicating that crossovers generated in the absence of the mei-MCM complex are MEI-9-independent.

Because recKS mutants exhibit the same distribution and number of crossovers as wild-type flies (Figure 3B), we hypothesized that recKS crossovers are dependent on MEI-9. To test this, we examined genetic length across 2L in mei-9; recKS double mutants (Figure 4). Mutants for mei-9; recKS exhibited a genetic length of 2.72 cM, which was significantly decreased compared to the recKS single mutant (P < 0.0001), but not significantly different from mei-9 single mutants (P = 0.94), showing that crossovers in recKS are indeed dependent upon MEI-9 nuclease. In contrast, we predicted that crossovers in recAD would be independent of MEI-9, similar to crossovers generated in rec null mutants. We observed that mei-9; recAD double mutants exhibit a genetic length of 1.1 cM, which is significantly lower than that of mei-9 single mutants (P < 0.001). Importantly, crossing over in the mei-9; recAD double mutant was not significantly different from in recAD single mutants (P = 0.23), demonstrating that crossovers in recAD are independent of MEI-9 (Figure 4).

From these data, we conclude that the crossovers in recKS mutants arise through the normal, MEI-9-dependent pathway, whereas mitotic nucleases generate the residual crossovers in recAD mutants. These data show that REC KS functions normally in the Class I pathway, but that this pathway is non-functional in rec null and recAD mutants. We suggest that the REC's ability to hydrolyze, but not bind, ATP is required for the formation of Class I crossovers.

**REC ATPase motifs are required to prevent Class II crossovers**

In wild-type Drosophila, most or all crossovers are generated through the Class I pathway (Hatkevich et al. 2017), and these crossovers are dependent upon the mei-MCM complex (Kohl et al. 2012). However, in Blm mutants, crossovers are generated exclusively through the Class II pathway (Hatkevich et al. 2017). In Drosophila Blm mutants, meiotic crossovers are decreased by 30%, suggesting that the Class II pathway is less efficient at generating crossovers than the Class I pathway, even though what may be the primary anticrossover protein, Blm helicase, is absent. It has previously been shown that loss of Blm suppresses the high NDJ of mei-218 and rec mutants (Kohl et al. 2012). However, in Blm rec double mutants, crossovers are increased significantly compared to Blm single mutants (Kohl et al. 2012), suggesting that REC and/or the mei-MCM complex has an anticrossover role in Blm mutants, and therefore in the Class II crossover pathway.

To further understand the role of REC in the Class II pathway, we investigated whether REC's predicted ATP-binding or -hydrolysis function is required for its Class II anticrossover function. To do this, we measured the crossovers across 2L in recKS and recAD in the background of Blm mutants. If REC ATP binding or hydrolysis is required for an anticrossover role in Class II, then the genetic length of Blm recKS or Blm recAD double mutants will be similar to that of Blm rec double mutants. Conversely, if REC ATP binding or hydrolysis is not required, then double mutants will exhibit genetic lengths similar to that of Blm single mutants.

Interestingly, Blm recKS mutants exhibit a genetic length of 43.3 cM, which is not significantly different from that of Blm rec mutants (P = 0.10) but is significantly higher than that of Blm single mutants (P < 0.0001; Figure 5). Similarly, Blm recAD double mutants have a recombination rate of 53.4 cM, which is not significantly different from Blm rec double mutants (P = 0.52), but is significantly higher than that of Blm single mutants (P < 0.0001). These results suggest that
CEC's predicted abilities to bind and hydrolyze ATP are both required for the inhibition of crossovers at REC-associated Class II recombination sites. Therefore, it appears that REC forms different complexes within the Class II and Class I pathways. It is unknown whether this Class II REC-associated complex requires the other mei-MCM proteins, and additional genetic studies will be valuable to discern this.

In summary, the mei-MCMs are a family of diverged proteins that help to establish the recombination landscape in D. melanogaster by promoting Class I crossovers and inhibiting Class II crossovers. Results obtained in this study have further elucidated meiotic recombination roles for two mei-MCM proteins, MEI-218 and REC. While the N-terminus of MEI-218 is dispensable for crossover formation (Figure 2), REC's predicted ability to bind and hydrolyze ATP exhibits differential requirements for the regulation of Class I and Class II crossover formation. From our genetic analyses, we suggest that the Walker B motif of REC, but not the Walker A motif, is required for promoting the formation of Class I, MEI-9-dependent crossovers (Figure 3 and Figure 4). The weakly antimorphic phenotype of recDA demonstrates that an impaired REC Walker B mutant renders a poisonous complex; a complex that we propose cannot be released from recombination sites. Both Walker A and Walker B motifs block crossovers in the Class II pathway, suggesting that REC forms different complexes to execute its pro- and anticrossover functions. Biochemical and cytological studies are needed to support or refute these hypotheses.

Acknowledgments

We thank Juan Carvajal Garcia, Carolyn Turcotte, and anonymous reviewers for thoughtful comments. This work was supported in part by a grant from the National Institute of General Medical Sciences to J.S. under award 1R35 GM-118127. K.P.K. was supported in part by National Institutes of Health (NIH) grant P20 GM-103499. T.H. was supported in part by NIH grants ST32 GM-007092 and 1F31 AG-055157.

Literature Cited


Iyer, L. M., D. D. Leipe, E. V. Koonin, and L. Aravind, 2004 Evolutionary history and higher order classification of General Medical Sciences to J.S. under award 1R35 GM-118127. K.P.K. was supported in part by National Institutes of Health (NIH) grant P20 GM-103499. T.H. was supported in part by NIH grants ST32 GM-007092 and 1F31 AG-055157.


Communicating editor: B. Calvi