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Title:

Plasticity of meiotic recombination rates in response to temperature in Arabidopsis

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ABSTRACT

Meiotic recombination shuffles genetic information from sexual species into gametes to create novel combinations in offspring. Thus, recombination is an important factor in inheritance, adaptation and responses to selection. However, recombination is not a static parameter; meiotic recombination rate is sensitive to variation in the environment, especially temperature. That recombination rates change in response to both increases and decreases in temperature was reported in *Drosophila* a century ago, and since then in several other species. But it is still unclear what the underlying mechanism is, and whether low and high temperature effects are mechanistically equivalent. Here we show that, as in *Drosophila*, both high and low temperatures increase meiotic crossovers in *Arabidopsis thaliana*. We show that, from a nadir at 18C, both lower and higher temperatures increase recombination through additional class I – interfering – crossovers. The increase in crossovers at high and low temperatures however appears to be mechanistically at least somewhat distinct, as they differ in their association with the DNA repair protein MLH1. We also find that, in contrast to what has been reported in barley, synaptonemal complex length is negatively correlated with temperature; thus, an increase in chromosome axis length may account for increased crossovers at low temperature in *A. thaliana*, but cannot explain the increased crossovers observed at high temperature. The plasticity of recombination has important implications for evolution and breeding, and also for interpreting observations of recombination rate variation among natural populations.

INTRODUCTION

The vast majority of eukaryotes rely on meiosis to produce gametes. One important process within meiosis is the crossing over of homologous chromosomes, which in most eukaryotes is essential for stable chromosome segregation (Zickler and Kleckner 1999). Recombination also shuffles the genetic complements of the two parents of an individual and is thus important in generating novel genetic combinations in gametes and ultimately offspring. The extent and pattern of genetic reshuffling via homologous recombination has important implications for evolution and adaptation, as well as population genetics and breeding (e.g.: Barton 1995; Charlesworth and Barton 1996; Otto 2009; Campos *et al*. 2015). Recombination is not a static parameter between, or even within taxa. Meiotic recombination rate is known to be sensitive to a variety of environmental factors, particularly temperature (Plough 1917; Elliott 1955; De Storme and Geelen 2014; Bomblies

et al. 2015; Modliszewski and Copenhaver 2015; Phillips *et al.* 2015). Extreme temperatures can cause meiotic recombination to fail outright due to structural disruptions of e.g. the spindle, the chromosome axes, or the synaptonemal complex (Bilgir *et al.* 2013; Bomblies *et al*. 2015; Morgan *et al*. 2017). We refer to the temperatures at which such defects become cytologically evident as "failure thresholds." Less extreme temperature fluctuations that do not cause outright failures, can nevertheless affect the genome-wide recombination rate in diverse taxa (Plough 1917; Elliott 1955; De Storme and Geelen 2014; Bomblies *et al.* 2015; Modliszewski and Copenhaver 2015; Phillips *et al.* 2015). Understanding the nature and strength of these effects has important implications for better understanding and predicting inheritance and evolution, especially in a time of climate change, and also for managing breeding programs. Understanding the effect of temperature on recombination also provides opportunities to manipulate recombination in a targeted and reversible way (e.g. Phillips *et al*. 2015).

That both temperature increases and decreases can affect meiotic recombination rates has been recognized for 100 years (Plough 1917). The first investigation into the effect of temperature on meiotic recombination rate suggested a U-shaped response in *Drosophila* (Plough 1917; Smith 1936), meaning that mid-range temperatures (which at least in the case of *Drosophila* correspond to common rearing temperatures) have the lowest recombination rate, and both increases and decreases in rearing temperature are associated with elevated recombination. Since the original discoveries, a variety of trends have been reported, including no effect, increases with increasing temperature, and decreases with increasing temperature (Elliott 1955; Stern 1926; Jensen 1981; Francis *et a*l. 2007; Phillips *et al*. 2015), reviewed in (Bomblies *et al*. 2015). We and others have previously suggested that while there may well be biological differences among taxa, distinct reported trends can also result from differences in experimental design (Wilson 1959; Bomblies *et al*. 2015), e.g. from only sampling a sub-section of the relevant temperature range, or by including temperatures beyond the meiotic failure limits where recombination declines sharply. Many species appear to have U-shaped curves (Wilson 1959; Bomblies *et al*. 2015), but it has remained unknown whether the low and high temperature effects are mechanistically distinct.

An important aspect of understanding the effects of temperature on recombination is to know what type of crossovers are responsible, as this has important implications for the patterning that may result. Crossovers come in two major classes. Class I crossovers represent the

majority of crossovers in most species (Lynn *et al.* 2007). These crossovers rely on a class of proteins called ZMM proteins (Börner *et al*. 2004; Lynn *et al*. 2007; Mercier *et al*. 2014), and are subject to crossover interference. Crossover interference deters crossovers from forming in close proximity, and thus causes recombination events to be more widely spaced than expected if they occurred randomly (Berchowitz and Copenhaver 2010). A second class are called the class II crossovers. These occur through a variety of pathways but share the important property that they are not subject to crossover interference and can be spaced randomly (Lynn *et al*. 2007; Higgins *et al*. 2012). In most species, it is not known whether temperature affects one or the other type of crossover preferentially. In barley, where temperature causes a change in the positioning of crossovers to more proximal locations (Higgins *et al*. 2012; Phillips *et al*. 2015), immunological staining suggests that class I crossovers are affected. In yeast, temperature also has effects on ZMM-dependent (class I) crossover designation (Börner *et al*. 2004). Whether temperature effects operate primarily through altering class I or class II crossovers has implications for crossover positioning and spacing.

In *Arabidopsis thaliana*, a positive relationship between temperatures from 19-28°C and male meiotic recombination was previously described (Francis *et al*. 2007). However, this temperature range represents only the upper portion of the viable range; *A. thaliana* can flower and produce seeds also at much lower temperatures. Here we study the effect of temperature on male meiotic recombination in *A. thaliana* across a wider temperature range than it has been previously examined. We test whether lower and higher temperatures affect class I and/or class II crossover frequency, and also explore whether changes in the length of the chromosome axes and synaptonemal complex might suffice to explain the effects of temperature on recombination rate in *A. thaliana*.

MATERIALS AND METHODS

Plant growth

Col-0 plants were grown under long day growth conditions (16h day 19-21˚C / 8h night 15˚C) until the primary inflorescence began to emerge from the rosette. Plants were then transferred to a range of small, constant temperature, long-day growth chambers at the experimental temperatures (5˚C-30˚C). For cytology, plants were grown to the same developmental age and height after flowering and then transferred to growth chambers at 8˚C, 18˚C or 28˚C for 1 week before material was collected to make slides. As the duration

of meiosis has previously been demonstrated to last 33 hours at 18.5˚C (Armstrong *et al.*, 2003), 1 week was chosen to be long enough to complete meiosis at each temperature without causing a significant impact on the developmental trajectory of the plants.
For flow cytometry, after transferring to constant temperature chambers, plants were grown until at least 5-6 inflorescences had emerged and flowered, thus providing sufficient pollen for flow cytometric analyses: 28˚C, 23˚C – 1 week, 18˚C – 2 weeks, 13˚C – 3 weeks, 8˚C – 5 weeks.

Seed set

Seed set was quantified as seeds per silique. For each temperature seeds were counted for 3-10 siliques for each of 3-4 biological replicates (plants). All siliques originated from the primary inflorescence.

Pollen viability

Method 1: For each temperature pollen viability was determined by Alexander staining for 2-4 plants. For each plant ~200 pollen grains were counted. All flowers originated from the primary inflorescence. Pollen viabilities reported are the means of the biological replicates for each temperature. *Method 2:* When analyzing flow cytometry data, single pollen grains were subdivided into two populations (viable and non-viable) based on SSC/FSC (Figure S9A-C). To confirm their composition, the two populations were sorted using a MoFlo ASTRIOS (Beckman-Coulter), stained using Alexander's stain (10%) and viewed under a light microscope (Figure S9D-G). While the presumed non-viable population consisted solely of non-viable pollen grains, the presumed viable population contained both viable and non-viable pollen grains (Figure S9D-H). This method therefore provides an output proportional to pollen viability, but systematically over-estimates pollen viability.

Pollen fluorescence detection

For each Flourescent Tagged Line (FTL) and each temperature, flowers were collected for a minimum of three pools of three plants, each pool representing one biological replicate. Pollen was isolated and analysed as described in Yelina et al. (2013). An LSR Fortessa (BD) was used for analysis, with 440nm, 488nm and 561nm lasers and 470/20, 530/30 and 582/15 bandpass filters used for detection of eCFP, eYFP and dsRED respectively. A standard run consisted of 50,000-100,000 pollen grains for each biological replicate.

Analysis of flow cytometry data

Single viable pollen grains were first subset based on size and granularity parameters, forward scatter (FSC) and side scatter (SSC) respectively (Figure S9A-C). Due to loss of fluorescent signal (but not loss of the respective transgene) in a significant proportion of pollen grains, a gating strategy was first used to eliminate potential false negatives prior to recombination analysis. Using this strategy, pollen grains were first subset based on detection of the "control" fluorophore and then scored for recombination based on the presence/absence of the "diagnostic" fluorophore (Figure S10A-D). The fluorophore used as the control had the less stable signal and the diagnostic fluorophore had the more stable signal. This ensured that for pollen grains used in analysis, loss of signal was due to recombination (i.e. true absence of the transgene) rather than a false negative loss of signal (Figure S10E-F).

A similar approach using two diagnostic fluorophores was used to detect double crossovers (DCOs, Figure S11). Although reciprocal results (e.g. $eCFP^{+}/eYFP^{+/-}$ vs $eYFP^{+}/eCFP^{+/-}$) gave relatively consistent recombination frequencies (Figures S10-11), there were some discrepancies. To assess which fluorophore detection regime gave the most accurate results we exploited the fact that for intervals Ia and Ib: $SCO_{Ia} + SCO_{Ib} = SCO_{Iab} + 2*DCO_{Iab}$. For each regime we assessed the concordance between $(SCO_{Ia} + SCO_{Ib})$ and $(SCO_{Iab} + 2*DCO_{Iab})$ and used the regime that gave the most concordant results in all further analyses (e.g. Figure S12).

Beam film modelling and analysis

Best-fit parameters for the FTL intervals on chromosomes 3 and 5 were determined using MADpatterns (White *et al*. 2017) and custom perl scripts, using an approach based on that described in (Zhang *et al*. 2014). Parameter value ranges (Smax: 1 - 8.5; L: 0.7 - 1; T2 Prob: 0.0025 - 0.011; cL: 0.9 - 1.6 and cR: 0.9 - 1.6) were chosen based on parameter values described in Zhang et al (2014) and comparison of ad hoc simulations with analysis of a large Arabidopsis whole genome recombination dataset described in (Basu-Roy *et al*. 2013). Final best-fit parameters for the FTL intervals were identified by comparing simulated data with the experimental FTL data.

Crossovers were simulated using a range of parameter combinations (50,000 bivalents per parameter set): parameters Smax, L, T2 Prob, cL and cR were varied, while parameters B, Bsmax, A and M were set at appropriate default values (Zhang *et al.* 2014). The number of precursor sites (N) was calculated based on the total number of DSBs expected per meiosis in

Arabidopsis (~250) multiplied by the proportion of the genome length contributed by the chromosome being simulated. Appropriate values for the position and strength of recombination "black holes" (Bs, Be, Bd) – corresponding to recombination suppressed centromeres – were chosen based on the analysis of experimental data in (Basu-Roy *et al*. 2013). Simulated chromosomes were analysed for crossover distribution and coefficient of coincidence (CoC) in the regions of the simulated chromosomes corresponding to the respective FTL intervals using the procedure outlined in (White *et al*. 2017). For each parameter set, the simulated recombination frequencies and CoC values were compared to values derived from the experimental FTL data. Importantly the experimental data are gamete data, while the MADpatterns program simulates (and outputs) bivalent data (i.e. for a chromosome pair). Therefore, all simulated bivalent crossover frequencies were halved to convert to gamete crossover frequencies. Parameter sets were then ranked, first based on the difference between the simulated and experimentally determined CoC values [$Score_{CoC} = (CoC_{sim} - CoC_{FTL})^2$] and secondly based on the difference between the observed FTL recombination frequencies and the simulated (gamete) recombination frequencies of the two intervals [$Score_{RF} = abs\{log2(RFI1_{sim}/RFI1_{FTL})\} + abs\{log2(RFI2_{sim}/RFI2_{FTL})\}$]. The final parameter values chosen (Table 1) were those with the lowest rank-sum. At least three rounds of analysis, with progressively smaller step-sizes between values were used to arrive at the final parameter values.

Finally, we modelled the effects on CoC, of increased crossovers caused by changes in a single parameter of the MADpatterns program (either Smax, L or T2 prob). For each parameter, the value was adjusted until a ~13% increase in COs had been achieved (i.e. the average increase in COs observed between 18ºC and temperature extremes; Table 1), the changes in CoC predicted for each parameter change were then compared to those observed experimentally (Figure 2).

Cytological procedures

Immunolocalisation slides using fresh material and DAPI stained spreads using acid fixed material were prepared as described previously (Caryl *et al*. 2000; Armstrong *et al*. 2002). The following antibodies and dilutions were used: anti-AtMLH1 (rat, 1/200 dilution) (Higgins *et al*. 2005), anti-AtHEI10 (rat, 1/200 dilution, rabbit, 1/200 dilution) (Lambing *et al*. 2015), anti-AtZYP1 (rabbit, 1/500 dilution, guinea-pig, 1/500 dilution) (Higgins *et al.* 2005), FITC anti-guinea-pig (1/100, Abcam), alexa-fluor 488 anti-rat (1/500, ThermoFisher), alexa-fluor 594 anti-rabbit (1/500, ThermoFisher), alexa-fluor 555 anti-rat (1/800, Abcam)

and alexa-fluor 647 anti-rabbit (1/800, Abcam). Epifluorescence microscopy was carried out using a Nikon 90i Fluorescence Microscope (Tokyo, Japan) and image capture, analysis and processing were conducted using NIS-Elements software (Nikon, Tokyo, Japan). Structured illumination microscopy was carried out using a Zeiss Elyra PS1 and image reconstruction and channel-alignment were carried out using ZEN black software (Zeiss). SC length measurements were made by measuring total SC length in three dimensions using the simple neurite tracer plugin to imageJ with Z-stacked images of pachytene nuclei stained for ZYP1 (Longair *et al*. 2011). Measurements were only taken from cells in which 5 complete bivalents could be measured to ensure cells were fully synapsed and the 5 bivalent lengths were combined to give a total SC length for each cell. MLH1 and HEI10 foci were identified as bright, round foci that overlapped with the SC in the x, y and z planes and were observed in late pachytene/early diplotene cells which were identified as either being fully synapsed or mostly synapsed with some small regions of SC disassembly, respectively. Note, HEI10 and MLH1 foci numbers in *Arabidopsis* have previously been shown to remain constant from late pachytene through diplotene (Chelysheva *et al*. 2012). Mann-Whitney U-tests were used to compare MLH1 and HEI10 foci counts and total SC lengths as described previously (Ziolkowski *et al*. 2017). This was appropriate as bulked anthers from multiple plants exposed to the same temperature treatment were used when making each immunolocalisation slide and therefore each cell was treated as an independent observation.

Data availability

Data are available by request from the authors.

RESULTS

Crossover rates in Arabidopsis are lowest in the middle of the fertile temperature range

We measured recombination both in meiocytes and in gametophytes. In the latter, recombination rate estimates can be confounded because: (1) recombination declines sharply due to structural failures when temperatures exceed failure thresholds, thus a biased view can arise if temperatures past the failure points are included, and/or (2) estimates can be biased due to failures in later stages of gametophyte development. Both sources of bias can be averted at least to some extent by avoiding temperatures that cause a decline in fertility. Thus, we first estimated the informative temperature range for *A. thaliana* by measuring seed set and pollen viability at temperatures from 5˚C to 30˚C. At the high end,

seed set dropped significantly from 28˚C to 30˚C (Figure S1). At at 8˚C seed set was no different from seed set at moderate temperatures (18˚C, p = 1; 23˚C, p = 1; t-test, Bonferroni corrected), however there was no seed set at 5˚C (Figure S1). The latter is consistent with previously observed post-meiotic defects following 4-5˚C cold-stress (De Storme *et al*. 2012). Therefore, for our purposes, we defined the "fertile range" of *A. thaliana* in our conditions as 8˚C to 28˚C and focused on this range to assay recombination. Within this temperature range there was no significant decrease in pollen viability at temperature extremes, although variance increased at higher temperature (Figure S2). We also ascertained that we had not exceeded failure thresholds using cytological observations. In plants exposed to 8˚C, 18˚C or 28˚C for 1 week synapsis, CO formation and chromosomal segregation proceeded without appreciable errors in male meiocytes (Figure S3) and at neither temperature extreme were obvious differences evident relative to 18˚C.

To initially score recombination rates at different temperatures in high throughput, we capitalized on a previously developed transgenic tool that uses fluorescent markers to score male meiotic crossovers in pollen grains (Francis *et al*. 2007). We scored male crossover frequency in Fluorescent Tagged Lines (FTLs) that flank two pairs of adjacent intervals on chromosome 3 (I3b and I3c) and chromosome 5 (I5a and I5b). While the FTL loci showed subtle differences in the responses at different temperatures (Figure 1 & S4-S5), the overall shapes of the I3bc and I5ab distributions were not significantly different after normalizing for the different sizes of the intervals (p = 0.873, Two-sample Kolmogorov-Smirnov test). Both pairs of intervals followed the same general trend with a minimum recombination rate at ~18˚C and higher frequencies at both higher and lower temperatures (Figure S4-S5). The combined genetic length of the four intervals shows a clear U-shaped trend of recombination rates across the temperature range (Figure 1C). Using a Mann-Whitney-Wilcoxon Rank Test (unpaired Wilcoxon test) on combined data from the four intervals, we found crossover rates were significantly lower (10-15 %) at 18˚C, the center

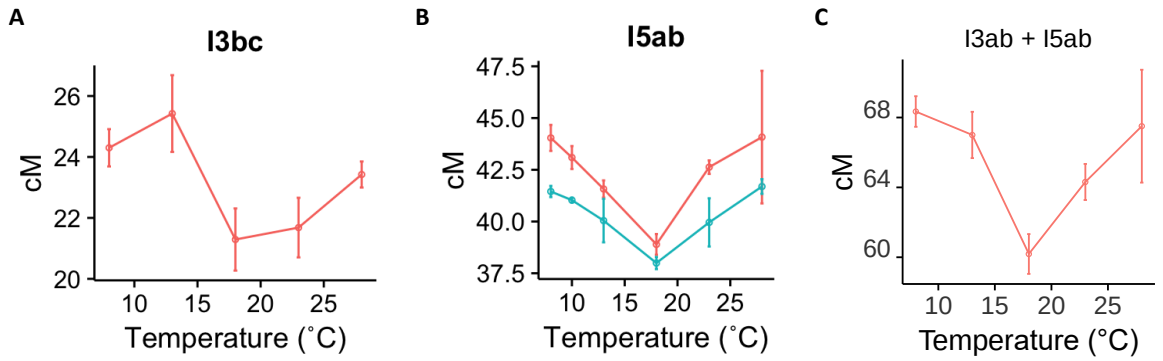

Figure 1. Meiotic recombination has a U-shaped response to temperature in Arabidopsis. Data from intervals I3bc and I5ab demonstrate a U-shaped response in recombination rate to temperature **(A & B)**. For interval I5ab **(B)**, the same trend is observed when plants have different numbers of secondary bolts and branches across the temperature range (red) or if all plants are harvested when they have 5-6 inflorescences (blue). The combined genetic length of intervals I3bc and I5ab is shown in **(C).** Error bars indicate 95% confidence intervals.

of the fertile temperature range, than at either 8˚C or 28˚C ($p = 7.76e^{-6}$ and $p = 2.22e^{-5}$ respectively). The upper half of the trend recapitulates previous findings in *A. thaliana* (assayed with markers on a different chromosome) of a positive trend from 19-28˚C (Francis *et al*. 2007). Since recombination rates can also be sensitive to developmental age (Francis *et al*. 2007) we tested whether this trend was merely a consequence of differences in overall development at the different temperatures (Figures 1B & S6). By assaying only plants at comparable developmental stages i.e. all plants with 5-6 inflorescences (Figure S6B), we showed that the increase in recombination rate at lower as well as higher temperatures is still evident. This indicates that *A. thaliana*, like *Drosophila* and several other species (Bomblies *et al*. 2015), has a U-shaped relationship between temperature and recombination rate.

Modeling predicts increased crossovers occur via the class I pathway

We next explored which crossover pathways might be affected. In *A. thaliana*, the majority (85%) of crossovers are class I crossovers; these rely absolutely on a group of proteins called the ZMM proteins and are subject to crossover interference, which prevents crossovers occurring in close proximity (Mercier *et al*. 2005; Chelysheva *et al*. 2007; Higgins *et al*. 2008; Chelysheva *et al*. 2012; 37–39). The remaining crossovers are collectively referred to

as class II crossovers; these occur via several pathways, and are not sensitive to crossover interference (Berchowitz et al. 2007; Higgins et al. 2008). When measured genetically (as here) the Coefficient of Coincidence (CoC) - the number of double crossovers observed, divided by the number expected in a given pair of intervals based on the single crossover rates – can provide insight into the relative contributions of the class I and class II crossover pathways (CoC should increase if additional crossovers are primarily class II non-interfering crossovers). For both pairs of intervals (I3b/I3c and I5a/I5b), we calculated CoC across the temperature range and observed no change, or a slight decrease in CoC at temperature extremes. This observation indicates that crossovers do not become noticeably more likely to occur near one another at higher or lower temperatures, suggesting that the increase in recombination rates may primarily involve class I (interfering) rather than class II crossovers (Figure 2A-B).

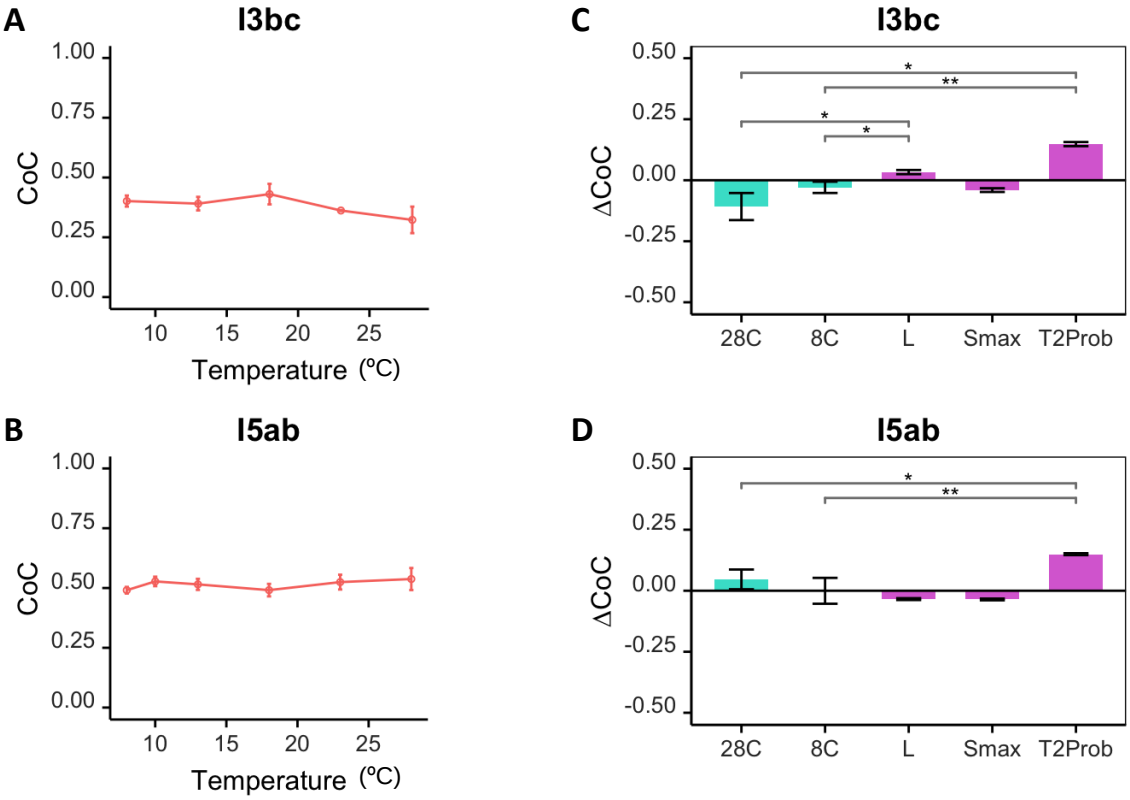

Figure 2. Observed and predicted CoC for intervals I3bc and I5ab. For I3bc (**A**) and I5ab (**B**), CoC values were mostly constant across the temperature range, although for I3bc CoC was slightly lower at 28˚C than at 18˚C ($p = 0.018$; pairwise t-test with Bonferroni correction). (**C** & **D**) The change in CoC observed between 18˚C and 28˚C or 8˚C is shown in teal; the change in CoC predicted by changes in a single beam film model parameter that

results in a 13% increase in COs (i.e. the average increase observed at temperature extremes) is shown in purple. Observed changes in CoC are consistent with changes predicted by altering beam film model parameters that affect class I COs – L, the proportion of the chromosome over which interference spreads and/or Smax, the (class I) crossover designation driving force. The observed changes in CoC are not consistent with changes predicted by altering the number of class II COs (T2Prob). Error bars indicate 95% confidence intervals.

We further tested this idea by simulating crossover patterning under the beam film model, a leading model of crossover designation and interference (White *et al*. 2017). The beam-film model proposes a mechanical basis of CO designation. Under this model, redistribution of mechanical stress along the chromosomes is the basis of CO interference. COs occur at precursor sites (i.e. meiotic DSBs) in regions of high stress, and locally relieve stress, preventing the formation additional COs nearby. Three important parameters of the beam film model are: "Smax" - the crossover designation driving force, "L" – the proportion of the chromosome over which interference propagates (i.e. proportion of the chromosome over which stress is relieved), and "T2prob" – the proportion of potential crossover sites that develop into non-interfering Class II crossovers. Changes in these parameters affect the crossover frequency and CoC predicted by the model. We determined the best-fit parameters for the intervals I5ab and I3bc in male meiosis (Table 1) using the experimental FTL data and a previously published large recombination dataset (Basu-Roy *et al.* 2013). We then adjusted single parameter values (Table 1) to model an increase in crossovers equivalent to that observed at higher and lower temperatures. We compared the observed CoC to the changes predicted by the beam film model under different parameter values. When extra crossovers were simulated to occur via the class I (interfering) pathway, the predicted effects on CoC were consistent with our observations (Figure 2C – Smax; Figure 2D – Smax, L), but when extra crossovers were simulated to occur via the class II (non-interfering) pathway, the predicted changes in CoC were not consistent with observed changes (Figure 2C-D). Consistent with the hints from the CoC trends, the modelling suggests increased crossovers observed as temperature changes in *A. thaliana* occur exclusively or primarily via the interference sensitive class I (ZMM) pathway.

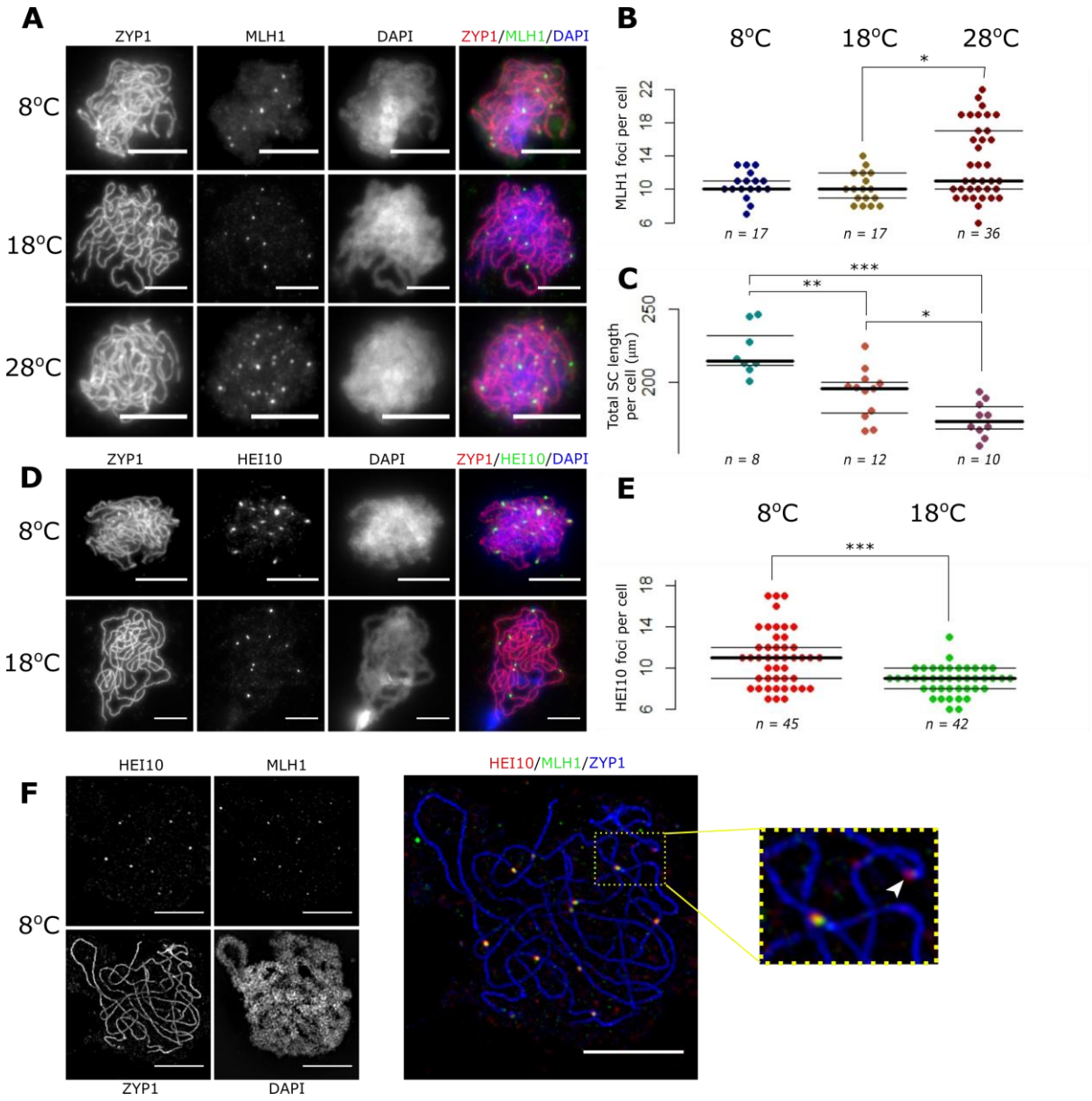

Figure 3. An increase in total class I CO frequency is observed at high and low temperature extremes and increasing temperature is associated with shorter SC length. MLH1 foci were counted in pachytene cells stained for ZYP1, MLH1 and DAPI (A) from plants grown for 1 week at 8, 18 and 28 °C. A plot showing MLH1 foci counts (B) demonstrates a significant increase in total class I CO number at 28 °C compared to 18 °C. Total SC lengths per cell in µm (C) also decrease significantly with increasing temperatures. HEI10 foci were also counted in pachytene cells stained for ZYP1, HEI10 and DAPI (D) from plants grown for 1 week at 8 or 18 °C. A plot showing HEI10 foci counts (E) demonstrates a significant increase in total class I CO number at 8 °C compared to 18 °C. A cell stained for HEI10, MLH1, ZYP1 and DAPI and imaged using structured-illumination microscopy (F) confirms that additional HEI10 foci are present that are not

associated with corresponding MLH1 foci (indicated by arrowhead) in plants grown for 5 weeks at 8 ^{o}C. Scale bars = 5 µm. *$p < 0.05$, **$p < 0.005$, ***$p < 0.0005$.

Increased crossovers occur via the class I pathway

To empirically test whether the class I / ZMM dependent crossovers are indeed responsible for the observed increases in recombination at high or low temperature, we quantified the number of MLH1 foci. MLH1 is a member of the MutL complex together with MLH3 and marks sites of class I crossovers (White *et al*. 2017). We counted MLH1 foci in pachytene nuclei from plants exposed to 8˚C, 18˚C or 28˚C for 1 week (Figure 3A). We found a significant increase in MLH1 foci when comparing 18˚C and 28˚C (Mann-Whitney U Test, $p = 0.01681$) indicating that high temperature does cause an increase in Class I crossovers as predicted by the modeling. However, we did not observe an increase in MLH1 foci at 8˚C (1 week or 6 weeks) compared to 18˚C (Mann-Whitney U Test, $p = 0.4299$ & $p = 0.503$ respectively; Figure 3B & S7).

While the low temperature results are at first pass puzzling in the context of modeling predictions, there is some evidence that MLH1 independent class I crossovers can occur in Arabidopsis: loss of any of several ZMM proteins (and hence all class I crossovers) result in an 85% reduction in crossovers (e.g., Stern 1926; Wilson 1959) while loss of MLH3, and therefore functional MutL complex (MLH1/MLH3), results in only a 60% reduction (Jackson *et al*. 2006). Thus, we reasoned that low temperature might increase recombination rate via such MLH1-independent class I crossovers. We therefore quantified foci of another class I crossover associated protein, HEI10 (Figure 3D) at both 8˚C and 18˚C. In contrast to MLH1, which is observed from pachytene and only marks sites of future crossovers (White *et al.* 2017), HEI10 foci are observed early in meiotic prophase I and initially mark many precursor sites not destined to become crossovers (Chelysheva *et al.* 2012). The number of HEI10 foci then reduces until only sites destined to become crossovers are marked by pachytene (Chelysheva *et al.* 2012). For this reason, we only counted HEI10 foci in late pachytene cells in which all five pairs of chromosomes were completely synapsed or in early diplotene cells in which the synaptonemal complex is just beginning to dissociate. We found a significant increase in HEI10 foci at 8˚C relative to 18˚C (Mann-Whitney U Test, $p = 0.0001316$). We also observed a significant increase in HEI10 foci compared to MLH1 foci at 8˚C (Mann-Whitney U Test, $p = 0.01543$) although no difference between HEI10 or MLH1 foci was observed at 18˚C (Mann-Whitney U Test, $p = 0.7198$). In agreement with a

higher number of HEI10 foci at 8˚C, most cells at 8˚C had 1-2 HEI10 foci that did not co-localize with MLH1 (Figure 3F). Taken together, these results suggest that in *A. thaliana* the increased crossover frequency at both high and low temperatures involves an increase in class I interfering crossovers, though the low and high temperature effects are mechanistically at least somewhat distinct.

The class II pathway does not contribute to increased crossovers

Though our modeling suggested that Class II crossovers are not likely to be involved in the temperature trends we observed in *A. thaliana*, in yeast, class II crossovers had been previously reported to increase in number with low temperatures in some mutant contexts (Mercier *et al*. 2014). Thus we also wished to test whether class II crossovers might contribute to the temperature effect on recombination in our study. Since there is no robust cytological marker for non-interfering crossovers in *A. thaliana*, we used recombination assays in mutant lines that lack class I crossovers. First, we repeated the pollen based recombination assay for FTL line I3bc in a *zip4, fancm* double mutant. In *A. thaliana*, *zip4* mutants lack class I crossovers, leading to semi-sterility (Chelysheva *et al.* 2007) while *fancm* mutants have increased class II crossovers (Crismani *et al*. 2012). This increase in crossovers restores pollen viability to the double *zip4, fancm* mutant under standard growing conditions (Crismani *et al*. 2012), enabling the pollen based FTL assay to be used. In the *fancm, zip4* background, crossover levels were unchanged at 28˚C compared to 18˚C (Figure S8A; p = 0.986, pairwise t-test with Bonferroni correction), confirming that increased recombination at high temperature occurs exclusively or primarily via the class I pathway. Crossover number increased at low temperature with borderline significance (10˚C vs 18˚C, p = 0.058, pairwise t-test with Bonferroni correction, Figure S8A). However, pollen viability was also drastically reduced in these double mutants at temperatures below 18˚C, suggesting that FANCM becomes more important at lower temperatures, at least in the absence of class I crossovers (Figures S8B & S9).

While the results for *zip4, fancm* double mutants at low temperature might suggest an increase in Class II crossovers at low temperatures in *A. thaliana*, similar to that observed at low temperature in yeast *zmm* mutants, we were concerned that (1) low pollen viability may have introduced a sampling bias in the double mutant at low temperature or (2) the unanticipated requirement for FANCM at lower temperatures in the absence of Class I crossovers may have affected our results in complex ways that are not necessarily relevant

in a wild type context. We therefore used a second cytological assay to investigate the effect of low temperature on class II crossovers, performing chiasma counts on metaphase I cells from *msh5* mutants after exposure to either 8˚C or 18˚C for 1 week. MSH5, a ZMM protein, is absolutely required for class I crossovers, and the only chiasmata that remain in an *msh5* mutant occur via the class II pathway (Higgins *et al*. 2008). Unlike FANCM, MSH5 does not affect the class II pathway. We found that in this mutant there was no significant difference in chiasma counts between 8˚C (n = 56 cells, mean chiasma number = 1.44) and 18˚C (n = 85 cells, mean chiasma number =1.46; χ^2 Test, p = 0.792; Figure S7). Unlike the pollen-based recombination assay we used for the *zip4, fancm* double mutants, the metaphase I bivalent counts occur before any potential sampling bias is introduced due to low pollen viability, and therefore likely better represents the effect of temperature on class II crossovers. These results suggest that the number of class II crossovers remains essentially unchanged across the tested temperature range in *A. thaliana*.

Synaptonemal complex length is negatively correlated with temperature

A previous study in barley demonstrated that a slightly increased crossover frequency at higher temperatures was associated with a concurrent increase in chromosome length as measured by the length of the synaptonemal complex (SC), suggesting that the longer chromosome length might explain the increase in crossover rate at higher temperatures (Phillips *et al.* 2015). SC length is also known to positively correlate with CO numbers in mammals (Lynn *et al*. 2002). We therefore measured total SC length in our MLH1/ZYP1 stained pachytene cells from *A. thaliana* grown at different temperatures to ask whether the same trend is seen (Figure 3C) (ZYP1 is the synaptonemal central element protein of *A. thaliana*, (Higgins et al. 2005). In contrast to barley, we observed that in *A. thaliana* total SC length significantly *decreased* with increasing temperatures and that this was consistent (a linear decline) across the whole temperature range (Mann-Whitney U Test, 8˚C vs 18˚C p = 0.001064, 18˚C vs 28˚C p = 0.0169, 8˚C vs 28˚C p = 0.0000457). Thus in *A. thaliana* the increase in crossover number at elevated temperatures cannot be explained by an increase in SC length. However, the low temperature effect could be: When factoring in the observed 14% (28 ± 8 µm) increase in SC length at 8˚C relative to 18˚C, the beam film model predicts a 16% increase in class I crossovers (or a 14% increase in total recombination). This is consistent with the observed increases in recombination measured by the pollen-based assay (8–18% increase in total recombination) and HEI10 foci counts (14–34% increase in class I crossovers).

DISCUSSION

In this study, we demonstrate that male meiotic recombination rate increases at temperatures both above and below a nadir at 18˚C in the Col-0 strain of *A. thaliana*. We show that both the high and low temperature increase appear to result wholly or mostly from an increase in class I interfering crossovers, but that the high temperature and low temperature effects may be mechanistically at least somewhat distinct. The low temperature increase in HEI10-marked, but MLH1-negative foci may be explainable by a concomitant increase in axis length of about 14% at lower temperatures. At high temperatures, on the other hand, axis length decreases, and thus cannot explain an increase in MLH1 foci and recombination.

There are reasons to think the effect of temperature on recombination may be in large part biophysical. For example, the length and integrity of the synaptonemal complex, which is which correlates with recombination rates (Zickler and Kleckner 2015), is known to be affected by temperature (e.g. Phillips *et al*. 2015; Rog *et al*. 2017). The recent observation that the synaptonemal complex displays liquid crystal like properties (Rog *et al*. 2017) suggest one possible mechanism. Liquid crystal structures could be easily perturbed by temperature, and indeed, extreme temperatures can lead to aberrant synaptonemal complex polymerization into polycomplexes (see Morgan *et al*. 2013). But this could also have important implications in understanding how recombination responds to subtler temperature changes, since even minor perturbation in the synaptonemal complex can cause quantitative effects on recombination frequency (Higgins *et al*. 2005). Liquid crystal properties of the SC could also provide a possible explanation for our observation that low temperature may increase the frequency of a specific sub-set of MLH1-independent, but ZMM dependent (class I) crossovers. If the SC is less fluid at lower temperature it may be able to stabilize Holliday junctions without an absolute requirement for the MutL complex.

A variety of stresses other than temperature also affect recombination rates (De Storme and Geelen 2014; Bomblies *et al.* 2015). If we envision the perturbations in meiosis as direct effects of temperature on the relevant proteins, how can these other effects be explained? Stress from a wide range of sources affects the oxidative state of the cell, which can also affect protein function and stability directly. Interestingly, one protein that is known to be very responsive to oxidative state is the cohesin subunit REC8 (Perkins *et al*. 2016), which is important for axis emplacement and recombination (Molnar *et al*. 1995; Bai *et al*. 1999;

Cai *et al.* 2003). Cohesin failures can, in turn, mimic temperature-related failures, specifically in the aggregation of axis proteins. These similarities suggest cohesin may be a particularly sensitive component of meiosis and that its perturbation can have reverberating effects through the subsequent processes of axis formation and recombination. Other factors may also play a role. It is known, for instance, that abscisic acid signaling and chromatin decondensation increase in response to temperature stress (Pecinka *et al*. 2010; Finkelstein 2013), and both are associated with increased recombination (Yin *et al.* 2009; Henderson 2012).

Our data suggest that temperature affects exclusively or primarily class I interfering crossovers in *A. thaliana*. This is in line with reports in barley that Class I crossovers are repositioned under warmer temperatures (Phillips *et al.* 2015). The barley study did not examine class II crossovers, but in yeast, class II crossovers have been reported to increase under temperature stress (Börner *et al.* 2004). This contrasts our findings in *A. thaliana*, where Class II crossovers showed no response to temperature, suggesting there may be variation among taxa in the sensitivity of particular crossover pathways to temperature. Such variation could result if specific proteins involved in different aspects of meiosis have different thermosensitivities across taxa. In mice and lilies, for example, there is evidence that particular recombinases are directly sensitive to temperature (Hotta *et al*. 1985; Stern 1986; Hotta *et al*. 1988), which may play a role here too. Another possible explanation may be a shift in crossover maturation dynamics. Previous experiments in yeast demonstrated that low temperatures can affect the dynamics of early steps in meiotic recombination (Börner *et al*. 2004), which may cause some crossovers to mature earlier or later at low temperature, and could affect crossover rates as well as the presence of (or our ability to detect) MLH1 foci at late pachytene. In barley, a change in the dynamics of DNA replication, specifically the replication of heterochromatic DNA, can affect the ultimate positioning of crossover events, though in this species it has negligible effects on their number (Higgins *et al*. 2012). Together with results from yeast, this hints that the timing of different stages of early meiotic events can alter crossover outcomes, though the details of how temperature affects the timing of meiotic events in *A. thaliana* has yet to be described in detail. Another factor may be that the SC is longer at lower temperatures, which could provide more physical space for crossovers to form (e.g. Lynn *et al*. 2002; Phillips *et al.* 2015).

Our results are consistent with the idea that meiotic recombination is tuned to the environment of a given species (Bomblies *et al*. 2015; Wright *et al*. 2015). The change in recombination that occurs under temperature increases or decreases in most species is a plastic response that is either adaptive in itself (Ritz *et al.* 2017) and/or reflects unavoidable instability in the system (Morgan *et al*. 2017). Plasticity of recombination has been previously described as a possibly adaptive response in some circumstances to increase diversity in offspring (Modlizewski and Copenhaver 2015). However, considering how common it is, we favor the idea that recombination rate plasticity, rather than being a directly selected trait, is an unavoidable by-product of the thermosensitivity of core meiotic proteins and/or processes, and that any benefits that arise from the increase in recombination are inadvertent (Morgan *et al.* 2017). Nevertheless, even if it is just a happy accident, it may well be that increasing recombination under temperature deviations does in fact benefit future generations by facilitating rapid adaptation.

U-shaped curves in response to temperature suggest that in "optimal" conditions, organisms generally have lower recombination rates than under stressful conditions. This is somewhat surprising given that elevated recombination rates may be advantageous for adaptation in at least some circumstances (e.g. Barton 1995; Charlesworth and Barton 1996; Presgraves 2005; Otto 2009; Campos *et al*. 2015). Indeed, numerous empirical studies have shown that strong artificial selection for a wide variety of traits is correlated with an increase in recombination rates (e.g. Flexon *et al.* 1982; Korol and Iliadi 1994; Ross-Ibarra 2004). However, a potential explanation for why there might be a low-point in recombination is that in a stable environment to which an organism is well adapted, minimizing recombination (while still ensuring at least one crossover per bivalent) better maintains allelic combinations that have been selected in previous generations (Otto 2009). An additional possibility is that recombination, while important for chromosome segregation in most species, is also mutagenic, and thus may be selected against (Arbeithuber *et al.* 2015). Moreover, there is an important exception to the aforementioned trend that selection tends to increase recombination. For example, when selection is applied for high fertility in mice, recombination rates decline, suggesting that high recombination can decrease fertility and may thus be evolutionarily selected against (Gorlov *et al*. 1992), even if no obvious immediate defects are observed with even very high recombination rates (Girard *et al*. 2014).

There is evidence from several species that recombination rate may be linked with local adaptation. For example, in grasshoppers, individuals with lower crossover rates are more sensitive to temperature shock (Rees and Thompson 1958; Shaw 1971), while wild *Sordaria* growing in distinct habitats have different recombination rates when grown together in laboratory conditions (Saleem *et al*. 2001). There is also evidence that natural selection has acted in populations adapted to different habitats on core meiotic proteins that have the potential to affect recombination rates (Turner et al. 2008; Anderson et al. 2009; Wright *et al*. 2015). The notion that temperature affects recombination and that populations adapt to local prevailing climates, has important implications for interpreting observations of recombination rate variation among populations when these are measured at a single temperature in the lab. It may be, in at least some cases, that as populations adapt to distinct environments, the recombination response curves shift in concert. If this is the case, when measuring recombination rate at a single laboratory temperature, we may be sampling different points on a given genotype's response curve, and may not be reflective of what occurs in nature. For these reasons, it will be important to better understand both the causes and the consequences of the links between stress, temperature, and meiotic recombination (Bomblies *et al.* 2015) both from a mechanistic and evolutionary perspective.

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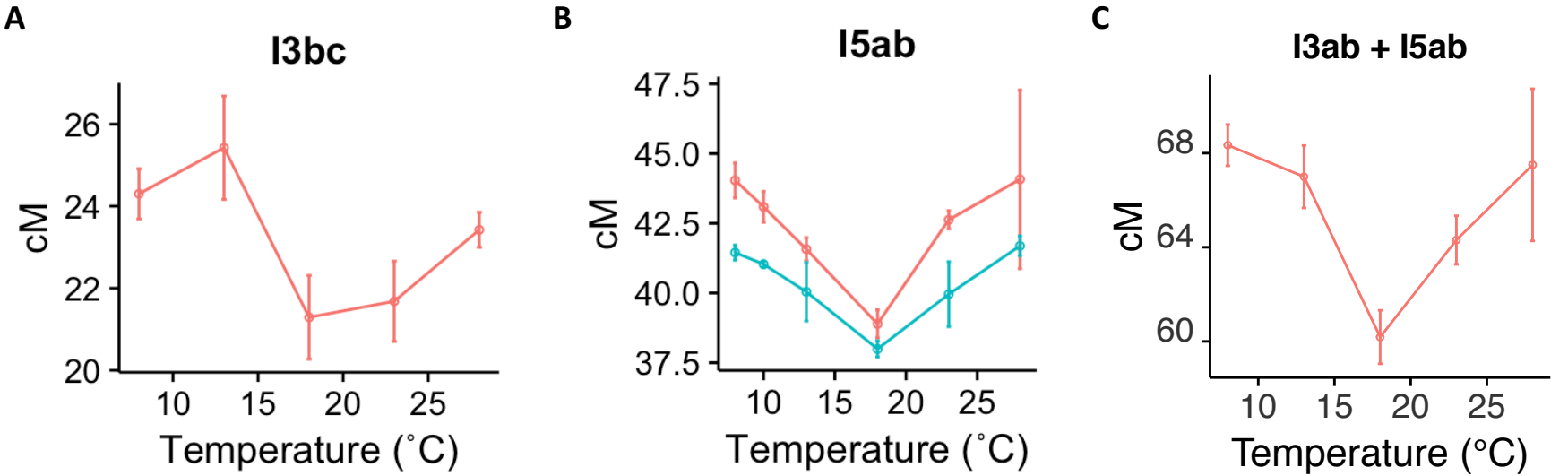
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Temperature (˚C)
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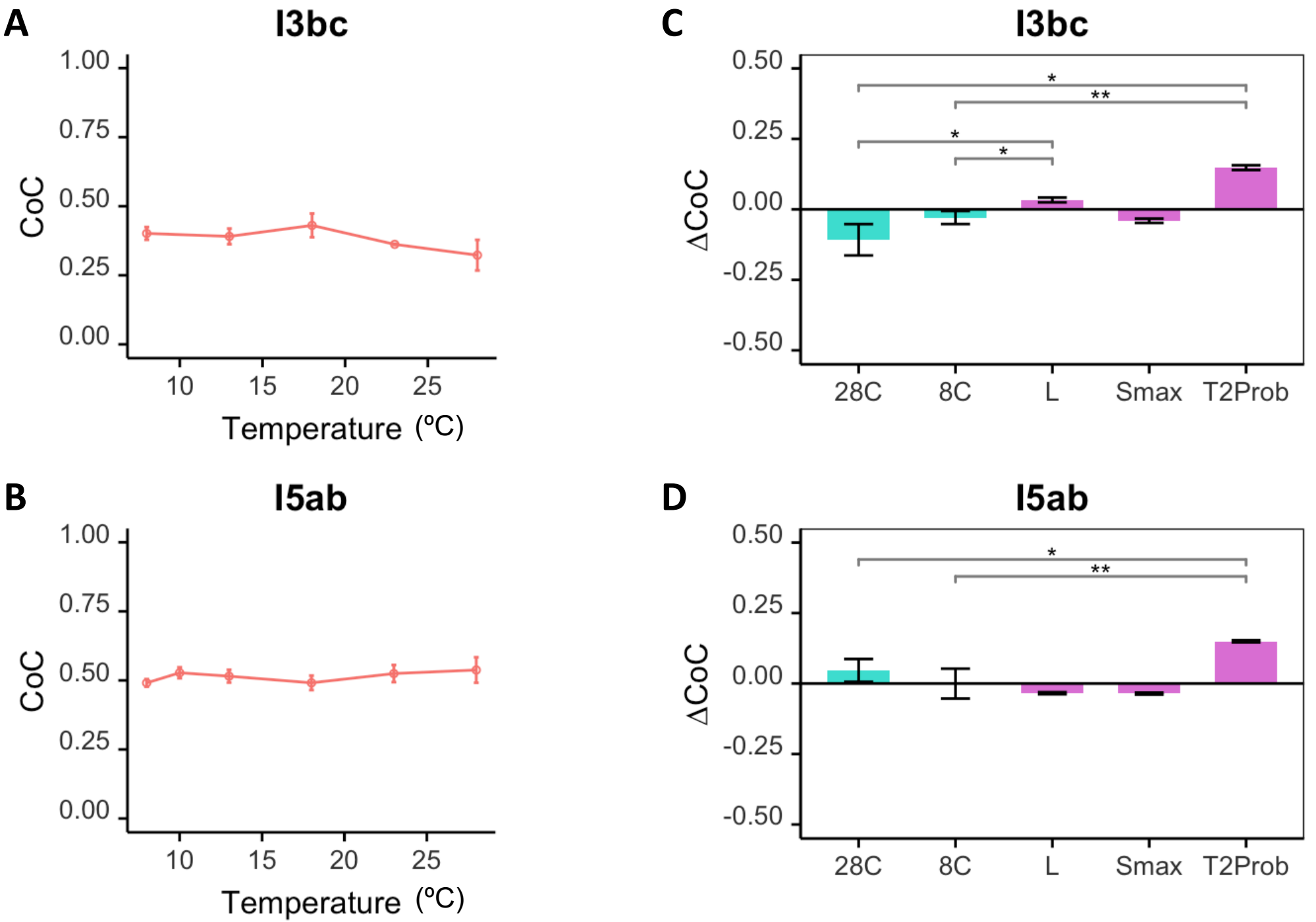
Temperature (°C)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CoC
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C
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28C
8C
L
Smax
T2Prob
D
I5ab
0.50
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-0.50
ΔCoC
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28C
8C
L
Smax
T2Prob

Table 1. Best-fit parameters* for chromosomes 3 and 5

Chr	N	B	E	Bs	Be	Bd	Smax	Bsmax	A	L	cL	cR	M	T2prob
5	56	1	0.6	0.4	0.5	0.01	4.5 (15)	1	1	1 (0.54)	0.8	1.05	1	0.0095 (0.0155)
3	49	1	0.6	0.5	0.65	0.01	1 (2.03)	1	1	0.9 (0.641)	1.5	1.5	1	0.01 (0.0162)

*whole chromosomes were simulated, with best-fit parameters based on FTL derived CO and CoC values

Values in brackets are those used to acheive a 13% increase in COs