Unexpectedly low recombination rates and presence of hotspots in termite genomes

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Abstract

Meiotic recombination is a fundamental evolutionary process that facilitates adaptation and the removal of deleterious genetic variation. Social Hymenoptera exhibit some of the highest recombination rates among metazoans, whereas high recombination rates have not been found among non-social species from this insect order. It is unknown whether elevated recombination rates are a ubiquitous feature of all social insects. In many metazoan taxa, recombination is mainly restricted to hotspots a few kilobases in length. However, little is known about the prevalence of recombination hotspots in insect genomes. Here we infer recombination rate and its fine-scale variation across the genomes of two social species from the insect order Blattodea: the termites *Macrotermes bellicosus* and *Cryptotermes secundus*. We used linkage-disequilibrium-based methods to infer recombination rate. We infer that recombination rates are close to 1 cM/Mb in both species, similar to the average metazoan rate. We also observed a highly punctate distribution of recombination in both termite genomes, indicative of the presence of recombination hotspots. We infer the presence of full-length *PRDM9* genes in the genomes of both species, which suggests recombination hotspots in termites might be determined by *PRDM9*, as they are in mammals. We also find that recombination rates in genes are correlated with inferred levels of germline DNA methylation. The finding of low recombination rates in termites indicates that eusociality is not universally connected to elevated recombination rate. We speculate that the elevated recombination rates in social Hymenoptera are instead promoted by intense selection among haploid males.

Introduction

Meiotic recombination has two fundamental roles: It is essential for correct disjunction of chromosomes during cell division and it generates new combinations of genetic variants that form the raw material of evolution (Hartfield and Keightley 2012). However, recombination can also be deleterious, as it can generate structural mutations and break up favourable combinations of alleles. Recombination varies among species, with optimal recombination rate in a genome likely determined by the optimal trade-off of its positive and negative evolutionary and mechanistic effects (Stapley et al. 2017).

45 The highest recombination rates in metazoans observed so far are found in social insects
46 (Wilfert et al. 2007; Stapley et al. 2017). However, until now recombination rate has only
47 been studied in social insects from the order Hymenoptera, to which the majority of social
48 insects belong. Among Hymenoptera, the highest rates are found in the genus *Apis*: the
49 Western honey bee *Apis mellifera* (20.8 cM/Mb) and its relatives *Apis cerana* (17.4 cM/Mb),
50 *Apis florea* (20.8 cM/Mb) and *Apis dorsata* (25.1 cM/Mb) (Beye et al. 2006; Shi et al. 2013;
51 Liu et al. 2015; Wallberg et al. 2015; Rueppell et al. 2016; Kawakami et al. 2019). Other
52 social Hymenoptera also have high rates including the bumblebee *Bombus terrestris* (8.9
53 cM/Mb) (Liu et al. 2017; Kawakami et al. 2019), the stingless bee *Frieseomelitta varia* (9.3 –
54 12.5 cM/Mb) (Waiker et al. 2021), the wasp *Vespula vulgaris* (9.7 cM/Mb) (Sirviö et al.
55 2011a) and the ants *Pogonomyrmex rugosus* (11.1 cM/Mb) (Sirviö et al. 2011b) and
56 *Acromymex echinatior* (6.1 cM/Mb) (Sirviö et al. 2006). In contrast, the solitary bee
57 *Megachile rotundata* and the solitary wasp *Nasonia* have relatively low rates (1.0 and 1.5
58 cM/Mb, respectively) (Niehuis et al. 2010; Jones et al. 2019). For comparison, the average
59 recombination rate of 15 insect species outside of Hymenoptera is 2.2 cM/Mb (Wilfert et al.
60 2007).

61 We can learn about the forces shaping the evolution of recombination rates in general by
62 understanding why high recombination rates have evolved in social Hymenoptera. Several
63 hypotheses have been proposed to explain this observation. One set of explanations
64 focusses on the effects of recombination on intra-colony genetic diversity. For example,
65 increasing the genetic diversity of a colony could promote task specialization among
66 workers (Kent et al. 2012; Kent and Zayed 2013). Similarly, elevated genetic variation in a
67 colony could prevent invasion by pathogens or parasites due to diversification of immune
68 genes (Fischer and Schmid-Hempel 2005). Recombination could also reduce variance in
69 relatedness between nestmates, thereby reducing potential kin conflict within colonies
70 (Sherman 1979; Templeton 1979; Wilfert et al. 2007). Additionally, it has been proposed
71 that high recombination rates could have facilitated the evolution of eusociality over a
72 longer evolutionary timescale, because recombination between genes that take on
73 functions in different castes permits them to evolve more independently (Kent and Zayed
74 2013). Several studies have addressed these hypotheses (Kent et al. 2012; Liu et al. 2015;
75 Wallberg et al. 2015; Rueppell et al. 2016; Liu et al. 2017; Jones et al. 2019; Waiker et al.

2021; Kawakami et al. 2019) but so far none is strongly supported. It is also not clear whether eusociality *per se* selects for higher recombination rates, or whether high rates are a specific feature of eusocial Hymenoptera.

The main characteristics of eusocial insect species are the presence of castes that forgo reproduction in order to care for brood or defend other colony members (workers and soldiers). Eusocial insects are found mainly in Hymenoptera, among bees, wasps and ants, and also Blattodea, in which all termites (Infraorder: Isoptera) are eusocial but exhibit varying levels of social complexity. These insect orders likely diverged ~400 million years ago (Misof et al. 2014) and there are substantial differences between social insects from the two orders (Korb 2008; Korb and Thorne 2017). Hymenoptera belong to the superorder Holometabola, which is the most diverse insect superorder and contains 11 orders including Lepidoptera (butterflies, moths), Coleoptera (beetles), and Diptera (true flies), which all undergo complete metamorphosis. Blattodea is a hemimetabolous order, which undergoes partial metamorphosis. Hymenoptera have haplodiploid sex determination in which males develop from haploid, unfertilized eggs and females derive from diploid, fertilized eggs. In Blattodea, both males and females are diploid. Members of the worker caste in eusocial Hymenoptera are all female, whereas eusocial Blattodea workers are of both sexes. Hymenoptera colonies are headed by one or a small number of queens, whereas Blattodea colonies contain both a king and a queen.

The hypotheses proposed to explain the high recombination rates observed in eusocial Hymenoptera predict that recombination should be elevated in all social insects. However, so far it is unknown whether social insects from other orders also have high rates. As described above, there are fundamental differences in the sex determination system and colony compositions of social insects from Hymenoptera and Blattodea. The robustness of the association between eusociality and high recombination rates can therefore be addressed by assessing mean genomic recombination rates in social Blattodea (termites).

In addition to variation between species, the rate of recombination also varies along chromosomes. In mammals, crossover events are mainly restricted to regions that contain specific motifs that act as binding sites for the PRDM9 (PR/SET domain 9) protein that marks regions for double-stranded breaks, which are repaired by recombination during meiosis (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010). Species with an active PRDM9

107 protein include nearly all mammals and many vertebrate taxa (Baker et al. 2017). In species
108 without PRDM9, recombination can be directed to hotspots defined by other features, such
109 as CpG islands and promoters that have open chromatin. Such hotspots have been
110 characterised in the genomes of diverse taxa including yeast, birds, and dogs (Axelsson et al.
111 2012; Lam and Keeney 2015; Singhal et al. 2015; Berglund et al. 2014). In insects, the
112 prevalence of recombination hotspots is not well studied. Fine-scale recombination maps in
113 the fruit fly *Drosophila melanogaster* and honey bee *A. mellifera* indicate a paucity of
114 recombination hotspots (Chan et al. 2012; Smukowski Heil et al. 2015; Wallberg et al. 2015),
115 whereas hotspots appear to be present in the genome of the butterfly *Leptidea sinapis*
116 (Torres et al. 2023).

117 Several other factors may also modulate recombination rate along chromosomes, such as
118 germline DNA methylation. Many vertebrate species have elevated recombination in CpG
119 islands, which are usually unmethylated in the germline (Axelsson et al. 2012; Singhal et al.
120 2015; Berglund et al. 2014). In insect genomes, methylation is not always present, but
121 commonly restricted to gene bodies (Arsala et al. 2022; Wang et al. 2013; Lyko et al. 2010;
122 Ventós-Alfonso et al. 2020; Bewick et al. 2019; Harrison et al. 2018). In the honey bee *A.*
123 *mellifera* and solitary bee *M. rotundata,* recombination is reduced in genes, particularly
124 those inferred to have the highest levels of germline methylation (Wallberg et al. 2015;
125 Jones et al. 2019). In addition, some studies have identified correlations between caste-
126 biases in gene expression and recombination. In honey bees, genes with worker-biased gene
127 expression have been found to have elevated recombination rates (Kent et al. 2012) but this
128 is likely an indirect result of differences in germline methylation between sets of genes
129 (Wallberg et al. 2015).

130 Here we estimate recombination rate and its fine-scale variation across the genomes of two
131 distantly related termite species with contrasting social complexities (Korb and Hartfelder
132 2008; Korb and Thorne 2017). *Macrotermes bellicosus* (Termitidae: Macrotermitinae) is a
133 fungus-growing termite with a high level of social complexity, with colonies of several
134 millions of individuals and sterile workers. It belongs to the foraging (multiple-pieces
135 nesting) termites, where workers leave the nest to forage for food. The drywood termite
136 *Cryptotermes secundus* (Kalotermitidae) has a low level of social complexity. Its colonies
137 consist of a few hundred individuals and totipotent workers from which queens and kings

138 develop (Hoffmann et al. 2012). It belongs to the wood-dwelling (one-piece nesting)
139 termites that nest in a single piece of wood that also serves as their food source.

140 The study has three main aims. Firstly, we aim to test the robustness of the association
141 between sociality and high recombination rate. If sociality is a universal driver of high
142 recombination rates, we would expect both termite species to have elevated recombination
143 rates, and that it is particularly elevated in *M. bellicosus*, which has a higher level of social
144 complexity. Secondly, we aim to determine whether recombination hotspots exist in the
145 two termite genomes, and infer whether active full-length *PRDM9* genes are present in their
146 genomes. Thirdly, we aim to analyse the factors that govern recombination rate variation
147 across the genome, in particular whether it is associated with patterns of methylation and
148 gene expression as has been reported in other studies.

149

150 **Results**

151 *Genetic variation in two termite species is typical for social insects*

152 We utilized genome assemblies of two termite species: *M. bellicosus* and *C. secundus*. The
153 genome assembly of *M. bellicosus* (Qiu et al. 2023) is 1.3 Gbp in total length across 275
154 scaffolds with scaffold N50 of 22.4 Mbp. The genome assembly of *C. secundus* (Csec_1.0)
155 (Harrison et al. 2018) is divided into 55,483 scaffolds with a scaffold N50 of 1.2 Mbp and a
156 total length of 1.0 Gbp.

157 We sequenced 10 unrelated individuals each of *M. bellicosus* and *C. secundus* to a mean
158 depth of 34x and 31x per sample, respectively (Supplemental Table S1). We mapped reads
159 to the appropriate genome assemblies and called variants in each species. In *M. bellicosus*
160 we called 5.6 million SNPs and in *C. secundus* 15.1 million SNPs (Table 1). One individual of
161 *C. secundus* (CS_8) was excluded due to a low proportion of mapped reads, poor mapping
162 quality and strand bias in mapping. Estimates of variation based on θ_W per bp (Watterson
163 1975) are 0.14% and 0.44% in *M. bellicosus* and *C. secundus* respectively, which are broadly
164 comparable to levels of variation in the honey bee *A. mellifera* (0.3 - 0.8%) (Wallberg et al.
165 2014).

166 We used these estimates of genetic variation to estimate effective population size (N_E) for
167 each of the sampled populations (Table 1). These rely on an estimate of mutation rate, μ, in

168 each species. As there is no estimate of μ for Blattodea, we considered a range of estimates
169 from insects compiled by (Lynch et al. 2023) based on experimental assays that includes
170 estimates from Diptera (*Drosophila*) (Keightley et al. 2009, 2014), Hymenoptera (Liu et al.
171 2017; Yang et al. 2015) and Lepidoptera (Keightley et al. 2015). These estimates range
172 between a minimum of 2.7 x 10^{-10} $bp^{-1}gen^{-1}$ in *Acyrthosiphon pisum* (Fazalova and Nevado
173 2020) to a maximum of 8.1 x 10^{-9} $bp^{-1}gen^{-1}$ in *Drosophila pseudoobscura* (Krasovec 2021).
174 The average of multiple estimates in *Drosophila melanogaster* is 4.5 x 10^{-9} $bp^{-1}gen^{-1}$, which is
175 typical of insects (Lynch et al. 2023). A mutation rate of μ = 1.85 x 10^{-9} $bp^{-1}gen^{-1}$ has been
176 estimated in the orchid mantis, *Hymenopus coronatus* (Huang et al. 2023) based on
177 inference from levels of interspecific divergence. This species is a member of the order
178 Mantodea, which contains the closest relatives of Blattodea.

179 Our estimates of N_E based on θ_W and the various mutation rates are ~43,000 – 1,279,000 in
180 *M. bellicosus*, which has high social complexity, and ~137,000 – 4,081,000 in *C. secundus*,
181 which has a lower level of social complexity (Table 1). Estimates of N_E assuming the typical
182 mutation rate of 4.5 x 10^{-9} $bp^{-1}gen^{-1}$ are 77,000 and 245,000 respectively. Assuming the
183 mutation rate of *H. coronatus* gives an N_E of 187,000 for *M. bellicosus* and 596,000 for *C.*
184 *secundus*. These estimates are consistent with previous evidence that eusocial species with
185 large colonies and high social complexity tend to have lower effective population sizes and
186 the values are broadly comparable to levels of N_E found in social and solitary Hymenoptera
187 (Leffler et al. 2012; Romiguier et al. 2014).

188 *Low average recombination rate in termite genomes*

189 We next examined the decay of linkage disequilibrium (LD) based on the statistic r^2. Both
190 termite species show more extensive LD compared to *A. mellifera*, which has an extremely
191 high recombination rate (Wallberg et al. 2015) (Figure 1). As N_E is broadly similar in all these
192 species, these differences are expected to largely represent differences in recombination
193 rates, and indicate that the two termite species do not exhibit the elevated genome average
194 recombination rate that is observed in honey bees.

195 We estimated variation in the population recombination rate, ρ, in both datasets using
196 LDhelmet (Chan et al. 2012) and LDhat (Auton and McVean 2007) (Table 1). Average rates of
197 ρ/kbp in *M. bellicosus* and *C. secundus* are 1.7 and 4.8 respectively from LDhat and 4.28 and

198 16.39 respectively from LDhelmet. These estimates can be converted to cM/Mb using
199 estimates of N_E, which gives average recombination rates of 0.033 - 0.986 cM/Mb in *M.*
200 *bellicosus* and 0.030 - 0.885 cM/Mb in *C. secundus* from LDhat and 0.084-2.49 cM/Mb for *M.*
201 *bellicosus* and 0.1 - 2.99 cM/Mb for *C. secundus* from LDhelmet. Using a mutation rate close
202 to the average for insects, the recombination rates in *M. bellicosus* and *C. secundus* are
203 0.550 and 0.494 cM/Mb respectively from LDhat and 1.39 and 1.67 cM/Mb respectively
204 from LDhelmet. Using the mutation rate from *H. coronatus*, the recombination rates are
205 0.23 and 0.20 cM/Mb from LDhat and 0.57 and 0.69 cM/Mb from LDhelmet for *M. bellicosus*
206 and *C. secundus*, respectively. Even though these estimates vary depending on the
207 algorithm used for estimating ρ and the assumed mutation rate, they are all substantially
208 lower than estimates from eusocial Hymenoptera (6-25 cM/Mb; (Sirviö et al. 2006) and
209 more similar to rates found in other insects (Wilfert et al. 2007). This represents the first
210 estimation of recombination rate in social insects outside of Hymenoptera and
211 demonstrates that eusociality is not a universal driver of high recombination rates. The
212 Spearman correlation between the results from LDhat and LDhelmet, using 10 kbp windows,
213 was $\rho = 0.946$ and $\rho = 0.947$ for *M. bellicosus* and *C. secundus*, respectively, with $p < 2.2 \times$
214 10^{-16} for both species. For the remaining analyses, results from the software LDhelmet were
215 used.

216 *Evidence for active recombination hotspots in termite genomes*

217 Recombination rates are highly variable across the genomes of *M. bellicosus* and *C.*
218 *secundus* (Figure 2). We characterised the distribution of recombination events across the
219 two termite genomes using a cumulative distribution plot (Figure 3). We found that 50% of
220 the recombination occurs in 0.4% of the genome in *M. bellicosus* and 0.2% of the genome in
221 *C. secundus*. This indicates that the majority of recombination events are restricted to a
222 much smaller portion of the genome than observed in *A. mellifera*, where 50% of
223 recombination events occur in 32% of the genome (Wallberg et al. 2015).

224 We further investigated whether recombination hotspots are present in the two termite
225 genomes by looking at the distribution of ρ in windows of 1 kbp, 10 kbp and 100 kbp across
226 the genome (Supplemental Figure S1). For all window sizes, a small subset of windows was
227 observed with ρ greatly exceeding the mean in both termite species. For example, the
228 percentage of 1 kbp windows with recombination rate at least four standard deviations

229 above the genome wide mean value is 0.2% for *M. bellicosus* and 0.6% for *C. secundus*. By
230 contrast, *A. mellifera* has no windows above this limit for any window size, consistent with a
231 lack of recombination hotspots.

232 We next defined hotspots as 2 kbp regions with more than 5-fold higher recombination rate
233 than the surrounding 100 kbp and used STREME (Bailey 2021) to identify 8 to 20-mers that
234 were enriched in hotspots compared to the rest of the genome. This yielded significantly
235 enriched motifs in both species (4 motifs for *M. bellicosus* and 1 motif for *C. secundus* after
236 compensating for multiple hypothesis testing; Supplemental Tables S2 and S3). However,
237 none of the motifs we identified are present in more than 5% of hotspots or exhibit more
238 than 2-fold difference in frequency of occurrence relative to the background, suggesting
239 they are not viable candidate motifs for promoting recombination in hotspots.

240 *Identification and characterization of the PRDM9 gene in termites*

241 We searched the *M. bellicosus* and *C. secundus* genomes for evidence of complete *PRDM9*
242 genes, which could potentially govern the presence of recombination hotspots in these
243 genomes, as it has been shown to do in mammalian genomes (Myers et al. 2010; Baudat et
244 al. 2010; Parvanov et al. 2010). The *C. secundus* genome contains a *PRDM9* homolog
245 (XP_023708049.2) with annotated KRAB, SSXRD, SET and zinc finger domains (Figure 4).
246 There is no complete homolog of *PRDM9* in the *M. bellicosus* annotation. We therefore used
247 BLAST to search for sequences homologous to the conserved functional domains from *C.*
248 *secundus*. We identified a putative *PRDM9* orthologue on Scaffold 42 of the *M. bellicosus*
249 genome assembly, containing all domains in the correct order. We identified retroviral
250 conserved domains in an intron 5' of the zinc-finger domains in this gene, which are not
251 predicted to alter the transcript. We confirmed the presence of a full-length transcript as
252 well as presence and correct order of conserved domains by alignment of the *Zootermopsis*
253 *nevadensis* PRDM9 protein sequence to the *M. bellicosus* genome using GeneWise (Madeira
254 et al. 2024)(Figure 4 and Supplemental Table S4).

255 We used a zinc-finger prediction algorithm (Persikov and Singh 2014) to predict DNA binding
256 motifs from the zinc-finger domain present in PRDM9 in the *M. bellicosus* and *C. secundus*
257 genome assemblies. The most probable consensus motifs were
258 TATGGAACGACAGGAACAACGACATCATCAGCCGCCTAAT and TAATAAGTAGAATCGTTTAG for
259 *M. bellicosus* and *C. secundus* respectively. Base probability matrices for these motifs are

260 shown in Supplemental Table S5. We tested whether the presence of these motifs
261 corresponded to elevated recombination considering 1 kbp around each motif. However,
262 recombination rate was not significantly elevated around these predicted motifs for either
263 species, either when searching based on the most likely motif, or by searching based on the
264 probability matrices.

265 *Genomic correlates of recombination rate*

266 We analysed genomic correlates of recombination rate in 10 kbp windows. There is a
267 significant correlation between recombination and $CpG_{O/E}$ in both species with Spearman's
268 $\rho = 0.24$, $p < 1 \times 10^{-4}$ for *M. bellicosus* and Spearman's $\rho = 0.10$, $p < 1 \times 10^{-4}$ for *C. secundus*
269 (Supplemental Figure S2). A reduction of recombination rates in regions of low CpG content
270 is consistent with interference of germline methylation with recombination. However, as
271 the correlation coefficients are low, the explanatory power is weak. Correlations of similar
272 magnitudes were observed between recombination and GC content (Spearman's ρ=0.23 for
273 *M. bellicosus*, $p < 1 \times 10^{-4}$ and Spearman's ρ=0.017 for *C. secundus*, $p < 1 \times 10^{-4}$). This
274 correlation has been associated with an effect of recombination in driving GC through GC
275 biased gene conversion but the relatively low correlation coefficients could indicate that this
276 force is not strong in termites. By contrast, the correlation between GC content and
277 recombination rate is much stronger in honey bee ($R^2 = 0.506$), which is likely caused by high
278 recombination rates and intense GC-biased gene conversion (Wallberg et al. 2015).

279 There is a weak but significant correlation between overall repeat element density and
280 recombination rate in *C. secundus* (Spearman's ρ= = 0.02, $p < 1 \times 10^{-4}$) but not for *M.*
281 *bellicosus*. There is a weak but significant correlation between simple repeats and
282 recombination in both genomes (Spearman's $\rho = 0.051$, $p < 2.22 \times 10^{-16}$ for *M. bellicosus* and
283 Spearman's $\rho = 0.055$, $p < 2.22 \times 10^{-16}$ for *C. secundus*). SINE and LINE elements are also only
284 weakly associated with recombination rate in both genomes (SINEs: Spearman's $\rho = -0.012$,
285 not significant for *M. bellicosus* and Spearman's $\rho = 0.02$, $p < 1 \times 10^{-4}$ for *C. secundus*; LINEs:
286 Spearman's $\rho = -0.02$, $p < 1 \times 10^{-4}$ for *M. bellicosus* and Spearman's $\rho = 0.002$ not significant
287 for *C. secundus*). There is a significant negative correlation between gene density and
288 recombination for the *M. bellicosus* genome (Spearman's $\rho = -0.185$, $p < 2.22 \times 10^{-16}$), but no
289 significant correlation for *C. secundus*. We also tested whether hotspots differ from the

290 background with respect to GC content. The GC content does not differ substantially
291 between hotspots and the rest of the genome in either species (means of 40.1% and 41.0%
292 for *M. bellicosus* and 40.2% and 40.3% for *C. secundus*).

293 We found a significant correlation between nucleotide diversity (π) and recombination in
294 both species (Supplemental Figure S2), with Spearman's $\rho = 0.48$, $p < 1 \times 10^{-4}$ for *M.*
295 *bellicosus* and Spearman's $\rho = 0.31$, $p < 1 \times 10^{-4}$ for *C. secundus*. This correlation is found
296 across a wide range of eukaryotic taxa and is generally accepted to be caused by the
297 interaction between recombination and linked selection (Nachman 2001; Begun and
298 Aquadro 1992).

299 *Recombination and gene expression patterns correlate with $CpG_{O/E}$*

300 Analysis of the distribution of $CpG_{O/E}$ in both termite species showed that it is bimodally
301 distributed, with substantially lower values in introns and exons compared to flanking
302 noncoding regions (Supplemental Figure S3). This indicates that germline DNA methylation
303 is biased towards gene bodies in the two termite genomes, a pattern that is also found in
304 honey bees and other insect genomes with functional DNA methylation (Harrison et al.
305 2018; Elango et al. 2009; Sarda et al. 2012). We found that exons have lower $CpG_{O/E}$
306 compared to introns, which are both lower than flanking regions (Figure 5, top row; all
307 comparisons $p < 0.001$ after Bonferroni correction) consistent with higher levels of germline
308 methylation in exons (Supplemental Table S6). We next analysed how recombination rate
309 varies among genomic features. We found that ρ/kbp is also significantly reduced in genes
310 compared to flanking regions for *C. secundus,* with exons also showing reduced ρ/kbp
311 compared to introns (Figure 5, bottom row, all p-values <0.005 after Bonferroni correction).
312 The same trends are observed in *M. bellicosus* although they are not significant. The
313 correlation between $CpG_{O/E}$ and recombination rate among genes is higher than for the
314 genome overall (Spearman's $\rho = 0.315$, $p < 2.22 \times 10^{-16}$ for *M. bellicosus*; Spearman's ρ =
315 0.196, $p < 2.22 \times 10^{-16}$ for *C. secundus*).

316 We next investigated whether patterns of gene expression between castes and sexes
317 (hereafter, for short 'caste-biased gene expression') were correlated with $CpG_{O/E}$ and
318 recombination rate using gene expression data from two studies (Lin et al. 2021; Elsner et
319 al. 2018). It has been proposed that it is evolutionarily advantageous for genes with worker-

320 biased expression to be located in regions with elevated recombination (Kent et al. 2012).
321 Comparisons of $CpG_{O/E}$ and recombination rate for the original gene expression categories
322 reported by (Elsner et al. 2018) for *M. bellicosus* are shown in Supplemental Figure S4. We
323 also reclassified the genes into the following expression categories: queen-biased, king-
324 biased, worked-biased, male-biased, female-biased, reproduction-biased, and differentially
325 expressed (see methods for details). For *C. secundus*, only worker-biased and queen-biased
326 genes were identified (Lin et al. 2021). We find that mean $CpG_{O/E}$ in gene bodies shows
327 significant variation between gene expression categories in both *M. bellicosus* and *C.*
328 *secundus* (Figure 6). However, this variation is not consistent between species. In *M.*
329 *bellicosus*, queen-biased and female-biased genes have low $CpG_{O/E}$ and king-biased and
330 male-biased genes have high $CpG_{O/E}$. In *C. secundus*, queen-biased genes have higher than
331 average $CpG_{O/E}$.

332 The differences in $CpG_{O/E}$ between caste-biased gene expression categories are mirrored by
333 differences in ρ/kbp (Figure 6). Gene expression categories with elevated $CpG_{O/E}$
334 consistently show elevated ρ/kbp, and this pattern is found in both species. Studies in the
335 honey bee have found that worker-biased genes have lower CpG and higher recombination
336 rates (Kent et al. 2012; Wallberg et al. 2015). In *M. bellicosus,* we find that worker-biased
337 genes have slightly elevated $CpG_{O/E}$ and ρ/kbp. However, in *C. secundus*, these values are
338 reduced in worker-biased genes, whereas queen-biased genes have a slightly elevated
339 $CpG_{O/E}$ and ρ/kbp in this species.

340 We investigated the relative roles of $CpG_{O/E}$ and gene expression in determining ρ in genes
341 using linear models, with $CpG_{O/E,}$ ρ in flanking region and expression categories as
342 explanatory variables. In both *M. bellicosus* and *C. secundus*, we found that $CpG_{O/E}$ was the
343 strongest predictor of recombination rate variation among genes (Supplemental Tables S7
344 and S8) in line with the analyses above. We found that caste-biased expression had no
345 significant impact on the recombination rate. $CpG_{O/E}$ is a better predictor of ρ/kbp in genes
346 than ρ/kbp in flanking region and variation in ρ/kbp among expression categories mainly
347 reflects differences in $CpG_{O/E}$.

348

349 **Discussion**

350 The main findings we present here are 1) that two distantly related termite species with
351 varying social complexity both have relatively low genomic average rates of meiotic
352 recombination, 2) both genomes possess recombination hotspots and likely contain full-
353 length copies of *PRDM9* and, 3) there are reduced levels of recombination in genomic
354 regions depleted in CpG sites. Our findings contrast with the extremely elevated
355 recombination rates observed in eusocial Hymenoptera, which are likely to be generated by
356 a feature that is specific to these taxa. The finding of recombination hotspots is one of the
357 first in insects. This could reflect a conserved function of PRDM9 in initiating recombination
358 events in both vertebrates and invertebrates. Our results also support a role for germline
359 methylation in suppressing recombination.

360 *Low recombination rates in termites*

361 Data from a wide range of taxa indicate that at least one crossover per chromosome tetrad
362 is essential for correct chromosomal segregation during meiosis (Fernandes et al. 2018). The
363 chromosome numbers of *M. bellicosus* and *C. secundus* are 2n = 42 and 2n = 40, respectively
364 (Jankásek et al. 2021). Considering their assembly lengths, this indicates that a minimum
365 average genomic recombination rate of 0.92 cM/Mb and 1.01 cM/Mb, respectively, would
366 be necessary for accurate meiosis to occur in the two termite species. Our estimates of
367 recombination rate per meiosis based on analysis of LD depend on several factors, including
368 the algorithm to estimate ρ and the estimate of mutation rate. As no estimates of the
369 mutation rate in termites were available, we considered a range of estimates from other
370 insects. These estimates vary by more than an order of magnitude between different insect
371 species (Lynch et al. 2023) and higher estimates of the mutation rate give higher estimates
372 of the recombination rate. Our estimates based on LDhat are all less than 1 cM/Mb for both
373 species, even when considering the highest estimate of mutation rate. Using estimates from
374 LDhelmet and the average of experimentally determined mutation rate estimates in insects
375 gives estimates of recombination rate of 1-2 cM/Mb. The species most closely related to
376 termites for which a mutation rate estimate was available was *H. coronatus (Huang et al.*
377 *2023)*. Using this estimate and ρ from LDhelmet, the recombination rate per meiosis was
378 estimated to 0.57 cM/Mb for *M. bellicosus* and 0.69 cM/Mb for *C. secundus*, i.e. both
379 slightly lower than expected based on the requirement of one crossover per chromosome.
380 Taken together, these results indicate that recombination rates in these two termite species

381 are substantially lower than the elevated values found in eusocial Hymenoptera (6-25
382 cM/Mb) (Wilfert et al. 2007).

383

384 It should be noted that our estimates of recombination rate are sex-averaged rates. It is
385 possible that recombination is absent in one of the termite sexes, which would make a
386 lower sex-averaged recombination rate more feasible. In addition, sex-linked contigs have
387 not been identified in the termite genome assemblies utilized here. *M. bellicosus* and *C.*
388 *secundus* have X1X2/Y1Y2 and X/Y sex-determining systems respectively (Jankásek et al.
389 2021). The inclusion of sex chromosomes in the analysis leads to errors in determining the
390 genome-wide recombination rate per meiosis because they have lower N_E than the rest of
391 the genome. In addition, sex chromosomes are more prone to assembly and read mapping
392 errors, due to reads aligning with the incorrect copy of the chromosome. However,
393 considering that sex chromosomes only comprise a minor portion of the genome, this is
394 unlikely to substantially alter our results. It has also been observed that some chromosomes
395 form ring or chain structures during meiosis in certain termite species (Bergamaschi et al.
396 2007), which could plausibly relax the requirement for one crossover per chromosome per
397 meiosis.

398

399 *Eusociality is not a universal driver of high rates of meiotic recombination*

400 Elevated genomic rates of recombination are characteristic of all eusocial Hymenoptera so
401 far investigated. Several hypotheses have been advanced to explain this phenomenon,
402 which are all based on an evolutionary advantage of recombination in eusocial species
403 (Wilfert et al. 2007). For instance, it has been suggested that elevated recombination could
404 increase genetic diversity in a colony. This could promote diversity in the workforce,
405 enabling more efficient task specialisation among workers (Kent et al. 2012). Alternatively, it
406 could render the colony less susceptible to invasion by parasites and pathogens (Fischer and
407 Schmid-Hempel 2005). Elevated recombination might also favour rapid evolution of caste-
408 specifically expressed genes (Kent and Zayed 2013). In addition, increased recombination
409 could lead to reduced variance in relatedness, which could prevent kin conflict in colonies
410 (Sherman 1979; Templeton 1979).

411 All these hypotheses predict that recombination rate should be elevated in all eusocial
412 insects. Here, however, in the first report of recombination rate in social insects outside of
413 Hymenoptera, we find overall low levels of recombination. Both termite species studied
414 here are eusocial, and in particular *M. bellicosus* has extremely large and complex colonies
415 characteristic of eusociality (Korb and Thorne 2017). The low recombination rate inferred in
416 the two termite genomes prompts re-evaluation of hypotheses connecting eusociality with
417 high recombination rates. Although both termites and social Hymenoptera share many
418 traits, they differ in others that reflect their different ancestries.

419 The chromosome numbers of both termite species (*M. bellicosus*, 2n = 42; *C. secundus*, 2n =
420 40) are typical for termites, although variation exists between taxa (Jankásek et al. 2021).
421 These values do not differ from those observed in Hymenoptera, which have a similar range
422 (e.g. *A. mellifera*, 2n = 32) and do not vary between solitary and eusocial taxa (Cardoso et al.
423 2018; Cunha et al. 2021; Ross et al. 2015). This suggests that differences in chromosome
424 number are unlikely to be relevant in explaining the differences in recombination rates
425 among these taxa.

426 One proposed advantage of sex and recombination is that it is associated with sexual
427 selection and a higher intensity of selection on males. This could be advantageous because
428 differential male mating success can reduce mutational load in sexual populations by
429 causing deleterious mutations to segregate at a lower equilibrium frequency on average
430 (Siller 2001; Agrawal 2001). Recombination is essential for effective purging of deleterious
431 alleles as it unlinks deleterious variants from nearby beneficial ones thus preventing
432 selection interference (Hartfield and Keightley 2012). Selection has been found to be
433 stronger in males than females across animal species (Janicke et al. 2016; Winkler et al.
434 2021). Species with a male-biased sex ratio are expected to experience particularly intense
435 selection on males. It is therefore possible that recombination rate could be particularly
436 elevated in species in which males face intense competition as this increases the
437 evolutionary advantage of recombination.

438 Another proposed advantage of sex and recombination in general is that it is associated
439 with the intensity of sperm competition. Maynard Smith (1976) presented a model that
440 explains how sib-competition can produce an immediate evolutionary advantage to sex and
441 recombination, which occurs when several offspring of a single female compete within a

442 patch. This model was extended by Manning and Chamberlain (1997) who argued that it is
443 analogous to intra-ejaculate competition among sperm, in which recombination increases
444 the variance of fitness. Under these conditions, if inter-ejaculate competition also exists, it is
445 predicted that there will be selection for increased recombination rate. This model predicts
446 a significant correlation between recombination rate and gamete redundancy (excess sperm
447 production), which is observed in mammals (Manning and Chamberlain 1997).

448 Many social Hymenoptera produce highly male-biased reproductive offspring and
449 thousands of haploid male drones compete to fertilise a small number of female queens
450 (Winston 1991; Koeniger et al. 2011; Baer 2005). This situation is similar to sperm
451 competition as haploid males can be considered analogous to gametes. However, as many
452 more genes are expressed in adult haploid males compared to gametes there are more
453 targets of selection. Selection against deleterious alleles is particularly effective in haploid
454 males because recessive deleterious alleles are exposed (Hedrick and Parker 1997). It is
455 therefore possible that the male-biased sex ratio observed in many eusocial Hymenoptera
456 could favour elevated recombination rates in the species so far studied, due to elevated
457 competition between males.

458 Male-biased sex ratios are particularly strong in the genus *Apis*, which is also the genus in
459 which the most extreme recombination rates have been inferred (Beye et al. 2006; Shi et al.
460 2013; Liu et al. 2015; Wallberg et al. 2015; Rueppell et al. 2016; Kawakami et al. 2019).
461 Male-biased sex ratios are also observed in other social bees and wasps. Both male and
462 female biased operational sex ratios have been observed in ants, but are difficult to
463 measure because workers invest more resources in female offspring and may manipulate
464 sex ratios. In non-social Hymenoptera, females lay roughly equal numbers of haploid and
465 diploid eggs (Trivers and Hare 1976). The sex ratio of reproductive males and females is also
466 relatively even in most termite species (Roisin 2001).

467 Further research is needed to determine the cause of variation in recombination rates
468 among social and non-social insects. For example, simulations could be used to determine
469 the effect of selection on haploid males on recombination rates, considering different sex
470 ratios. In addition, it is necessary to estimate recombination rate in a wider range of social
471 and non-social species to determine whether the strength of selection on males is a key
472 factor in determining these rates.

473 *Full length PRDM9 gene and recombination hotspots in termite genomes*

474 Our results are also indicative of the presence of recombination hotspots in the two termite
475 genomes. The fine-scale distribution of recombination rate in both termite genomes shows
476 that 50% of the recombination happens in less than 0.5% of the genome, which is even
477 more extreme than for humans where this corresponds to ~6% of the genome (Myers et al.
478 2005). This contrasts to the honey bee and solitary bees where fine-scale maps are available
479 and recombination is relatively uniformly distributed in the genome (Wallberg et al. 2015;
480 Jones et al. 2019).

481 Two main mechanisms have been shown to lead to recombination hotspots. The first, which
482 is best understood in human and mouse, is governed by the PRDM9 protein. A zinc-finger
483 domain recognises a specific DNA sequence motif and then performs a histone modification
484 in the vicinity, which marks the sequence for a DNA double-stranded break that is repaired
485 by recombination during meiosis (Baudat et al. 2010; Myers et al. 2010; Parvanov et al.
486 2010). In species with this mechanism, both the PRDM9 zinc-finger domain and the
487 sequences present in hotspots are fast evolving, which results in a rapid turnover of hotspot
488 locations (Myers et al. 2010). Full-length PRDM9 orthologues are present among a range of
489 highly-diverged vertebrates including many fish, reptiles and mammals, but many full or
490 partial losses of the gene have also been inferred. In a study of 225 vertebrate genomes, a
491 minimum of six partial and three complete losses were inferred (Baker et al. 2017).
492 However, it is unclear whether PRMD9-hotspots are common in invertebrates.

493 A second mechanism is found in vertebrates that lack PRDM9, in which recombination
494 hotspots are localised to regions of open chromatin such as CpG islands and promoters. This
495 is found in dogs and in most or all birds, in which PRDM9 has been lost, and results in
496 hotspots with stable rather than rapidly evolving locations (Axelsson et al. 2012; Singhal et
497 al. 2015). A similar pattern is also observed in the yeast *Saccharomyces cerevisiae* in which
498 recombination preferentially occurs in promoter regions (Wu and Lichten 1994). PRDM9-
499 independent hotspots can be identified in CpG islands in some vertebrate genomes even
500 when PRDM9 is present (Joseph et al. 2024). In invertebrates such as *Drosophila* and
501 *Caenorhabditis elegans*, recombination hotspots appear to be absent (Coop and Przeworski
502 2007; Chan et al. 2012; Smukowski Heil et al. 2015). In insects, fine-scale maps of social and

503 solitary bees have not revealed recombination hotspots (Wallberg et al. 2015; Jones et al.
504 2019), but there is evidence for hotspots in a butterfly genome (Torres et al. 2023).

505 We find evidence that recombination is directed towards hotspots in both termite species.
506 We also identify a full-length *PRDM9* gene in both species, containing all of the domains
507 needed to initiate recombination. However, we are unable to demonstrate that PRMD9 is
508 responsible for the presence of recombination hotspots in the two genomes. We used a
509 motif prediction algorithm to predict the zinc-finger binding motif in *M. bellicosus* and *C.*
510 *secundus*, but we did not observe elevated recombination rate around instances of the
511 motif in either of the genomes. Furthermore, we did not identify any common sequence
512 motifs that were strongly enriched in recombination hotspots in either of the termite
513 genomes. A plausible interpretation of these observations is that the PRDM9 protein indeed
514 initiates recombination in hotspots in both species, but that positive selection leads to
515 frequent shifts in the target motifs, which results in a lack of a strong association between a
516 specific motif and LD-based hotspots (Myers et al. 2010). It is also possible that the
517 sequences of the zinc-finger motifs are not correctly represented in the genome assemblies,
518 which could result from problems with assembly around minisatellites. However, an
519 unknown mechanism could also be responsible for hotspots in termites.

520 *Evidence that germline DNA methylation suppresses recombination*

521 In insects with a functioning DNA methyltransferase machinery, the $CpG_{O/E}$ statistic shows
522 substantial variation along the genome, which mainly reflects variation in levels of germline
523 DNA methylation (Elango et al. 2009). In contrast to vertebrate genomes, methylation is
524 strongly skewed towards gene bodies in the genomes of insects (Glastad et al. 2011). In the
525 two termite genomes studied here, we find lowest values of $CpG_{O/E}$ in exons, whereas
526 noncoding flanking regions are biased towards higher values, indicative of lower levels of
527 DNA methylation (Figure 5, Supplemental Figure S3). Exons, introns and noncoding flanking
528 regions all display a predominantly bimodal distribution of $CpG_{O/E}$, likely reflective of the
529 presence of methylated and unmethylated regions. We find that recombination rate is
530 reduced in gene bodies compared to flanking regions in one of the two termite genomes,
531 but the overall genomic correlation between $CpG_{O/E}$ and recombination rate, although
532 significant, is weak. This could reflect the fact that the majority of the genomes are not
533 methylated, so that much of the variation in $CpG_{O/E}$ on the genome scale is not strongly

influenced by methylation. Our inference of reduced recombination rates in exons could also be influenced by lower N_E in these regions due to the effects of linked selection, which could result in more extensive LD (Charlesworth 2009). However, the observation that differences in $CpG_{O/E}$ among genes are associated with recombination rate indicates that linked selection is unlikely to be a major factor driving the observed differences in recombination rate and that germline DNA methylation is more important.

~~W~~e identified $CpG_{O/E}$ as the factor with the strongest influence on recombination rate variation among genes, with no significant effects of than differences in gene expression patterns across castes, a result that was also observed in the honey bee genome (Wallberg et al. 2015). This indicates that recombination rate variation is not modulated by differences in gene expression in these genomes, which might be expected if natural selection favours increased recombination rates in certain genes. For example, it has been proposed that natural selection could favour elevated recombination rates in genes with roles in worker behaviour or in immune function due to their important roles in colony function (Wilfert et al. 2007; Kent et al. 2012). However, the results presented here suggest that differences in recombination rate between genes with caste-biased patterns of gene expression are mainly due to underlying differences in methylation levels among genes.

A direct effect of germline DNA methylation in suppressing recombination could influence variation in recombination landscapes among vertebrates and invertebrates. Vertebrate genomes are usually highly methylated with the exception of CpG islands. In vertebrate genomes that lack a functional *PRDM9* gene, recombination events tend to localise to CpG islands (for example in dogs and birds) (Singhal et al. 2015; Axelsson et al. 2012). The effect of DNA methylation on recombination rate variation in invertebrates is less clear, but the results presented here also support a role of germline methylation in suppressing recombination.

Materials and Methods

Sample collection

M. bellicosus samples were collected from colonies in Kakpin, next to the Comoé National Park in Côte d'Ivoire (coordinates 8°39′N 3°46′W) (Elsner et al. 2018). *C. secundus* colonies

564 were collected from dead *Ceriops tagal* mangrove trees near Palmerston-Channel Island
565 (Darwin Harbor, Northern Territory, Australia; 12°30′S 131°00′E). Colonies were then kept
566 in *Pinus radiata* wood blocks in climate rooms in Germany, providing 28 °C, 70% relative
567 humidity, and a 12-h day/night cycle (Lin et al. 2021). For each species, each of the 10
568 collected samples came from a different colony.

569 *Population sequencing*

570 The termites were cut in two, approximately between head and thorax. DNA was extracted
571 from both parts using the QIAGEN Blood and Tissue Kit following the standard protocol,
572 including treatment with 4 µL RNase and 25 µL Proteinase K. The DNA extraction product
573 was cleaned and concentrated with ZymoResearch Genomic DNA Clean & Concentrator kit.
574 For most samples, the RNase treatment was repeated prior to cleaning and concentrating.
575 One DNA sample from each individual was chosen, based on the DNA amount and quality,
576 to be sequenced. Sequencing libraries were produced using the Illumina DNA PCR-free
577 library preparation kit according to the manufacturers protocol, using an input DNA quantity
578 of 200 ng per sample. This protocol yields insert sizes of approximately 350 bp. We
579 performed Illumina short-read sequencing on the libraries using NovaSeq 6000 S4 flow cell
580 with 2 x 150 bp paired end reads.

581 *Read mapping and variant calling*

582 The sequence data from the two termite species were mapped to the reference genomes
583 for *M. bellicosus* (Qiu et al. 2023) and *C. secundus* (Csec_1.0) (Harrison et al. 2018)
584 respectively, using Burrows-Wheeler alignment tool BWA version 0.7.17 (Li & Durbin 2009)
585 with the BWA-MEM algorithm. Sorting and indexing of the BAM-files was done with the
586 SAMtools package version 1.17 (Li et al. 2009), followed by adding read groups and marking
587 duplicate reads with Picard toolkit version 1.118 (http://broadinstitute.github.io/picard/).
588 After mapping, we excluded all scaffolds < 1 kbp from the *C. secundus* genome, which in
589 total correspond to 2% of the genome size, as they are potentially of lower quality and not
590 informative for analysis of linkage disequilibrium or recombination. For *M. bellicosus* there
591 are no scaffolds shorter than 1 kbp, but we excluded the following five scaffolds, which
592 together correspond to 3.78% of the genome length, due to unexpectedly high
593 heterozygosity: 93, 62, 41, 35 and 32.

One of the *C. secundus* individuals did not map well to the reference genome (71% mapped reads, unequal distribution between forward and reverse strand and an average mapping quality of 35 while all the other samples had an average mapping quality >45). This individual was excluded from all further analyses and hence the total number of termite individuals analysed in this study is 19, including 10 *M. bellicosus* and 9 *C. secundus*.

Variant calling was done using the tools HaplotypeCaller, GenomicsDBImport and GenotypeGVCFs from GATK version 4.3.0.0 as described in their best practices workflow (https://gatk.broadinstitute.org/hc/en-us/articles/360035535932-Germline-short-variant-discovery-SNPs-Indels-, last accessed 2023-07-11). The variants were filtered in multiple steps, first removing extended regions of low mapping quality or deviating read depth as those regions are likely to be unreliable. This was done based on statistics from the SAMtools mpileup and depth tools, respectively, removing 100 kbp windows with mean mapping quality below 70 or mean read depth more than two standard deviations from the genome-wide mean. Indels were removed using VCFtools version 0.1.16 (Danecek et al. 2011) before GATK VariantFiltration was run with the following limits, which are all equal to or stricter than the ones recommended (https://gatk.broadinstitute.org/hc/en-us/articles/360035890471-Hard-filtering-germline-short-variants, last accessed 2023-07-11) and adapted to the observed distributions of the corresponding statistics: QD<2; FS>50; MQ<40; ReadPosRankSum< -4; ReadPosRankSum>4; SOR>3; ExcessHet>5 for both species as well as MQRankSum with limits -5 and 5 for *C. secundus* and limits -6 and 4 for *M. bellicosus*. This was followed by additional filtering with VCFtools to select only bi-allelic sites with a minimum quality score of 30 and maximum of 40% missing genotypes. The SNPs with mean read depth in the lowest or highest 2.5% of the depth distribution were also filtered out, which translates to a depth below 10 or above 34 for *C. secundus* and below 5 or above 40 for *M. bellicosus.* For the recombination rate calculations, the SNPs were also filtered for a minor allele count >= 2, as rare variants appearing on only one chromosome have a relatively high false positive rate and are not informative regarding LD. The average proportion of missing genotypes per individual was 4.5×10^{-5} for *C. secundus* and 1.2×10^{-4} for *M. bellicosus*. After variant calling and filtering, the data was phased and imputed using Beagle version 5.1 (Browning and Browning 2007; Browning et al. 2018).

Estimation of LD decay

625 The decay of linkage disequilibrium, r^2, with increasing physical distance was estimated with
626 the software PopLDDecay version 3.42 (Zhang et al. 2019) over a maximum distance of 10
627 kbp. For this analysis, sequence data from *A. mellifera scutellata* was included for
628 comparison (Wallberg et al. 2017). The *A. m. scutellata* sequences were mapped to the
629 Amel_HAv3.1 reference genome (Wallberg et al. 2019) and processed and filtered in the
630 same way as described above for the termite data (GATK VariantFiltration with the limits
631 QD<2, FS>25, MQ<40, MQRankSum<-4, MQRankSum>4, ReadPosRankSum<-4,
632 ReadPosRankSum>4, SOR>3, ExcessHet>5 and VCFtools to select bi-allelic sites with mean
633 read depth between 5-13, quality score >= 30, minor allele count >=2 and <=40% missing
634 genotypes). For *M. bellicosus*, the reference genome contains some gaps of unknown size
635 and in order to avoid estimating r^2 across those gaps, scaffold breaks were introduced at the
636 corresponding positions.

637 *Estimation of population recombination rate*

638 We estimated the population-scaled recombination rate, ρ, using two methods: LDhat
639 (Auton and McVean 2007) and LDhelmet (Chan et al. 2012). The complete, interval and stat
640 functions of LDhat (https://github.com/auton1/Ldhat, downloaded 2023-04-19) were used
641 with 10 million iterations, sampling every 5000th iteration, taking the first 20 samples as
642 burn-in. We used a block penalty of 1 as this has been used previously with LDhat in similar
643 studies (Wallberg et al. 2015; Jones et al. 2019).

644 The recombination rate was also estimated using the software LDhelmet version 1.10 (Chan
645 et al. 2012), which uses a reversible-jump Markov Chain Monte Carlo algorithm to estimate
646 ρ. In order to prepare the input files for LDhelmet, the filtered vcf-files were converted into
647 multiple-sequence fasta-files using the vcf2fasta function from vcflib version 2017-04-04
648 (Garrison et al. 2022) and to the related file formats .snps and .pos with the - -ldhelmet
649 option from VCFtools (version 0.1.16). The first step of the LDhelmet workflow is to create
650 haplotype configuration files with the find_confs tool, followed by generation of likelihood
651 lookup tables with the tool table_gen and computation of Padé coefficients with the tool
652 pade. These tools were run with the recommended parameters, meaning that find_confs
653 was run with a window size of 50 SNPs, table_gen was run with a grid of ρ-values ranging
654 from 0 to 100 with increments of 0.1 up to 10 and increments of 1 for the remaining grid
655 and pade was run to generate 11 Padé coefficients. Scaffolds shorter than or equal to the

656 window size of 50 SNPs were removed, corresponding to 1% of the sequence length in *C.*
657 *secundus* and even less for *M. bellicosus*. The tool rjmcmc which contains the main
658 algorithm was run with a burn-in of 100,000 followed by 1,000,000 iterations with a block
659 penalty of 50 as recommended (Chan et al. 2012). For each species, the rjmcmc tool was run
660 three times with different seeds and the convergence between the replicates was evaluated
661 in terms of Spearman's rank correlation coefficient, which was > 0.95 with $p < 2.2 \times 10^{-16}$ for
662 all pairwise comparisons of both species. The binary output from rjmcmc was converted to
663 text, extracting the mean ρ-value between each pair of SNPs, using the tool post_to_text.

664 The outputs from LDhat and LDhelmet give the value of the parameter ρ between each pair
665 of consecutive SNPs. Those values were converted to equally sized windows across each
666 scaffold, as well as the coordinates of individual genomic features, by taking a weighted
667 average of values from overlapping intervals. The *M. bellicosus* scaffolds contain a few gaps
668 of unknown size and the values between SNPs across such gaps were removed.

669 The parameter ρ is proportional to the recombination rate *r* and the effective population
670 size N_E, which in turn can be estimated based on the mutation rate μ and the number of
671 segregating sites, *K*. In order to convert ρ to *r*, the following equations were used, where *n* is
672 the number of haploid sequences. The number of segregating sites (*K*) was calculated before
673 the filter on minor allele count >=2 was applied, as this filter likely removes many true SNPs
674 as well, which could affect the estimates.

675 θ_W was estimated for each sample using the equation below from (Watterson 1975):

$$\theta_W = K \Big/ \sum_{i=1}^{n-1} \frac{1}{i}$$

676 We used the value of θ_W to estimate N_E using:

$$N_E = \frac{\theta_W}{4\mu}$$

677 We estimated N_E using a range of mutation rates estimated from other insect species
678 (Keightley et al. 2009, 2014, 2015; Yang et al. 2015; Liu et al. 2017; Lynch et al. 2023). We
679 then estimated the recombination rate using the following equation, assuming a range of
680 values of N_E.

$$r = \frac{\rho}{4N_E}$$

681

682 *Cumulative plot of rho* ρ/kbp

683 A cumulative plot of the proportion of recombination events versus the proportion of the
684 physical distance along the genome was constructed based on estimates of ρ/bp for the two
685 termite species and previous estimates for *A. mellifera* (Wallberg et al. 2015; PRJNA236426).
686 The ρ/bp estimates between markers were placed in decreasing order before multiplication
687 with the respective physical distances between the markers. Then cumulative sums were
688 calculated for the ρ-values as well as the corresponding physical distances and divided by
689 the total genome-wide sums.

690 *k-mer enrichment in recombination hotspots*

691 In order to identify *k*-mers associated with elevated recombination rate, we defined
692 recombination hotspots as 2 kbp segments with at least five-fold elevated recombination
693 rate compared to the local background, as defined by 50 kbp flanking up and downstream of
694 the segment, resulting in 39837 regions for *M. bellicosus and* 40894 regions for *C. secundus.*

695 Then, we used these hotspots to search for motifs associated with elevated recombination
696 rate by comparing against an equivalent number of randomly chosen 2 kbp regions from the
697 rest of the genome. This was done using STREME 5.5.4 (Bailey 2021) using a minimum and
698 maximum size of *k*-mer of 8 and 20, (--minw 8 ; --maxw 20) and otherwise default options.
699 From all motifs with significant enrichment after adjusting for multiple testing, we then
700 considered only motifs present in more than 5% of all hotspots and an at least two-fold
701 enrichment compared to the background as credible candidates.

702 *Identifying PRDM9 orthologues in M. bellicosus and C. secundus*

703 A full-length copy of PRDM9 is present in the *C. secundus* genome annotation, but not in *M.*
704 *bellicosus*. Using OrthoFinder (Emms and Kelly 2019), and the genome annotation files for
705 both species, we identified a single orthologue to the *C. secundus* PRDM9 in *M. bellicosus*.
706 We analysed this region using the NCBI conserved domain search (Wang et al. 2023). We
707 also searched the *M. bellicosus* assembly for the PR/SET domains derived from *C. secundus*
708 and *Zootermopsis nevadensis* using BLAST (Camacho et al. 2009) and subsequently for all

709 other PRDM9 domains (KRAB, SSXRD, ZF-Casette) to identify hits that contain all other
710 PRDM9 domains in the vicinity in the correct order. We used GeneWise (Madeira et al.
711 2024) with default options to perform gapped alignment of a the PRDM9 protein sequence
712 from *Zoothermopsis nevadensis* against the target region to predict exon-intron borders.

713 *Predicting binding sites from zinc-finger-motifs*

714 Using the ZF-motifs from *C.secundus,* we obtained letter probability matrices for predicted
715 binding motifs using a webserver (http://zf.princeton.edu/index.php ; (Persikov and Singh
716 2014) which were used to search for binding sites across the genome using FIMO (Grant et
717 al. 2011) with default options. Subsequently, the mean rho for the surrounding 1 kbp bin
718 was used to test for a difference in mean rho between bins associated with a suspected
719 binding site, and a similar number of randomly chosen bins without association. For
720 significance testing, we repeated this draw 10.000 times to compare the associated bins
721 against the 95% confidence interval of the resulting distribution.

722 *Analysis of genomic correlates of recombination*

723 We divided the genome into 10 kbp windows in which average ρ and other genomic
724 features were estimated. Windows shorter than 5 kbp (half of the specified window size),
725 which appear in short scaffolds or at the ends at longer scaffolds, were excluded from the
726 analyses (excluding less than 1% of the sequence for each species). Correlation coefficients
727 were estimated with Spearmans ρ, with significance estimated by permutation tests with
728 10,000 iterations.

729 In order to determine the repeat content across the *M. bellicosus* and *C. secundus* genome
730 assemblies, we first generated custom repeat libraries for each species with RepeatModeler
731 (Flynn et al. 2020) using default options. This was then combined with Repbase 29 (Bao et
732 al. 2015) and Dfam 3.8 (Storer et al. 2021) and used to run RepeatMasker with default
733 options on each genome. We estimated the proportion of sequence in each repeat class in
734 10 kbp windows and used Spearman's rank correlation to correlate this with estimates of
735 recombination rate.

736 *Per gene recombination rate and $CpG_{O/E}$ ratio*

737 The observed/expected frequency of CpG sites ($CpG_{O/E}$) and mean ρ were calculated on a
738 per-gene basis, as well as for exons and introns, and 50 kbp flanking regions 10 kbp

739 upstream and downstream of the gene, akin to Wallberg et al (2015). For recombination
740 rate, estimates of ρ between markers were used, utilising a weighted mean when the
741 element spanned multiple markers. For visualisation, extreme $CpG_{O/E}$ values due to low GC
742 content were set to a maximum of 4.

743 We tested for significant difference in mean between ρ and $CpG_{O/E}$ in flanking regions, exons
744 and introns using paired *t*-tests corrected for multiple testing using a Bonferroni threshold.

745 *Differential expression data*

746 We classified genes in both species according to their caste-biased patterns of expression
747 from two studies (Elsner et al. 2018; Lin et al. 2021). Elsner et al. (2018) analysed four castes
748 of *M. bellicosus*, with two age classes of each: major and minor workers, queens and kings.
749 They analysed differences in gene expression among these classes using RNA-seq data. We
750 reclassified the differential expression data by grouping the direct caste-vs-caste
751 comparisons as "queen-biased", “king-biased”, “worker-biased”, “reproduction-biased”,
752 "male-biased" or "female-biased" if they were differentially upregulated for this caste (or
753 group) in comparison to other castes (or groups). Since Elser *et al.* (2018) initially mapped
754 the *M. bellicosus* reads against the *Macrotermes natalensis* genome, We used OrthoFinder
755 (Emms and Kelly 2019) to identify the *M. bellicosus* orthologues corresponding to the
756 differentially expressed genes. Only single-copy genes were considered for this analysis.

757 Lin et al. (2021), performed RNA-seq on samples of workers and queens. Here, we used the
758 data from untreated queens and workers. Differentially expressed *C. secundus* genes were
759 classified as “worker-biased” or “queen-biased” if they were differentially expressed with a
760 bias to the respective caste, or unbiased if they were not, and subsequently compared
761 between classes. The lists of genes we identified in the caste-biased categories in both
762 species are provided as Supplemental Tables S9 and S10.

763 *Correlates of recombination rate variation among genes*

764 In order to assess the relative importance of $CpG_{O/E}$ and differential expression patterns on
765 recombination rate in genes (genic ρ/kbp), two ordinary least squares models were built
766 using statsmodels (Seabold and Perktold 2010) for each termite species. Genic $CpG_{O/E}$,
767 differential expression categories and flanking region ρ/kbp were used as exogenous

768 variables. In the first model, we included flanking region ρ/kbp and $CpG_{O/E}$. In the second
769 model, we included all available biased expression categories for each species.

770

771 **Data access**

772 The Illumina whole-genome sequencing data generated in this study have been submitted
773 to the NCBI BioProject database (https://www.ncbi.nlm.nih.gov/bioproject/) under
774 accession number PRJNA1021607. Custom scripts are available on GitHub
775 (https://github.com/troe27/termite-recombination-rate) and as Supplemental Code.

776

777 **Competing interest statement**

778 The authors declare no competing interests.

779

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794 conducted according to the Nagoya protocol. MTW designed and led the research; TE and
795 TR conducted the analysis; MTW, TE, TR and JK wrote the paper; DE and JK contributed data
796 and samples; AO, YL, and TL performed lab work.

797

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1071

1072 **Figure Legends:**

1073

1074 **Figure 1.** Genome-wide decay of LD measured as r^2 versus distance (bp) between SNPs for
1075 the two termite species (*M. bellicosus*, dark red; *C. secundus*, yellow) and honey bees (*A.*
1076 *mellifera scutellata*, blue; data from Wallberg et al. 2017).

1077 **Figure 2.** Variation in recombination rate estimated as ρ/kbp across representative genomic
1078 scaffolds in a) *M. bellicosus* and b) *C. secundus*. Estimates of ρ/kbp are calculated in 10 kbp
1079 and 100 kbp windows.

1080 **Figure 3.** Cumulative plot of proportion of recombination events versus proportion of the
1081 genome for the two termite species *M. bellicosus* and *C. secundus* compared to the honey
1082 bee *A. mellifera* (Wallberg et al. 2015). Dashed lines show the proportion of the genome
1083 where 50 % of the recombination occurs, which for *M. bellicosus* is 0.4 %, *C. secundus* is 0.2
1084 %, and *A. mellifera* is 32 %.

1085 **Figure 4.** PRMD9 structure and predicted zinc-finger motifs in the *M. bellicosus* and *C.*
1086 *secundus* genomes. A) Predicted structure of the PRDM9 protein sequence in *C. secundus.* B)
1087 Predicted structure of the PRDM9 gene in *M. bellicosus* identified by homology searches.
1088 Exons and conserved functional domains are marked. The mapped exons from
1089 *Zoothermopsis nevadensis* are also shown. C) Structure of PRDM9 gene in *C. secundus*.
1090 Exons and conserved functional domains are marked. D) Predicted zinc finger binding motif
1091 in *M. bellicosus,* E) Predicted zinc finger binding motif in *C. secundus*.

1092 **Figure 5.** Boxplots showing variation in levels of $CpG_{O/E}$ and recombination rate (ρ/kbp; rho)
1093 in genic and flanking regions in the *M. bellicosus* and *C. secundus* genomes. The differences
1094 between all categories are significant.

1095 **Figure 6**. Boxplots showing variation in levels of $CpG_{O/E}$ and recombination rate (ρ/kbp) in
1096 the coding region of genes in the *M. bellicosus* and *C. secundus* genomes classified according
1097 to their patterns of gene expression (Q = queen-biased, K = king-biased, W = worker-biased,
1098 F = female-biased, R = reproductive-biased).

1099

1100

Table 1. Estimates of levels genetic variation, effective population size and recombination rate in two termite species.

						LDhat		LDhelmet	
Species	Assembly length (Mb)	No. SNPs	θ_W/bp	μ bp^{-1} gen^{-1}	N_E	ρ/kb	r (cM/Mb)	ρ/kb	r (cM/Mb)
M. bellicosus	1,139	5,581,662	0.14%	2.7 x 10-10	1,278,982	1.69	0.033	4.28	0.084
				4.5 x 10-9	76,876		0.550		1.392
				8.1 x 10-9	42,898		0.986		2.494
C. secundus	992	15,037,468	0.44%	2.7 x 10-10	4,080,725	4.85	0.030	16.39	0.100
				4.5 x 10-9	245,280		0.494		1.671
				8.1 x 10-9	136,869		0.885		2.994

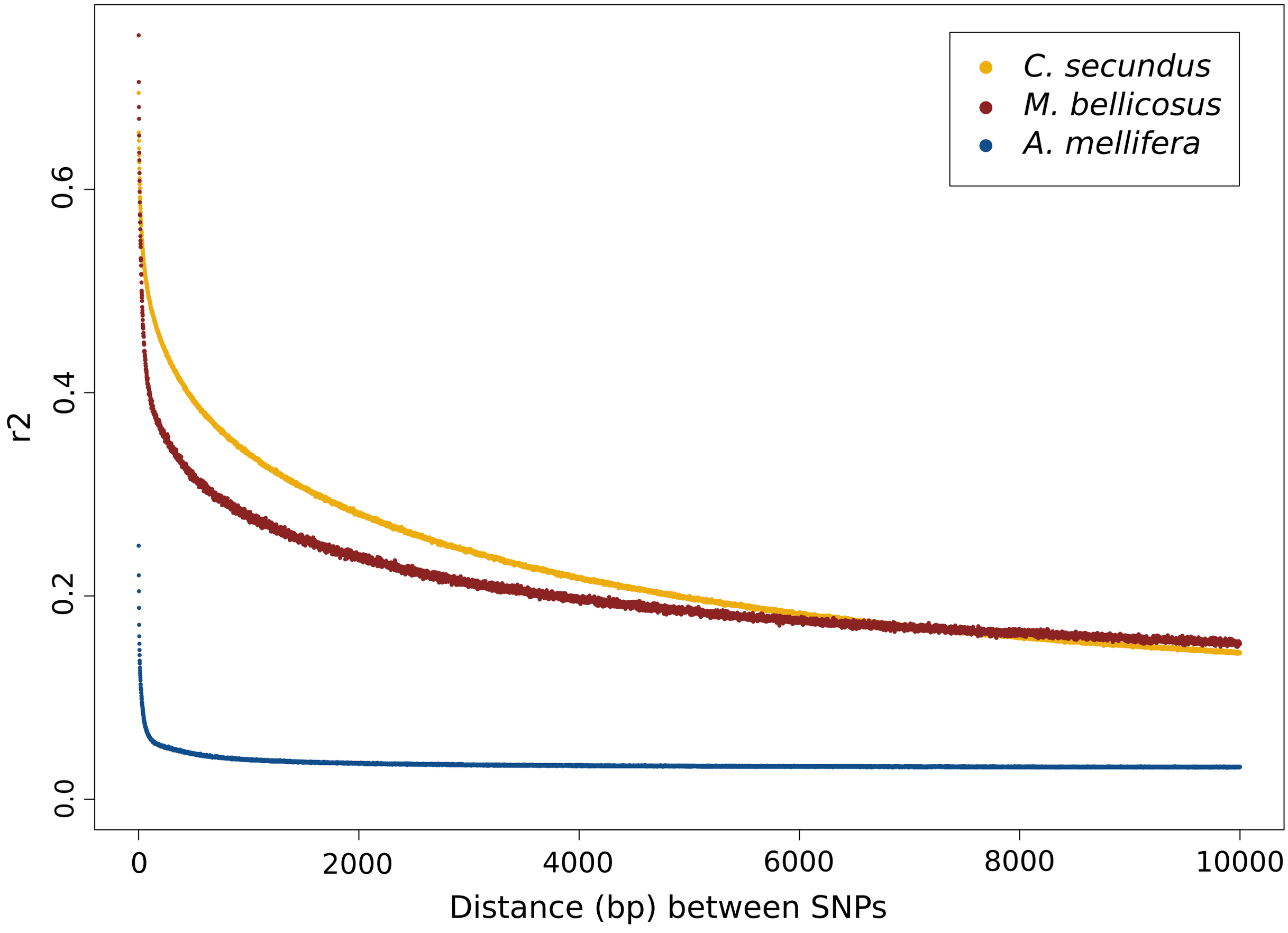
θ_W/bp - Watterson's θ per base pair

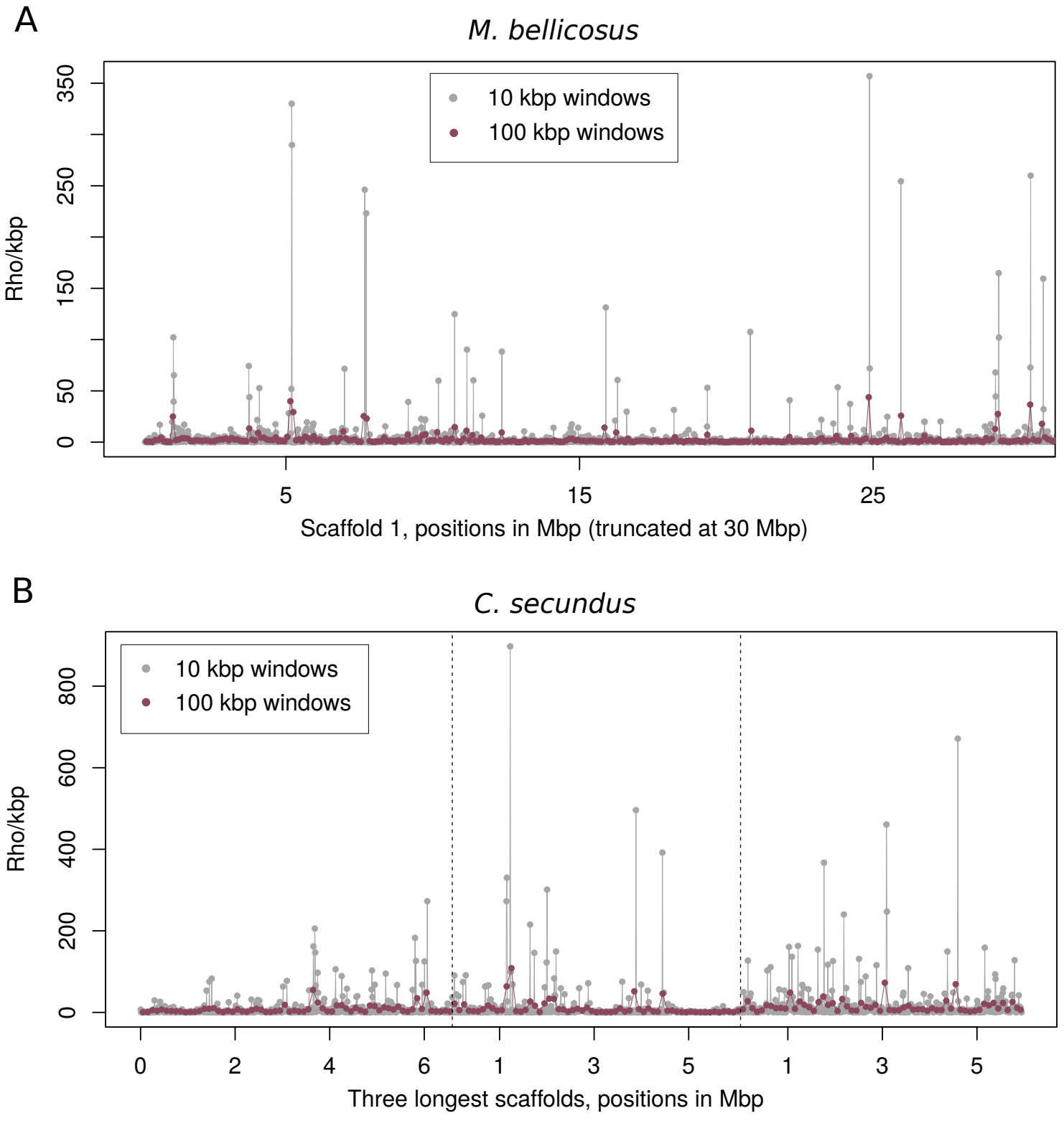
ρ/kbp - population recombination parameter, ρ, per kilobase

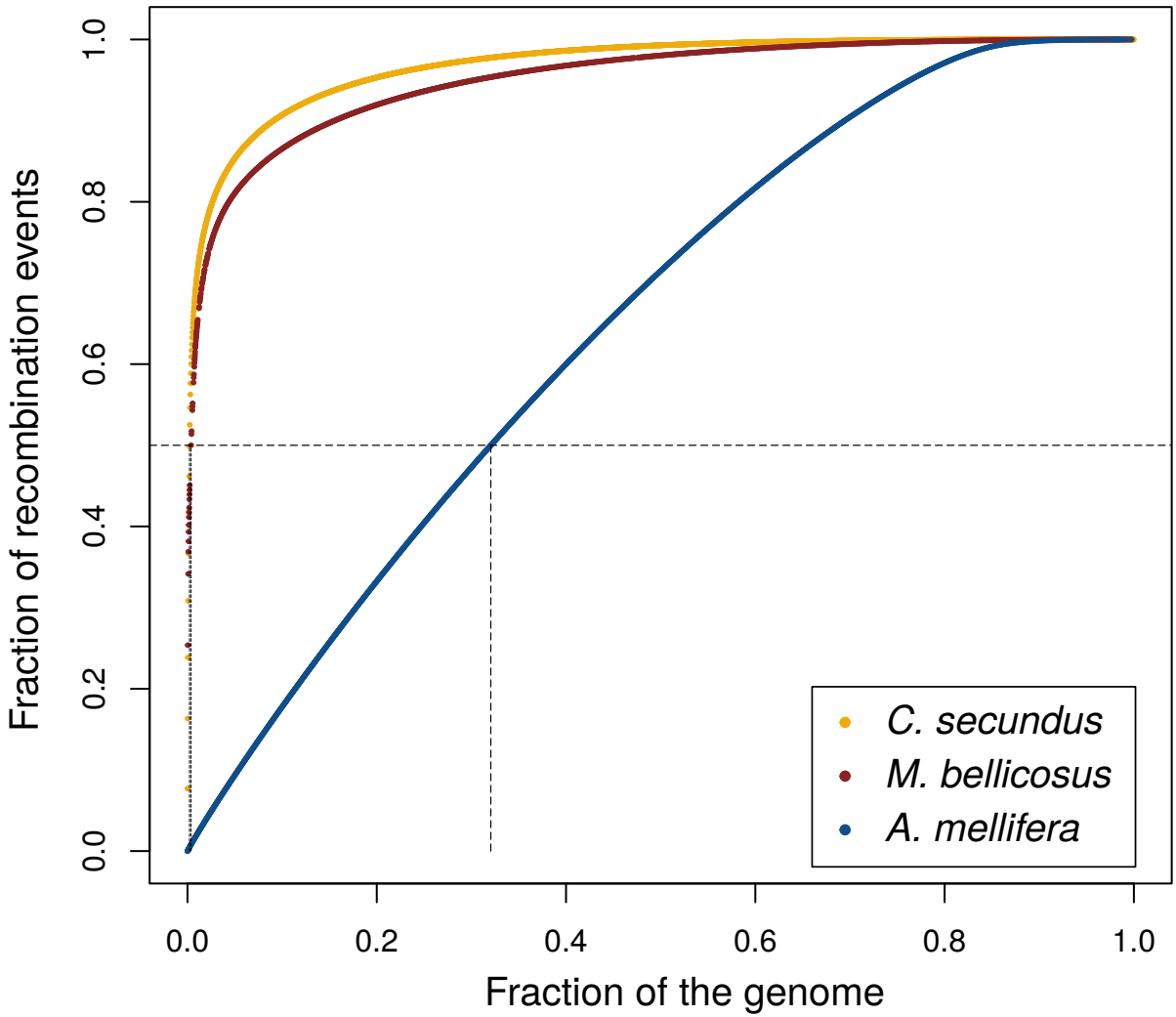
μ bp^{-1} gen^{-1} - mutation rate per base pair per generation taken from literature. Estimates correspond to *Acyrthosiphon pisum* (2.7 x 10^{-10}), *Drosophila melanogaster* (4.5 x 10^{-9}) and *Drosophila pseudoobscura* (8.1 x 10^{-9})(Lynch et al. 2023).

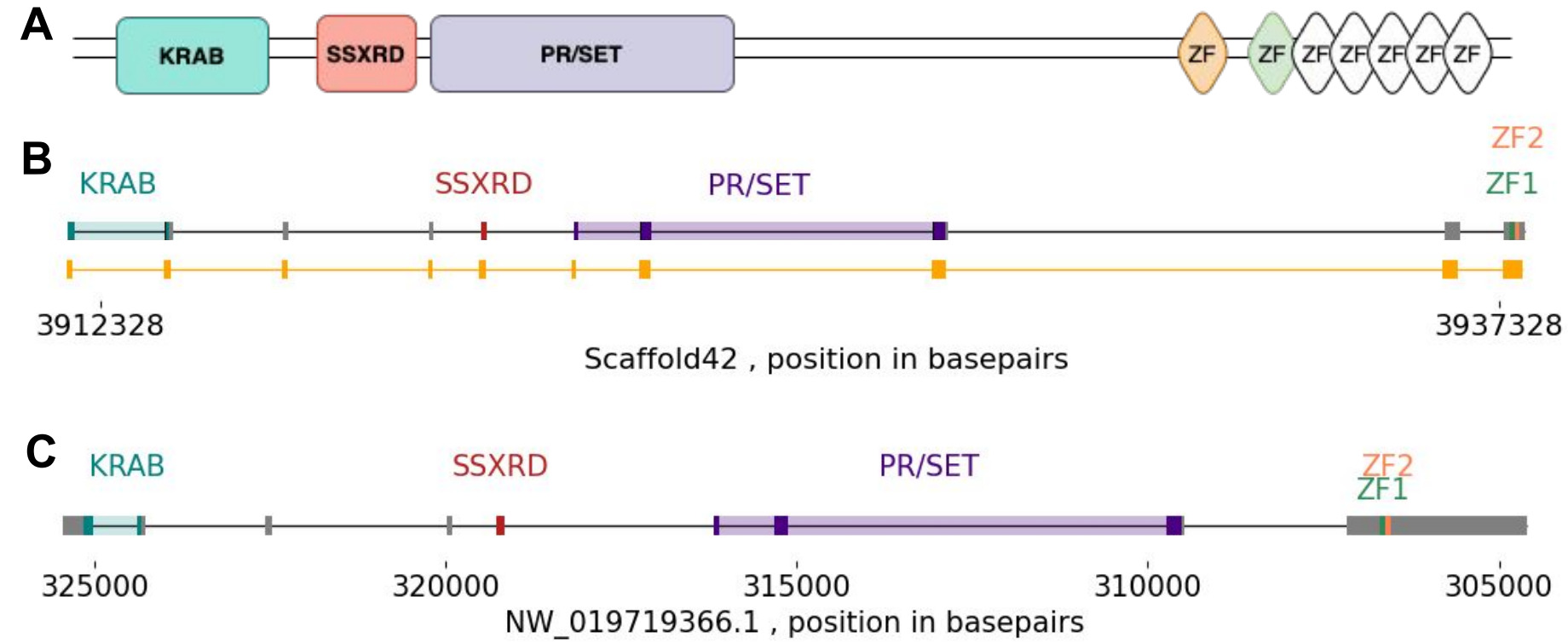
N_E - effective population size

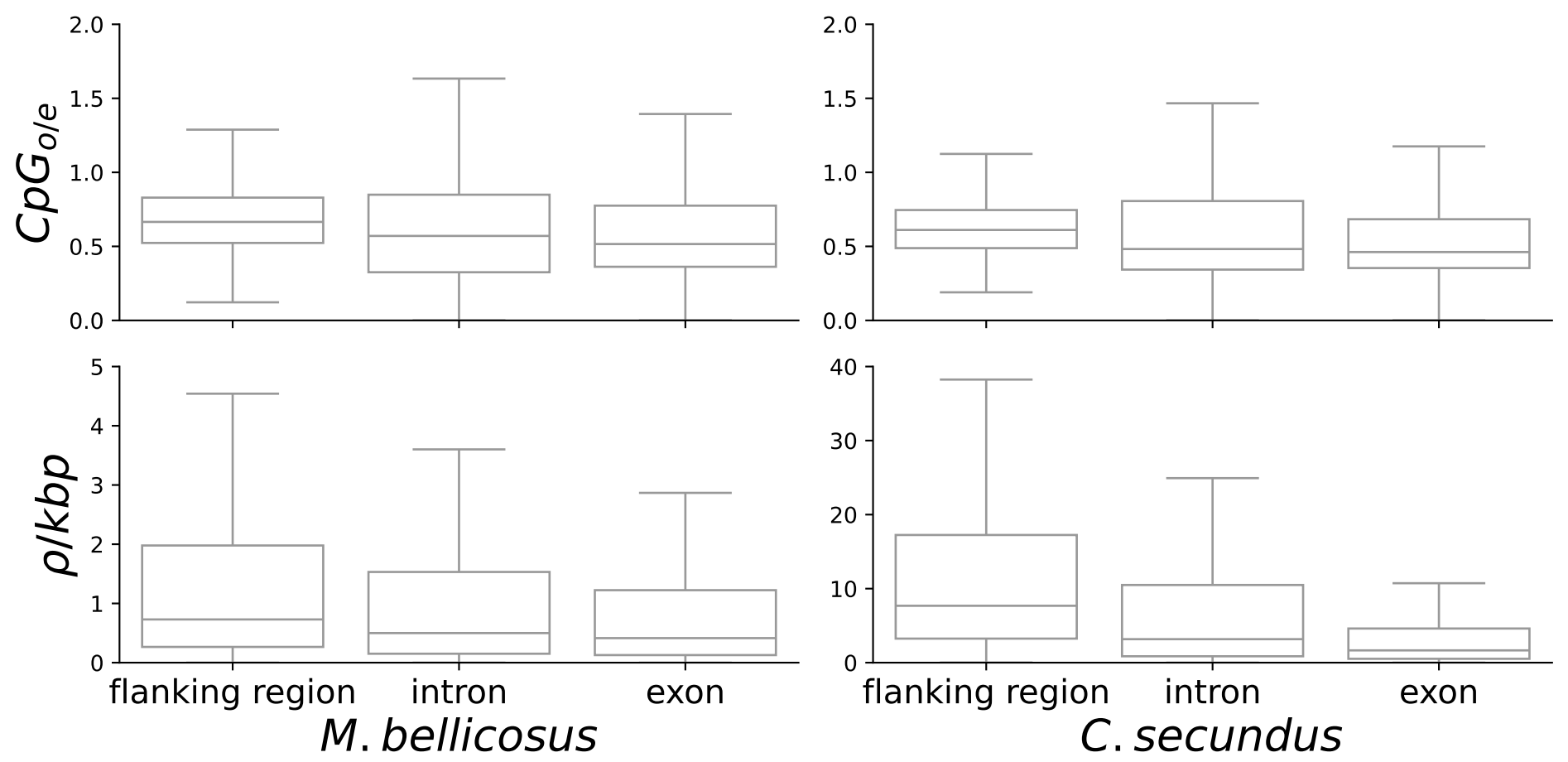
r (cM/Mb) - recombination rate in centimorgans per megabase


C. secundus
M. bellicosus
A. mellifera
r2
0.0
0.2
0.4
0.6
0
2000
4000
6000
8000
10000
Distance (bp) between SNPs


A
M. bellicosus
10 kbp windows
100 kbp windows
Rho/kbp
0
50
150
250
350
5
15
25
Scaffold 1, positions in Mbp (truncated at 30 Mbp)
B
C. secundus
10 kbp windows
100 kbp windows
Rho/kbp
0
200
400
600
800
0
2
4
6
1
3
5
1
3
5
Three longest scaffolds, positions in Mbp


Fraction of recombination events
0.0
0.2
0.4
0.6
0.8
1.0
Fraction of the genome
0.0
0.2
0.4
0.6
0.8
1.0
C. secundus
M. bellicosus
A. mellifera


A
KRAB
SSXRD
PR/SET
ZF
ZF
ZF
ZF
ZF
ZF
ZF
B
KRAB
SSXRD
PR/SET
ZF2
ZF1
3912328
3937328
Scaffold42 , position in basepairs
C
KRAB
SSXRD
PR/SET
ZF2
ZF1
325000
320000
315000
310000
305000
NW_019719366.1 , position in basepairs
D
bits
2.0
1.0
0.0
5
10
15
20
25
30
35
40
E
bits
2.0
1.0
0.0
5
10
15
20


$CpG_{o/e}$
ρ/kbp
2.0
1.5
1.0
0.5
0.0
5
4
3
2
1
0
40
30
20
10
0
flanking region
intron
exon
flanking region
intron
exon
M. bellicosus
C. secundus

$CpG_{o/e}$
ρ/kbp
2.0
1.5
1.0
0.5
0.0
3.0
2.5
30
20
10
0
Q
K
W
M
F
R
unbiased
$M. bellicosus$
$C. secundus$