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# Discussion Draft v1

The higher instance of rapid evolution in recombination rates could be attributed to a difference in effective population size. Selection becomes less effective due to mutation-drift balance, in small populations (cite).

In this scenario, modifiers which increase recombination rates will be selected for since they increase the efficiency of selection (find citation, Otto?).

In the house mouse species complex – differences in Ne have been estimated for the three main subspecies, Mm domesticus, castaneus, and musculus -- musculus was found to have the lowest Ne and castanesus had the largest Ne [@**geraldes2011**]

(the Ne was associated with genetic differentiation

, mm domesticus has a higher predicted Ne compared to mm musculus and mm molossnius (which is predicted to have the lowest.

2. hybridization – may // historical contact – hybrization contact may – select for the evolution of higher recombination rates to purge deleterious introgressed DNA

We think its’s notable that the three high-recombining strains identified in this study all have a connection to hybridization (from natural populations). Musculus^PWD^ was sampled from the house mouse hybrid zone in central Europe, musculus^SKIVE^ was sampled for the northern section of the hybrid zone and has musculus nuclear genome and domesticus mitochondria (cite). The subspecies molossinus is a natural hybrid of musculus and cataneus (Geraldes et al 2008, Geraldes et al 2010).

However not all strains had increased recombination rate, additional hybrid Musc

(additionally, new musc samples from eastern Europe GOR have shown higher rates (Beth Dumont )? (ask if we can publish this)

(Carl Veller paper -- <https://www.biorxiv.org/content/10.1101/846147v1.full.pdf> -- this may be more about a connection to variance in genetic relatedness

~~three modifier models and two functional and cell physiology models (table X).~~ We choose To place our results in the broader context of recombination rate variation we examine a number of models related to recombination landscapes and evolution of the genome wide recombination rate to compare to our results (Table X). The three modifier models were built to explain variation in genome wide recombination rates between sexes (heterochiasmy), while the chromosome oscillatory movement (COM) model was built to describe positive interference. While some aspects of our results fit existing models, the combination of unexpected patterns motivates a new model based on selection at the metaphase I spindle. ~~This spindle based selection model was developed to explain the results resented in this manuscript~~.

Evolution of reversed heterochiasmy direction

In our results and more generally in the literature, female biased heterochiasmy is the most common pattern, however male biased heterochiasmy is not especially rare (Brandvain and Coop 2012).

**~~Our results extend previous reports of male biased heterochiasmy (B. L. Dumont and Payseur 2011) to new subspecies of house mouse (~~*~~molossinus~~*~~) and emphasize the short evolutionary period.~~**

Our results emphasize the rapid evolution and extend previous reports of evolved recombination rates in wild derived strains (Dumont, Forjt) by reporting i) framing the recombination rate evolution within a larger number of strains and ii) adding female-specific data for more strains (which historically have less empirical results). Whether these instances of evolution of genome-wide recombination rates are due to independent events or segregating genetic variation within house mouse subspecies requires further study. Regardless, the faster male evolution in genome-wide recombination rates suggests that even for species in female biased heterochiasmy species, selecting for higher male specific genome wide recombination rates may be the most effective way to increase the sex-averaged recombination rate for a genetic background. This insight could be important for animal breeding programs (Battagin et al. 2016).

~~The direction of heterochiasmy under the two locus modifier model is dependent on female specific recombination modifier suppresses or increases recombination, if the modifier is linked to the driving locus, and the meiotic stage (reduction or equatorial division) when the driver acts (see Table 1 of Brandvain and Coop (2012)).~~

Under the spindle based model, faster male evolution of the genome wide recombination rate, is primarily driven by a efficient spindle assembly checkpoint (SAC) acting on chromosome structures at metaphase I alignment. The SAC prevents aneuploidy by ensuring all bivalents are correctly attached to the microtubule spindle, (bi-orientated) before starting the metaphase-to-anaphase transition ((Lane and Kauppi 2019), subramanian and Hochwagen , J. Dumont and Desai (2012)).

A stable chromosome structure requires, i) kinetochores attached to opposite poles of the cells and ii) at least one crossover to create tension across a proportion of sister cohesion (Lane and Kauppi 2019). Genetic variants will be selected in a manner to optimize the process of bi-orientation and prevent SAC from delaying cell cycle or triggering apoptosis. Multiple lines of evidence indicate that the effectiveness of SAC in spermatogenesis is greater compared to oogenesis (Lane and Kauppi 2019), Subrahman), which are connected to conserved features of gametogenesis; centrosome spindle (So et al. (2019), J. Dumont and Desai (2012)) and cell volume (Kyogoku and Kitajima 2017).

**The more stringent SAC in spermatogenesis will be more effective at removing genetic variants which interfere with bi-orientation compared to females.**

~~This model nominates conserved differences in in the~~

This dynamic can give rise to sex-specific genetic variants which in turn can result in **~~context of meiosis between males and females as the primary source of~~ distinct evolutionary trajectories in genome wide recombination rates**.

### Conservation in sexual dimorphism in between cell variation in crossover number (cite Lenzi et al)

Regardless of whether these hypotheses are true, Our observations of between cell variation fail to support a basic prediction of (the relationship between mean and variance) a higher mean will be associated with a higher variance. Across all strains, including the high-recombining strains, musc^PWD^, musc^SKIVE^ and mol^MSM^, females consistently have higher between cell variance for crossover count. These results add to previous findings in mice and humans that oogenesis has increased variance for crossovers (Lynn et al, Gruhn) and precursors to crossovers (Lenzi et al ) compared to spermatocytes. **This** feature of heterochiasmy supports evolutionary theories predicting distinct reproductive strategies between females (diversifying offspring) and males (maintain successful haplotypes) (Trivers and others 2002).

In the spindle based selection model, the less efficient SAC in oocytes leads to relaxed selection on the metaphase I chromosome structure. This will result in increased variance in chromosome structure and crossover number per cell, not just across strains, but across cells within individuals. Oocytes at metaphase I, have an acentriolar spindle comprised of diffuse network of microtubules with multiple microtubule organizing centers (Schuh and Ellenberg 2007). Centrosomes spindles are in spermatogensis and mature sperm cells delivers centrioles (most mammals) or centrosome material (rodents and rabbits) to the egg during fertilization (Manandhar, Schatten, and Sutovsky (2005)). This is another way the spindle based selection model is linked to conserved sex differences in gametogenesis (Ross and Normark 2015).

### Conservation in sex-specific recombination landscape

Our results extend (the mountain / plethora) or previous data reports for broad scale sex difference in the recombination landscape (Sardell) – data comprised mostly of highly divergence species / large evolutionary distances. In contrast our results demonstrate that this pattern is maintained across much shorter evolutionary distances and even with rapid evolution in the genome-wide recombination rate.

We argue that this conservation of the male chromosome end bias // recombination landscape is one of the most conserved features of heterochiasmy and could be connected to fundamental aspects of gametogenesis.

As reviewed in (Sardell and Kirkpatrick 2020), sexual dimorphism in the broad scale recombination landscape is a highly conserved trait. The two locus modifier and SACE models predict sexual dimorphism in the broad scale recombination landscape, for diminishing the effect of drive systems and maintaining larger chromosome blocks under linkage in males respectively. The COM model, predicts the sex differences in the recombination landscape via interference is due to a combination of the length of the axis and differing strengths of chromosome movements during the pairing process (Hultén 2011).

Under the spindle based model we hypothesize that the sexual dimorphism in the recombination landscapes hinges on sex differences on the requirements for chromosome cohesion in late meiosis I. The irreversible process of the metaphase to anaphase transition is initiated by the protolytic decay of the sister cohesion connecting homologs (Lane and Kauppi 2019), subramanian and Hochwagen , J. Dumont and Desai (2012)]. The number and placement of crossovers alter the distribution of sister cohesion and the resulting chromosome structure when bivalents are aligned and bi-oriented on the metaphase plate (Veen and Hawley 2003, Altendorfer et al. (2020)). Differences in timing of cell cycle between oogenesis and spermatogenesis imposes the different selective pressures on how sister cohesion affects chromosome structure. Faster spermatogenesis may select for synchronization of the separation homologs (cite?). While in oogenesis, the slower cell cycle and multiple arrest stages may require chromosome structures with greater stability on the MI spindle, especially for those with dicyate arrest (Lee 2019).

~~A consequence of the sexual dimorphism in broad scale recombination landscapes is that the male chromosome end bias (will have observation/ will be detected under more approaches) while the female pattern will – is more difficult to detect (since it is uniform)/.~~

~~recombination pattern drives deviation from an uniform distribution in any sex averaged recombination landscape~~ (Sardell and Kirkpatrick 2020). ~~Elevated recombination rate at the chromosome ends is a conserved trait across animals and plants and has a consequence of higher genetic diversity near chromosome ends (Haenel et al. 2018). (this pattern is driven by the male recbination landscape (Sardell and Kirkpatrick 2020). )~~

The higher levels /increased genetic diversity and recombination rates at chromosome ends (Haenel et al. 2018)– suggests that this is driven by the male-specific recombination landscape (Sardell and Kirkpatrick 2020). (giving rise to interesting evolutionary predictions).

### Conservation of sex differences in chromatin structure

Our results from musculusMSM and musculusPWD demonstrate that chromatin compaction are uncoupled from the direction of heterochiasmy in house mice. These results slightly depart from predictions which nominate chromatin compaction as the primary driver of recombination rate variation (Petkov et al. 2007). Chromatin compaction could explain variation in heterochiasmy, which is driven by the distinct meiotic contexts across sexes but is a weak predictor for recombination rate variation within the sexes. Our results indicate the sexual dimorphism in chromatin compaction is conserved in house mouse (e.g. females have longer SC than males) and that the rapid male-specific evolution in crossover number per cell proceeded through another aspect of crossover regulation (see below).

Only the COM model predicts sexual dimorphism in chromatin structure and attributes the source to greater cell volume in oocytes. This prediction model might fit broader pattern such as in *Arabidopsis thalania* where pollen is the larger cell and has longer axis length (Cahoon and Libuda 2019).

As outlined in Haenel et al. (2018), sexual dimorphism in chromatin organization translates to interference strength measured in base pairs (linkage maps).

From empirical data in mice (Petkov et al. 2007, Lynn et al. (2002) and humans (Gruhn et al. 2013), there seem to be to general configurations for chromatin structure: longer axis and shorter loops in females; shorter axis and longer loops in males. thought to be SC, which is built on top of the regardless of the loop size. Supporting this is the observation that As a consequence, since more base pairs are sequestered into the radial loops per unit of the linear central axis, chromatin organization with longer DNA loops (and shorter axis), as seen in males, will have a signal of stronger interference when measured in base pairs compared to ‘the typical female chromatin configuration. Stronger interference in males, has been noted across many sex-specific linkage maps (cite) strengthening the hypothesis that sexual dimorphism in the chromatin organization is widespread, however this has only been confirmed by cytological data in mice and humans. (Also large difficulties in observing sperm cells through meiosis).

~~Stronger interference strength in base pairs for male specific linkage maps is indirect evidence that sexual dimorphism in chromatin organization however this has yet to be confirmed in cytological data from both sexes in species beyond mice and humans.~~

### Evolution of interference strength in males

An expected consequence of our observed elevated genome-wide recombination rate is lower LD across the genome, which may increase the efficiency of selection and impact the dynamics of introgression (cite). Given that the higher genome-wide recombination rates are paired with stronger interference these predicted pattern may have heterogeneous signal along chromosomes.

Examples of evolution of interference strength are rare and may be complicated by changes in the underlying karyotype structure (Segura et al 2014). The general pattern of empirical measures of interference strength is that it has a negative correlation to the genome wide recombination rate (Otto and Payseur 2019). This fits the logic of the chromosome axis acting as the ‘real estate’ for DSBs and aligns with known molecular mechanisms (cite). Two examples of the opposite direction, a positive correlation of interference strength and genome-wide recombination rate, involve descriptions of observations at the single bivalent level; the between lab-raised and wild mice of *Peromyscus leucopus* from (Peterson, Miller, and Payseur 2019) or large effects on genome wide recombination rates across a short evolutionary differences; the within-sex comparison of two breeds of cattle with different genome wide recombination rates (Ma et al. 2015). **~~We propose that there is a difference in resolution and power between these two groups of empirical results with the positive and negative relationship between genome wide recombination rates and interference strength~~**~~.~~

We propose that the spindle based selection model can explain the positive correlation via selection on the amount of sister cohesion connecting homologs at **metaphase**. The evolution of genome wide recombination rates in our study is driven by a transition of the majority of bivalent having single crossovers to an enrichment of bivalents with two crossovers. All else being equal, interference strength would be expected to be equal or even weaker. Our results show that the two crossovers are spaced further apart when SC length is controlled for and chromosome size effects are minimized, in the strain enriched for two crossover bivalents. Assuming that chromatin compaction between pachtyene and metaphase is uniform along chromosomes, an outcome of this further spacing of two foci results in an increased area of sister cohesion connecting homologs (Figure X).

The COM model predicts that interference and the recombination landscape arises from known oscillatory movements during prophase, however it lacks a mechanism for a evolutionary based predictions. While the SACE modifier model does not explicitly model evolution of interference strength we note that a logical outcome of the main prediction of maintaining larger chromosome blocks in males, would be a recombination landscape with stronger interference strength.

We have focused on the model involving direct selection on the recombination pathway, which has an impact on the fitness of an individual, but we acknowledge connections to other models involving indirect selection on recombination rates which involve the fitness outcomes of offspring. A model from Goldstein et al, reviewed in (Otto and Payseur 2019) and Veller, Kleckner, and Nowak (2019), predict that interference strength evolves whenever increased recombination rates evolve. The simulations under this model indicate that the space across multiple loci or between multiple crossovers increases in a positive manner with the genome wide recombination rate. A distinguishing feature of this model from other **modifier** models is that the number of crossovers per chromosome is kept constant. **Empirically**, the range of crossovers per chromosome is quite limited, 1-3, for the majority of chromosomes across most taxa (Otto and Payseur 2019, Stapley et al. (2017)). Constraining the number of crossovers per chromosome in models may fit empirical data better than those where recombination rate across an abstracted genetic space is unconstrained.

### Future steps

There are still many un-known aspects regarding heterochiasmy (Lenormand) , these novel results suggest – we hope ppl we follow up . (fitness – evolutionary dynamics – role in linked selection)

We make three suggestions for future steps in studying recombination variation. First consider the when comparing sex specific meiotic traits consider that evolutionary distinct trajectories due to the fundamental differences in gametogenesis. Second certain systems can be leveraged to overcome limitations inherent in some approached. For example, identifying chromosomes across cells in cytological data requires chromosome specific probes, (e.g. FISH) but chromosome specific data can be collected from organisms with diverse karyotypes (birds, peromyscus, humans) or backgrounds with Robertsonian trans-locations.

Third we encourage the cross-pollination of physiology based models and more abstract model such as population genetic models with testable hypotheses **(Dapper Paysuer)**. A goal of such merging of models could be to connect empirical findings across scales.

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