Another thing to point out / regarding this model -- is the connection to sex difference in interference strength. Our results of conserved within strain raw IFD lengths - yet when the IFDs are controlled for total SC length, we observed sexual dimorphism with males having longer IFD^normalized^ (stronger interference), mirror those observed in [@petkov2007].

The model / explanation proposed in that paper is that The chromatin structure which has longer loops (and shorter axis) will have more DNA bps folded / sequestered into the DNA loops. Thus the strength of interference will be stronger because with each step (count) along the 2D axis, more bases pairs are being skipped above the axis. These findings point out two things, This part of heterochiasmy generates testable prediction: First, the interference strength measured in chromosome axis units (or SC) is generally conserved between sexes. Second the sex with longer axis and shorter loops will have weaker interference compared to the other sex. Or conversely, the sex with stronger linkage map based interference would have chromatin organization with shorter axis compared to the other sex. There is a plethora of data of sexual dimorphism in linkage map based interference strength indicating sexual dimorphism, but comparative cytological data is lacking (difference in perparness of some sexes and complications due to identification of specific chromosomes between cells.)

## The CONTEXT of MEIOSIS

the study confirmed preivously identified sexual dimorhisc patterns in regard to the recombiantion landscape (in mammals) -- in the goal of unifying all of these results, we sough to investigate physiologycal aspects of gametogenesis which have conserved sexual dimorphic features. A fundamental difference in meiosis (MI) for males and females is the presence of the centrosome which serves as a nucleation site for MT at each pole (and changes the shape of the spindle). (Our hypothesis is that the tension in a centrosome spindle is stronger (or more uniform) since all MT-KT are anchored at single points across cells (the two centrosomes). This will also make prediction for the spindle assembly checkpoint (SAC), which is stronger/stricter in smaller gametes with centrosomes. (the SAC is more sensitive to achiasmate bivalents on the spindle / better at detecting a lack of tension).

Whereas in the acentrosome spindle is more diffuse (across a larger area) and the tension across bivalents are anchored by multiple MTOCs, resulting in weaker tension force or less uniform strengths across all the bivalents within the cells. The SAC in eggs seems to be weaker/leakier, that is more achiasmate bivalents are required to trigger the SAC (stop the division).

\*\*main sex differences in spindle\*\* are the anchoring of MT at opposite poles

in males there are centromsomes for Mi and MII divisions

where are in oocytes, a (universal) conserved feature of oogenesis in many species is that they loose centrosomes -- instead the MTs are anchored at mulitple aMTOCs.

There is potential for these aMTOC to be unevenly distributd across the cortical and central side of the spindles (Wu et al, Schuh and ellenberg) --- (could be an origin of different tension / pulling )

The survalence of SAC in oocytes might be decreased due to large volumne difusing the signals.

#CO placement translates to bivalent shape

\*\*still an open question of if and how the CO number and placement of crossovers translates to different fitness values for segregation rates\*\*

the metric / amout of sister cohesion might be an good place to start

the ultimate goal is proper disjunction of chromosomes, the main checkpoint is spindle assembly checkpoint (SAC) which responds to the tension signal across chiasmata

we like this model because it can be applied to \*\*both our results\*\* for i) sexual dimorphism variation and ii) the fast male evolution in gwRR and recombination landscape.

Uses / centers around one of the best known selection factors on meiotic division, anneuploidy. Several other facors related to meiotic recombiniation center on \*\*segregation\*\* (obligate chiasmata, lower bound of the genome wide rate) it's not unbelievable that the recombination

Consequences of evolution in the number and placement of crossovers / evolution of interference strength:

Spindle / SAC model: The number and placement o­­­f crossovers changes the resulting amount of sister cohesin involved the tension signal, which affects the tetrad/chiasmata structure at MI when the homologs are pulled apart (Hollis et al 2020, Lee et al 2019). This model predicts a difference in the meiotic spindles or division mechanism between high and low rec strains.

ii. SACE: For the 2CO in the high rec males, larger blocks of chromosomes are kept together in the next generation.

This model would predict greater reproductive variance for males.

#blah

<5. Model prediction

The models above which predict directional selection on the recombination landscape in males: SACE and Spindle based selection are most parsimonious for the models review in this paper. The reduction principle wouldn't predict males diverge in genome wide rates and two locus modifier doesn't predict males gwRR would be higher than females.>

<3.Two-locus (protect for drivers)

This second modifer model was persented in [@brandvain2012scrambling] the basics of the model are that females will have a longer genetic map and more centromere biased recombination landscape compared to males.

A strength of this model is that is presents a clear driver / source of differential fitness (ie meiotic drivers can decrease fitness/fertility). This model also accounts for the general female pattern,

However, this model doesn't explain the borad scale pattern for the male pattern.>

<Also:

-These results are different from the sex differences because the difference is seen in both the raw and normalized IFD, indicateing the mechanism / physcial strength (interference strength (signal) mediated through the SC has evolved.>

<Some of the traits related to faster male evolution -- distinguish in which models can redict them: the reverseal of heterochiasmy direction and the correlated evolution of gwRR and interference strength.

\*\*DSB evolved but, don't included as an examined trait, since most evolution based models don't make predictions for this stage of meiosis.\*\*

\_the propotion of DSB repaired into crossovers hasn't evolved, the total number of DSBs has evolved\_ (following the tethered lop model of DSBs formation -- this would suggest that in the high rec strains, assuming no large difference in the Mb size of the chromosomes,

during chromatin remodeling in prophase, in the high rec strains the chromosomes have longer axis, allowing a higher number but shorter DNA loops (for SPO11 to make the DSBs). Our results mirror those found in Baier et al [@baier2014]

Our results show that the ratios of DSB : CO

\*\*range from X to X which is similar to those presented in [@baier2014] (which report X to X) \*\*

These conserved ratios suggest that the increase in DSB numbers are accompanied by proportional increase in crossovers.

This shifts support away from evolution at the CO:NCO decision to an earlier prophase stage such as when the chromatin compaction is set up. \*\*increase in DSBs is driven by the number of DNA loops\*\* and due to the inverse relationship of loop and chromatin axis length, this would result in longer sc lengths (which reflect the underlying chromatin axis length).>

<Petkov paper -- states that the sexual dimorphism for interference strength is due to the chromatin structure (meiotic chromosome organization) with the increased interference strength in males being due to longer chromatin loop lengths.

same pattern in humans (Gruhn et al 2013)

(exceptions, birds (fish?) plants?) -- examining this is hard due to chromosome size effecs

- This also assumes that the DNA loop sizes have uniform size along and between chromosomes

2. Short axis / longer DNA loops will have stronger interference

This prediction combines the findings of chromatin compaction and interference differences which are intertwined by the transmission of interference along the chromosome axis and the inverse relationship chromatin compaction (axis length and DNA loop sizes).

In physical units (micron) the counting model fits interference well to the 2D linear space of the axis these measures of interference are conserved across sexes in mouse. This is because the counting units are the BASES of DNA loops which is conserved along the 2D length of chromatin axis. When this space is transformed to account for all of the DNA base pairs which are sequestered into the DNA loops above the axis, the strength of interference will vary depending the on underlying chromatin structure.>

<We focused on the largest axis of variation, the faster evolution of genome wide recombination rates in males. One of our primary objectives was to identify other traits which correlate (could explain the increase).>

<Baier et al found significant differences in sc legnths for

The tests in our study - show moderate to low significance in the differences in SC lengths. (this is because we have more noise-can't distinguish individual chromosomes)

a study of in house mouse -- using different markers for DSBs and intermediates (markers for the recombination pathway (from DSB to mature crossover))

-different DSB marks, distinct inbred strains two classical lab strains and a wild derived strain from castenus, used FISH for chromosome specific measures

our results are similar in several ways

- correlation of final MLH1 and DBS counts, SC measues correlate with the DSB number (even tho the differnces we observe in our study are -- slight / less significant -- we attribute that to chromosome specific noise )>

<We can't distinguish if this is 3 independent instances of evolution in gwRR OR if the patterns are due to shared standing variation, incomplete lineage sorting, but these points are for describing the general patterns.>

<extends the lenomand focusing on two conditions. first that the stength of epistatsis in dependant on the cis or trans nature. the authors note that this would apply to gene archtechture (and increase with in cis ) -- where the regulatroy region and coding region of a gene evolve (together). second that the relative interference strengths differnt between male and female. This can apply to (genes acting in sexual antagonism) or can be mediated via imprinted genes.

originally proposed/outlined by Trivers [] and refined /formalized in [@lenormand2003]. This model describes a system where gametes are competing or selection is acting in the haploid stage to cause difference in genome wide recombination rates between males and females. This is a modifier model of three loci, where the recombination rate between two loci is determined by a third locus (or modifier)>

<2. Review the assumptions for measuring CO interference in different ways.

The logical model: Crossover interference is a mechanism of suppressing crossovers, negative relationship between interference strength and gwRR. More crossovers can fit along the chromosomes and results in more crossovers overall.

Examples of empirical results supporting this pattern; Otto Payseur, (Ruiz-Herrera? Bomblies?)

Quantifing using the gamma distribution:

Caveats, This doesn't make since for the general recombination landscape: i) finite chromosome length and ii) limited range of crossovers per chromosomes (1 to 4).

Alternative interference characterization: i) the number of crossovers are held constant and ii) transform / generalize the rec landscape, (focus on how the rec landscape would change instead of the genome wide rate) iii) assume crossover assurance.

-The Goldstein model, models predicts a positive correlation with interference strength and higher recombination rate. A modifier which changes the probability of the recombination landscape having 0 crossovers to 2 crossovers, (driven by crossover assurance)>