1. **HetC causes distinct Evo trajectories --- (the table)**

--it all comes down to gametogenesis (focus on universal aspects of how gamtogenesis types differ)

**2. Evo in the male specific rates**

**a. DSB –SC / before**

**b. 2CO higher interference**

**3. NEXT STEPS!!**

**1. Heterochiasmy driven by fundamental aspects of gametogenesis**

Logic of RR not needing to be different / rec landscape not needing to be different…

-indirect vs direct (define these differences)

Indirect review:

1.-Reduction hypothesis (equilibrium) / haploid selection

2. Two locus drive model (brandvain and Coop, females evolve to disrupt drive systems (Akira et al?)

3. sexual antagonism –cis epistatsis, (SACE)

Direct selection forces

-Review cell biology background,

-Differences in **constraints**

Relaxed SAC constraints in females

-INEFFECTIVE SAC (leaky)

-(some oocytes rescue aneuploidy (some ref cite that there is less aneuploidy than expected)

(female spindle) -the driving centromeres and lazy / topsy turny spindle

-(mostly) fundamental gametogenesis differences

- Division/Size (asymmetrical (Big) vs symmetrical (small) )

- centrosome contribution (+sperm, -egg)

-(timing?)

SPINDLE, CENTROMERE, KITOCHORE, (structure at the metaphase plate)

(holocentric, how spindle is attached to kinetochore,

Review the models –

Indirect selection, prophase based models, metaphase based models (-can I merge these tables?

-can I clean up the tables / make them punchier / connect them more closely to my results?)

**2.A** the DSB differences have proportional CO differences – this suggests that the changes (evolution) happened before the DMC1 foci are laid down.

This evidence shifts the support away from evolution at the point of CO:NCO decision to earlier, when the str of meiotic chromosomes is build (the programming of the // the initial restructuring of the meiotic chromosomes )

**2.B strong interference is the best predictor of gwRR evolution**

-background / logic of the negative correlation with COI and gwRR

Empirical measures from PayseurOtto

-Bauer et al (half sib lines ) pooled data(chromosomes/populations) – find significant negative correlation of gwRR and COI strength (as expected with the basic logic ) (but when data subdivided this relationship not sig (low power)

-Caveats – only type I COs – the measures of interference from ALL COs might be different –but it’s outside the scope of this study to (figure this out)

<gamma metric – the gamma metric also incorporates the variance of interfocal differences – we observe that – outliers IFD weigh / effect the gamma estimate (to a large degree)>

(strong interference (gamma) – not just larger IFDs, but also low variance across IFDs), --

- Evolution of interference (how expectations for evolution of gwRR translate)

Otto Payseur – present empirical measures of interference and gwRR for a bunch of species and find a negative correlation (this is also a logical prediction)

(review in Otto Payseur – of Goldstein et al simulations,

when the (total recombination rate or number of COs is held constant – evolution of crossover interference and recombination rate in the same direction (positive correlation)

(our results / findings of the 2CO IFDs – (artificially?) hold the number of crossovers constant

(tie into the functional (direct) selection predictions from the HetC section) ---

-caveats on the chromosome size and chromosome specific effects -- (independent of chromosome identity) (haenel et al 2018)

-can any of the models from above be re-used here?

**(holocentric chromosomes have strongest – interference) – limit kinetochore point of attachment)**

**Discussion Outline**

Heterochiasmy take away pattern

* Distinct recombination landscapes between sexes – suggest distinct evolutionary trajectories (relaxed vs directional)

**Recombination rate evolution (males)**

-Strain evolution – traits that change in both females and males (

-- is it polymorphism (standing variation) and 3 independent instances of evolution in gwRR

OR

shared standing variation // incomplete lineage sorting, // the same history

- (distinct evolutionary trajectories – males have more directional pattern;

Within male

- evolvability, less effective in females due to the increased (within animal variance

- (what would have driven the rapid 30% drive gwRR (enrichment of 2CO bivalents)…?

-are their gene candidates (signatures of selection (CAST / WSB/DOM vs PWD + MSM ?)

- **CONSTRAINTS** on gwRR

House mouse – (close to the minimum) –

Most species close to minm (1-3 CO per cell )

Consequences

- linked sites (indirect)

- change in the cohesin landscape

**Future steps**

Don’t use sex-averages / acknowledge that sex average data can obscure distinct patterns (Haenel et al biggest offenders)

-focus on interference