Sex-specific evolution in genome wide recombination rates

## Intro outline

-definition of HetC

-“Here we define heterochiasmy as sexual dimorphism in recombination rates in dioecious species where both sexes recombine.”

- HetC is a ‘made-up’ metric from sex specific measures. Here we define it as the ratio of average female to male mean genome-wide rec rate.

-caveats and how they will be addressed

-Heterochiasmy definition should encompase correlated traits to gwRR (SC axis length, NCO:CO, DSB number)

-The common pattern of heterochiasmy are: (overall magnitude and position of COs)

1. female higher rec levels compared to male (female-biased)

2. females more uniform CO positions across chromosomes

(3. females have longer SC/Axis, (exceptions in some fish and bird species)

-Theories for evol of heterochiasmy have focused on indirect selection

Summarize Trivers, Lenormand, BrandvainCoop, SardellKirkpatrick

- Fewer models focus on direct selection driving evolution of heterochiasmy. (segregation of chromosomes; euploidy or efficient homolog pairing)

- some gametogenesis patterns that are universally sexually dimorphic

-asymetrical vs symmetrical cell division results in big size differences in gametes

- anastral vs astral microtubule organization / acentrosomic vs centrosomic

-differences in gametogenesis could result in sexual dimorphism in meiotic recombination rates

## Result outline

1. **MLH1 results**

**A.1 General Patterns for the Mean MLH1 counts**

Table 1 (MLH1 statistics)

Figure 1 (MLH1 strain means)

Rapid male specific evolution in PWD and MSM, two subspecies

Mixed model (Sup Table 1)

-No significant (and consistent) effects of subspecies or sex

Post hoc investigation for strain effects (PWD and MSM)

GLM (all fixed effects) for strains

Sex-specific evolution (nuanced female patterns)

**A.2 General Patterns for variance in MLH1 counts**

(Figure X of mouse level variance)

Mixed Model for variance

Sex is a significant effect. Variance for gwRR is higher in female mice.

B. **DMC1** **results**

Figure 3. (DMC1 distribution)

1) ANOVA, strain effect across mice holds for L but not Z cells.

2) post-hoc – t-tests between high and low groups

t-test between the ‘High’ and ‘Low’ MLH1.group is significant for L cells, but not Z

**C. Heterochiasmy patterns incorporating total SC, IFD, and relative CO placement**

(How do High recombine strains differ from low, How do the sexes differ from each other)

(Figure 4 (HetC plot)?

Figure 5 chromosome class proportion plot

Figure X total SC scatter plot, relative CO position plot, and IFD scatter plot

Review caveats with heterochiasmy definitions

Heterochiasmy values adjusted for female XX bivalent

**D. Predictions of selection on bivalent structure**

*Purifying selection for bivalent structures to converge on metaphase spindle in spermatocytes*

*(For males, in high recombining strains the REC landscape is evolving to increase sister-cohesion-tension area and low recombining strains REC is evolving to minimize that area)*

1. There should be less variance (within mouse and strain) in relative CO positions and raw SC length in males relative to females.
2. Given that high recombining strains have ~1:1 proportions of 1CO and 2CO bivalents, the relative position of 1CO foci will be less telomeric. (1COs in high recombining strains will be distinct from 1CO in low recombining strains).
3. The interfocal distances for 3COs in males should be less symmetrical than in females. The distances between foci will maximize or minimize the amount of sister cohesion tension area.

## Discussion

Table X, Current models and their predictions for the evolution of heterochiasmy

Table X, results from proposed predictions

(Figure X, cartoon of difference in bivalent on spindle for 1CO and 2COs)

1. Review main patterns
   1. Male specific polymorphism for gwRR in musculus and molossisnus, may not be a species wide optimum for gwRR
   2. More variance in females for meiotic features, resulting in greater variation in gwRR
   3. Rapid male specific evolution upstream of CO repair stage
2. SACE predictions and bivalent selection models are not mutually exclusive,
3. Importance of broad scale patterns for recombination

(centromere effects for mis-segregation rates) - (high rate of robertsonian translocation in Dom, and absent in Musc – maybe something about centromeres (encourages transloactions + suppresses 2CO (rec near centromere) in DOM

(that has changed in Musc, REC near centromere suppresses rates of robertsonian translocation)