**General mlh1 pattern / description (cells level) and Estimates of gwRR from (House mouse species complex)**

- number of cells, mice, strains, subsp, repeatability

- (Our results are similar to previously reported measures, and report novel measures from wild derived inbred strains in house mouse.

- Sex specific evolution is the major pattern.

-male: PWD, MSM, and SKIVE have significant strain effects. They are grouped into the ‘High Rec’ group. PWD, MSM, and SKIVE have evolved 20, 30% and 10% higher than other means respectively.

- female: G has significant strain effect. G female are 7% higher than other female means.

- The degree of hetC is pretty low there is a reversal of the female biased gwRR, for 2 of the High Rec strains. This is uncommon between closely related species.

**Analysis using a Mixed model framework for examining pattern of heterochiasmy**

-Logic for the Model choices (multiple models ), sex effect, subsp, interaction, and random strain effects are used for distinguishing subsp (a proxy for divergence) and strain (a proxy for polymorphism).

-Mixed model 2 (now 1), sex and interaction effects with subsp were significant () AND the random strain effect is significant. Variance due to strain effect is not 0. ---lack of support for uniform/ consistent divergence in the trait – lack of support for neutral evolution

After mixed models, we ran post hoc fixed effect models

-glm: The G strain effect is the largest effect for gwRR. The sex\*strain interaction effects for PWD, MSM and G effects are also significant. Additional glm models show that PWD\*male and MSM\*male increase the gwRR and G\*male decrease the gwRR. Qualitatively G female is distinct.

1. *Predictions for ‘uniform’ patterns across all Mus musculus strains are not met; (ie. strains within subspecies didn’t diverge uniformly)*
2. *Sex is a significant effect, but not in a uniform manner, the significant fixed effects are interactions (strain \* sex).*

**Within Mouse variance for MLH1 counts**

- (Within mouse variance –is an important aspect of the trait), Brief background on within mouse variance in CO (cite RWang, KVeller).

- All models support female having more within mouse variance in gwRR / MLH1 counts per cell.

-Models with the higher quality dataset support the pattern of greater variance in females.

**CO precursors indicate a correlation with higher gwRR (in males)**

- The majority of DSBs mature into NCOs (in the CO:NCO decision).

- Greater range of variation in total number DSBs than total COs (cite Cole, Baier et al).

- These results were from a subset of juvenile male samples for DMC1 staining.

- Early staged cells have more DSBs (leptotene cells have more DMC1 foci than zygotene).

- Musc PWD, MSM leptotene cells have more DMC1 foci than WSB and G leptotene cells.

**Genome wide RR variation translates to the chromosome level**

- The genome wide RR is a composite of number of COs per chromosome.

- Most species have a range of 1 to 3 COs per chromosome (Stapley et al 2017), this may be a limit of a mechanism of RR.

- The male high rec strains have more 2CO bivalents than low RR strains

*- This is motivation to investigate more traits at the chromosome level*

**Bivalent Level Results**

( these are the single bivalent – metrics we can assess in the dataset)

1. SC Length,
2. Normalized 1CO position (rec landscape)
3. CO interference via interfocal distance (IFD) of 2CO bivalents

Q1. sex specific patterns

Are there sex specific effects

1**.Sex specific patterns and predictions (background / intro)**

-outline the predictions and the relevant background

-SC length and 1CO / telomere bias are supported in the lit

- sex specific comparisons of IFD / interference in the physical scale are very rare – only De Boer et al 2006 (1 classical lab strain) --- but genetic map defined interference is well established

chromosome level aspects of Heterochiasmy

* SC length and the normalized 1CO position are conserved chrm level traits of heterochiasmy in house mouse
* Some IFD patterns are Sexually dimorphic, --
* (which lines of evidence support – unreg vs reg patterns in male and female bivalent patterns

**Q1. SC Length differences**

Dom – no differences (not met)

-for almost all models, sex is the only significant effect. \_\_ except in comparison of the Musc strains—where the SKIVE strain effect is also significant – because both male and female bivalents are shorter compared to PWD and KAZ.

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**Q1. normalized 1CO position**

-Norm F1 has significant sex effect (haven’t run the )

**Q1. IFD / interference**

Run on ‘long biv’ dataset

-there are sex differences in the IFDs (which strain has biggest ones)

**Framework for Q2**

Q2. (focus on male specific variation in gwRR) (dom < low.musc , low.mol < PWD MSM

Make predictions with the following bivalent level metrics;

-variation in

**Q2. SC Length differences**

-when all chrm classes are pooled, the general pattern is that the higher rec strains have longer bivalent SC lengths.

\*\*except SKIVE

Glm( SC ~ strain )

- All strains are significantly different in mean mouse SC lengths

- all strains have significant logistic regression – for SC predicting 1CO or 2CO

- The mean.pooled.SC lengths can significantly predict if the mouse is high or low group.

When bivalents are subsetted by chrm class the patterns are a bit nuanced – but fit an overall pattern of SC lengths having more clustered / less overlapping ranges in high rec strains. Higher rec 1COs are shorter than lower rec 1COs.

(generalish) pattern of high rec strains (PWD and MSM), not SKIVE

*Shaper clustering of SC lengths across chromosome classes in the high Rec males (1CO and 2CO have different means compared to low rec strains)*

**Q2. normalized 1CO position**

Single bivalent level

-WSB has the most terminal nrm.1CO.pos and MOLF has the most central nrm.1CO.pos

Mouse level pattern – differences less clear

-high rec strains have more central normalized F1 pos

\*\* long biv data set – also has kinda strange results (but number of observations isn’t balanced)

\*\* mol is a significant subsp fixed effect in M1 – driven by MOLF strain (most central)

**Q2. IFD / interference**

-High Rec strains have longer IFD