Results Outline

**Q1. SC – sex differences in SC length // SC area**

Motivating statement (sex differences known in other species)

SC area and gwRR – have been established as correlate meiotic traits ---

From the literature – female have more SC area (longer sc)

our data set provides an opportunity to test if the canonical pattern of females having higher gwRR and more SC area) – have been uncoupled in the instance of rapid male specific evolution in the gwRR of PWD and MSM.

A simple model might predict if SC area is the strongest predictor for gwRR / CO number, the high recombining males would have greater SC area proportional to the difference in CO number per cell.

Basic stats

- cells used in the final total SC data set (after filters and removing outliers)

– more total SC area (total SC)

Main general (boring results)

-positive correlation with SC lengths and number of foci on bivalents (not shown) --- confirmation of SC-AE length as being a strong predictor for MLH1 / CO number.

While the signals for

\*\*comparing the full single bivalent data sets – have very strong signal (support female longer) (NOT SHOWN),

<LOGIC for using mouse averages of 1) total.SC and 2) short bivalents>

BUT the interpretations are complicated

-the sex chromosomes (these data aren’t subdivided by foci number)

**Total sc area**

1. females have longer total SC area by t.test() per for all strains

2. IS the area is greater for BOTH sexes in a strain or subsp

**Use glm / lmer for mouse average sc area – to test if there has been evolution – and interaction across the subsp and sex**

From mixed model:

1.Sex effect confirmed --

2. strong rand effect (strain)

3. moderate – to strong subsp and strain effects

From glms M2 and M3

(sex effect confirmed)

1. Musc and mol subspecies effect (just MSM) –both sexes have longer /more SC than dom (except maybe SKIVE which has low power few observations)

2. greater differences between sexes in G (mirrors the gwRR pattern)

(can use mean short biv patterns – confirm this at single bivalent level – confirm with a metric without XX or XY) – mouse average short bivalent

**Short bivalent data set**

Get around the XX – reduced single bivalent data set – from shortest 5 bivalents from a single cell, the XX is thought to be 3rd longest in reference genome (mb). The XY in males and distinguishable and can be is filtered out from the single bivalent data set

**1.from t.test()**

All but SKIVE have significantly long SHORT biv means -- Dom has greater sexual dimorphism compared to Musc

SKIVE is not significant (p=.11) (this might be a low number of mouse samples / maybe lower quality of the cells) … noticeable the female means are lower compared to pwd and kaz

**2. from Mixed model**

Sex is still most significant factor, interaction slightly significant

**3. from glm**

-male most significant for both models, (M2 Skive strain slightly sig)

**Short biv interpretation -**

**Interpretation --**

1. <Simple model / prediction not met, suggesting a DECOUPLING of broad summaries of SC length and gwRR – female have longer SC metrics even in strains with males have more COs per cell. This is not a complete decoupling since in all strains the positive correlation of SC lengths across bivalent classes is held.

2. Longer SC-AE in females is – a consistent feature across all strains (t-tests, model’s (large sex effect)) for a cell wide summary and (a reduced single bivalent data set)

3. males from Musc and mol strains have significantly longer SC metrics than males from Dom. Suggests at chromatin compaction – between these subspecies and may (be a requirement for the rapid evolution seen in the 2 musc and mol strains)

**Q1. 1CO foci placement / foci position**

Background / lit –positional bias, another well documented why male and female rec landscapes differ

-Normalized positions to control for differences in SC length

Male telomeric, female middle / more uniform

-caveats / complications – chromosome size effects

Small chromosome (Mb physical) have more uniform landscape – either due to i) bias positions in absolute scale (thus more of small chrms) (Keeney) or ii) same mimimum requirement and less physical area for obligate CO to occur (--or there’s less space for the position to)

the minimum number of

genetic maps – less physical area in which the obligate CO can occur, resulting in – higher rate (cM/MB)