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 SC area – t.test() per strain

2. model frame work tells us – if 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)

**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

Basic states short bivalent area

**t.tests** female longer? In all strains?

**Lmer** (divergence / evolution within strains?)

**Glm M2 M3** (divergence / evolution within strains?)

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

1.from t.test()

Most female mouse averages are significantly longer – especially for the DOM strains, but not all

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

KAZ is in the expected direction but less significant, (p = 0.06)

(MSM not enough male short measures … (use / add in the whole cell manual)

2. from Mixed model

Sex is still most significant factor

3. from glm

MSM strain effect most significant, G

Male PWD, male MSM are significant int effect significantly longer

G male – sig (shorter)

Skive strain and skive male are significant factors

Interpretation --

< 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. >

Simple model / prediction not met>

(Mouse average for total SC area)

- looser chromatin compaction (all strains) --

Strain specific evolution of sex differences

Musc and mol --

Support for model of Divergence in sc area / chromatin compaction – musculus having longer compared to domesticus