Results Outline

Full MLH1

Basics stats -mean,

X cells, X strains from X subspecies

-tried to sample at least X mice per category (exceptions)

Mouse level statis are in table 2

-for each mouse, ~ 30 cells were tried to quantified

(the main summary statistics in Table 1) - - (the other / general patterns of the Figure 1)

( the Table 1 are the values displayed in Figure 1)

-Notes on error

-Comparisons to references / literatures

**- variance**

The variance and cv for within mouse MLH1 counts across cells are listed in Table 1

**DMC1-**

To connect / the variation in CO number across – the high and low rec strain – we quantified DMC1 foci in meiocytes.

-basic stats, strains quantified from juvenile mice, cells selected based on stage of prophase. Means and number of cells reported in table.

**1. evolution of early number of DSBs (leptotene or early zygotene), this results in higher correlation of mean Z to CO)**

- but the Z staged foci number are not significantly different across groups

Boring results;

1. Early staged cells have significant more foci (DSBs) than the later stage.

Unexpected / new results

1. The high rec group has more foci for the early L stage, the no significant difference is observed for the later Z stage There is a stronger correlation between the number of foci in the early L stage (r= 0.8736143) than the later Z stage (r = 0.284302).

The ratios (X more DSBs than CO

2. TABLE OF CO : NCO RATIOS ( DSB / MLH1 = estimated proportion of NCO. ) – **add correlation with MLH1**

L based ratios: WSB, G and KAZ: 7.3 and 6.5, 6.6\* PWD and MSM: 6.1 and 7.4

Z based ratios: WSB, G and KAZ: 5.4 and 5.9, 6.9 PWD and MSM: 4.8 and 5.3

**+ t.tests of ratios**

(For the L based strains, MSM has the highest proportion of NCO – but not significantly so), (there are fewer NCO for the Z based ratio in the High rec strains), (PWD has the lowest Z based NCOs, )

**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

t.tests

lmer

glm

1. short bivalent

-use the short bivalent dataset to control for XX in females

basic stats

t.test :

in all but SKIVE, the female mean length of short bivalents were significantly longer. For SKIVE (p= NS) qualitatively the female means are lower compared to the other musc female means (KAZ and PWD).

Lmer-- Sex is the most significant effect

Glm --- Sex is the most significant effect

**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)

<!-- -For almost all models, sex is the only significant effect for mouse averages of SC length.

The exception is in the Musc strains, where the SKIVE strain effect is also significant, because both male and female bivalents are shorter compared to PWD and KAZ.

-Female SC are longer than male even despite the XX. i) all bivalents are longer within cells (there isn’t a single longer bivalent), ii) shortest bivalents within cells are also longer in females. 

Transition, --- the SC-AE area can be thought of as the ‘area / available real-estate for COs

-- these results suggest that this area is ‘utilized’ in different ways across sexes and strains – so we next investigate the recombination landscape – (ie the relationship between the placement and number of COs along chromosomes).

We focus on two metrics/ aspects i) the placement of single foci along a bivalent (just 1CO) and ii) the placement of two foci on the same bivalent / the interfocal distance of 2CO bivalents (reflects crossover interference)

Notes, Sardell, Guppies:

Divide chrms into n segments of equal size (n varies from 2 to 20) ---

Devide chrms into equal segments – number of COs are the dependant variable

There model for testing the telomere and centromere effect was mied linear model

Number of COs by bin (per CO) ~ telomere\_dist + centromere\_dist + (1 | chrm)

I would try re-writing (within strains and sex?)

Norm\_CO \_pos ~ telomere\_dist + centromere\_dist + ( 1 | SC length)

(the sardell paper has more power because they pool number of COs per chrm bin across many meioses – I can’t pool across meiosis, with this data set – maybe with the Chap3 dataset)

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

General summary of Rec landscape –

Investigating evolution of ‘typical recombination landscape’ (from Sardell Kirkpatrick)

Has the typical rec landscape evolved in house mouse? (in terms of the sex specific patterns)

Are centromeres suppressing CO? and do telomeres promote clustering of COs at the telomeres? –beyond the scope of this paper

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

Sardell – separate maps, one for each sex // meta analysis; 51 species

-positional bias might be best example of sex-specific maps (does selection only act on the sex specific maps? Or a average… since the genomes pass through both sexes thru time)

-Male telomeric, female middle / more total COs in females and fewer in females (sardell defines as typical landscape) (exceptions; 2 marsupials, domes pig tomato, grasshopers, birds and maize don’t have much sex differences)

Causes: -sex specific centromere effects, telomere directed initiation

Guppies (Sardell,

Are centromeres suppressing CO? and do telomeres promote clustering of COs at the telomeres?

more uniform –predictions for this (generalization of rec landscape (metazoans)

-caveats / complications – chromosome size effects

(positions / landscapes differ between chromsomes

Framework notes

-Normalized positions to control for differences in SC length (across sexes)

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)

**Sex is the most significant factor influencing the normalized placement of single foci along a bivalent (by t-tests, mixed and linear models).**

**(--Dom strains more significant sex differences compared to musc?)**