**Lab meeting outline**

Background

New hetC measures (from adding new MLH1 measures)

1. 3 of 4 Musc male strains are male biased hetC (counting MSM as musc)
2. Musc male specific variation / “polymorphism” (spread in the x axis, and not y)
3. How do the musc male chromosome class proportions compare? (do the patterns match the MLH1 patterns)?

-Is the increase due to 1COs going to 2COs?

**Results**

**plot**

1. Dataset just scored about 10 cells from each. I scored male and female – but just focusing on male data for now.
2. (in Musc the high RR and low have clearly a different pattern. Most notably, enriched 2CO class
3. Low RR musc males more closely resemble Dom strains
4. -(this is sorta an expected result (and has been shown previously
5. Haven’t thought up a null expectation to test

**numbers**

show the values of the proportions might make the patterns clearer

1. dom pattern: low variation in MLH1 mean and hetC.

2.Musc pattern, In some male biased mice, there are more 2COs than 1COs

3. The chromosome class profiles differ between Dom and high RR musc males with

i. 1CO -> 2CO

ii. fewer 0COs are

4. This is small sample size and it’s unclear if the 3CO bivalents play a large role

**Last time**

1. Longer bivalents in high RR musc males
2. Weaker interfere in PWD (seems to also be the case in MSM)

**Total SC (regression SC with MLH1)**

I ran R’s algorithm on my images to get total SC on my image dataset and took the mouse average

1. Haven’t visually assessed the algorithms performance on my images, but this is within R’s ranges
2. Positive correlation
3. Czech male might not be of good quality (just 1 mouse)
4. The range of total SC in high RR male strains overlap with female total SC
5. In musc males – low and high RR strains cluster together.
6. **Total SC is decent predictor of RR for musc males**

**(SC / axis length and chrm proportions fit with expectations for increase in RR)**

**Why more 2COs in high RR Musc males?**

What enabled Musc males to have higher rec rates? (what constraint has changed/relaxed?)

What else happened? What facilitated this?

more SC?

smaller IFD?

DSBs?

- (the constraint is on the amount of sister cohesin) (not COs per )

-- a metric of sister cohesin would be the same

-across cells and chrm?

-across male strains

**Prelim Results**

Generally see positive cor for skel\_size (SC length) and nMLH1.foci (at cell level observations) for

IFD – (from preivous lab meeting) (PWD have longer IFDs than KAZ) (normalized positions are the same)

Regulation of chromatin packing (long SC)

Weaker interference (longer IFDs) in PWD

(these haven’t been confirmed in MSM) – PER IFDs are similar to PWD PER.IFD

DOM vs Musc

(don’t have full dom results yet)

But --- looks like --- I bet the IFD for Dom is shorter… and there are fewer 2COs

(these results all seem very logical … besides the longer IFD)

Strange new results / strange Musc male pattern

-higher gwRR from more 2COs comes with longer SC and longer IFDs (weaker interference)

-think of these results within CONSTRAINT framework

-is there another constraint?

Best known meiotic constraint is 1CO per chrm

-tetrad level

-during metaphase

-tension

Another constraint that acts/fits with this constraint? (1CO per bivalent is within sis-co-ten constraint framework)

Sister cohesion generated tension force (sis-co-ten)

CONSTRAINTS

1. Sister-cohesin as a constraint

SC length and interference evolve within sister-cohesin-tension constraint

(most biv numbers are at 1-3) (I’ll talk about 1 and 2)

Background – cell cycle

(contrast ideas pachytene

During early cell cycle, the homolog glue is SC. SC degrads after pactyene – so the only remaining glue is sister cohesin.

switches from SC

(use puppet)

1CO – the amount of sis-co-ten

Sister-co metric (for most chrms)

-2CO IFD1

- 1CO foci1 to end

Smaller chrms – would matter less

-centromere suppression

- more faint foci near centromere?

-combo of both

---- what now -----

---- chiasmata puppet ----

**Conclusions**

-my tests

-- is this strange interference pattern connected to sister cohesin?

Whats the best way to test this?

-- how do I develop the metric…