# Heterochiasmy -- Theory Comparison Framework

Can we find any models with fit a logic for the 4 conserved features of HetC of our dataset?

The conserved features are:

1. (-we proposed that (as noted in sardell) --- the **typical landscape** is the most conserved feature of heterochiasmy, we see it across all strains regardless of the direction of heterochiasmy (this is also seen in cattle and same rate strains) )

**2. SC compaction** differences also seem to be conserved features (for mammals –(birds are exceptions). Longer SC length (less dense CO placement / number)

**3. weaker interference** in females (normalized) The physical units of interference in SC seems consistent between sexes. (are the sc compaction and weaker interference connected??) (stronger interference in female cattle)

**4. more within mouse variance**! (seen in humans Lynn / Koehler et al – other species?)

(table of models/theories) and noting if we think they would lead to the (4 heterochiasmy patterns we observe ).

## Review of modifier (popgen models)

(indirect forces – common things for across all the modifier models

## Review of cell biology

-Look at conserved features of gametogenesis that distinguish male and females

**Different Centrosome spindle**

**Asymmetrical division**

# Predictors of Recombination rate evolution within (males)

<motivation – largest axis of variation, large for the short time scale, --- this motivation for this section – is to try and detect correlates of the (rapid evolution)

--The pattern of evolution in these mouse things: -- traits that change in both females and males (-- is it polymorphism (standing variation) and 3 independent instances of evolution in gwRR

OR

shared standing variation // incomplete lineage sorting, // the same history

- (distinct evolutionary trajectories – males have more directional pattern;

Within male

- evolvability, less effective in females due to the increased (within animal variance

- **CONSTRAINTS** on gwRR

House mouse – (close to the minimum) –

Most species close to minm (1-3 CO per cell )

Consequences

- linked sites (indirect)

- change in the cohesin landscape

## A. DSBs!! (plus moderate support for SC length differences

**2.A** the DSB differences have proportional CO differences – this suggests that the changes (evolution) happened before the DMC1 foci are laid down.

This evidence shifts the support away from evolution at the point of CO:NCO decision to earlier, when the str of meiotic chromosomes is build (the programming of the // the initial restructuring of the meiotic chromosomes )

1.there are more DSBs in the high rec strains

2. the ratios of DSB : CO are conserved, this implies that the increase in DSB numbers are accompanied by proportional increase in crossovers. We interpret—This is evidence that shifts support away from the CO:NCO decision to an earlier prophase stage.

3.-- candidate is the stage when the (basics) meiotic chromosome structure is laid down (the bottle brush / chromatin compaction / axis DNA loop structure

4.This is supported by the moderate support of longer SC length (pachytene stage in the high rec males)

## B. INTERFERENCE

<gamma metric – the gamma metric also incorporates the variance of interfocal differences – we observe that – outliers IFD weigh / effect the gamma estimate (to a large degree)>

(strong interference (gamma) – not just larger IFDs, but also low variance across IFDs), --

- Evolution of interference (how expectations for evolution of gwRR translate)

Otto Payseur – present empirical measures of interference and gwRR for a bunch of species and find a negative correlation (this is also a logical prediction)

# Future steps

Don’t use sex-averages / acknowledge that sex average data can obscure distinct patterns (Haenel et al biggest offenders)

-focus on interference