**Background for motivating and interpreting findings**

**Significance of question in field (motivation)**

A process that is the primary source of genetic variation – that shows multiple levels of variation – but still not really understood.

**Power of experimental design (how this overcomes weaknesses)**

A power of this experimental design (and dataset) is that it has data from both males and females. The cytological approach allows connection of other traits at the single cell level which are closer to /may pertain to cell and developmental differences in gametogenesis.

**Themes**:

Chromosome segregation is (an obvious /the primary) source of differential fitness. Chiasmata, from crossovers, and sister-centromere cohesion ensure proper chromosome segregation in the first and second division respectively.

- Sex is the most notable from of variation, Heterochiasmy main patterns; female biased gwRR and male telomere bias. (caveats achiasmy)

-No first principle which would predict the evolution of sexually dimorphic recombination rates (in species with two sexes).

Adaptive background / indirect selection / makes selection more efficient

- draft? / background selection

- Patterns of variation (across chroms, cells, individuals, sexes, pops, species)

Pathway / functional background

-Meiotic chromosome structure (axis-loop structure) and it’s connection to DSB formation. SC built on-top of chromosome axis.

- This loop-axis structure complicates translation to base pairs or linkage map estimates of RR complicated.

Along the chromosome, between short and long chromosomes, and between cells the loop length can vary. Consistent features are the density of anchoring of loops along the SC.

Petkov broman (haenel) (interference i) sex difference (broad scale sex differences in interference are due to chromatin compaction)

and ii) correlation with genome wide rate

-interference

-Components of gwRR (number of chromosomes and chromosome arms, size, (scale – hotspots)

Sardell kirkpatrick (heterochiasmy

-Genetic variation in genome wide- wild pops / genetic diversity and within species measures

-(my pero refs, honey bee RR, SOAY SHEEP

-optimum

-minim / max

-wild pops / genetic diversity and within species measures

-(my pero refs, honey bee RR, SOAY SHEEP

De Boer et al

**Novelty of this study**

Both Male and females in cytology approach – closets to fundamental gamete differences

Short evolutionary distances

meiotic recombination is one of the major sources of genetic variation (besides mutation).

genome wide recombination rates have X effect on genetic variation and population genetics.

heritable component to genome wide RR, assumed fitness effects for making gametes, and inter-population / interspecific variation. (genome wide recombination

rates can evolve). Evidence that these rates can evolves rapidly.

(Examples of variation in GWRR)

The source of this variation is not well understood or known. The purpose of this manusciprt is to document one of the major sources of

interspecific GWRR, heterochiasmy or the sexual dimorphism of gwRR.

#### points to make

- importance of GWRR (a distinguished from RR)

- 1 CO per chrm

- bounds of gwRR, not well understood

- HetC is not just sex chromosomes

- differences in gametogenesis

- not many empiracal measures, we find variation within subspecies

- within and across population framework

# Draft INTRO, first paragraph

**7/31/19**

Meiosis can be reduced to the expression of (2n -> 4n -> 2n -> 1n) which tracks the duplication of a diploid genome into haploid cell products. The meiotic program relies on crossovers and the process of recombination to ensure the correct separation of chromosomes. Under one of the most common forms of sexual reproduction, anisogamy where a species has distinct gametes, there is no first principle which would predict the evolution of sexually dimorphic recombination rates. Yet sexual dimorphism for this trait, called heterochiasmy, is commonly observed in dioecious species, suggesting that other meiotic traits which distinguish the gametes, for example symmetrical vs asymmetrical cell division, may impose selection for sexually dimorphic recombination rates.

(make a connection to the lg in cahoon libdua – about crossovers testing their metel at the first arrow).

Start out with anisogamy re-away – will need to address features / arguments about yeast / isogamgous species with recombination rate variation.

Notes:

Anisogamy may just refer to the gamete shape – while recombination doesn’t happen in gametes – it happens in cells upstream of gametes. –BUT the context of meiosis for making different gametes is distinct. (anisogamy refers to the final product / gamete – the upstream pathway are necessarily / fundamentally difference)

The first sentence is sorta general / abstract compared to later sentences that get more detailed.

Things to keep, Meiotic program, no first principle, (it is surprising that heterochiasmy exists given that the meiotic program is conserved)

“by meiotic program I mean”

# Questions (angle)

-Within species measures (polymorphism) (fitting hypotheses)

-more sex data // hetC long documented but not solved

-why hetC?

a. distinguish between primary causes being due to indirect or direct selection (pop gen or functional aspects common to anisogamy)

b. long documented not solved

c. (misconceptions about genetic diversity assuming single rate / male only pattern)

# Outline

Defining HetC

-Both sexes recombine,

-overall number

- anisogamous species (sperm and egg) / Celegans (hermaphrodite) dioecious species

HetC patterns

-female higher // but limited ~60% of species are within this range, X percent no difference in overall number

-bivalent level patterns

Defining evolution of HetC

one sex varies – other is static

Meiosis pathway – which part evolves / contributes to sexual dimorphism?

(this is what we did statement)

Sex specific measures for heterochiasmy

Tests / a couple models for evolution of heterochiasmy

-cell size difference

-DSB and precursors

- (tension force / amount of tension force at metaphase) – maybe chapter 3

**Aim 2, *Sexual dimorphism in genome-wide recombination rates within* Mus musculus**

The genome-wide recombination rate is a fundamental genomic parameter. Meiotic recombination facilitates proper chromosome segregation and creates novel genetic diversity. Sexual dimorphism in recombination rates is termed heterochiasmy. In dioecious species where both sexes recombine, often females have higher genome-wide recombination rates (i.e. female-biased heterochiasmy). However there are numerous examples of male biased heterochiasmy have been documented across species, suggesting that the direction and magnitude of heterochiasmy evolve.

# Draft writing sentence

--We look at (sex-specific patterns of variation with and between sub-species of house mice and related rodents --- to start to better understand

what // how heterochiasmy evolves. (how evolutionary forces are acting on gametogenesis to affect the average number of crossovers that are formed

in a meiocyte.