* The total number of COs per (4n meiotic) cell = genome wide recombination rate (gwRR)
* The gwRR regulates populations responses to selection, and determine the fate of novel mutations.
* This process shapes the genomic patterns of genetic variation.
* It is an integral part for proper chromosome segregation. With an obligate crossover per bivalent may act as the lower bound for gwRR.

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. The total number of COs per cell (at the 4n stage) is equal to the genome wide recombination rate (gwRR). The gwRR regulates populations’ response to selection, and determine the fate of novel mutations by transferring beneficial mutations onto novel genetic backgrounds or by breaking linkage of bad mutations from beneficial backgrounds.

This process shapes the genomic patterns of genetic variation, with high recombination areas of genome having more nucleotide variation while areas of low recombination have decreased genetic variation (Begun Aquadro, Nachmann, Payseur).

The lower bound/threshold is thought to be an obligate crossover per homolog pair -- is a checkpoint for proper chromosome segregation (Hunt Nagaoka, Hassold). While too much recombination (ectopoic recombination) and DNA damage preceding crossover formation (may be a constraint for an upper threshold. (cite other than Inoue, OttoPaysuer?).

**As the gwRR influences the evolution of other traits, it is important to document and understand the evolutionary patterns for the genome wide recombination rate itself.**

Sex is one of the most notable axes along which individuals vary

* Discovered over one hundred years ago (cite Morgan 1914)

Since, the heterochiasmy patterns has been shown to be more nuanced than just the direction of which sex has more recombination. Note that this paper focuses on evolution of sex differences where both sexes recombine, for achiasmy evolution see (citation).

* Sardell Kirkpatrick – broad scale recombination landscape differences (generally male telomere-bias)
* Carhoon Libdua, -- longer chromosome axis / longer loop-axis structure generally has higher recombination

-gap in the literature

* Above examples:
* 1) Not enough data for the loop-axis structures of both sexes (or gamete types) in more species.
* 2) Limited taxa diversity for heterochiasmy in broad scale recombination landscape. Exceptions to male-telomere bias might have fundamental altered meiotic programs. For example the lack of clear male-telomere bias in some fish species could be due to sequential hermaphrodism or chromosome chains in metaphase could change the pattern in marsupials.
* An understanding of how sex shapes the evolution of recombination cannot be achieved with available data. Comprehensive comparisons of female and male recombination rates usually come from outbred populations (human, dog, cattle, sheep, mouse collaborative cross REFS), in which the role of sex is confounded with the contributions of genetic variation. Although it is clear that the relationship between female and male recombination rates can differ among species, comparisons between and within closely related species are missing.
* Direct contrasts between females and males across a common, diverse set of genomic backgrounds would reveal whether the recombination rate evolves differently in the sexes.

**2.  The House Mouse is a great model for uncovering evolutionary patterns at a short timescale.**

* House mouse complex comes from a recent radiation providing an opportunity to interrogate variation at short evolutionary scales.

(this short evolutionary scale --- can be leveraged since it limits the scope of genetic mutations which lead to gwRR evolution.

Short evolutionary scale – makes it easier to narrow down genetic variation which leads to

Observing variation in gwRR across house mouse may suggest =-- meiosis has evolved with (due to a small number of few strong acting variant)

* Wild derived inbred strains generate the best comparison of females and males, besides the sex chromosomes, the mouse for each genome are almost identical. Additionally due to their global distribution allows us to compare samples of natural diversity from a broad geographic range.
* While there are strains with Robertsonian translocations, in house mouse and related murid species it is possible to assemble sets of strains with identical karyotypes, 20 pairs of acrocentric chromosomes.
* Classical lab strains of mice have generated a mountain of knowledge central to meiosis and outcomes on recombination through meiotic mutation studies (cite), previous crosses for recombination rate variation (Dumont, Murdoch, Wang).
* House mouse is well suited for single cell cytology approaches. The single cell level allows integration of data at a closer connection to the molecular pathway / meiotic program. In addition to the quantification of gwRR (this study quantifies precursors to crossovers, double strand breaks (DSBs), and meiotic chromosome morphology (across stages of meiosis) which would not be accessible to with genetic linkage data and crosses.

**3. What we accomplished in this paper**

* We report a rare, direct, evolutionary comparison of recombination rate in females and males (or something like this).
* For the first time in many of these strains, We report a rare, direct, evolutionary comparison of recombination rate in females and males

we quantify gwRR of both sexes, from 3 subspecies and outgroups with divergence spanning 0.5 mya to 3 - 5 mya respectively. (same phylogenetic tree)

* We use rare strains from a broad range of geographic locations of the species territory.
* The gwRR is made up of crossovers occurring on individual chromosomes within cells. Thus we quantified meiotic chromosome morphology (SC length) and placement of crossovers to comprise an approximate picture of the recombination landscape.
* Our results indicate rapid male specific evolution of gwRR occurred in a subset of house mouse lines. We observed up to a 30% difference (translating into approximately ~7 more crossovers per cell), a surprising amount considering the short evolutionary time scale.