**Main point**

- dioecious species has two genome wide recombination rates (recombination landscapes) – with-distinct evolutionary trajectories for the gwRR

- this no doubt affects the evolution of the species.

The answer to the

Question of genome wide recombination rate is adaptive may be dependent on which sex.

-although required for gametogenesis, gwRR varies across individuals, sex is most notable

-(evolutionary patterns, using closely related species – is powerful / useful tool for demonstrating selective dynamics)

-gap is that evolutionary patterns rarely compared for both sexes

-we fill this gap (with house mice

Background/approach was designed / chosen to create (the most) equivalent comparison of female and male rates AND comparison of effects from natural genetic variation

-inbred mouse strains raised in standard lab environment –access genetic variation

-immunocytology of single cells – (put/placed the counts measures within the same meiotic context)

-Additionally we decomposed the gwRR into single chromosomes component, and compared sex differences general recombination landscape of single chromosomes using Image analysis tools

-We found Discordant evolutionary patterns (verify explain)

Significant differences between strains for the female gwRR, magnitude smaller

Males two groups (high and low recombining strains) – INDICATING RAPID sex specific evolution of the gwRR in house mouse

-(this evolution) Male specific pattern – high and low recombining strains

-DSBs and IFD significantly separate the two groups,

-but IFD is not as expected

-(closing statement about fitting / comparison to models)

Our findings reveal that recombination experiences distinct evolutionary pressures in females and males. To explain these findings, we propose a model based on sex differences in bivalent and meiotic spindle structure.

-in males we narrow in on the male specific pattern – in order to identify other features that separate this groups

-the number of DSBs and relative spacing of double crossovers significantly distinguishes the two groups, while chromosome axis length and relative spacing of single crossover landscape do not.

- (positive correlation with DSBs and gwRR) but Surprisingly, a greater proportion of the chromosome separates crossovers in the high recombining strains compared to the low recombining strains.