**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.

The rapid evolution in male gwRR is significantly predicted/correlated by the number of double strand breaks and spacing of double crossovers.

However the relative spacing of double crossovers in the high recombining group is greater compared to the low recombining group – (that is the relative recombination landscape – is less dense – but has more recombination).

<understanding the pathway>