**Evolution of interference**

Some basics of the constraints bounds of interference are known, yet there are still many unknowns regarding the relationship of genome wide recombination rate and interference strength.  The non-random spacing of crossovers along the 2D length of chromosomes is the first level of quantification of crossover interference (cite gamma COI papers). Logically a negative correlation is expected; increasing the number of crossovers across chromosomes would most logically be done by more densely spacing crossovers along chromosomes and decreasing interference strength. This pattern has empirical support from the most species (Otto and Payseur) and fits well with the fundamental relationship between the SC area or axis length, the physical upper limit for the number of crossovers.

Our results support an opposite pattern, a positive correlation between interference strength and genome wide recombination rates; we find support that interference strength has evolved in the two groups of male strains. There is a small number of positive correlations between genome wide recombination rate and interference strength in the literature. The within sex comparison of two breeds of cattle with different genome wide recombination rates (Ma et al), between lab and wild mice of Peromyscus leucopus, in a previous house mouse cross (Dumont F2 cross,  preliminary data (HVR unpublished) and in human sperm (Veller et al 2018).

Few theoretical models have considered the evolution of interference strength. Neither the haploid selection or two locus modifier model make prediction for the evolution of interference strength. While the SACE modifier model does not explicitly model evolution of interference strength we note that a logical outcome of the main prediction of maintaining larger chromosome blocks in males, would be a landscape with stronger interference strength. The COM model predicts that interference and the recombination landscape arises from known oscillatory movements during prophase, it lacks evolutionary based predictions. We propose the spindle based selection model would support the evolution of interference strength in the positive direction via modulation of the amount of sister cohesion connecting homologs (figure).

Models from Goldstein et al (review in Otto and Payseur) suggest that if this pattern is widespread interference evolves whenever increased recombination rates evolve. Perhaps a distinguishing feature of models which come to this finding is that the number of crossovers is kept constant. The space across multiple loci (veller et al 2018?) or between multiple crossovers increases in a positive manner with genome wide recombination rates. Given that the empirical range of crossovers per chromosome is quite small (1-3  (Otto Payseur 2019, Stapley et al 2017) and the obligate crossover rule, the assumption of constraining the number of crossovers per chromosome fits well with empirical data.

(add paragraph on exceptions to positive interference:  experimentally increasing crossover number through mutants or fusion chromosomes  (Celegans, plants, fungi with negative interference.)