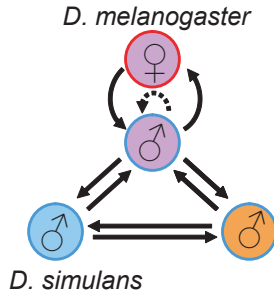
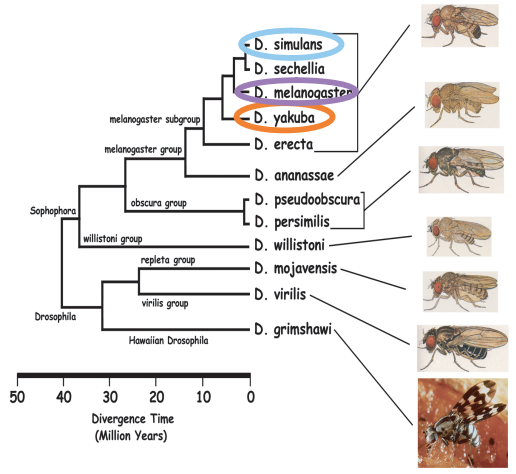
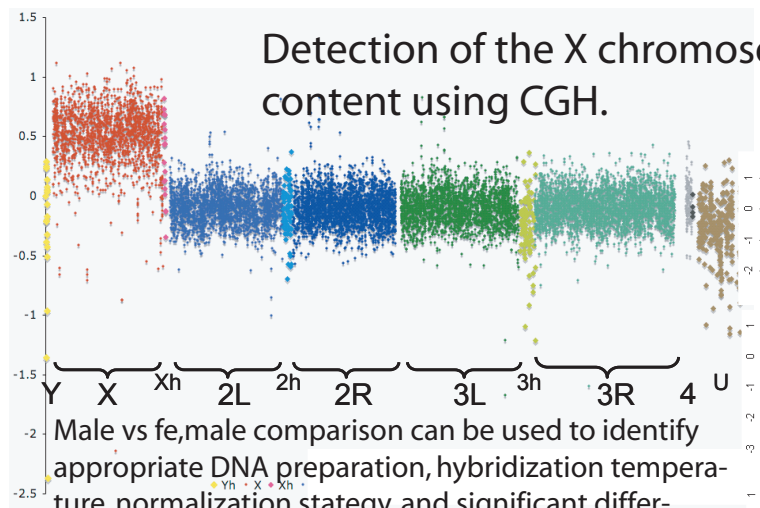


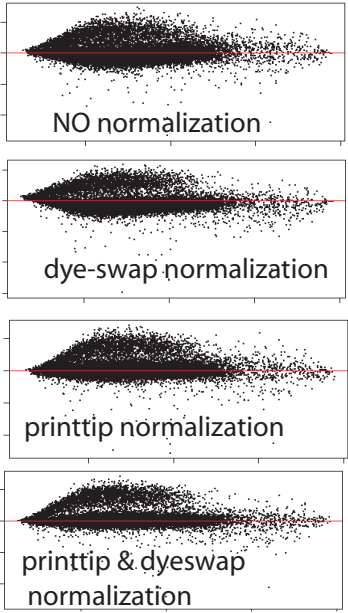
hCGH proof of principle using *Drosophila* species in collaboration with Rob Kulathinal (Fly Base)



Assembled genome sequence is (becoming) available for 12 *Drosophila* species.



Male vs female comparison can be used to identify appropriate DNA preparation, hybridization temperature, normalization strategy, and significant differences. By moving to other sequenced *Drosophila* species we can determine the degree to which sequence divergence compromises detection ability. Also by moving to non-sequenced *Drosophila* species we can investigate the movement of genes on and off of the sex chromosomes.

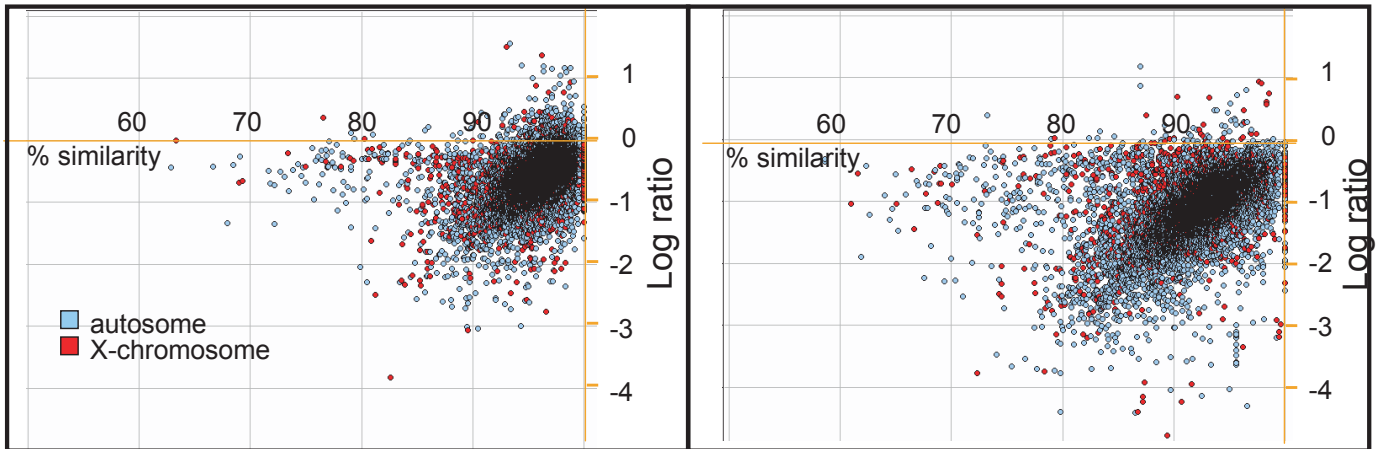


hCGH show a linear relationship between log ratio of Hybridization and % homology

D. simulans



D. yakuba



we are currently using bioinformatic approaches to identify the correlation between heterologous genomic hybridization ratio and different degrees as well as different types of sequence divergence (e.g. length of homology, % homology, small deletions and insertions, GC content, presence of orthologs) Additionally we are using gene ontology and pathway information to identify gene networks that may experience similar selection pressure

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