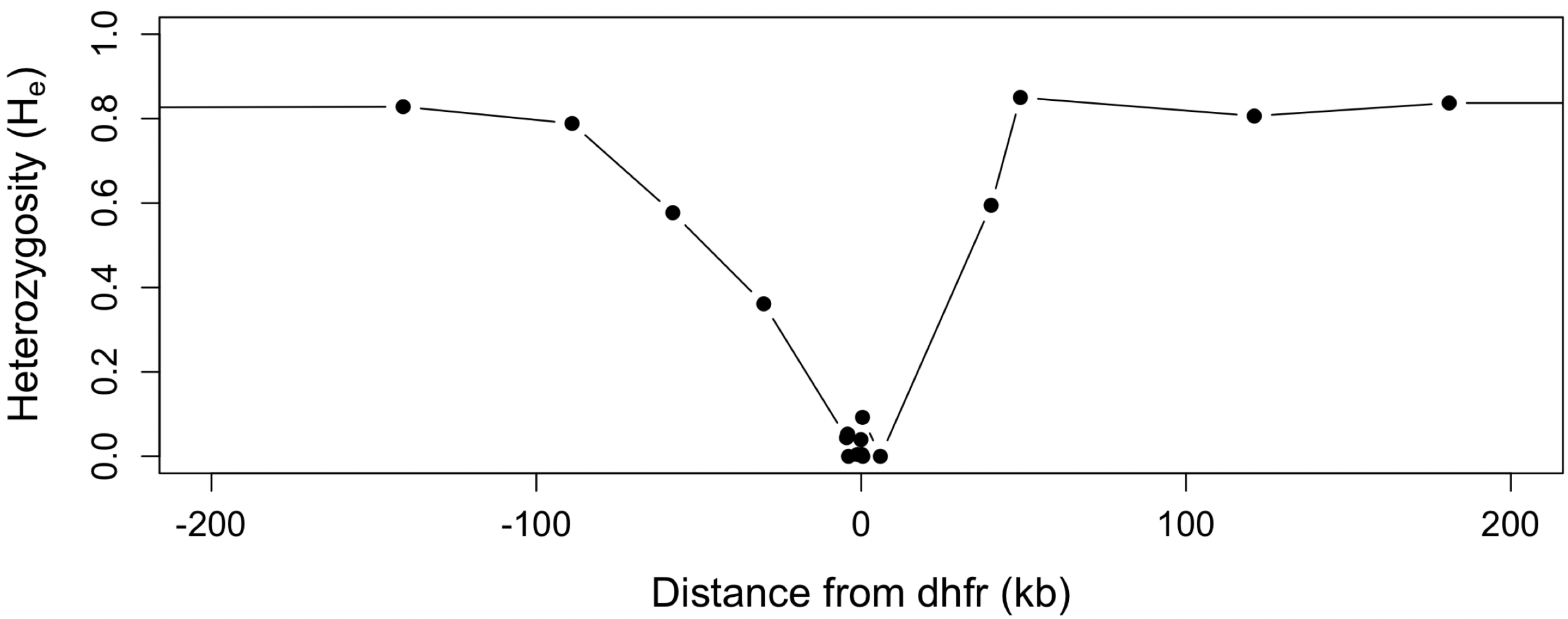
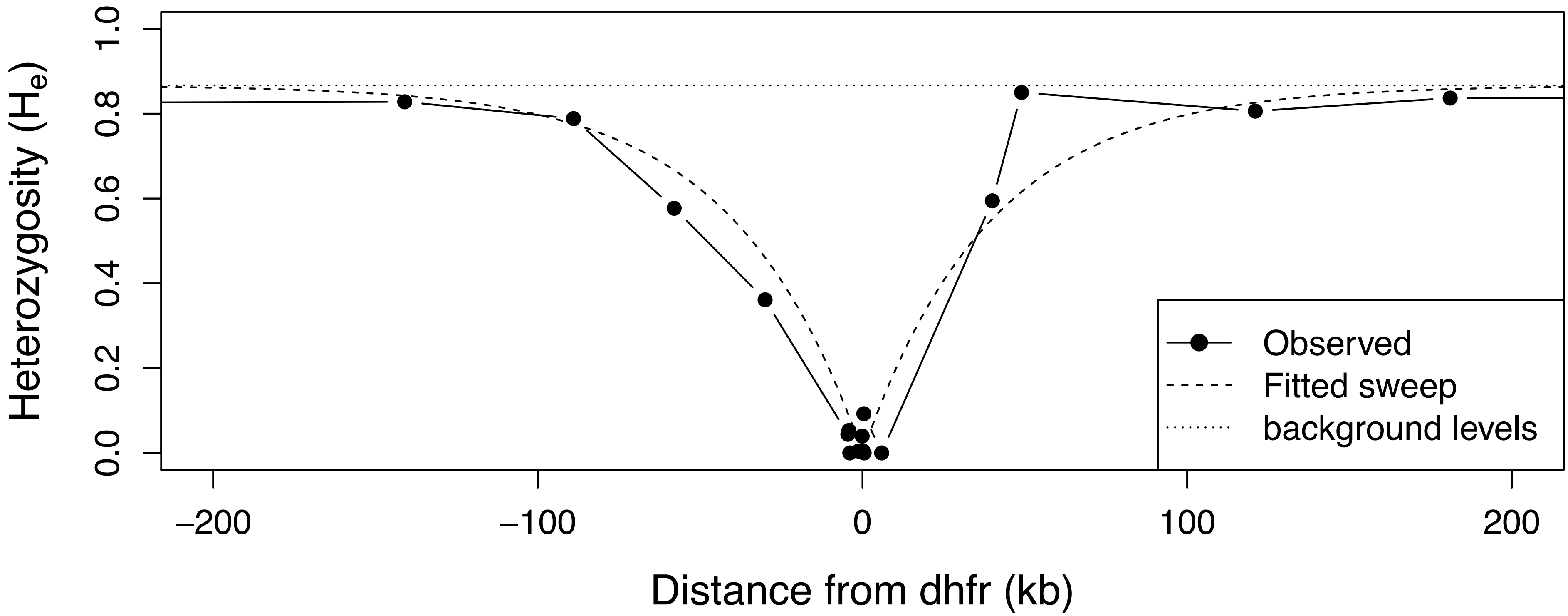
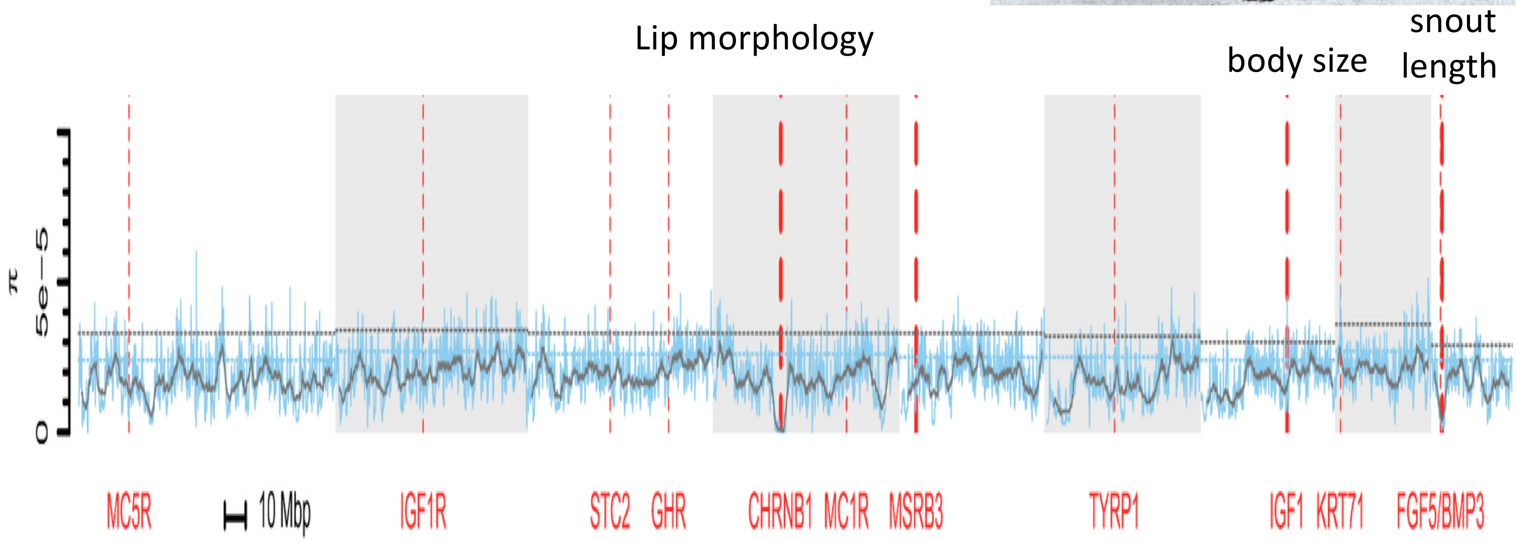

Heterozygosity (H_e)
1.0
0.8
0.6
0.4
0.2
0.0
-200
-100
0
100
200
Distance from dhfr (kb)

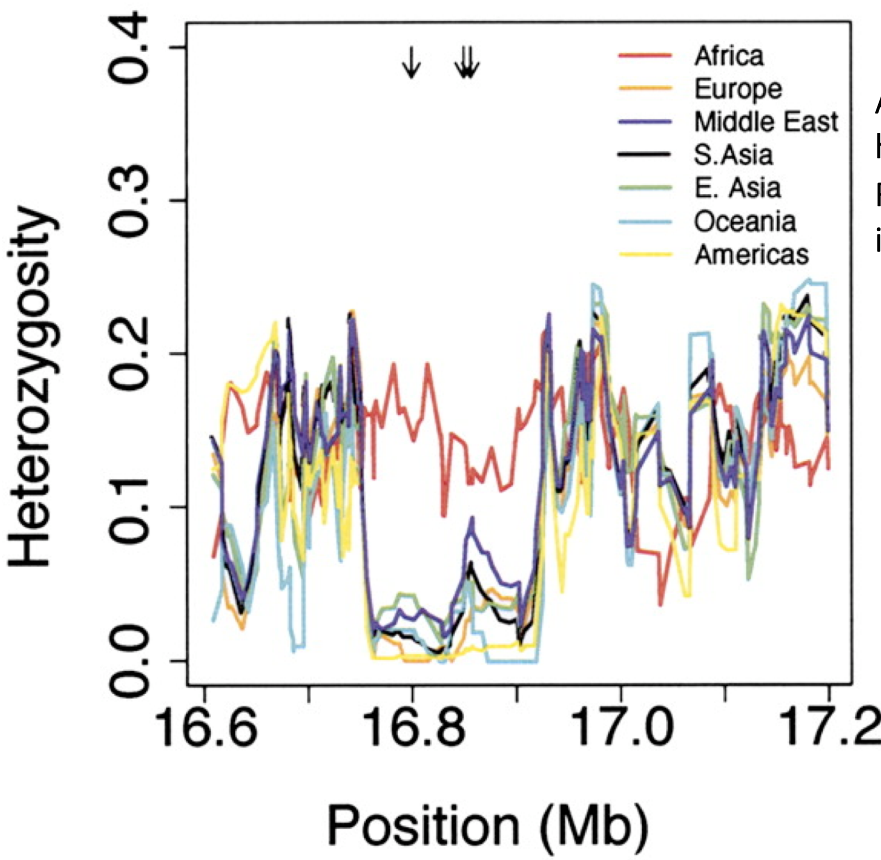


Heterozygosity (H_e)
1.0
0.8
0.6
0.4
0.2
0.0
−200
−100
0
100
200
Distance from dhfr (kb)
Observed
Fitted sweep
background levels

Evaluating the performance of selection scans to detect selective sweeps in domestic dogs

FLORENCIA SCHLAMP,*† JULIAN VAN DER MADE,* REBECCA STAMBLER,* LEWIS CHESEBROUGH,* ADAM R. BOYKO‡[1] and PHILIPP W. MESSER*[1]



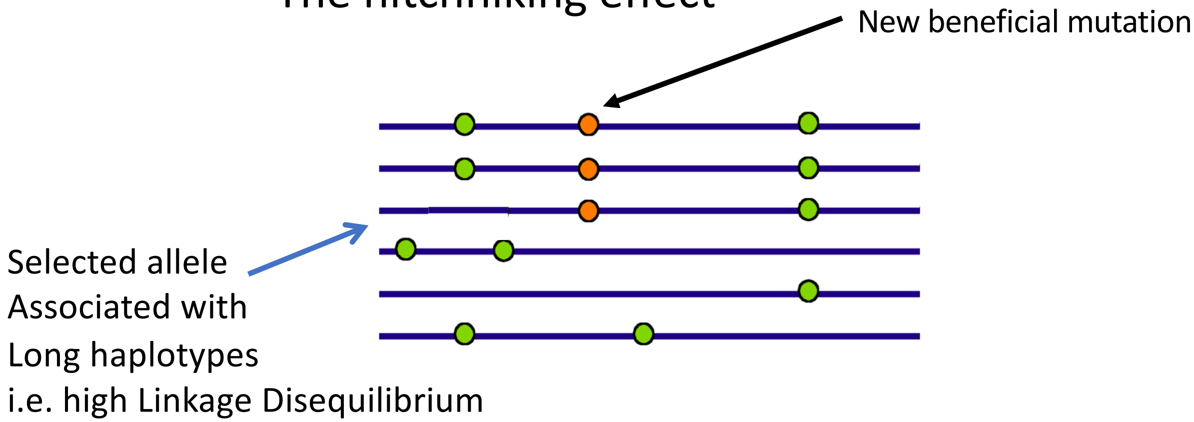


A selected allele has swept to high frequency in Eurasia Reducing levels of heterozygosity in a broad genomic region

Pickrell and Coop et al 2009

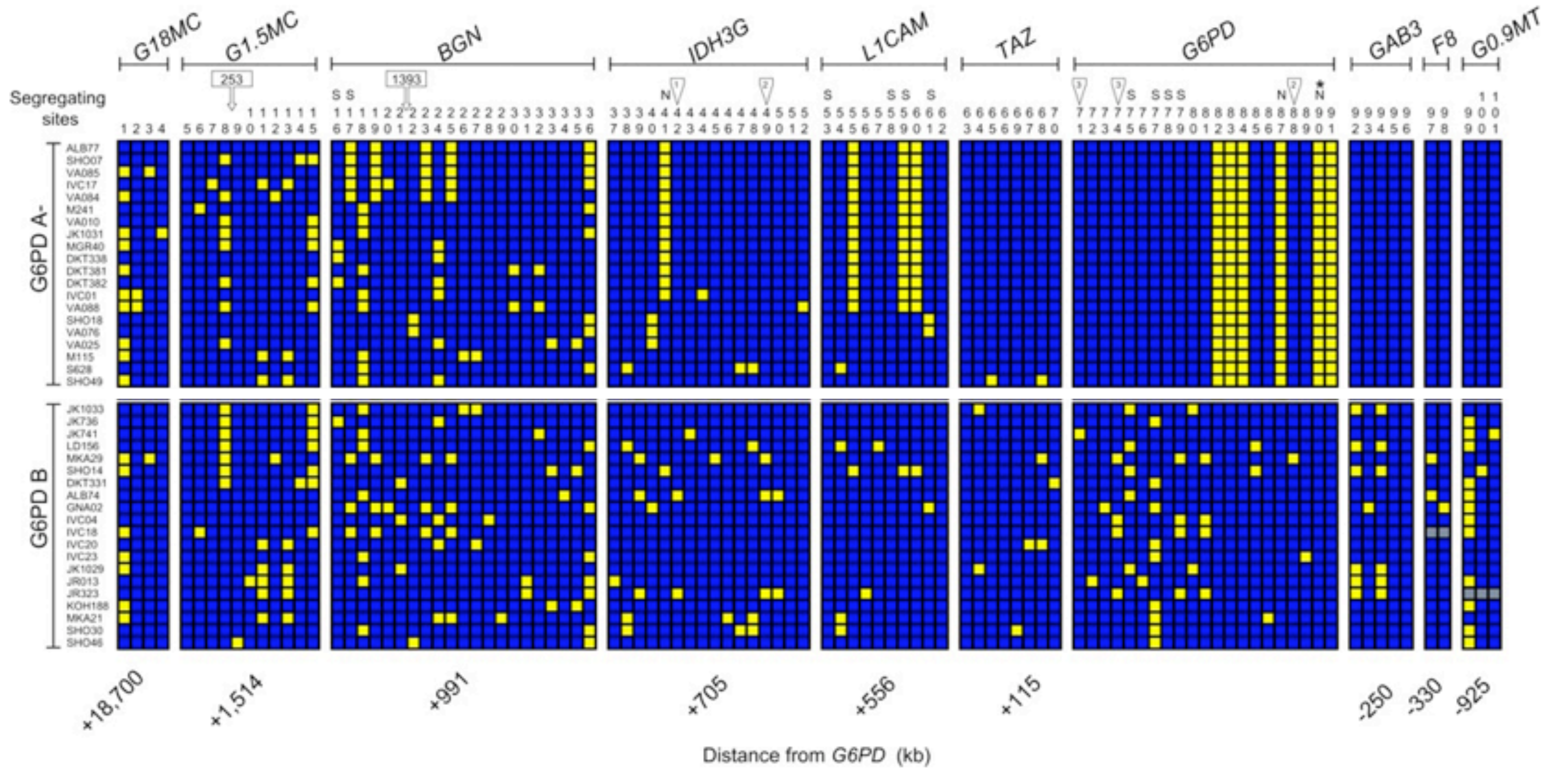
Genomic effects of directional selection

The hitchhiking effect



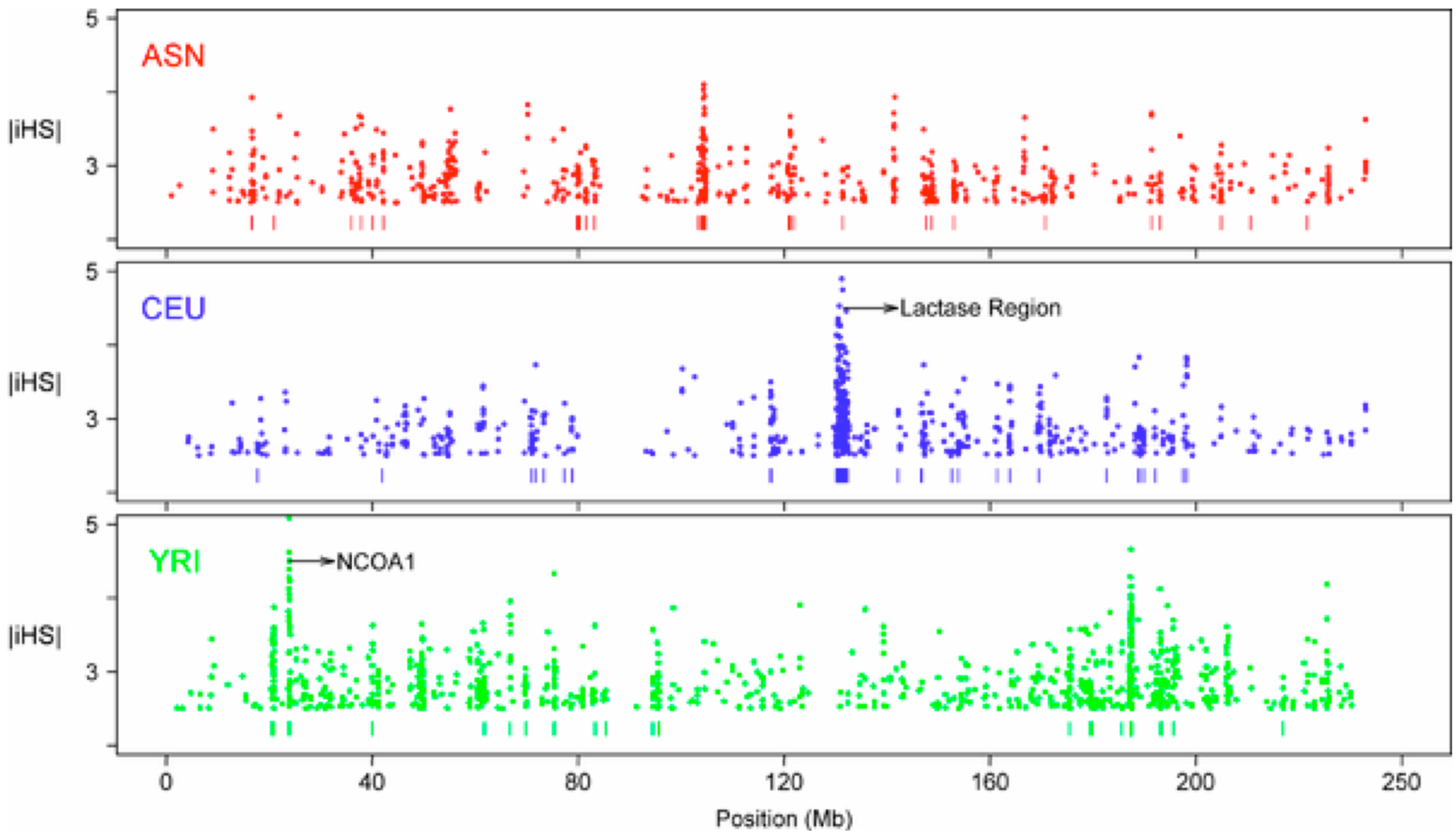
7

G6PD region in Africans



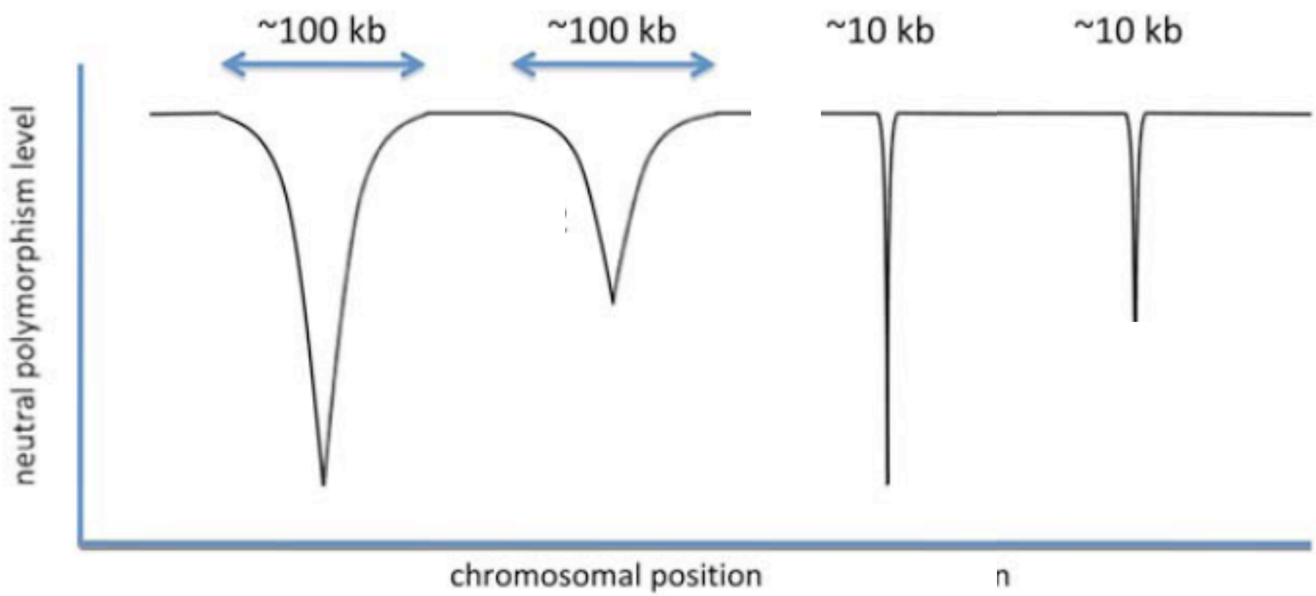
Tishkoff et al.

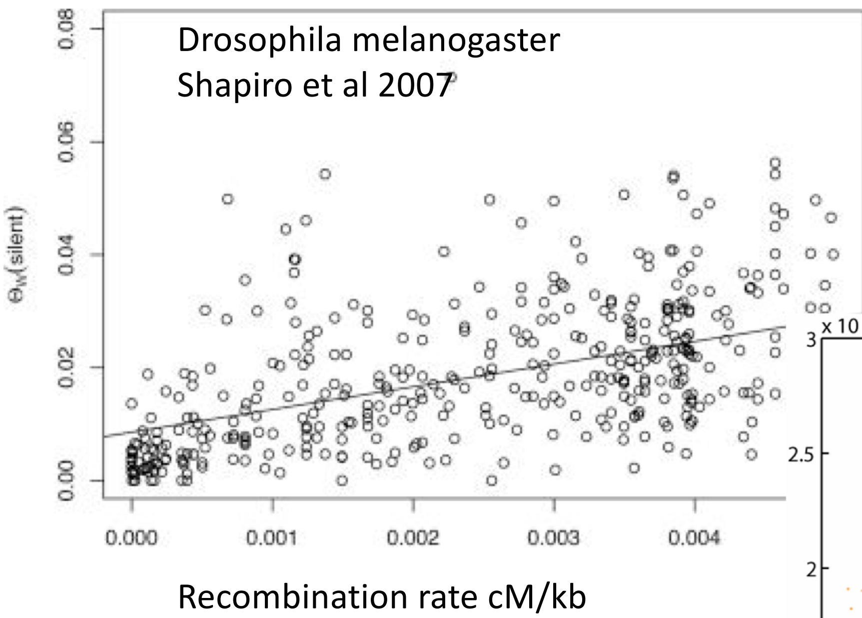
Voight et al Plot of human
chromosome 2: Scanning for partial sweeps

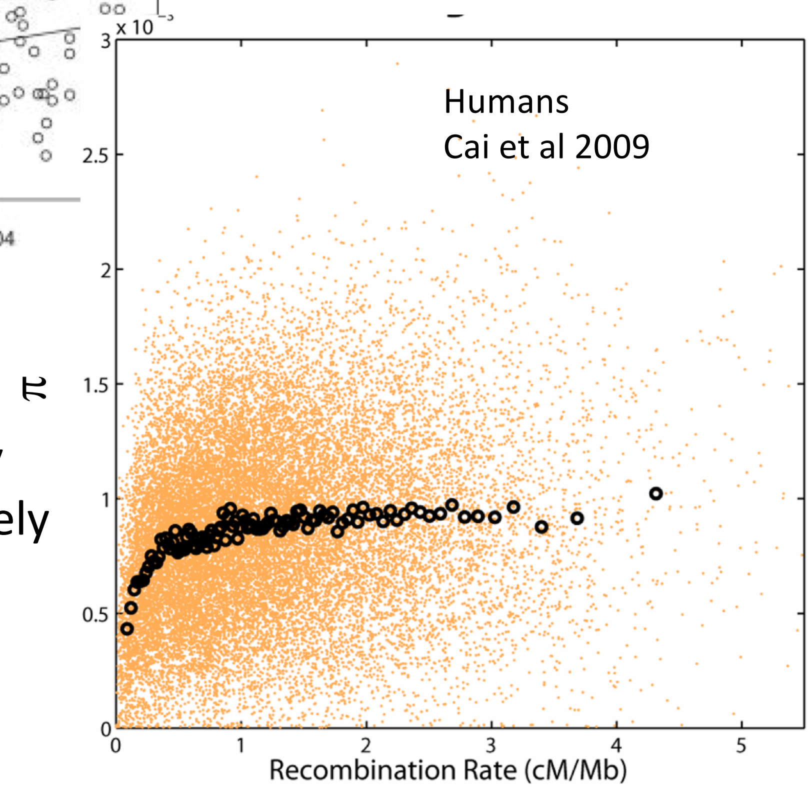


Genomic patterns

Low recombination rate region   High recombination rate region







Polymorphism levels are positively correlated with recombination, likely due to linked selection effect.

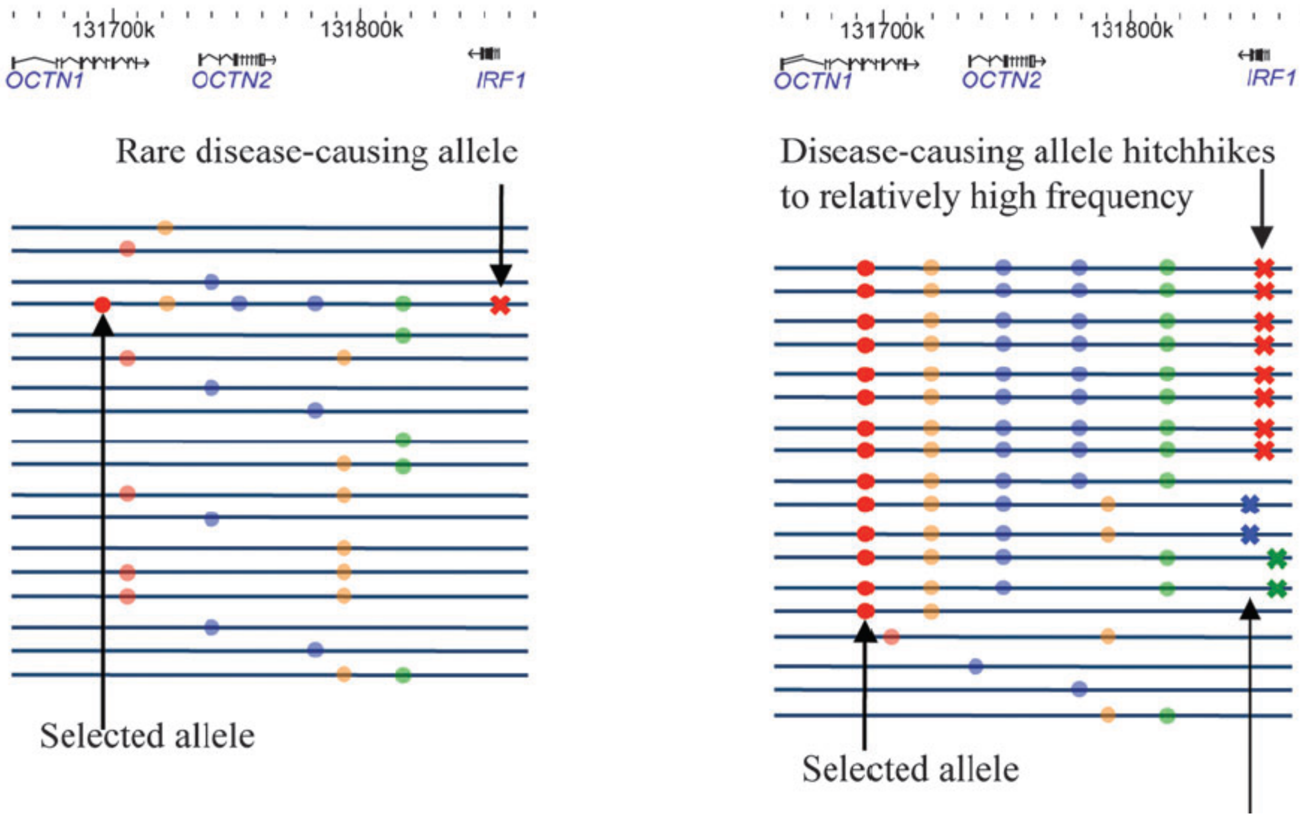
Genome-wide evidence
For selection shaping neutral polymorphism levels

Interaction between multiple selected loci and recombination

Interaction between selected alleles
& recombination

Why sex?
sex = meiosis = segregation and recombination
Why not have sex in particular places?
Why have sex?
Why not have sex?
Why not have sex with other groups of organisms?

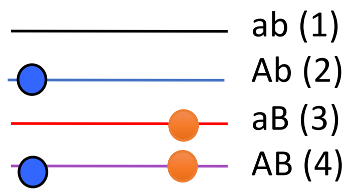
Interaction between selection & recombination
Hitchhiking of deleterious alleles



Crohn's Disease and Genetic Hitchhiking at IBD5

Chad D. Huff,*[,1] David J. Witherspoon,[1] Yuhua Zhang,[1] Chandler Gatenbee,[1] Lee A. Denson,[2]

Interaction between selection & recombination
Hitchhiking of deleterious alleles



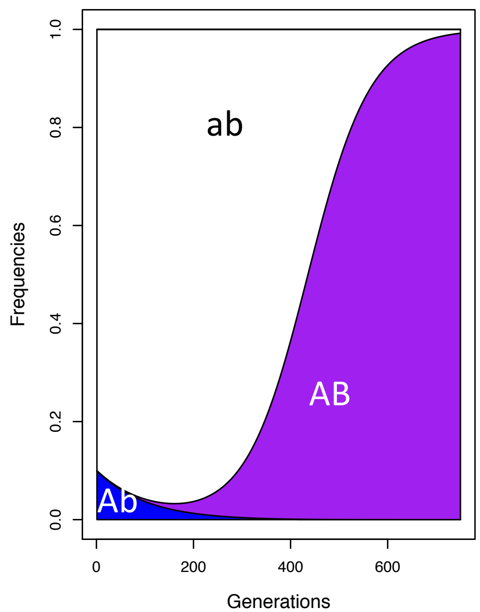
A deleterious ($-s_A= -0.02$)

B advantageous ($+s_B=0.05$)

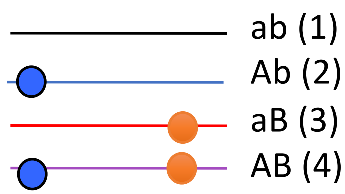
AB ($+s_B-s_A=0.03$)

$w_{aB} > w_{AB} > w_{ab} > w_{Ab}$

r=0



Interaction between selection & recombination
Epistasis among loci



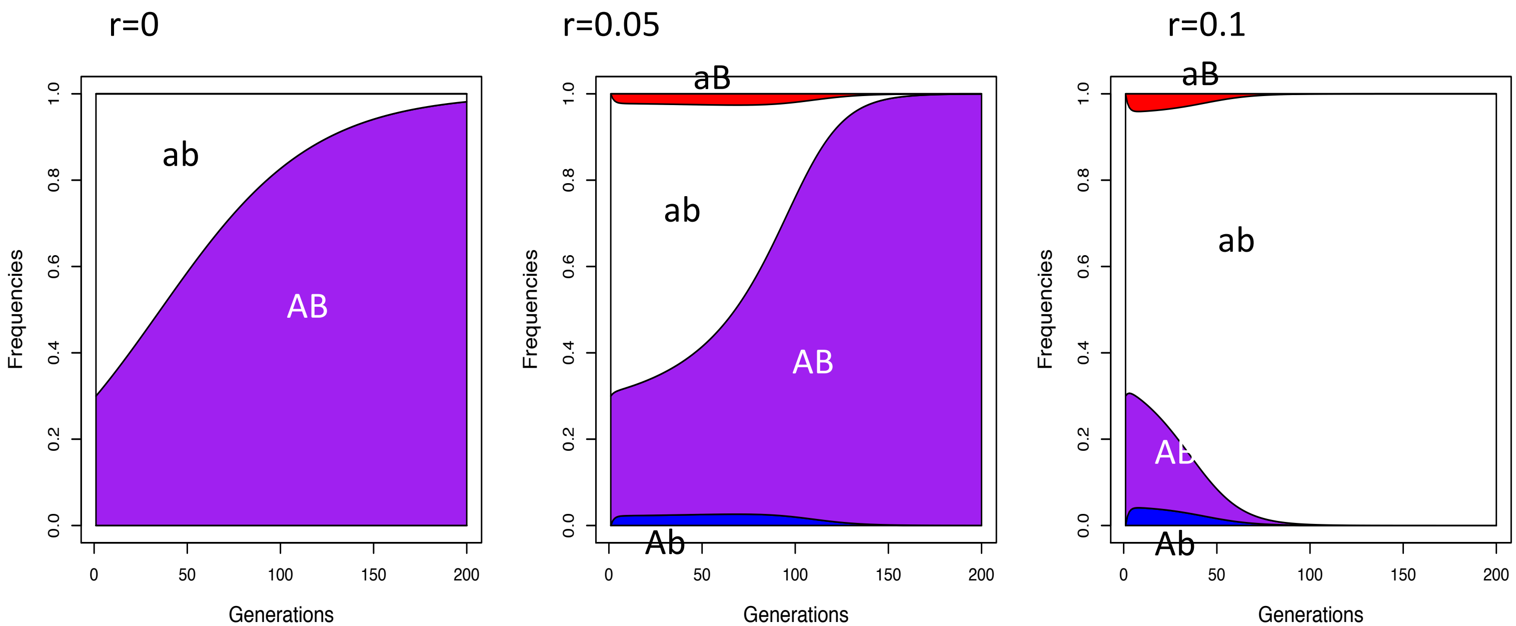
$w_{AB} > w_{ab} > w_{Ab} > w_{aB}$

$s_{AB} = 0.05$

$s_{Ab} = -0.9$

$s_{Ab} = -0.9$

$S_{ab} = 0$



Heliconius numata

f. silvana *f. bicoloratus*

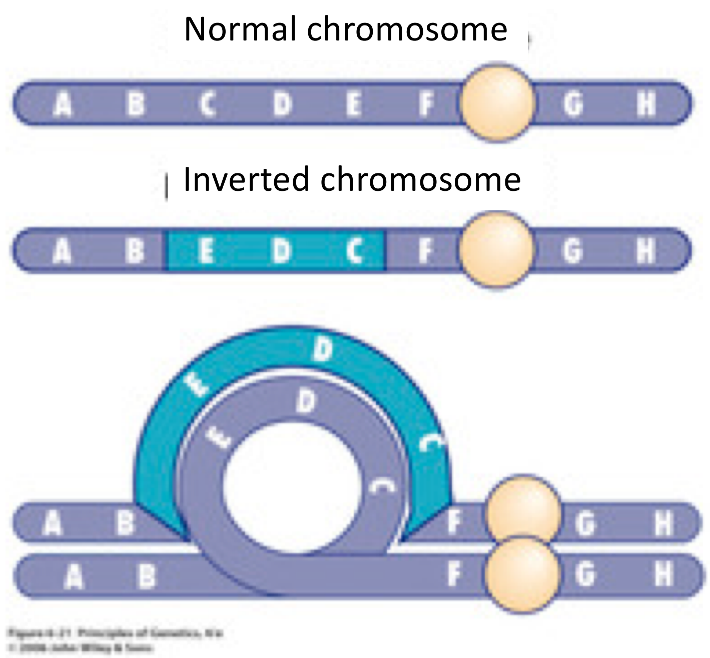
AB AB	AB or ab ab ab

Mimicry model

Melinaea ludovica *Melinaea marsaeus mothone*

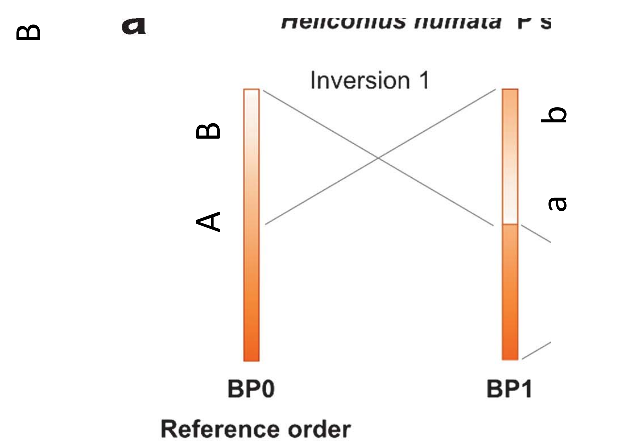
M J Thompson[1,2] and C D Jiggins[1]

Inversions block recombination in heterozygotes



Super genes

‘coadapted combinations of several or many genes locked in inverted sections of chromosomes and therefore inherited as single units.’
(Dobzhansky, 1970).



Heliconius numata

f. silvana *f. bicoloratus*

AB	AB or ab
AB	ab ab

Mimicry model

Melinaea ludovica *Melinaea marsaeus mothone*

Supergenes and their role in evolution

M J Thompson[1,2] and C D Jiggins[1]

Faeder-Independent inversion
4Mb

Structural genomic changes underlie alternative reproductive strategies in the ruff (*Philomachus pugnax*)

Sangeet Lamichhaney, Guangyi Fan, Fredrik Widemo, Ulrika Gunnarsson, Doreen Schwochow Thalmann, Marc P Hoeppner, Susanne Kerje, Ulla Gustafson, Chengcheng Shi, He Zhang, Wenbin Chen, Xinming Liang, Leihuan Huang, Jiahao Wang, Enjing Liang, Qiong Wu, Simon Ming-Yuen Lee, Xun Xu, Jacob Höglund, Xin Liu & Leif Andersson

A supergene determines highly divergent male reproductive morphs in the ruff

Clemens Küpper, Michael Stocks, Judith E Risse, Natalie dos Remedios, Lindsay L Farrell, Susan B McRae, Tawna C Morgan, Natalia Karlionova, Pavel Pinchuk, Yvonne I Verkuil, Alexander S Kitaysky, John C Wingfield, Theunis Piersma, Kai Zeng, Jon Slate, Mark Blaxter, David B Lank & Terry Burke

Fredrik Widemo

motto555/Thinkstock

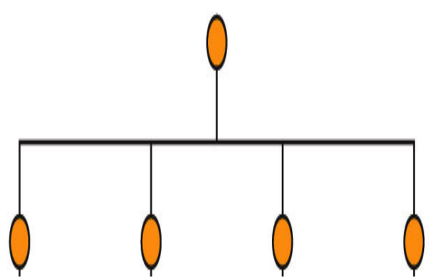
Melissa Hafting

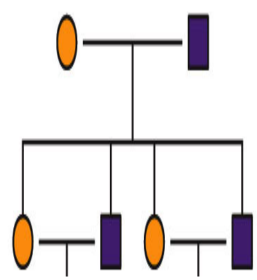
The cost of sex.

Why risk breaking it up a winning genotype.

Finding and attracting a mate are costly and may be impossible, and mating is dangerous

The two fold cost of sex





Sexual organisms only contribute ½ of their genome to their offspring While asexual organisms contribute their entire genome. This is sometimes called the cost of males

Despite this sexual reproduction persists.

- Why have sex?

Vast majority of eukaryotic organisms reproduce sexually

Many species are not obligate sexuals and can reproduce clonally (i.e. asexually)
e.g. Vegetative growth in plants.
However, they will only do so for a few generations

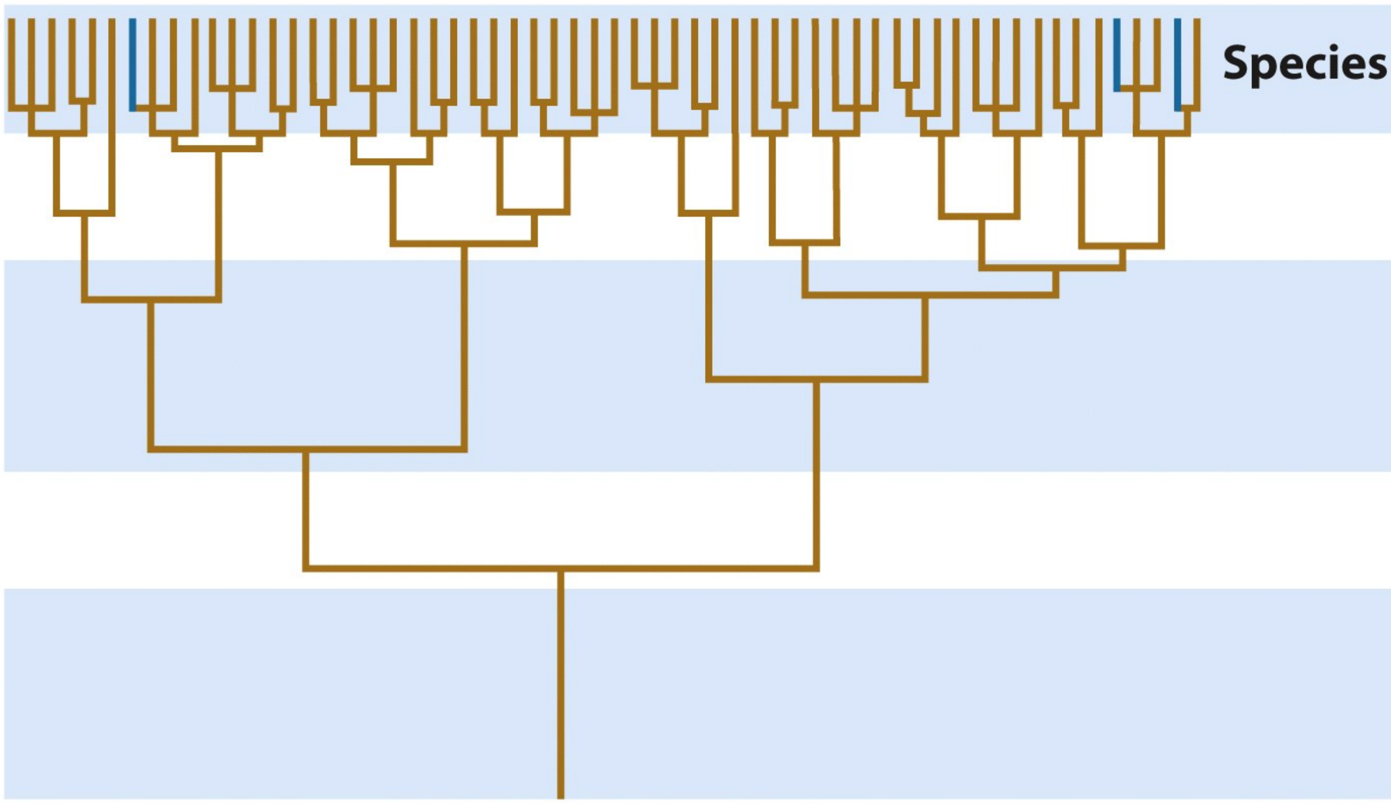
Vertebrate asexual species can evolve

Unisexual Cnemidophorus

Unisexual *P. formosa* (left) sexually parasitizes the sexual *P. latipinna* (right)

Despite this sexual reproduction persists.

Asexual species emerge often in animals/plants but are generally short-lived as species



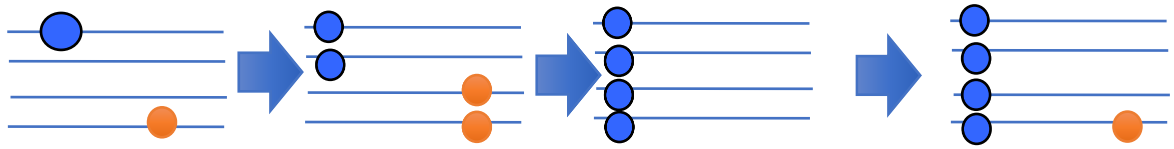
Evolution, 1/e Figure 16.9

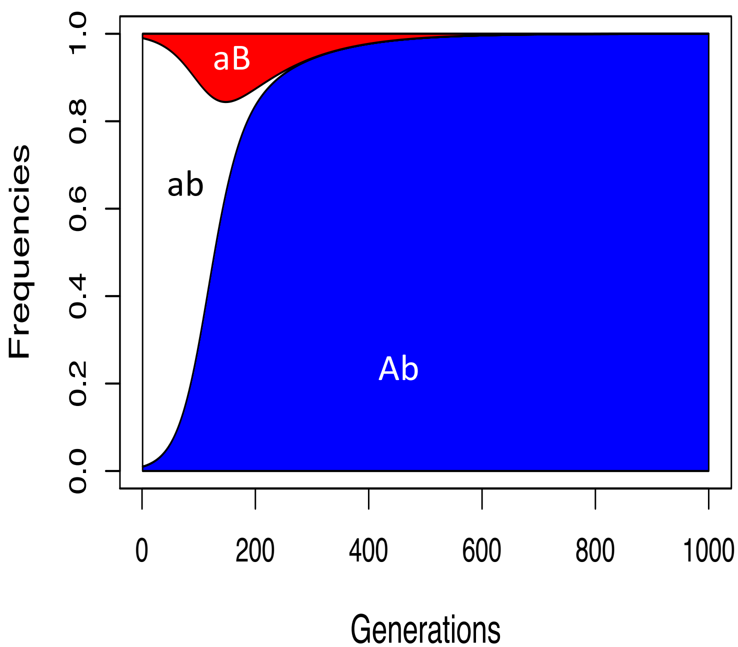
Hypotheses for the evolutionary advantage and maintenance of sex

- Asexual species accumulate deleterious mutations
    - Hitchhiking of deleterious mutations
    - Due to Muller's Ratchet
- Asexual species adapt slower
    - forced to fix advantageous mutations sequentially (Clonal interference)
    - Creation of novel haplotypes in asexuals is mutation limited. Hard to keep pace with rapidly evolving pathogens (Red queen hypothesis)

Clonal interference hypothesis

Selected alleles must fix sequentially in absence of sex

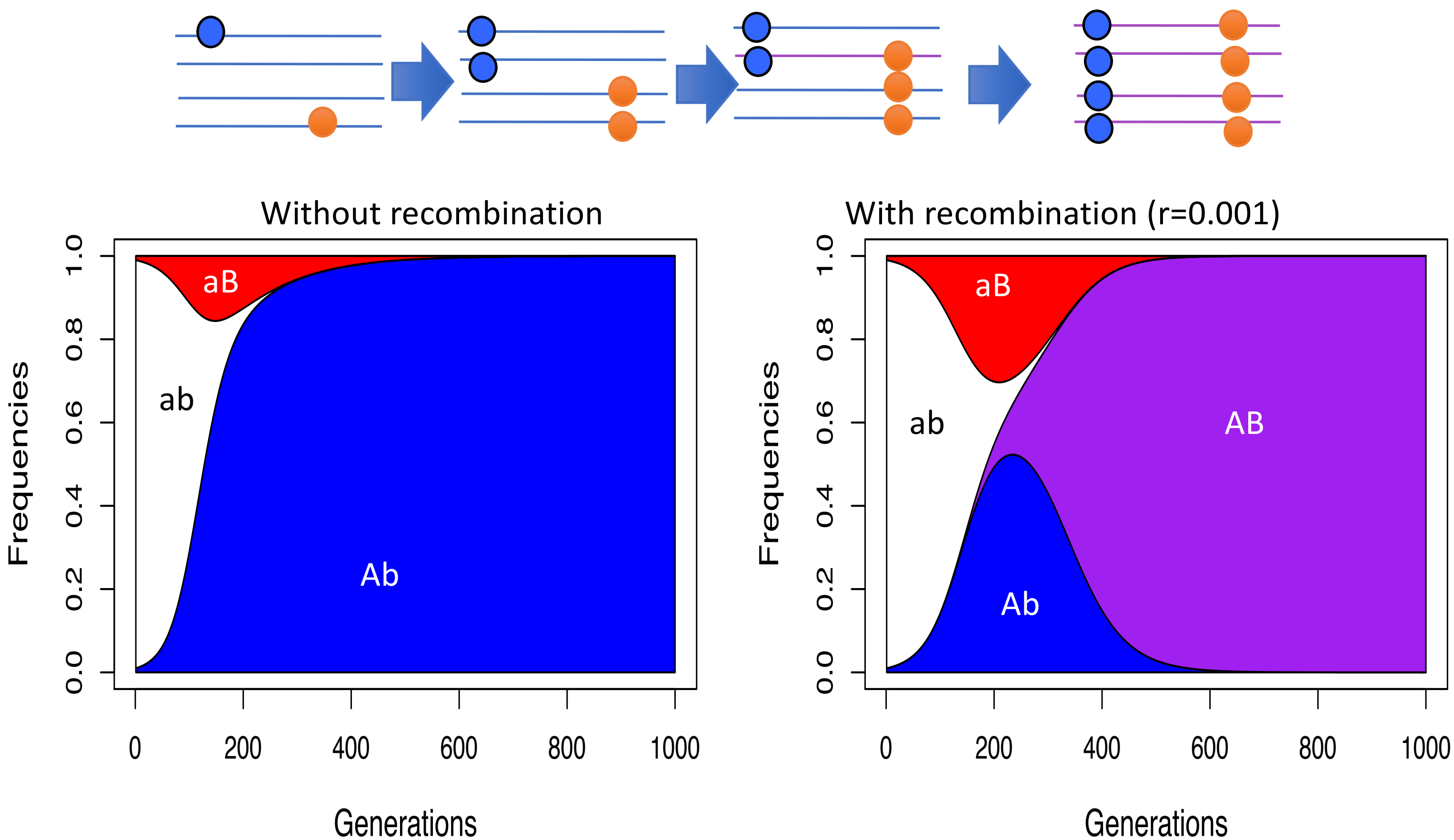




$s_A = 0.08$
$s_B = 0.06$
$s_{AB} = 0.14$

Clonal interference hypothesis

Selected alleles can fix simultaneously in presence of sex.



Evidence of Clonal Interference

doi:10.1038/nature12344

Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations

Gregory I. Lang[1]*†, Daniel P. Rice[2]*, Mark J. Hickman[3], Erica Sodergren[4], George M. Weinstock[4], David Botstein[1] & Michael M. Desai[2]

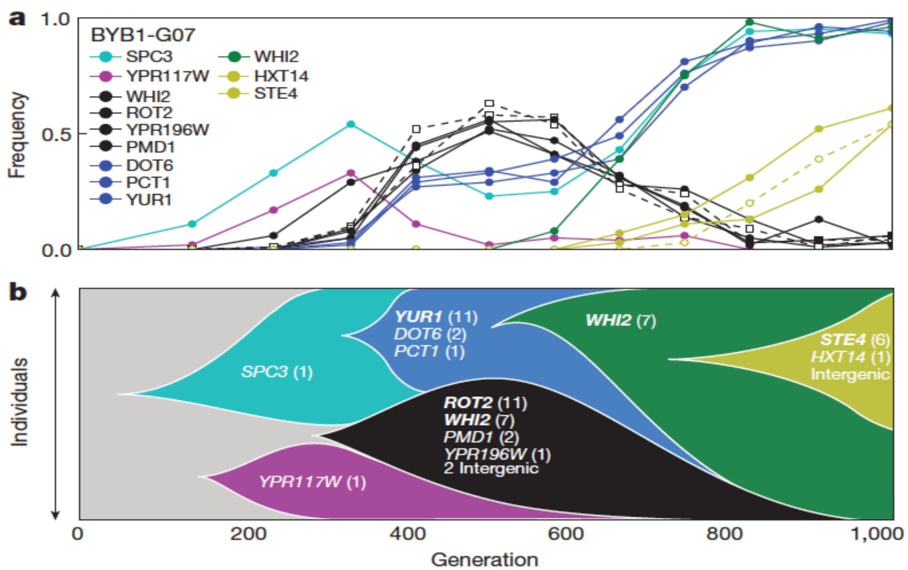
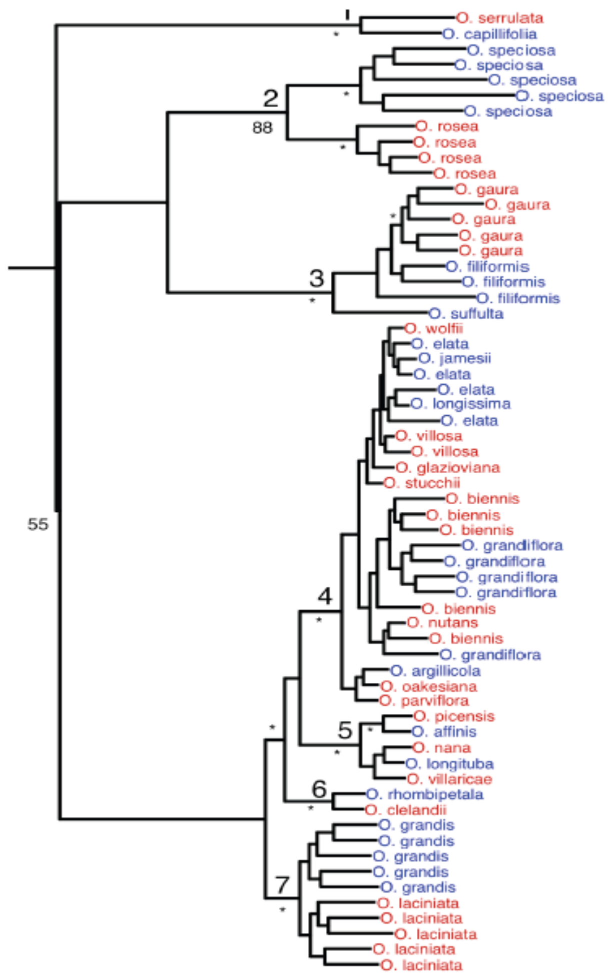


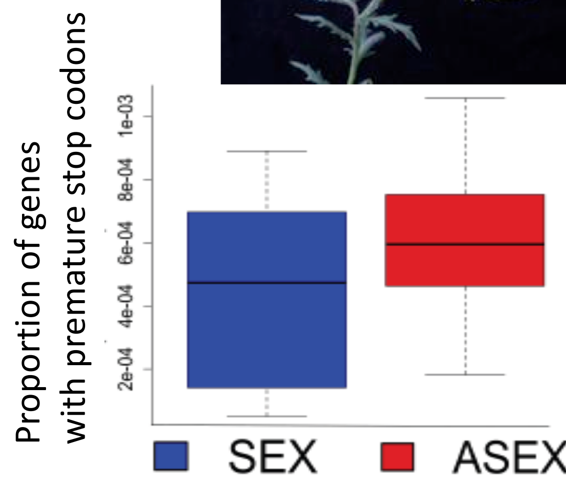
Figure 3 | The dynamics of sequence evolution in BYB1-G07. a, The trajectories of the 15 mutations that attain a frequency of at least 30%, hierarchically clustered into several distinct mutation 'cohorts', each of which i: represented by a different colour (Methods). **b**, Muller diagram showing the

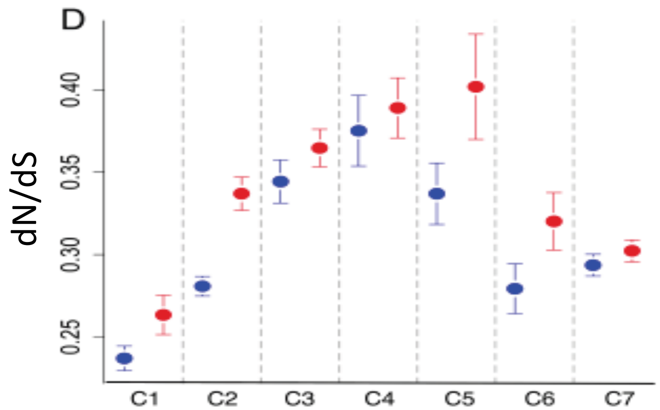
Clonal interference also plays a key role in thinking about evolution of drug resistance in pathogens.

Recurrent loss of sex is associated with accumulation of deleterious mutations in *Oenothera*

Jesse D. Hollister[1,2,*], Stephan Greiner[3], Wei Wang[1], Jun Wang[4], Yong Zhang[4], Gane Ka-Shu Wong[4,5,*], Stephen I. Wright[1,6], Marc T. J. Johnson[2,6]





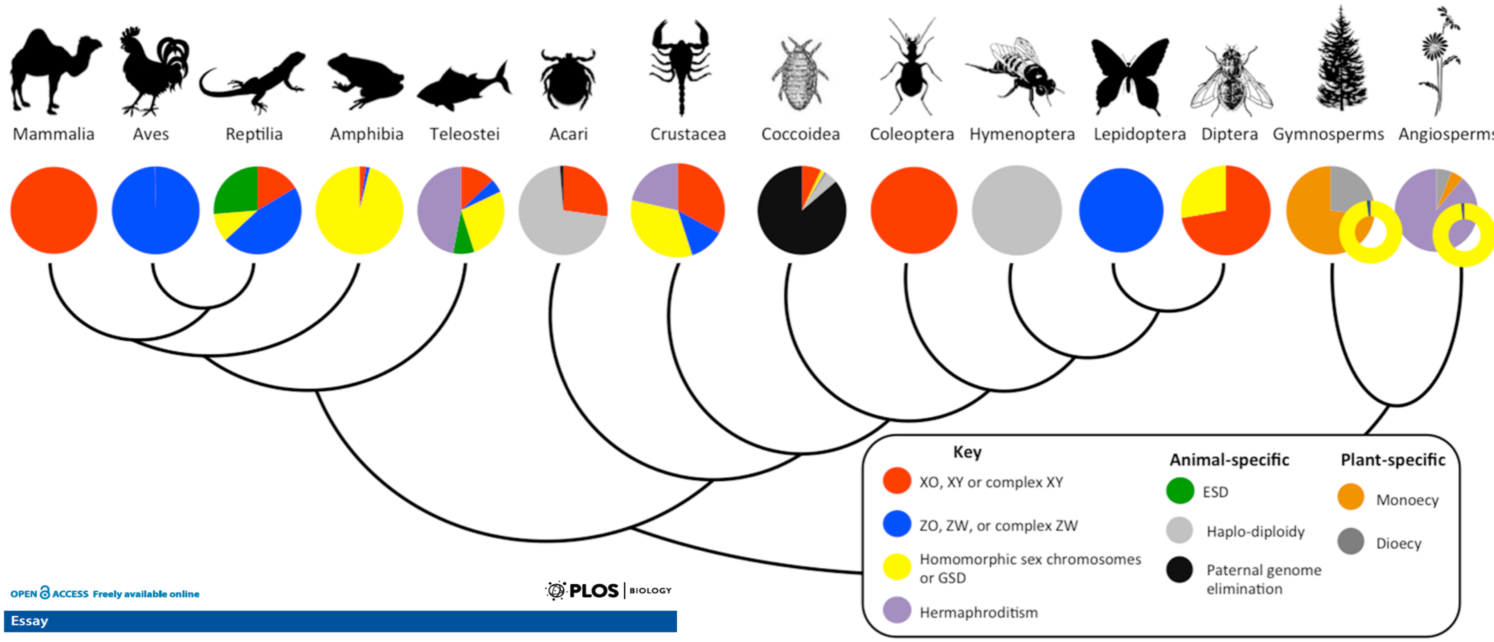


A species having sex is not the same as a species having different sexes

- The fundamental difference between male and female function is Anisogamy (Gametes differ in size)
- Male sexual function:
  - Small mobile gametes
- Female sexual function:
  - Larger less mobile gametes
  - Maternal provisions

Zimmer book

Male and female functions do not
necessarily mean sexes are separate individuals
But separate sexes have arisen many times
Perhaps because of:
Selection for specialization
or inbreeding avoidance.



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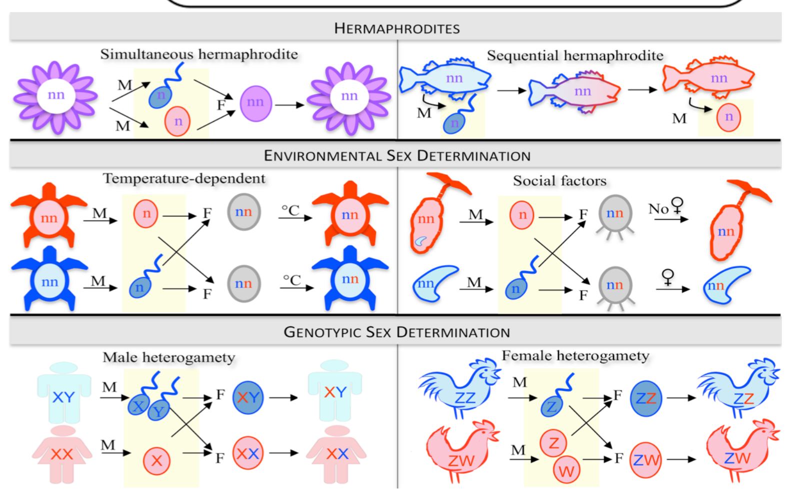
PLOS | BIOLOGY

Essay

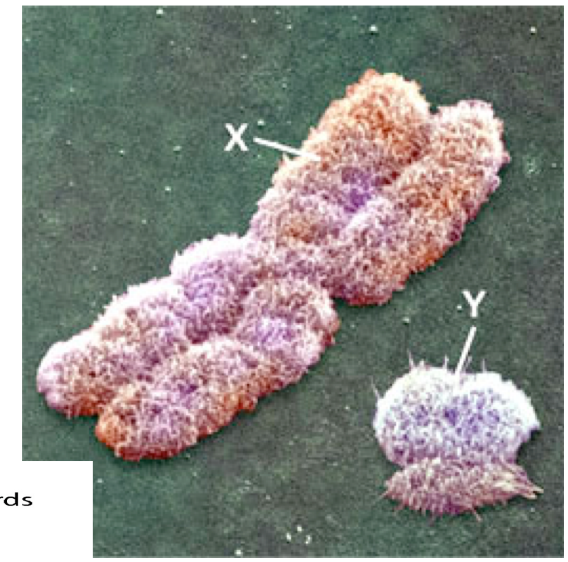
Sex Determination: Why So Many Ways of Doing It?

Doris Bachtrog[1*], Judith E. Mank[2], Catherine L. Peichel[3], Mark Kirkpatrick[4], Sarah P. Otto[5], Tia-Lynn Ashman[6], Matthew W. Hahn[7], Jun Kitano[8], Itay Mayrose[9], Ray Ming[10], Nicolas Perrin[11], Laura Ross[12], Nicole Valenzuela[13], Jana C. Vamosi[14], The Tree of Sex Consortium[¶]

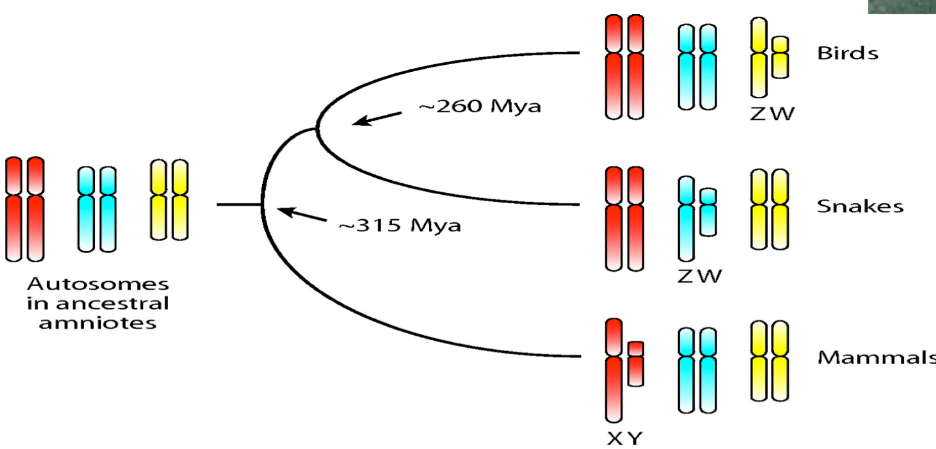


Evolution of sex chromosomes

In species with genetic sex determination
the chromosomes containing the sex determining factors
are often heteromorphic:
One is much reduced in
function and size.
And does not recombine.

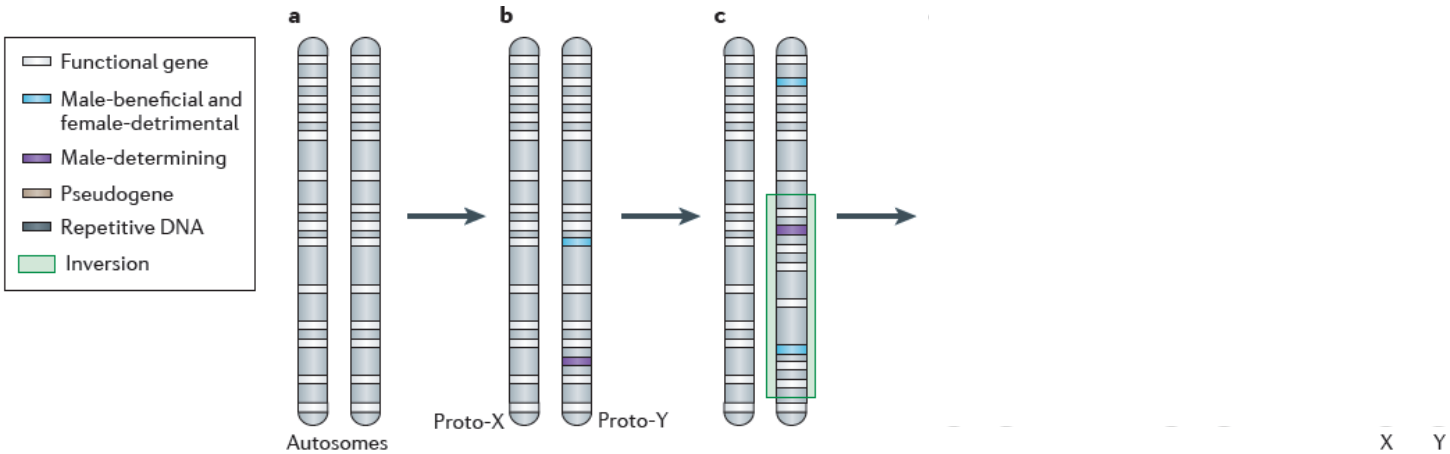


Human Y: 60 Mbp ~80 genes
Human X: 153 Mbp ~2000 genes



Heteromorphic sex chromosomes have evolved independently many times

The evolution of sex chromosomes



Sex determining allele arises (e.g. dominant male determining allele)
Recombination between sexually antagonistic allele and male-determining allele have lowers fitness.
Recombination between these loci suppressed by inversion