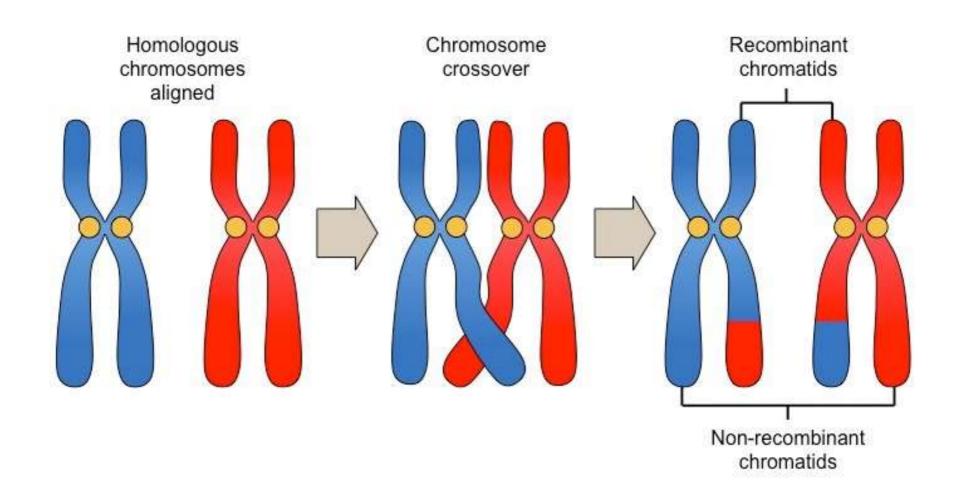
Interactions between several loci, Epistasis, Super Genes, Pleiotropy, Interactions Genes x Environment

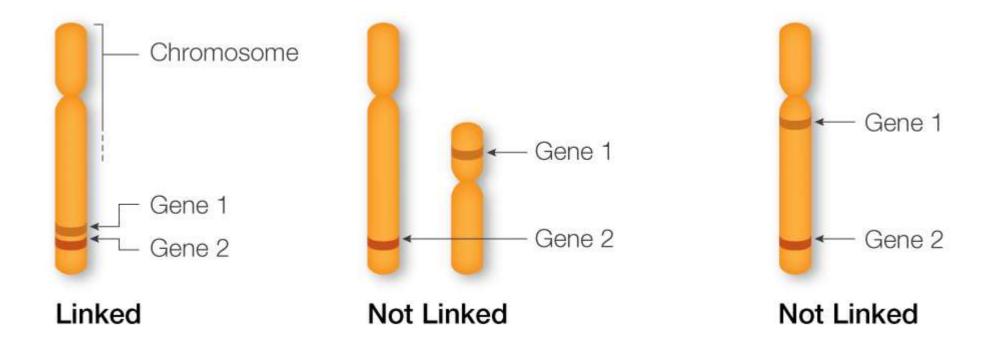
Virginie Courtier-Orgogozo Institut Jacques Monod, Paris

Genetic Linkage

Crossing overs

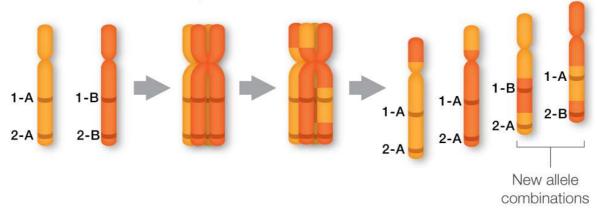


About one recombination event per chromosome arm

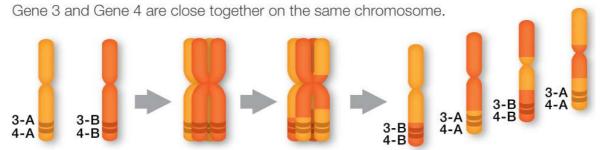


Not Linked

Gene 1 and Gene 2 are far apart on the same chromosome.



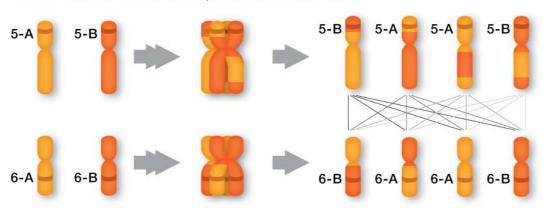
Linked



No new allele combinations

Not Linked

Gene 5 and Gene 6 are on separate chromosomes.



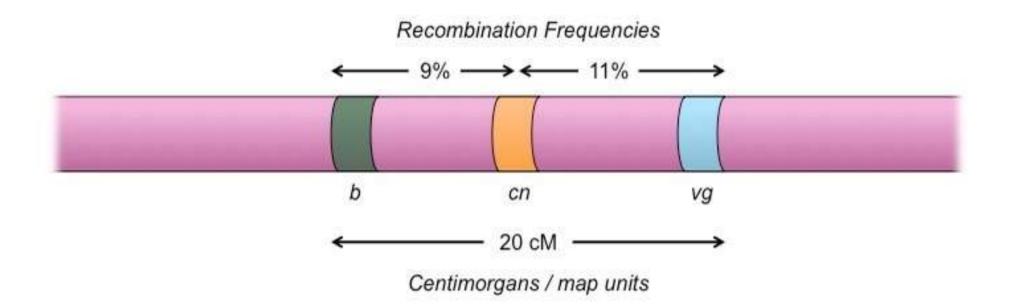
Alleles (on whole chromosomes) can be distributed to gametes in any combination.

One "centiMorgan"

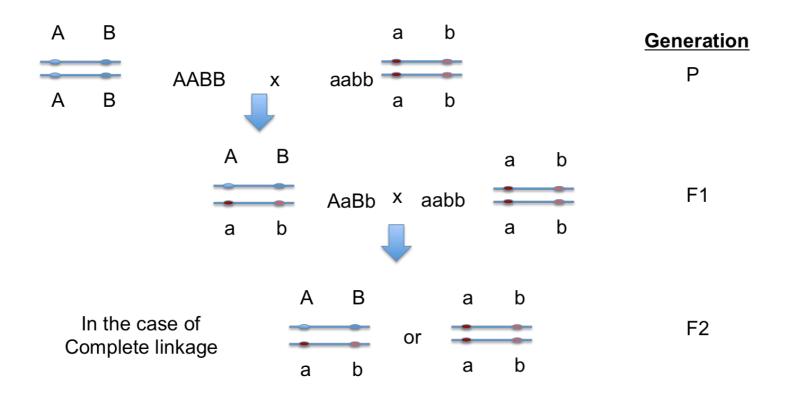
= genetic distance that produces a recombination frequency of 1%

Genetic distance (in cM)

= (# Recombinant gametes) X 100
Total gametes



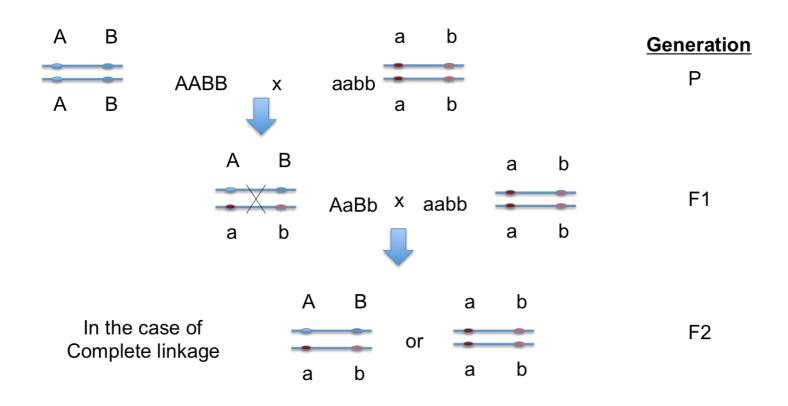
Measure of genetic linkage



Complete Linkage

50% AaBb 50% aabb

Measure of genetic linkage



Complete Linkage

50% AaBb 50% aabb

Genetic Linkage

40% AaBb 10% Aabb 10% aaBb 40% aabb

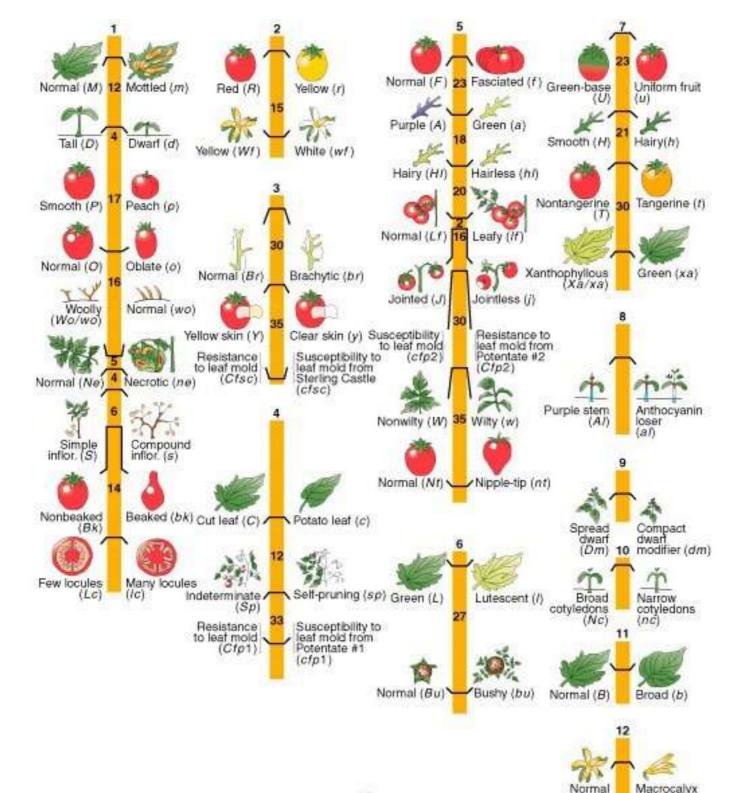
20% of recombinants so 20cM

Measure of genetic linkage

If y % recombinant gametes and y < 50% => y cM apart

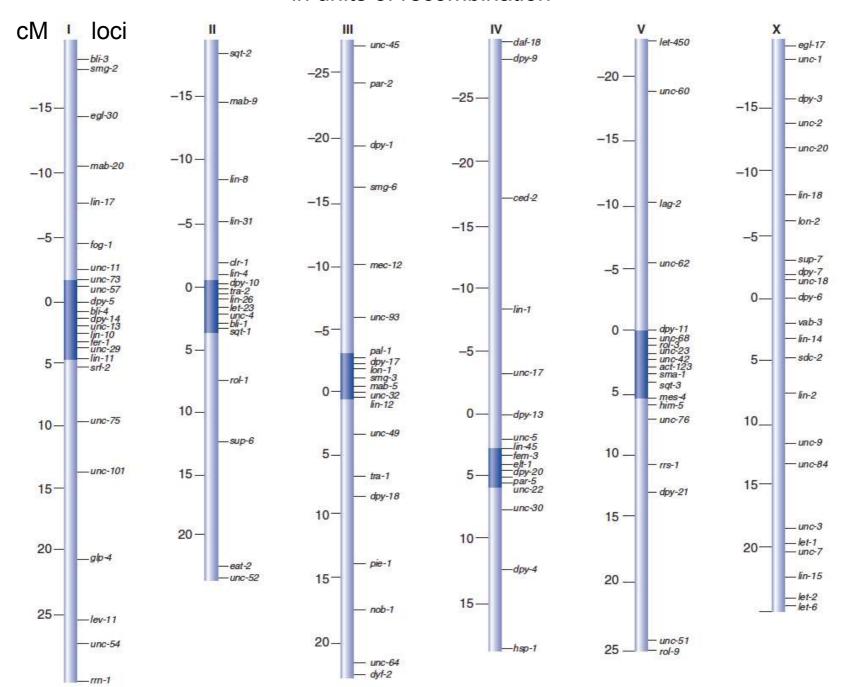
Due to double cross-overs and cross-over interference, genetic distances need corrections when long and are not fully additive

If the linkage group is longer than 50 cM, mutations at the two extremities are operationally unlinked



Genetic map

in units of recombination



Genetic Markers

Mark the region of interest through genetic linkage

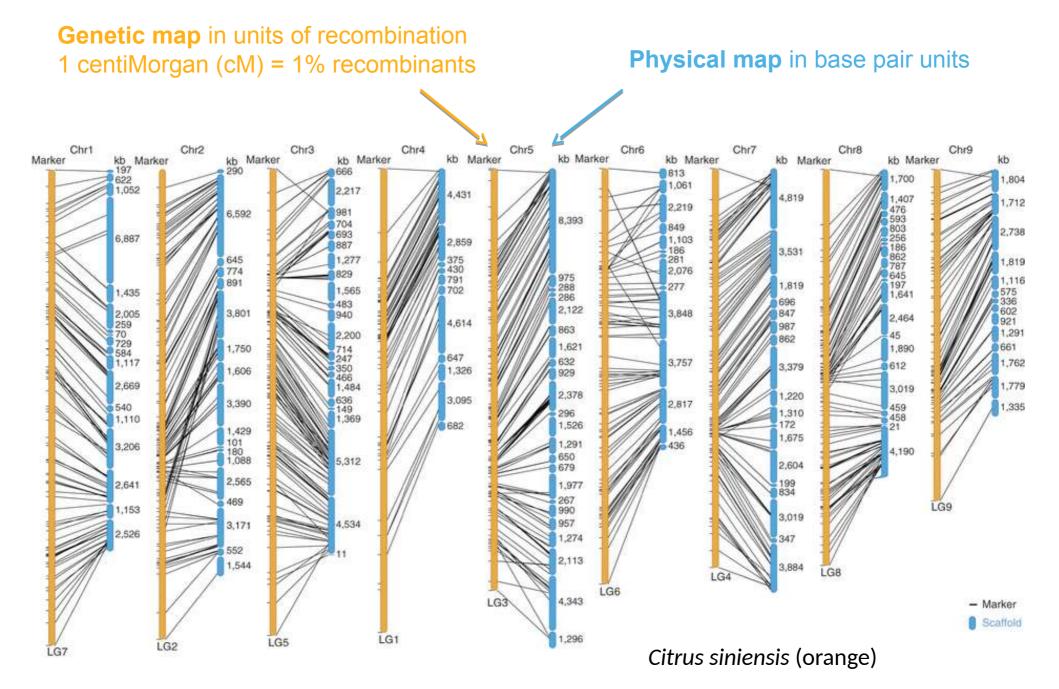
Are not causal (or only rarely) for variation in the phenotype of interest



Detected:

- through their phenotypic effect:
 white eyes, dumpy shape, GFP marker
- molecularly: PCR, sequencing transposon insertion, single-nucleotide polymorphism (SNP), indel

Alignment of genetic and physical maps



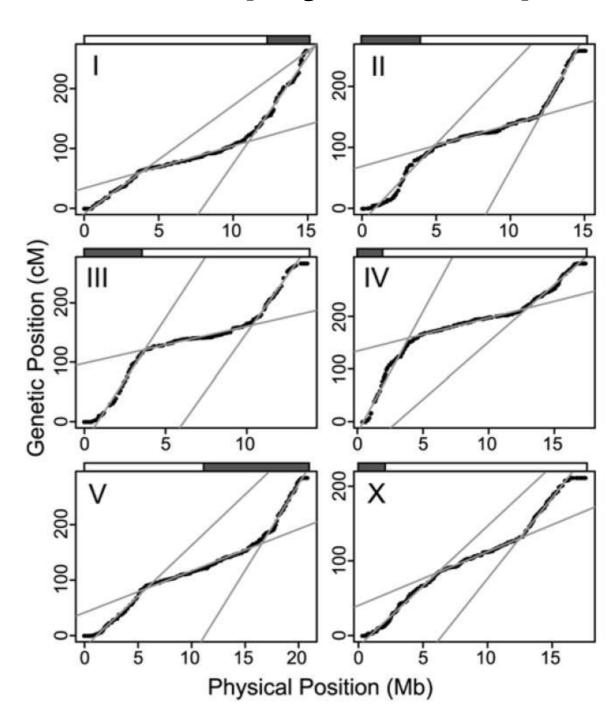
Alignment of genetic and physical maps

Marey map

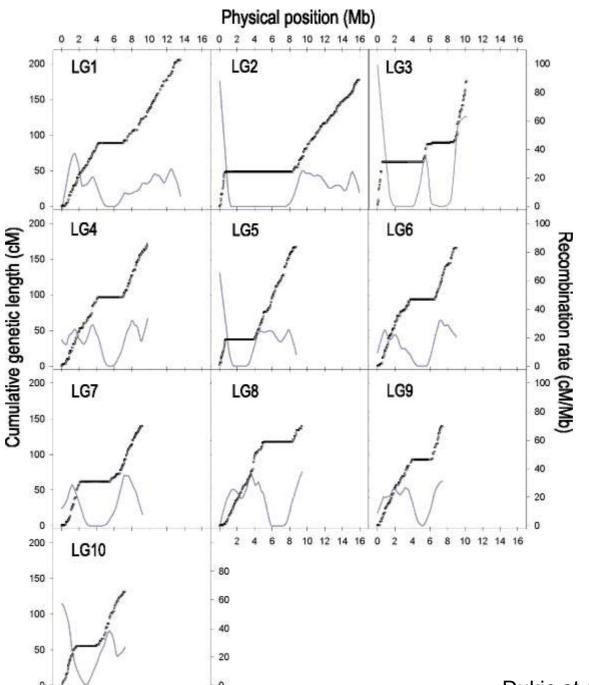
Genetic position was measured in centiMorgans based on a recombinant inbred advanced intercross line population, and not based on meiotic distances.

Recombination rate varies along the chromosome

C. elegans Rockman & Kruglyak PLoS Gen 2009



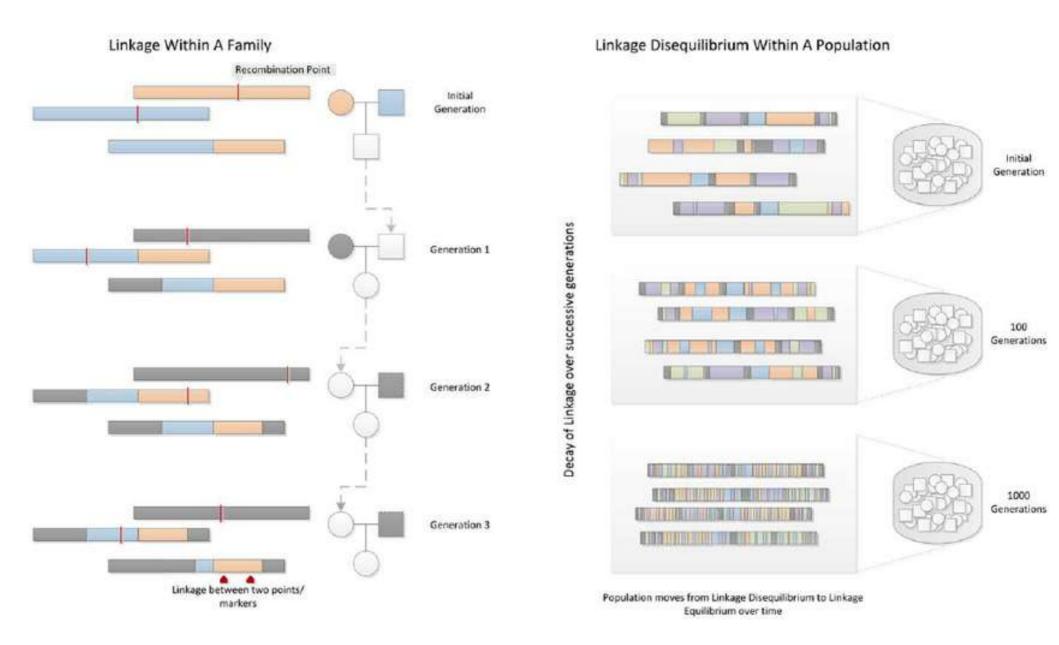
Marey maps in Daphnia



Dukic et al. 2016 BMC Genetics

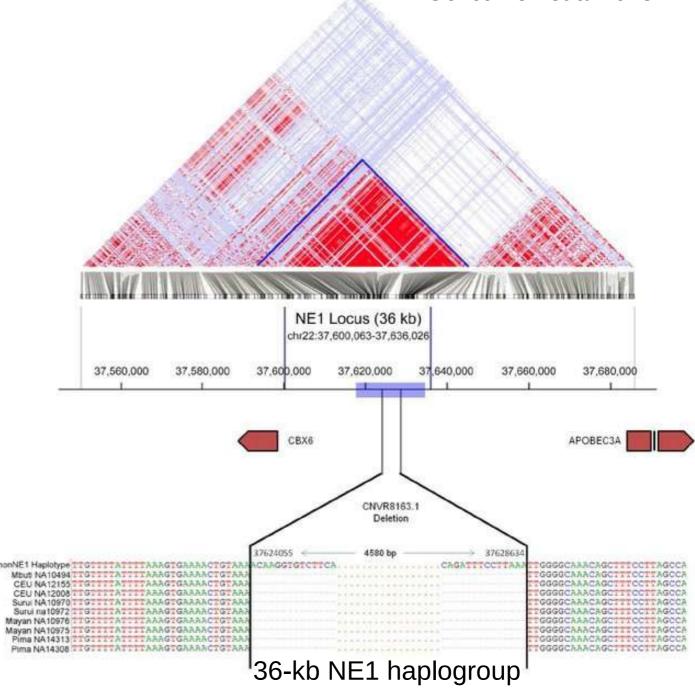
Linkage disequilibrium (LD)

non-random association of alleles at different loci in a given population



Gokcumen et al 2013

The Linkage
Disequilibrium (LD)
block was determined
using SNP data of the
CEU population from
1000 human Genomes



contains a 4.6-kb deletion in perfect linkage disequilibrium with 12 SNP aligns with Neandertal haplotype

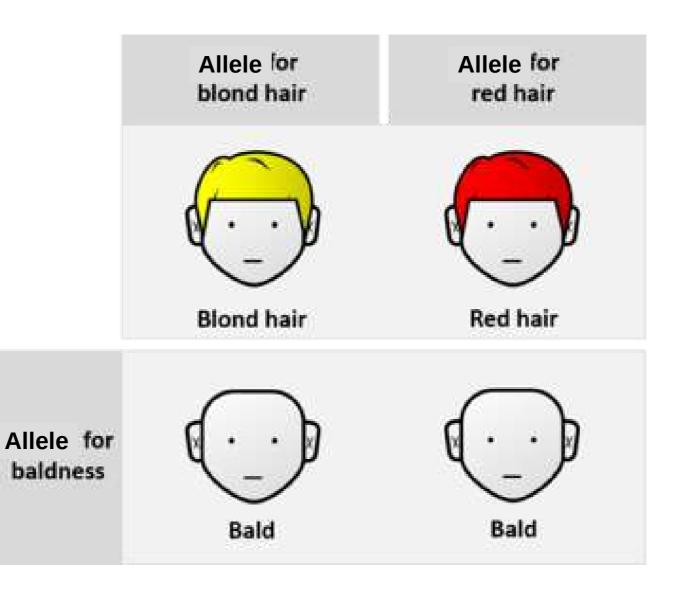
Variation in Linkage disequilibrium (LD)

LD is a function of age of alleles, outcrossing and recombination rates

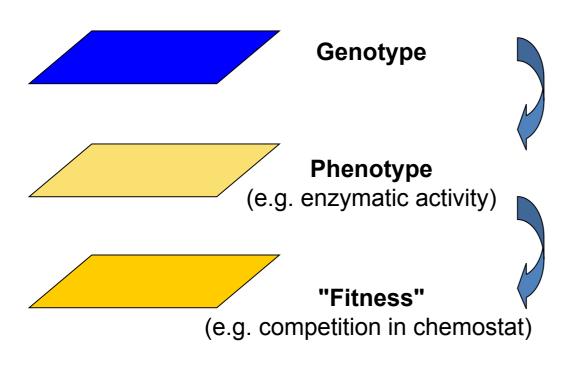
Depends on organism and genome region short-range = 100 bp *D. melanogaster*, *Caenorhabditis remanei* medium-range = a few kb: *Homo sapiens*, *Arabidopsis thaliana* long-range = Mb: *Caenorhabditis elegans*

Epistasis

= Non-additive interaction of alleles at different loci for a given phenotype

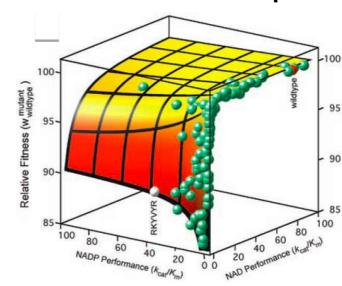


Additivity at one phenotypic level does not imply additivity at another level



additive

epistasis
due to enzyme saturation
=> non-linear relationship



Various meanings for Epistasis

Laboratory genetics, with null alleles

m1 is epistatic to m2if m1 m2 displays the M1 phenotype=> genetic pathway

Quantitative / evolutionary genetics "epistasis" used for "gene interaction"

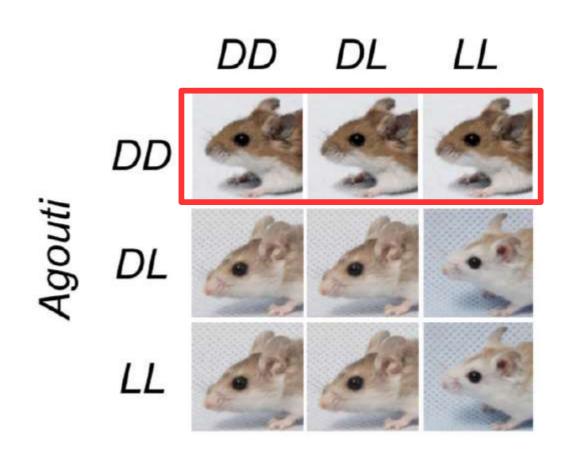
= non-additive effect for any combination (heterozygote, homozygote) non-additive mapping of genotype space to phenotype space

=> confusion between lab geneticists and evolutionary geneticists

Meaning of "epistasis" depends on the scientific context!

Agouti (D, L) and Mc1R (D,L)

Natural alleles 3 phenotypes



Agouti^D is epistatic over Mc1R alleles

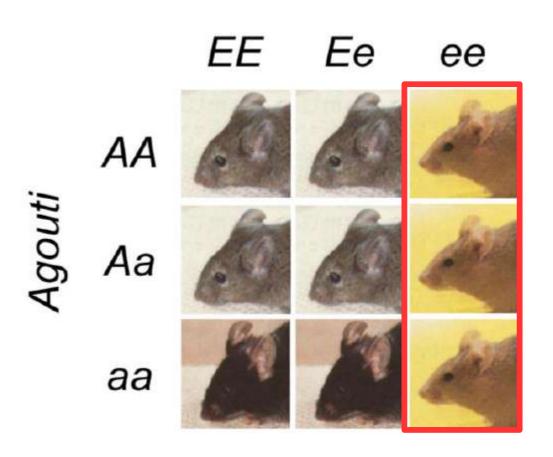
Agouti (A, a) and Mc1R (E,e)

Laboratory mutants 3 phenotypes

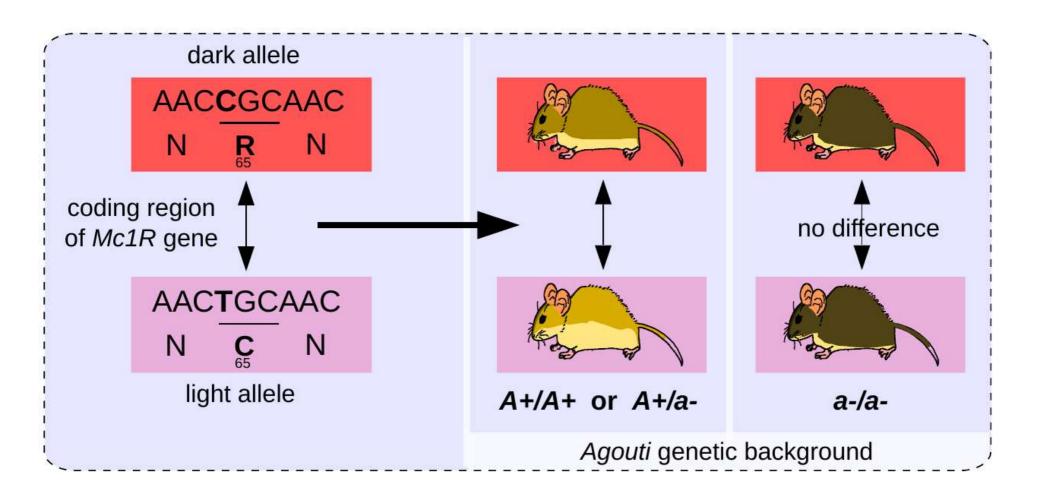


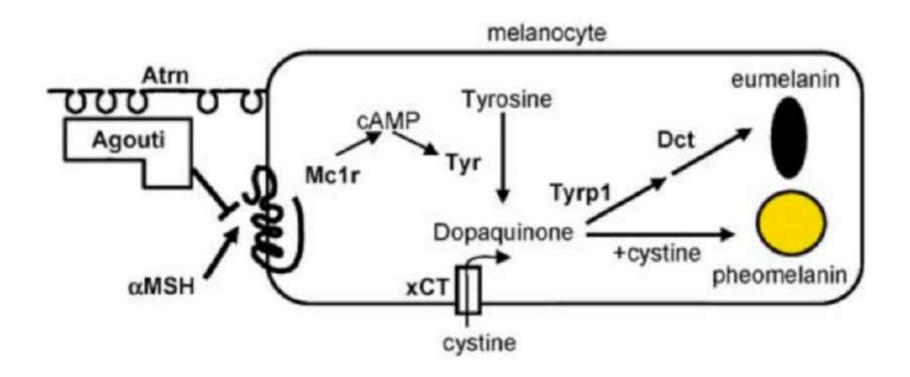


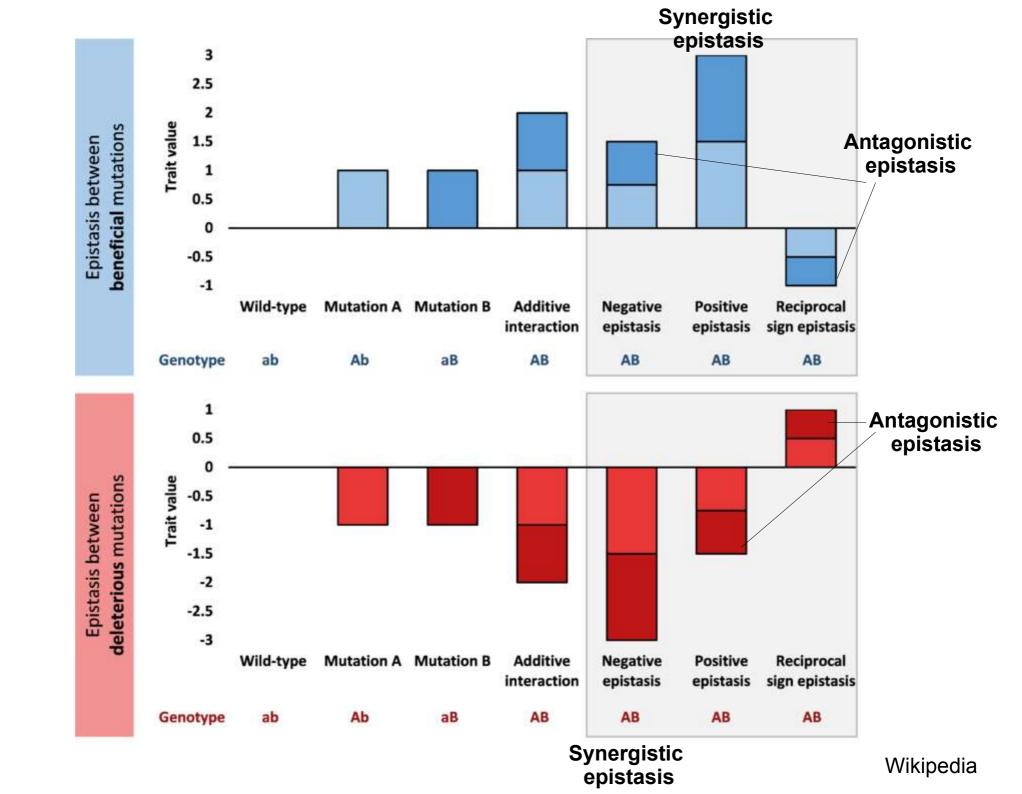




Mc1R^e is epistatic over Agouti alleles





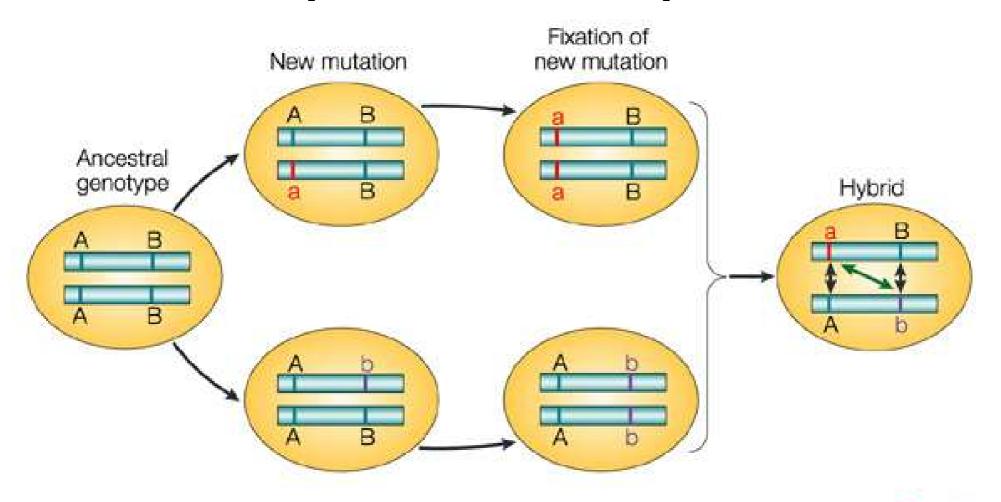


"Synergistic epistasis": the effects of both alleles
reinforce each other (more than the sum of their individual effects);
extreme case: synthetic phenotype (new phenotype)

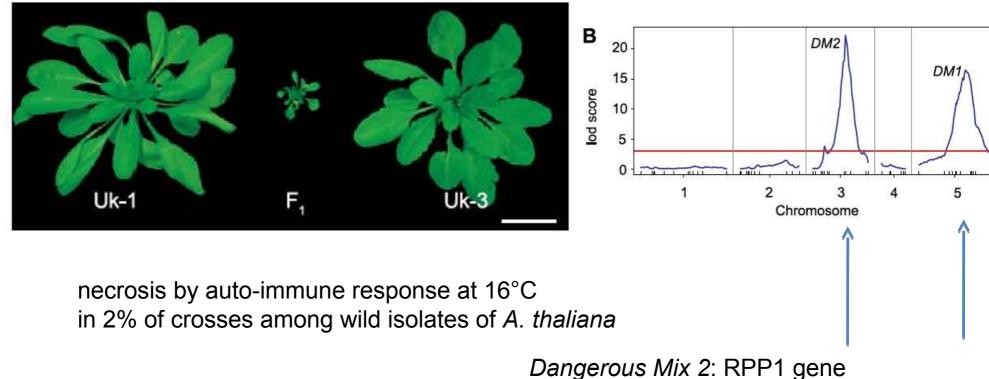
"Antagonistic epistasis": the effects of the two alleles partially compensate (less than the sum of effects of a2, b2)

"Positive or negative epistasis": the phenotypic value is either increased or decreased relative to additivity

Dobzhansky-Muller model of hybrid incompatibility A special case of epistasis



Hybrid incompatibility in A. thaliana



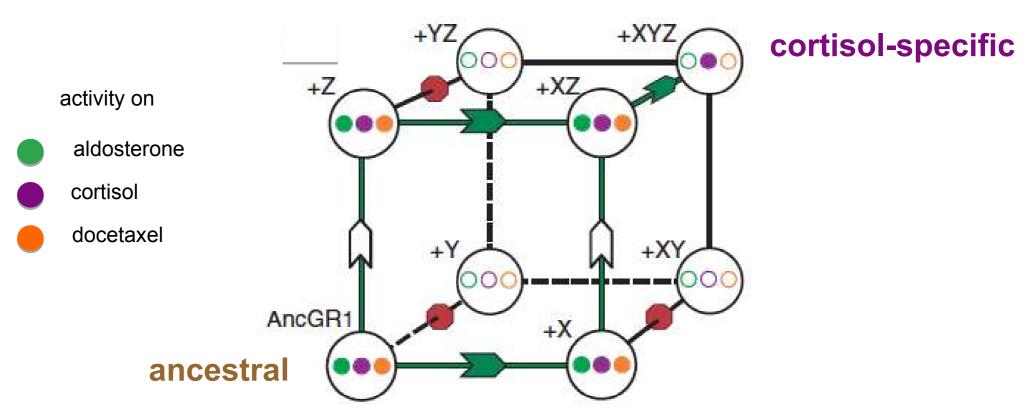
resistance against oomycete

Dangerous Mix 1: member of a large family of pathogen resistance gene NB-LRR

Intramolecular epistasis

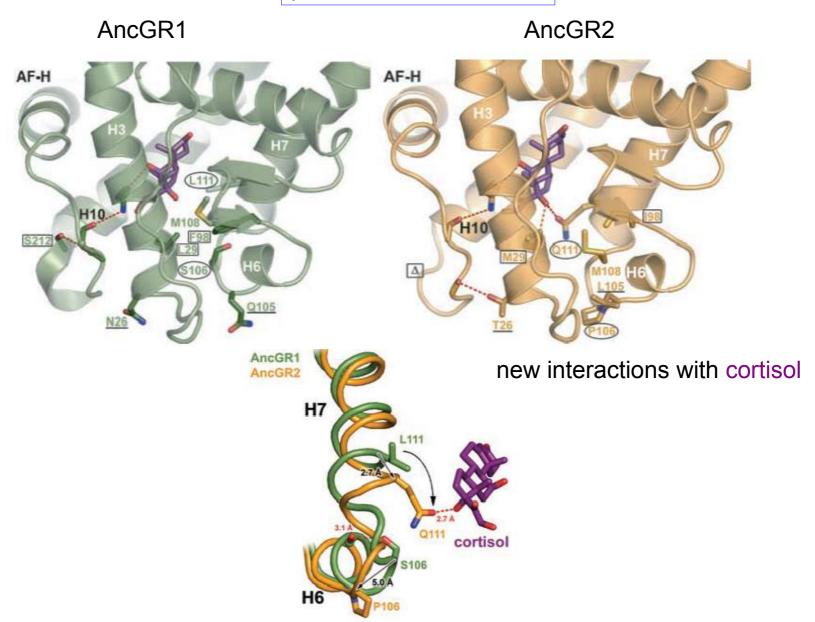
Reconstruction of ancestral protein sequence from phylogenetic analysis of extant family in databases

Vertebrate corticoid receptor family



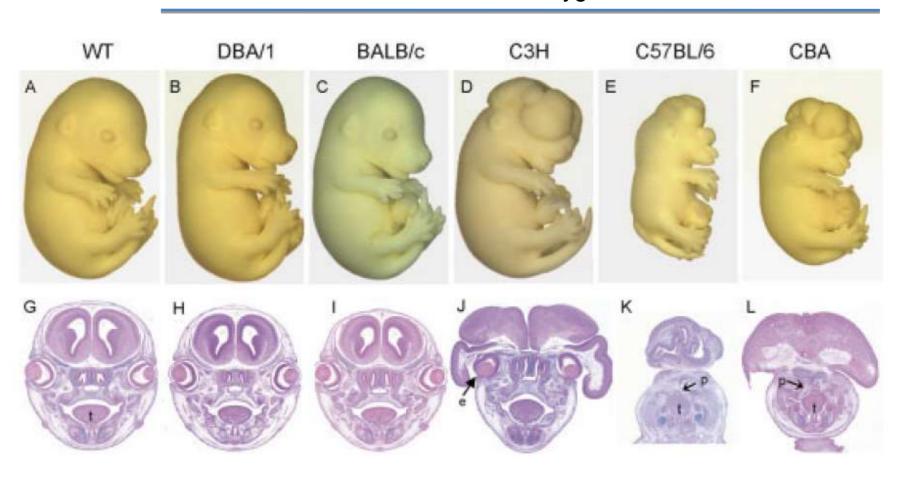
Ortlund et al. Science 2007

permissive substitutions



Expressivity of one mutation varies with wild genetic gackground

Tcof1/- heterozygote mice



Different kinds of GxG interactions

G x G between 2 laboratory mutations m1 m2

G x G between 2 natural alleles

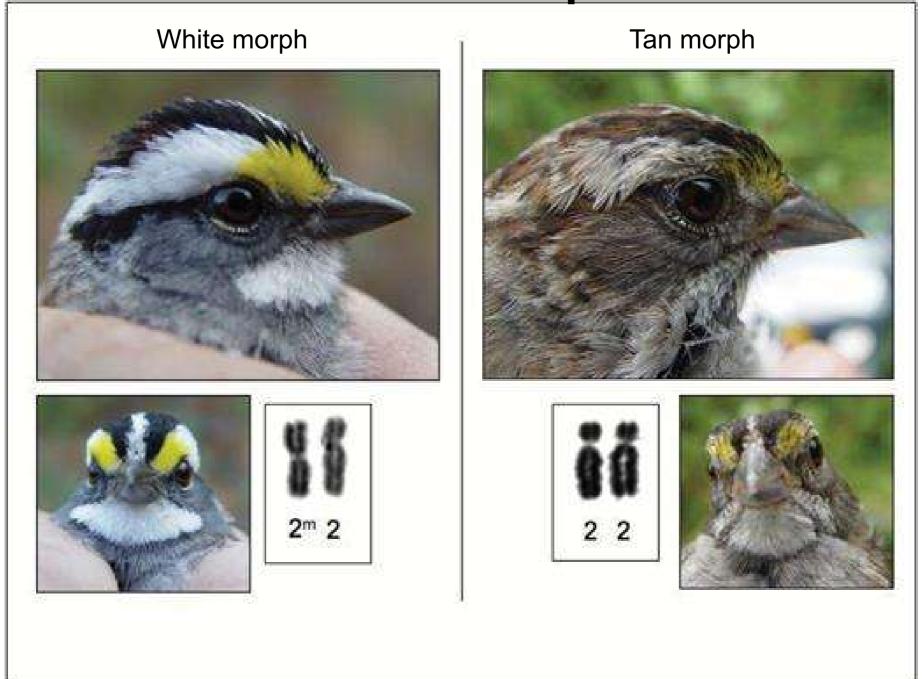
G1 x G2 one mutation in different wild genetic backgrounds "cryptic" variation

 $G \times G \times G > 2 loci$

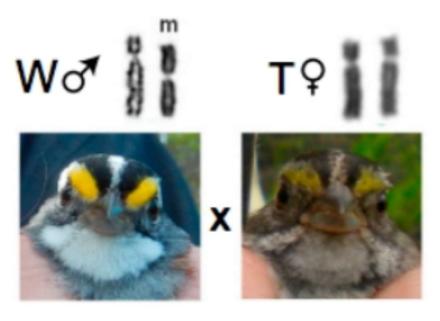
Gerke et al. 2010

Super genes

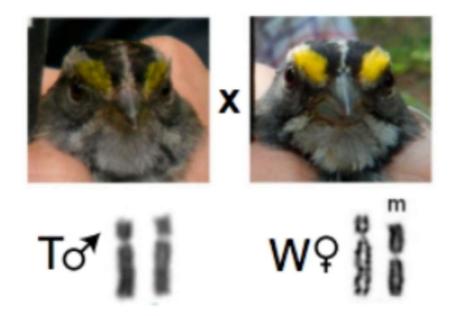
White throated sparrow



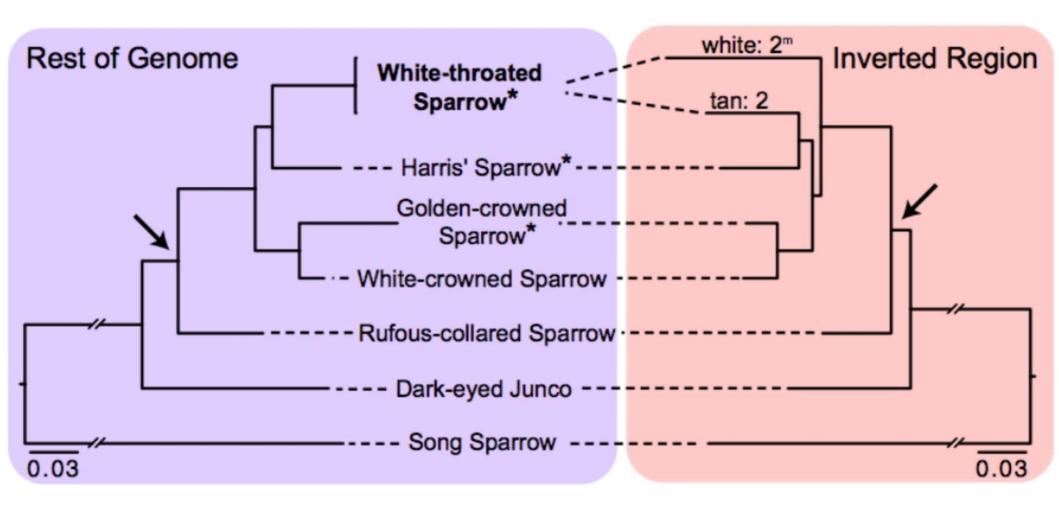
Disassortative mating

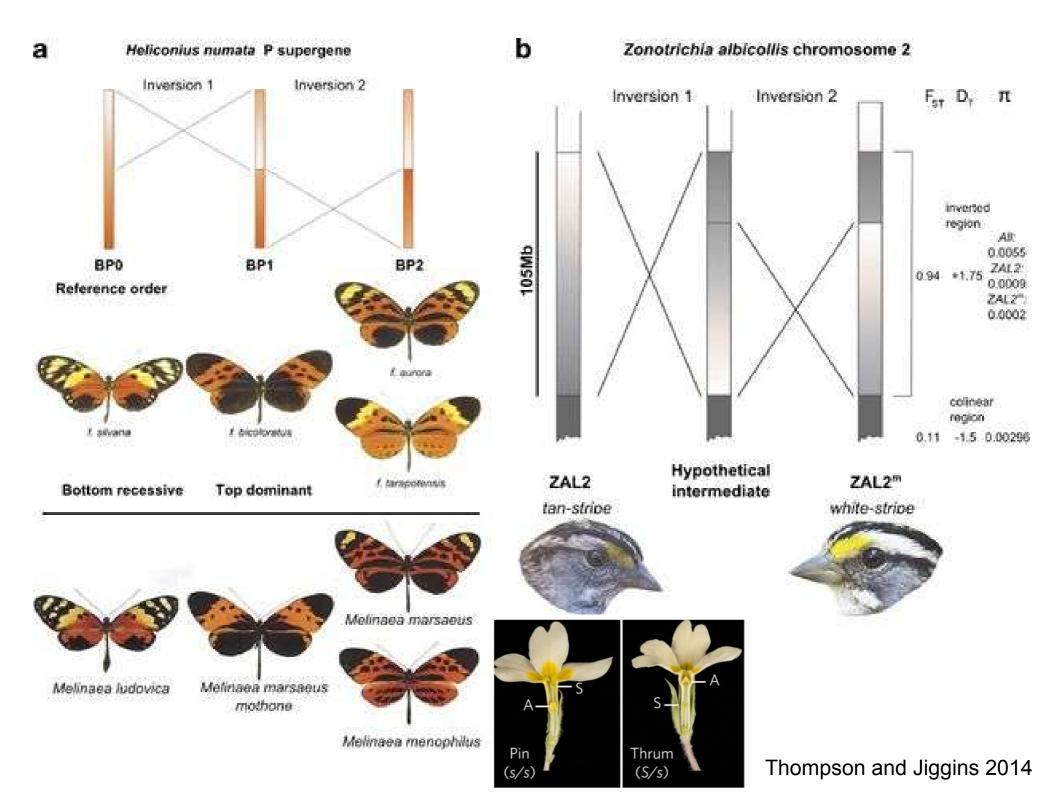


Never W male x W female Never T male x T female



Two sparrow morphs are determined by a supergene Alternative alleles are maintained by disassortative mating White Two supergene alleles have an ancient origin and may have come together via hybridization Tan Due to a lack of recombination on chromosome 2th. that version of the chromosome is degrading





Pleiotropy

= when a genetic change affects several phenotypes

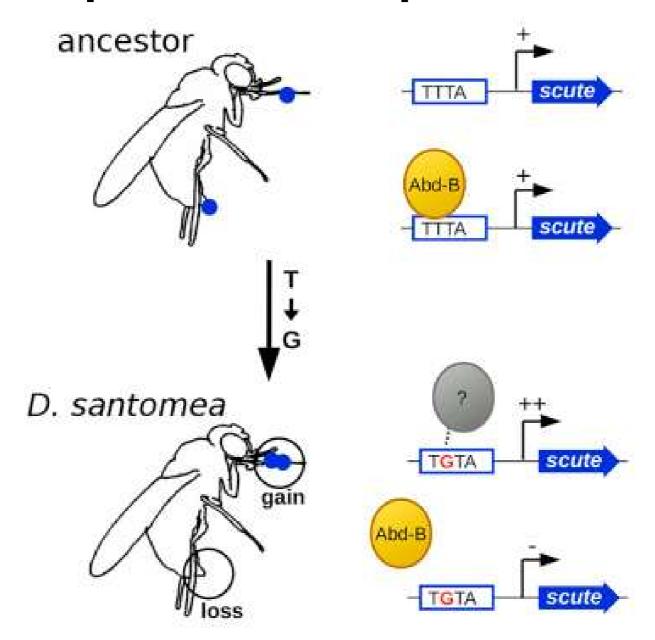
Various meanings for Pleiotropy

Pleiotropy of a gene (means pleiotropy of the *null* mutation)

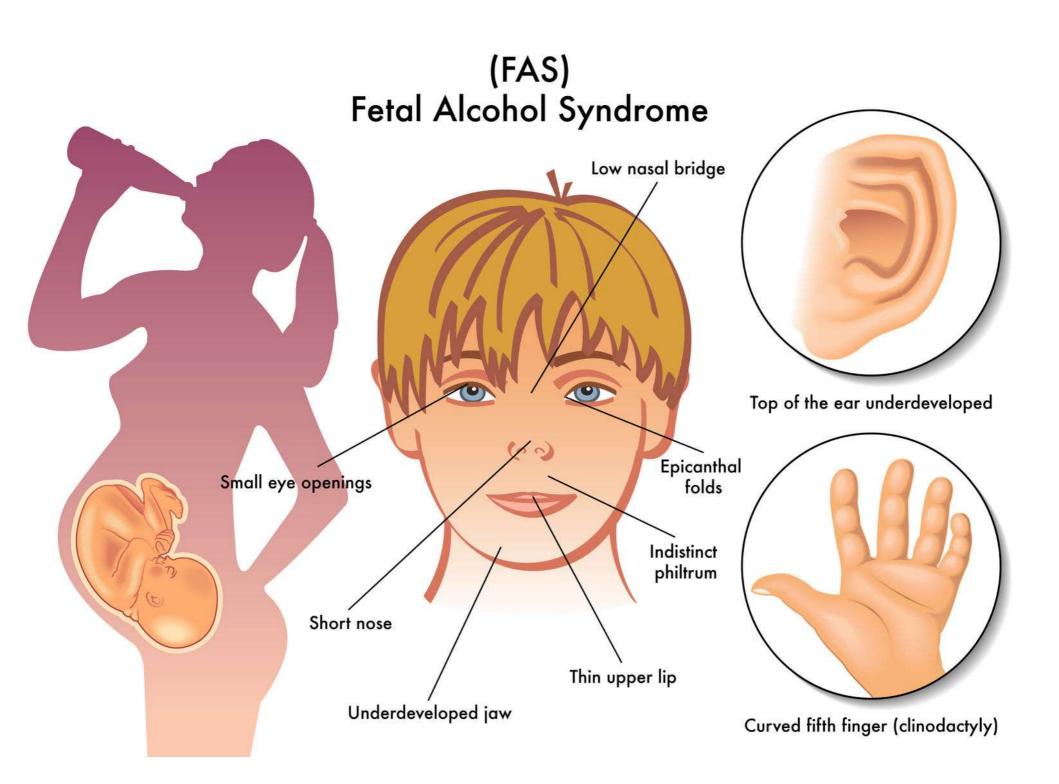
Pleiotropy of a cis-regulatory region (means pleiotropy of the *deletion* of the region)

Pleiotropy of a mutation

A pleiotropic cis-regulatory mutation responsible for species difference



GXE



Causes of skin color differences

Genetic

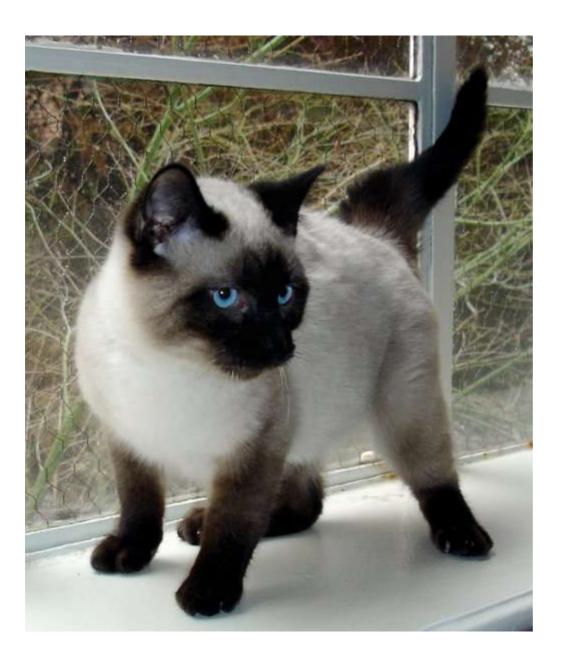






Phenotype = G + E + GxE

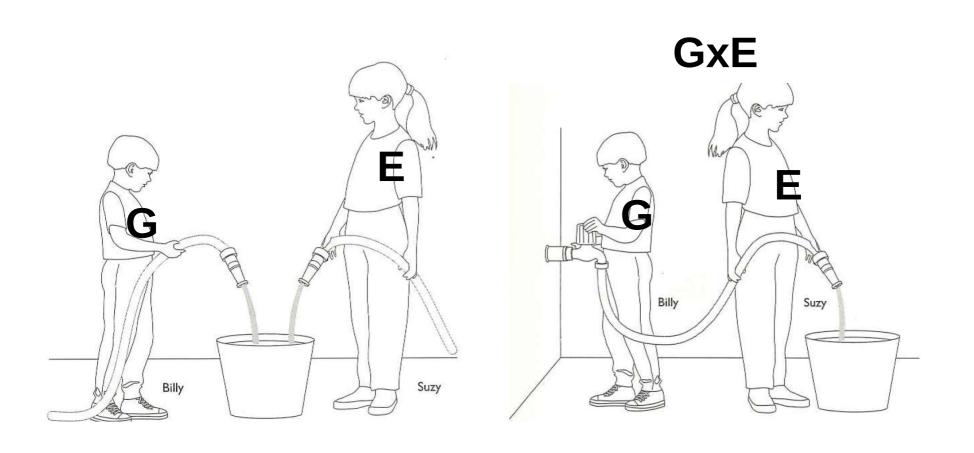
The Siamese cat An example of GxE



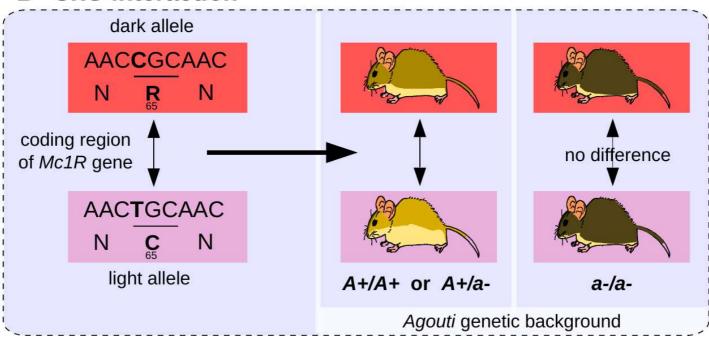


Mutation in *tyrosinase*Heat-sensitive
enzyme
No production of
melanin in warm body
parts

Contributions of the genotype (G) and the environment (E) to phenotypic variation

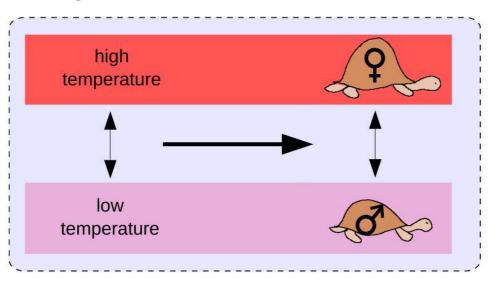


B GxG interaction

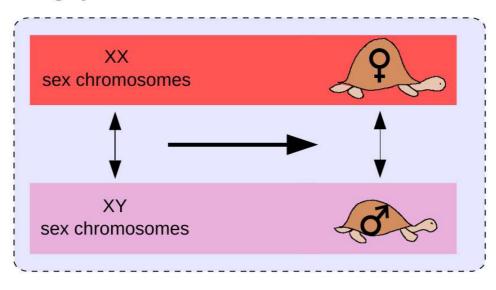


Comparing G and E effects

A enphe



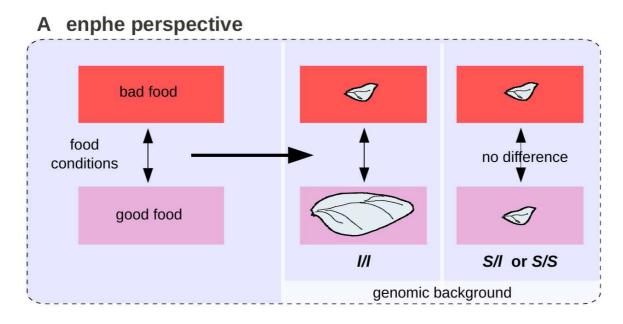
B gephe

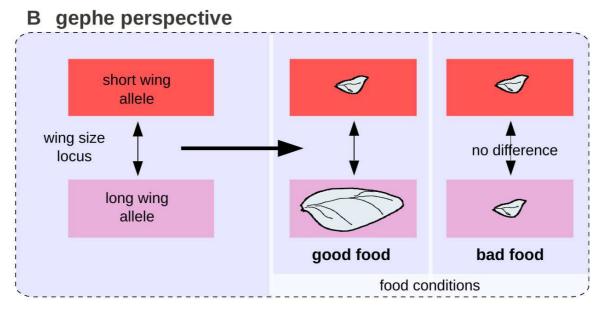


Intermingled G and E effects

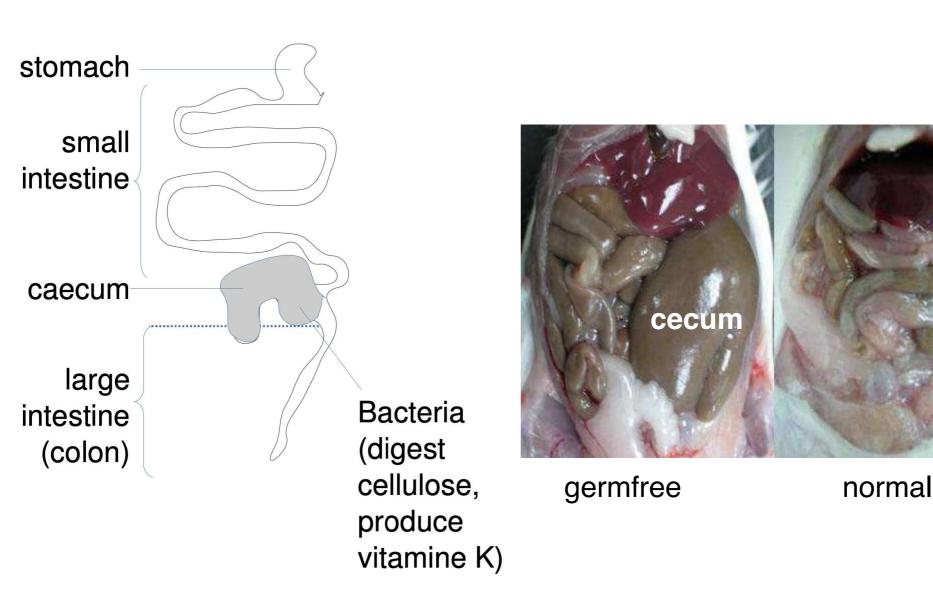
Calathus melanocephalus







Mouse caecum development An other example of GxE



Causes of phenotypic differences?

Heritable

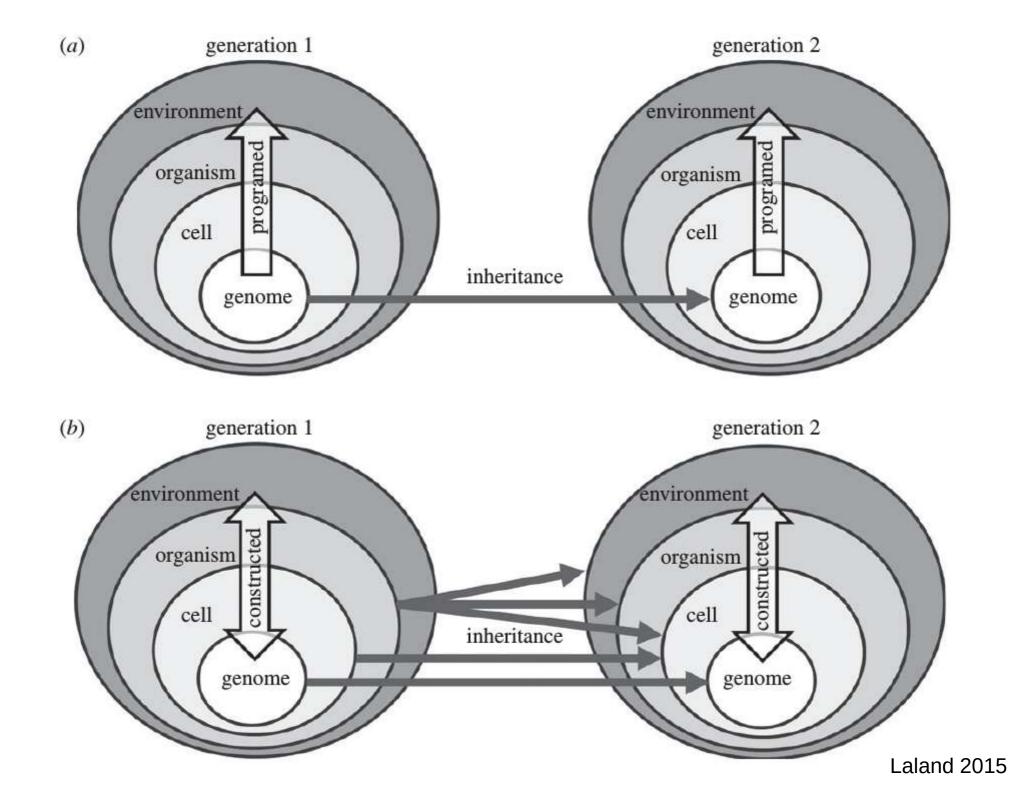
Non heritable





Phenotype = H + NH + HxNH

Like GxE but not always (Exceptions: DNA methylation, microbiome, langage, accent, culture, life style, parental care, maternal effet...)



Complexifications of the G-P map

Genetic Linkage

Epistasis

Supergene

Pleiotropy

GxE (introduction)