A. Allele frequencies among populations correlate with environmental variation at a candidate locus

allele frequency

differentiation

genetic

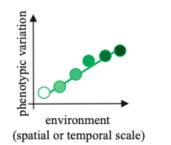
environment

(spatial or temporal scale)

 $^{\circ}$

genome positions

C. Phenotypic variation among populations at a candidate trait correlates with environmental variation



B. Genetic differentiation between extreme populations exceeds neutral expectation at a candidate locus

1

95% CI neutral

allelic differentiation

D. Phenotypic differentiation among populations exceeds neutral expectation at a candidate trait

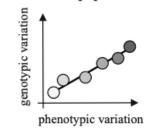
95% CI neutral

allelic differentiation

phenotypic differentiation

traits

E. Genotypic variation at a candidate locus correlates with phenotypic variation at a candidate trait across populations



F. Genotypic variation at a candidate locus associates with phenotypic variation at a candidate trait within populations

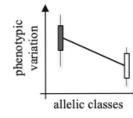
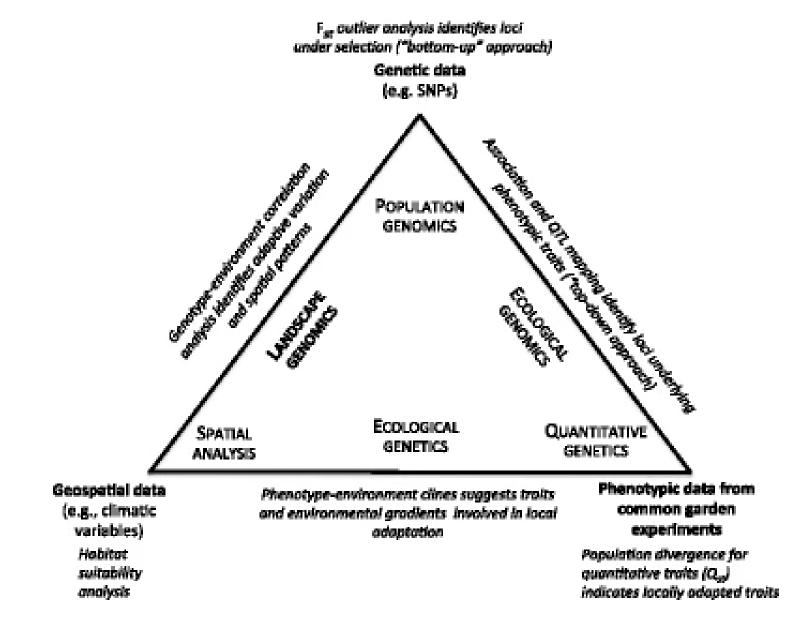


Fig. 1 Experimental approaches to detect potentially adaptive polymorphisms and traits using population genetic (**a**, **b**) or phenotypic (**c**, **d**) data, or combining both (**e**, **f**). A candidate polymorphism whose allele frequency among populations varies with spatial or temporal variation can be detected using correlation-based methods (**a**) or genome-wide scans, where it displays an elevated differentiation of allele frequencies compared with neutral (squares) loci (**b**). A candidate trait that covaries with spatial or temporal variation among populations can be detected using correlation-based methods (**c**) or when phenotypic differentiation measured in common environment(s) exceeds genotypic differentiation at neutral (squares) loci (**d**). A link between candidate loci and traits can be established by correlating genotypic and phenotypic variation measures in common environment(s) across populations (**e**), and within populations (**f**)

Approaches to the Study of Adaptive Genetic Variation



Sork et al. 2013 Tree Genetics & Genomes

OIL MEANS

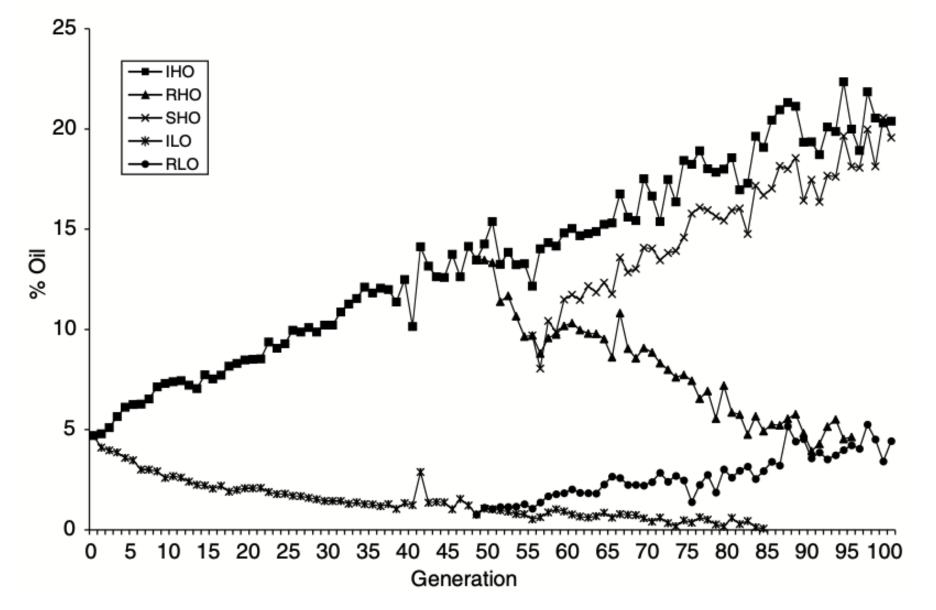


Fig. 5.1 Mean oil percentage plotted against generations for IHO, RHO, SHO, ILO, and Dudley et al (2010) Plant Breeding Reviews

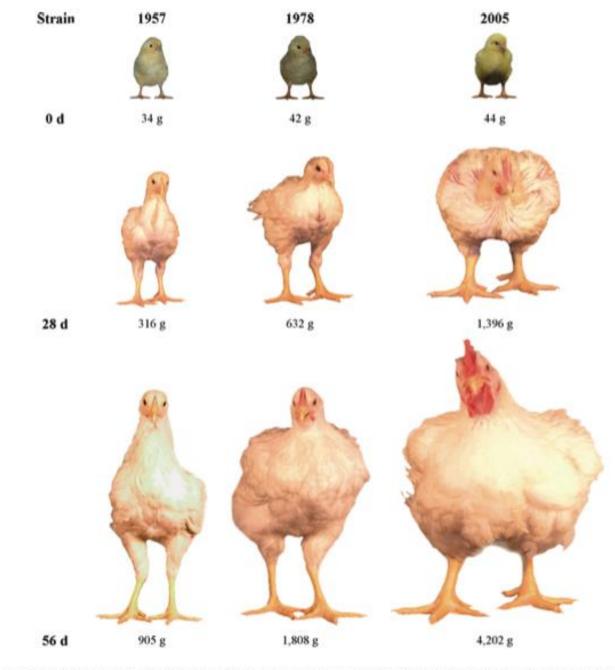
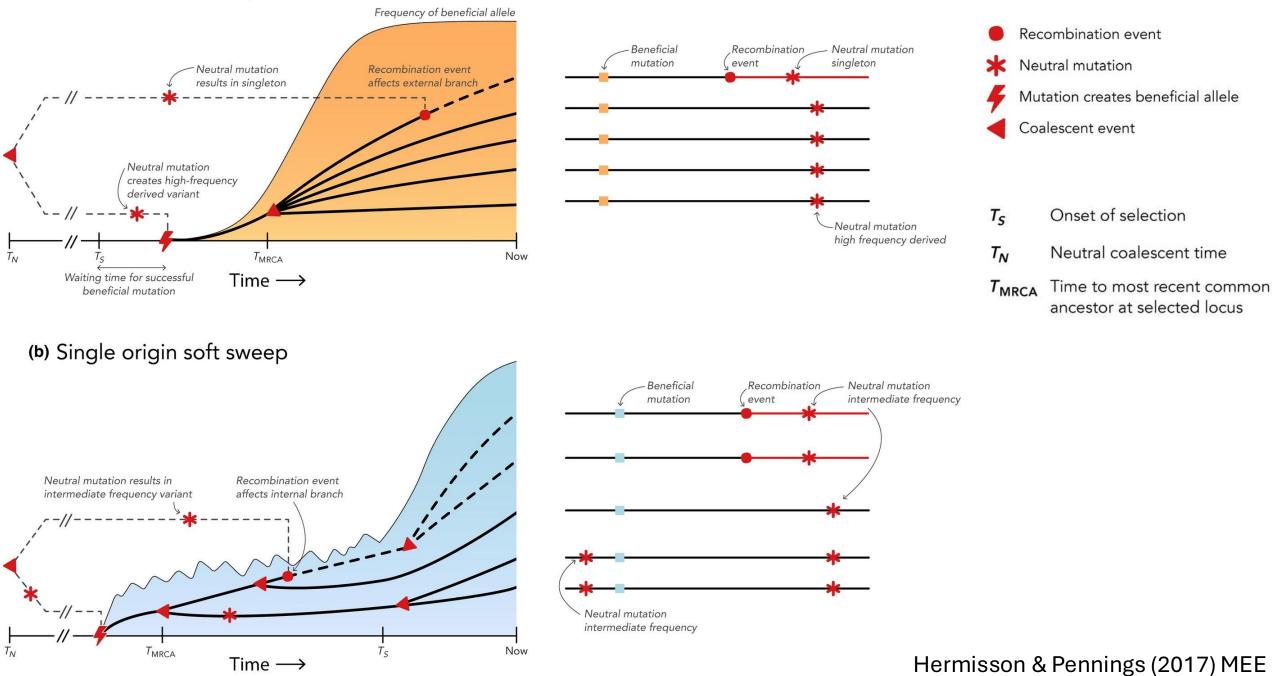
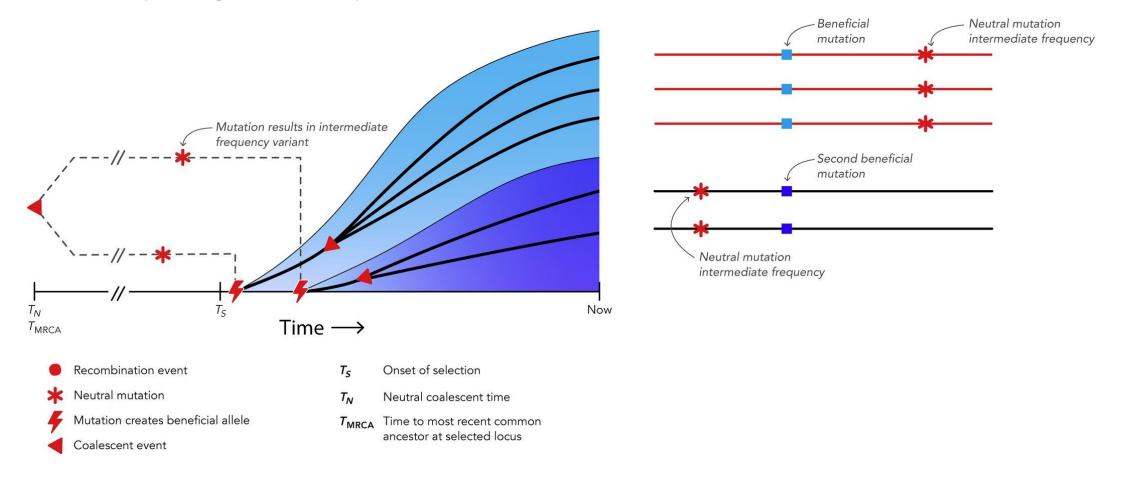


Figure 1. Age-related changes in size (mixed-sex BW and front view photos) of University of Alberta Meat Control strains unselected since 1957 and 1978, and Ross 308 broilers (2005). Within each strain, images are of the same bird at 0, 28, and 56 d of age. Color version available in the online PDF. Zuidof et al. 2014 Poultry Science

(a) Hard selective sweep



(c) Multiple origin soft sweep



Hermisson & Pennings (2017) MEE

Diversity in genes is not evolving neutrally, but instead is reduced by the impacts of selection on linked sites

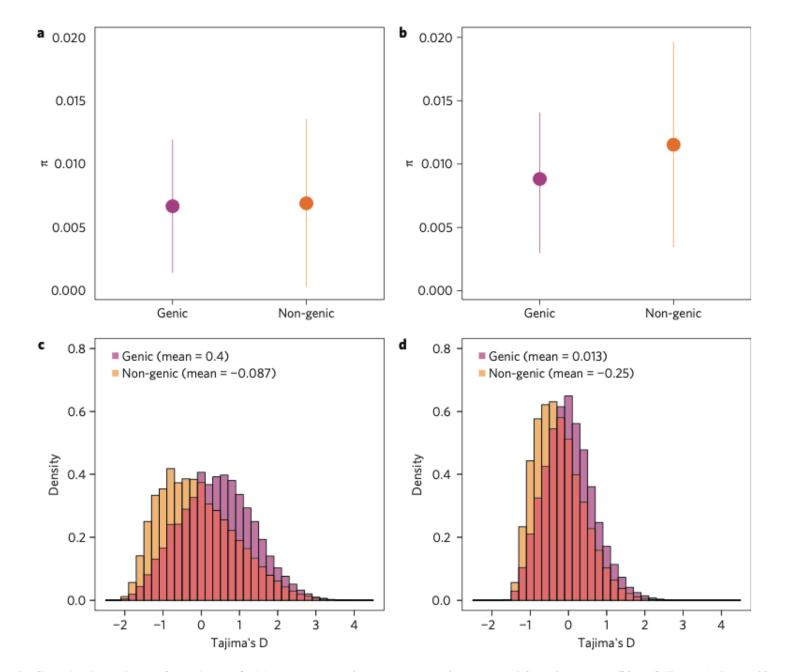


Figure 1 | Genetic diversity in maize and teosinte. a,b, Mean pairwise diversity $\pi \pm 1$ s.d. in maize (a) and teosinte (b). c,d, Tajima's D in 1 kb windows from genic and non-genic regions of maize (c) and teosinte (d). Bessinger et al. 2016 Nature Plants

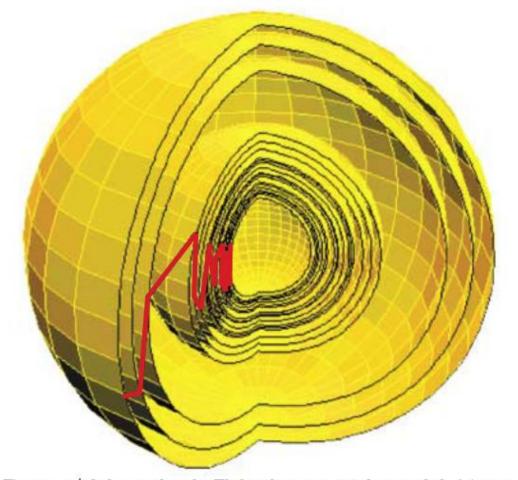
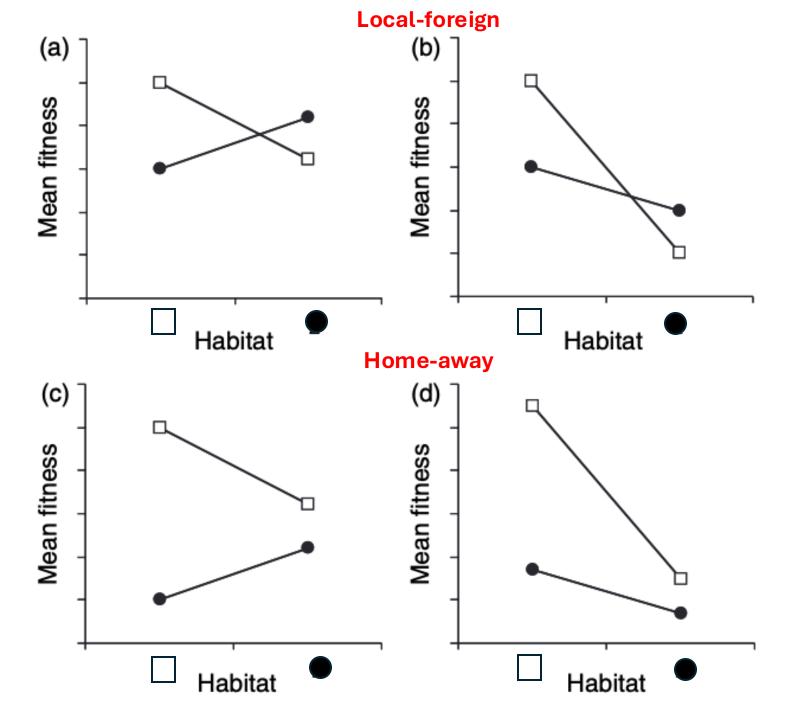


Figure. 1 | Adaptation in Fisher's geometric model. A bout of adaptation in Ronald A. Fisher's geometric model is shown. For simplicity, the organism that is considered comprises only three characters. The population begins on the surface of the sphere and, by substituting beneficial mutations (red vectors), evolves towards the phenotypic optimum at the centre of the sphere. The mutations that are substituted become smaller on average as the population nears the optimum. Modified, with permission, from REF. 41 © (2002) Macmillan Magazines Ltd. Domestication favors alleles of large effect from standing variation

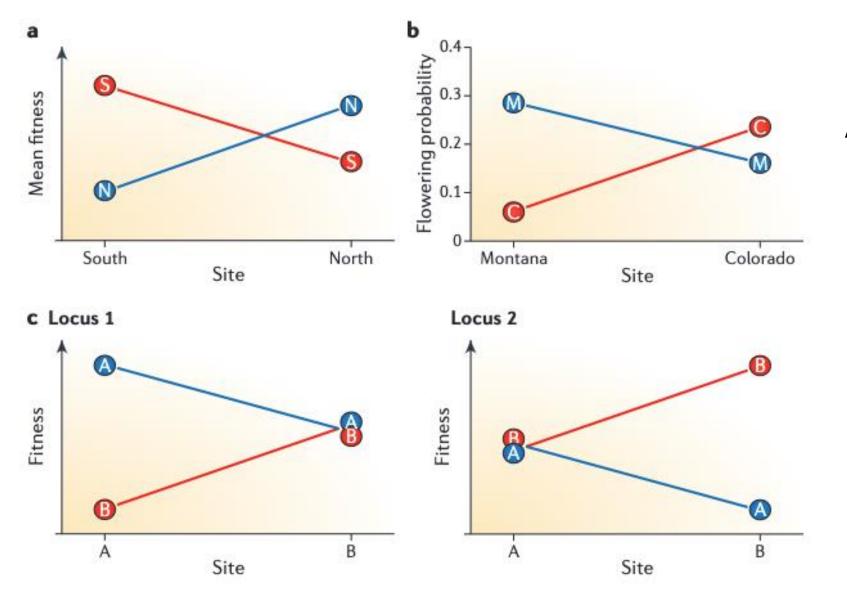
Orr (2005) Nat Rev Genet



Measures of local adaptation

Which is it: "Studies showed that highland maize landraces outperform lowland maize populations in their native environment but perform worse than any other population at lower elevation sites, suggesting strong adaptation for high altitude."

Kawecki & Ebert (2004) Ecol Lett



Antagonistic pleiotropy (b)

Conditional neutrality

Savolainen et al. (2013) Nat Rev Genet