



Lecture 8:

A theory for evolution

Course 410

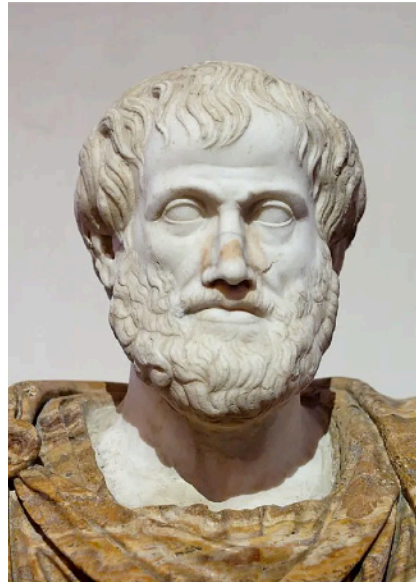
Molecular Evolution



History of evolutionary thought

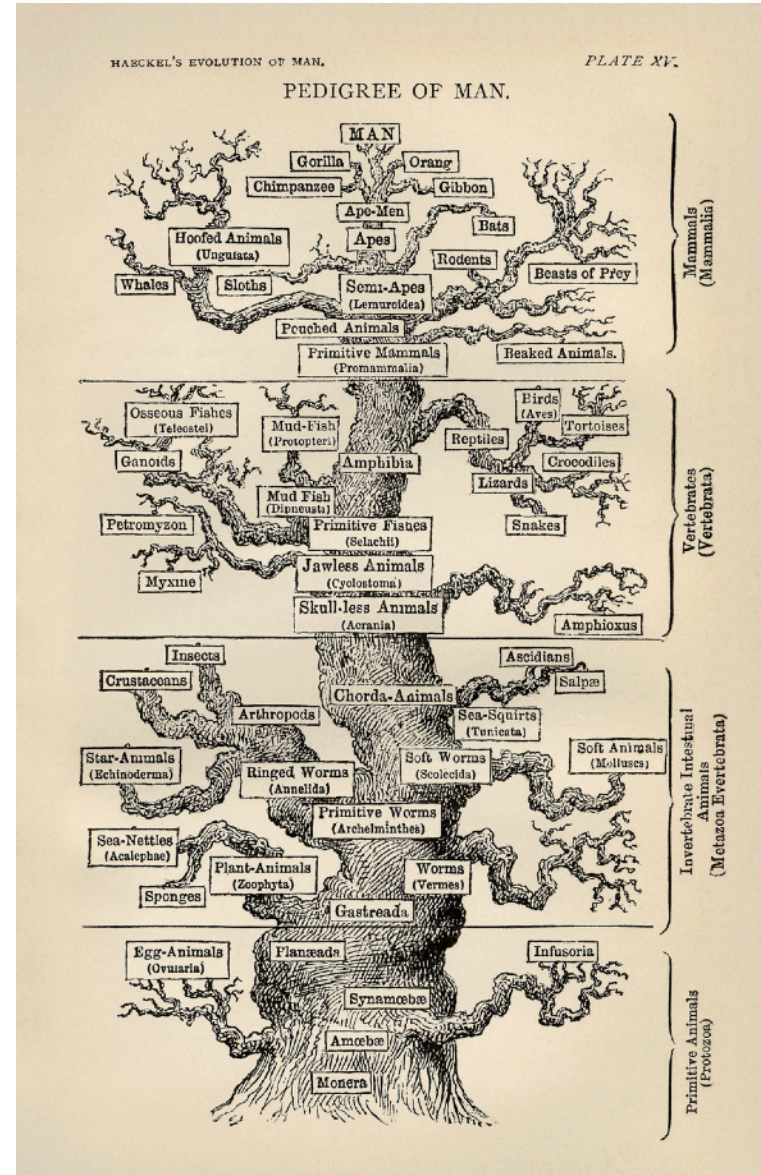


Plato:
essence fixity



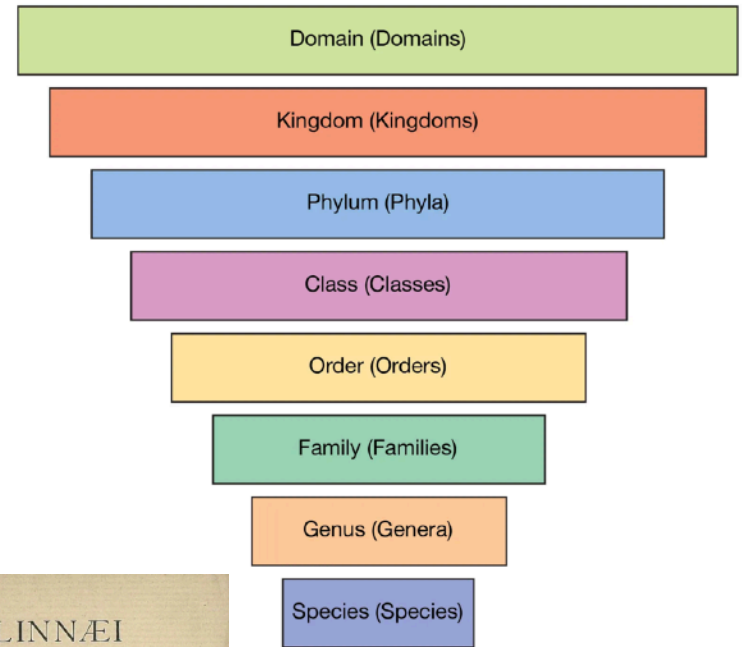
Aristotle:
Species fixity

Key concept:
orderly progression
from “lower” organisms
to “higher” forms.

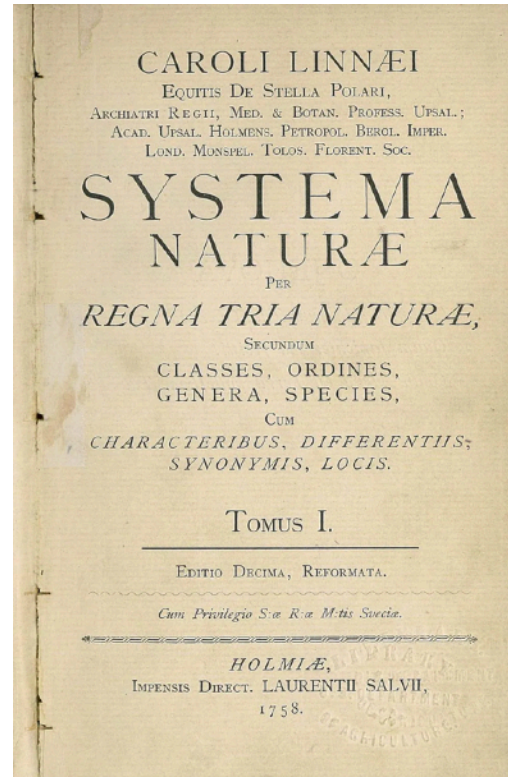




Carl Linnaeus



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The Species Concept of Linnaeus

*By James L. Larson**

The empirical element in Linnæus' species concept issues from two commonsense observations. The plants found in nature are admittedly individuals, but some individuals resemble one another more than they resemble the individuals who surround them. In favorable circumstances the seeds of such individuals produce plants resembling those which created them. In short, the characters of species members are relatively constant, and species members tend to breed true. A cursory examination of plants of the same species reveals, however, slight variations from individual to individual. In general, seeds reproduce plants very like the parent, but individuals are not absolutely alike; colors, sizes, figures, and so on, vary.

Linnaeus allowed for intra-specific variation





Mechanism for evolutionary change

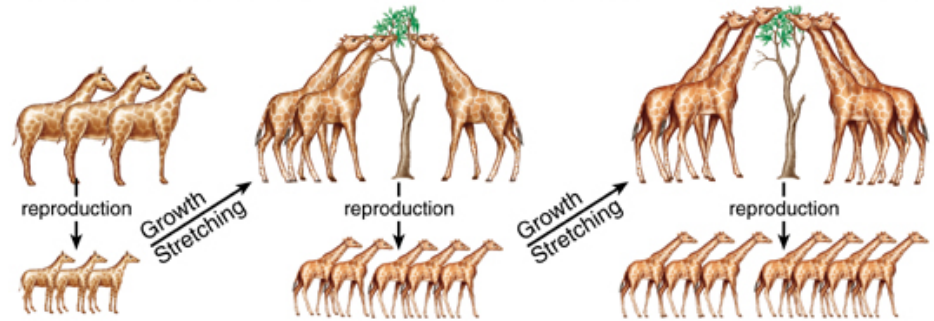
I. Lamarckian inheritance and evolution



Jean Baptiste Lamarck

Lamarck proposed the inheritance of acquired characteristics

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Proposed ancestor of giraffes has characteristics of modern-day okapi.

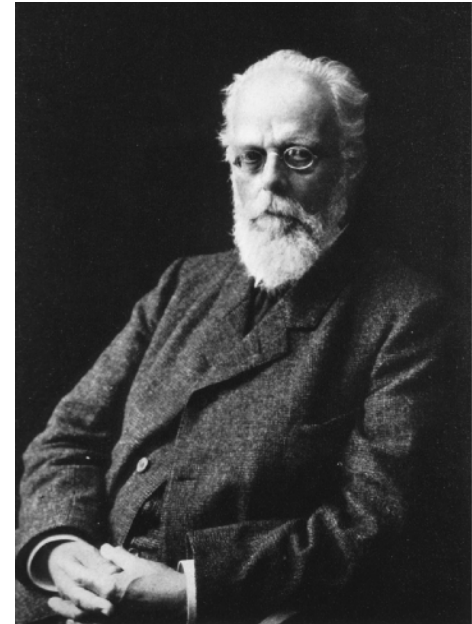
The giraffe ancestor lengthened its neck by stretching to reach tree leaves, then passed the change on to offspring.

(a) Lamarck's theory: variation is acquired.



Testing Lamarck's idea

- Weismann tested Lamarck's idea using mice.
- Cutting mice tails and breeding them.
- 5 generations!



August F. Weismann

What happened?

Mouse #899: Female

Mouse #900: Male

Mouse #901: Baby

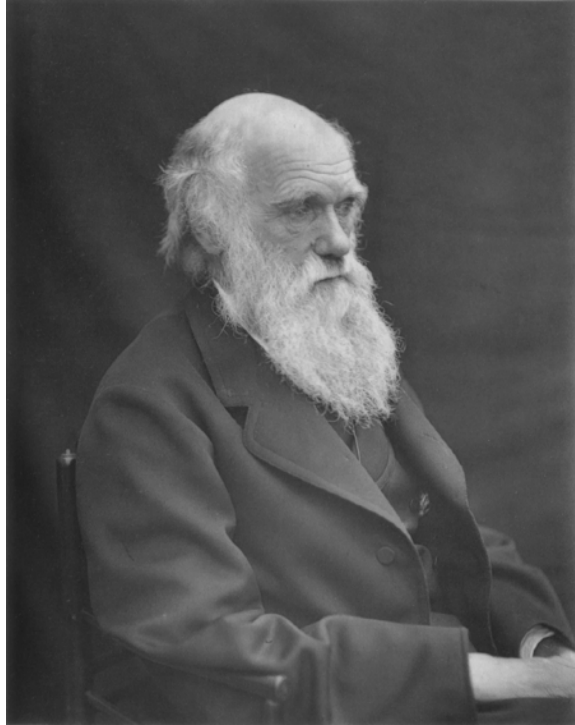


"Seriously, Weismann. Enough is enough!"

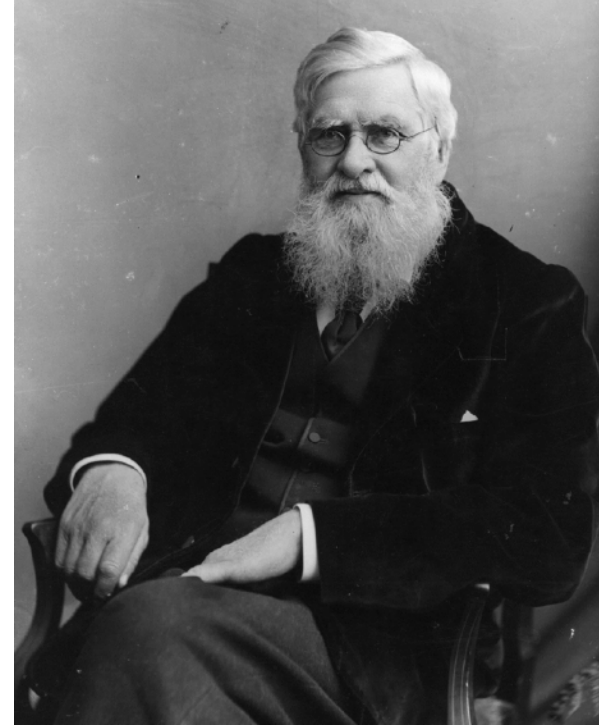




Mechanism for evolutionary change
II. Natural selection



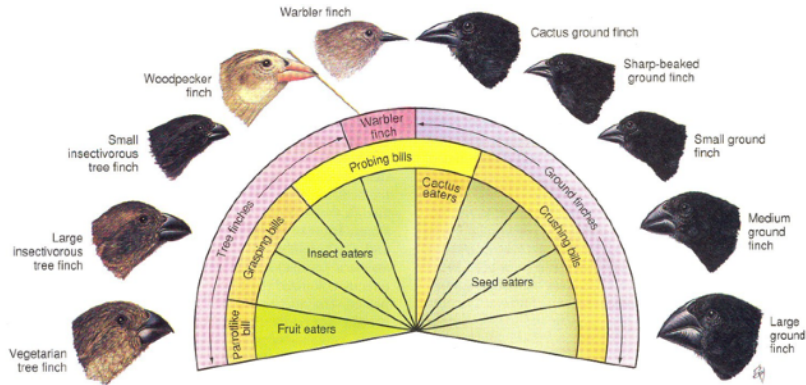
Charles Darwin



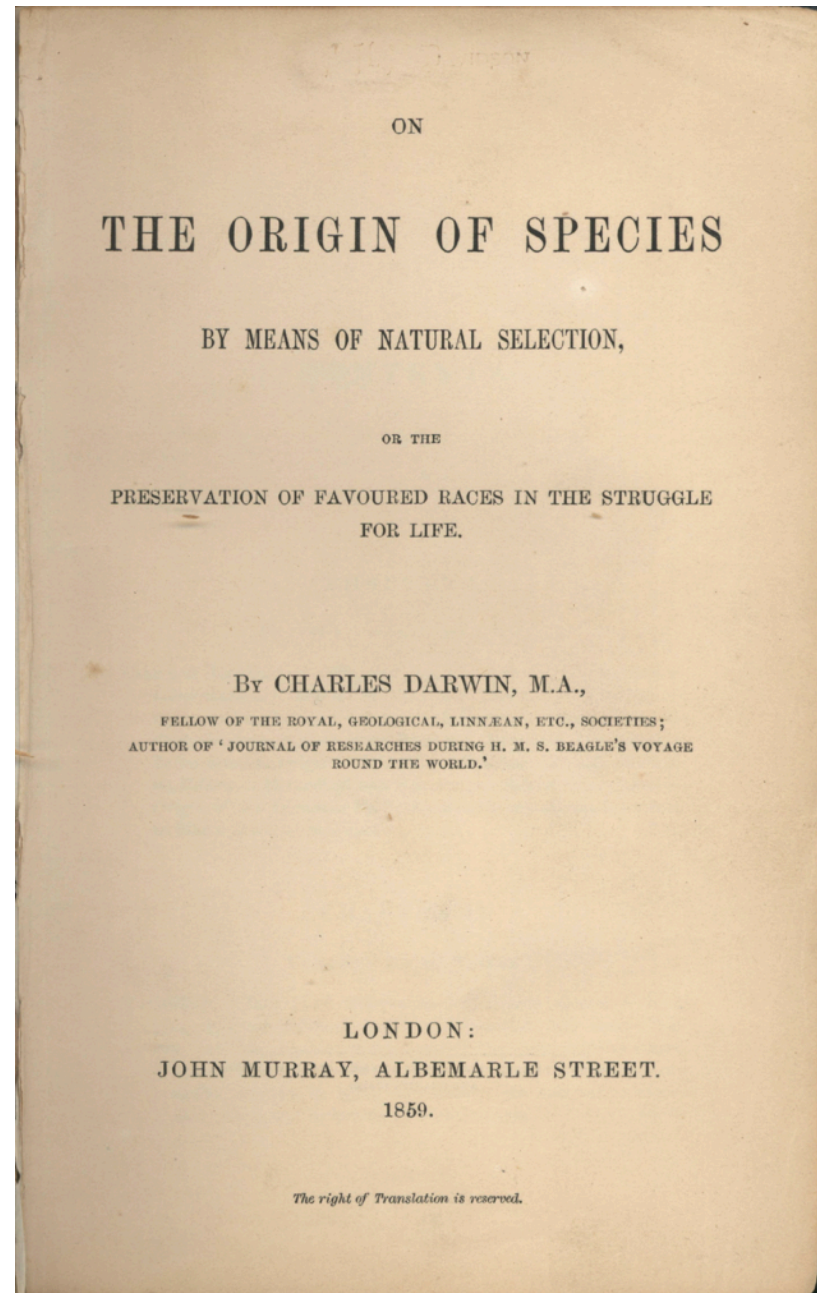
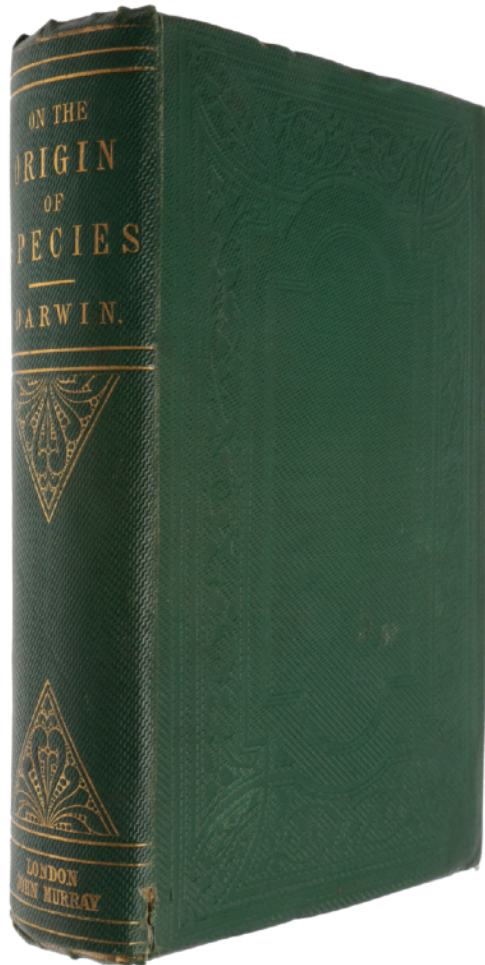
Alfred Russel Wallace

Darwin and Wallace, independently, proposed a theory of biological evolution and called it
“Natural selection”

Variation!



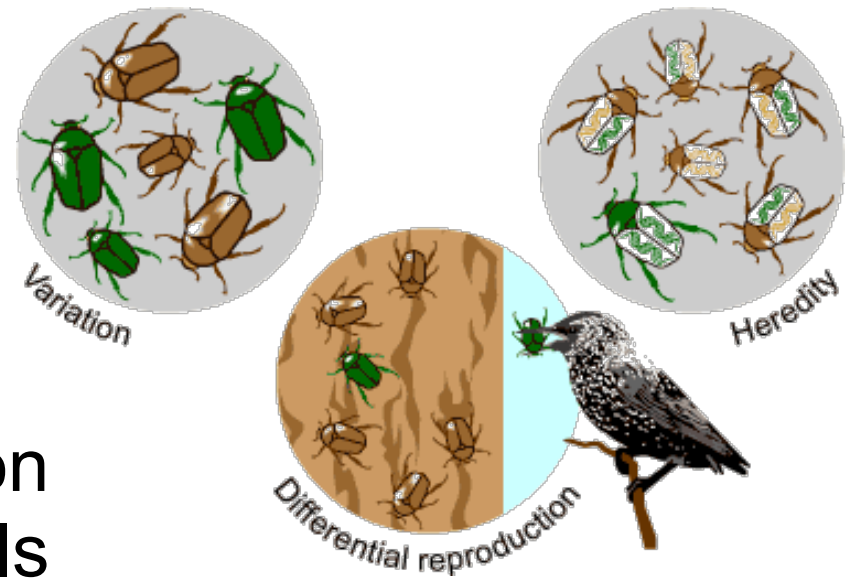
The book





Darwin's postulates

- 1) Individuals within a population are variable.
- 2) Variation is heritable (passed to offsprings).
- 3) Differential survival and reproduction.
- 4) Survival and reproduction is not random (individuals with best variation produce more offsprings - Naturally selected).






Testing Darwin's postulates



How does natural selection work?

- 
- 1) Natural selection operates on **individuals**.
 - 2) Effects of selection are only seen at the **population** level.
 - 3) Selection operates on **phenotypes**.
 - 4) Evolution is seen as a change in **allele frequencies**.
 - 5) Evolution is a response to **past** conditions.
 - 6) No adaptation to potential future conditions.
 - 7) New traits may appear, and be selected for, as a result of random mutations.
 - 8) Evolution is non-random.
 - 9) Evolution is not “progressive” (does not always involve a change to greater complexity).

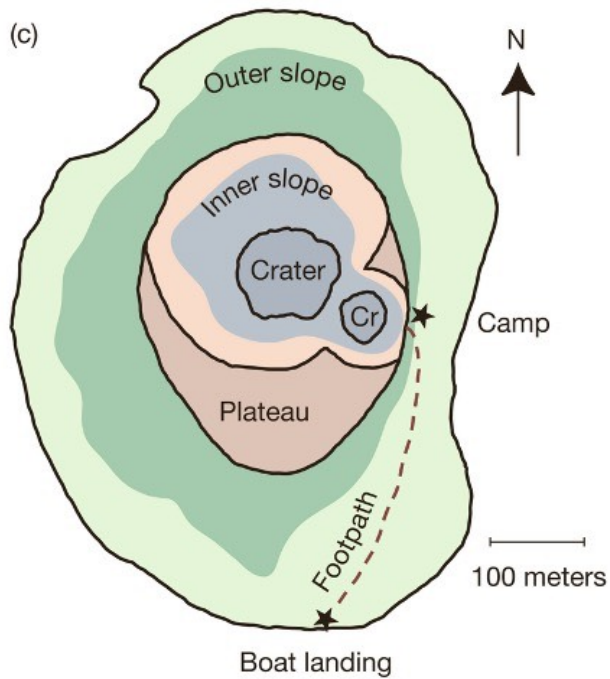
Testing Darwin's postulates

What Darwin's Finches Can Teach Us about the Evolutionary Origin and Regulation of Biodiversity

B. ROSEMARY GRANT AND PETER R. GRANT



Peter Grant and Rosemary Grant



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Research site: Daphne Major



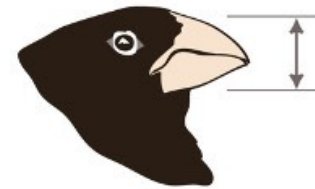
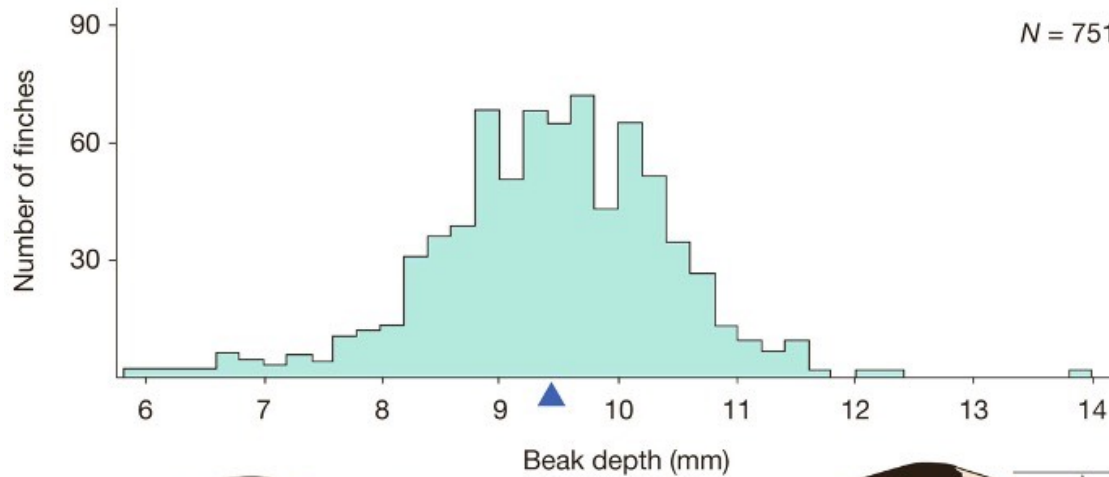
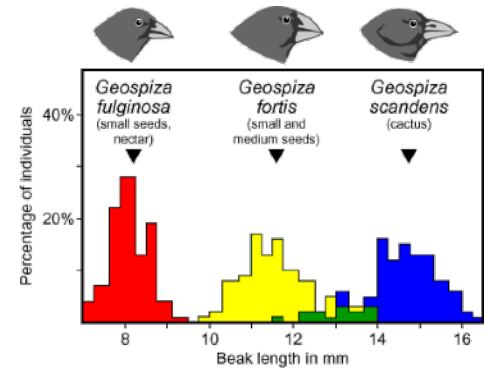
Data:

Morphometrics on finches (e.g., beak size)

Track multiple generations

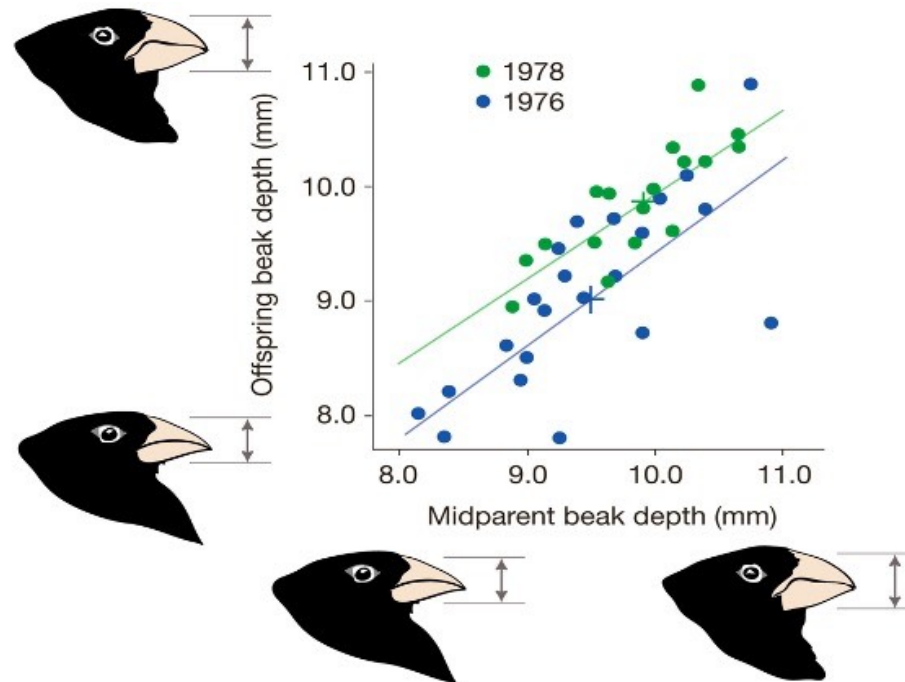
Measure survival and reproductive rates

1) Do finch populations vary?



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2) Is that variation heritable?



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3) Do individuals vary in survival and reproduction?

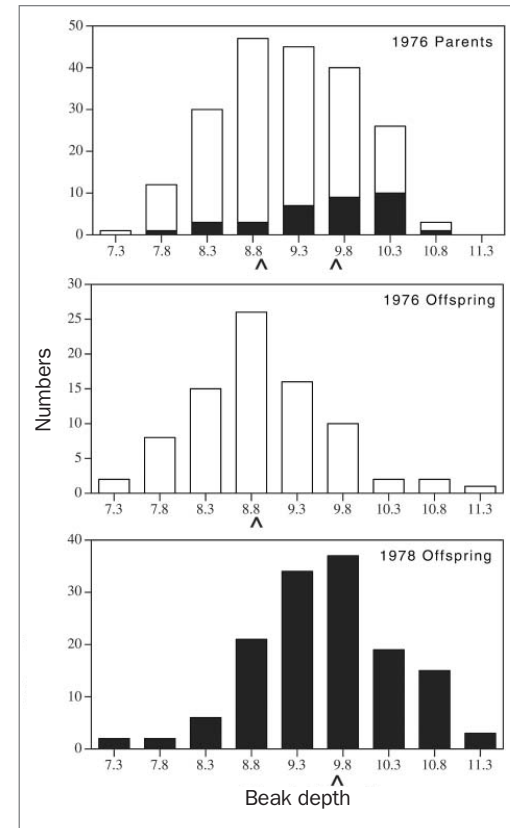
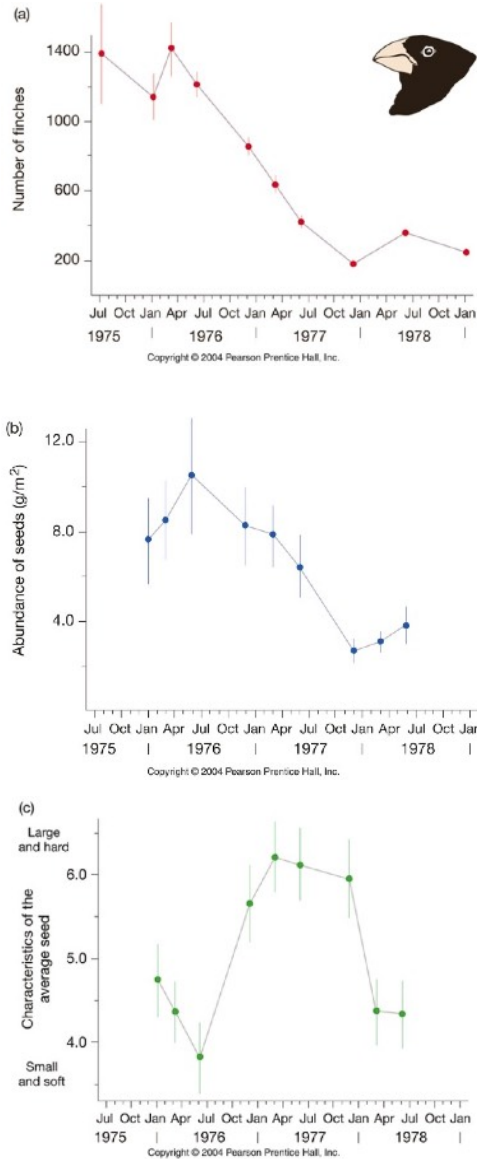
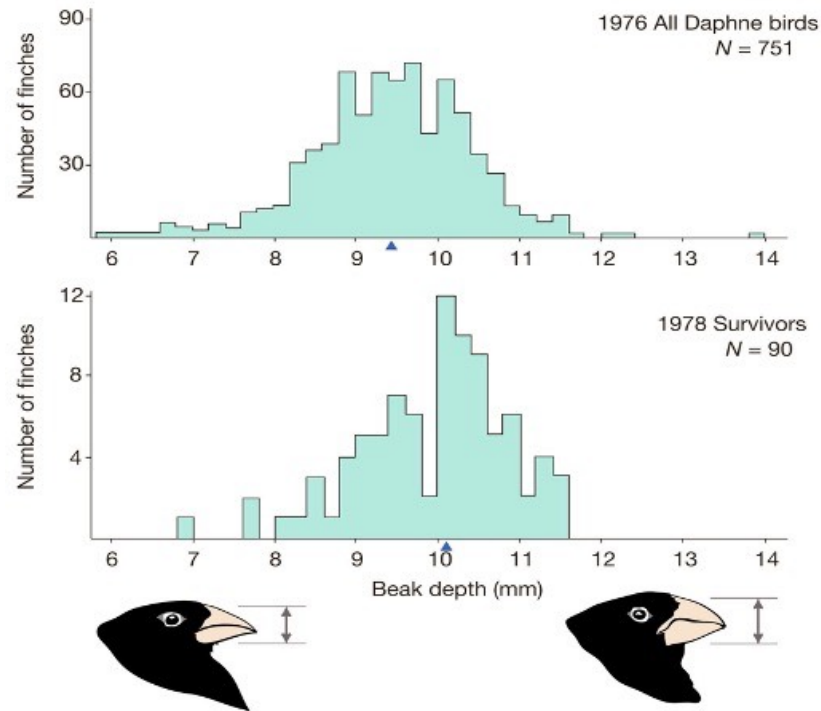


Figure 5. Evolutionary change in beak depth in the population of *Geospiza fortis* on the island of Daphne Major. The upper panel shows the distribution of beak depths in the breeding population in 1976, with the survivors of the 1977 drought that bred in 1978 indicated in black. The difference between the means, indicated by a caret, is a measure of the strength of natural selection. The middle and lower panels show the distributions of beak depths of fully grown offspring hatched in 1976 and 1978, respectively. Evolutionary change between generations is measured by the difference in mean between the 1976 population before selection and the birds hatched in 1978.

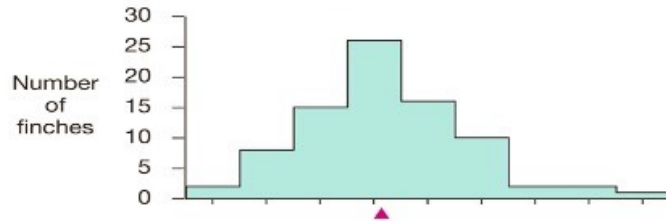
4) Are survival and reproduction non-random?



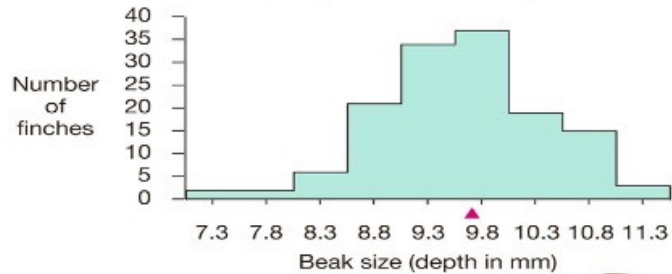
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5) Did the population evolve?

Finches hatched in 1976, the year before the drought



Finches hatched in 1978, the year after the drought



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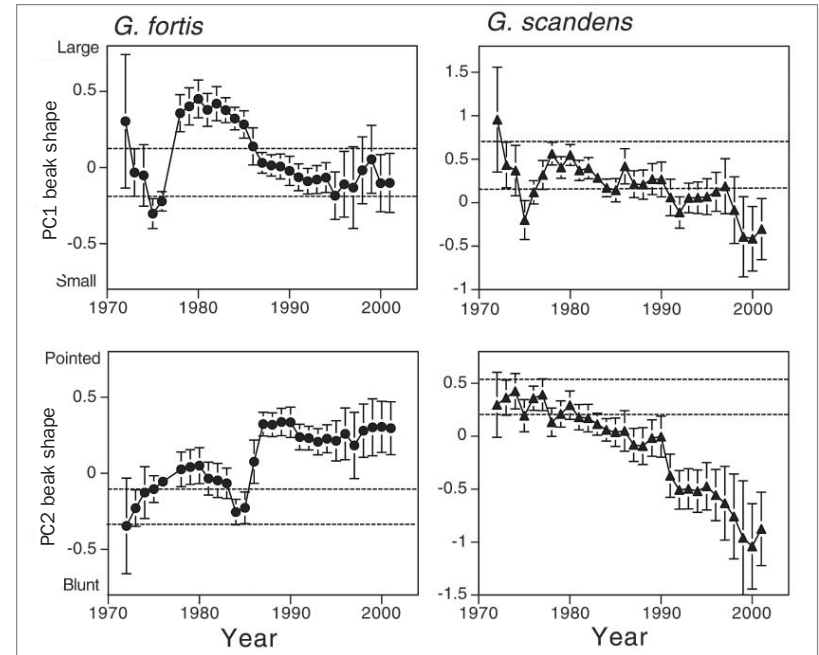



Figure 6. Changes in the beak size and shape of *Geospiza fortis* and *Geospiza scandens* on the island of Daphne Major. Mean trait values for each year are indicated by solid circles, and 95% confidence intervals are shown by vertical bars above and below the mean. In the absence of change, the means should remain within the 95% confidence intervals (horizontal broken lines) of the mean estimates from the 1973 samples. PC refers to principal component, obtained from a principal components analysis of size and shape variables. From Grant and Grant (2002a).



Restatement of Darwin's postulates

- 
- 1) New alleles arise as a result of mutation.
 - 2) Segregation and independent assortment reshuffle the genes.
 - 3) Individuals are variable for many heritable traits.
 - 4) Alleles are passed to offspring.
 - 5) Excess offspring are produced.
 - 6) Individuals with favorable allelic combinations preferentially reproduce.

Evolution of Darwin's finches and their beaks revealed by genome sequencing

Sangeet Lamichhane^{1*}, Jonas Berglund^{1*}, Markus Sällman Almén¹, Khurram Maqbool², Manfred Grabherr¹, Alvaro Martínez-Barrio¹, Marta Promerová¹, Carl-Johan Rubin¹, Chao Wang¹, Neda Zamani^{1,3}, B. Rosemary Grant⁴, Peter R. Grant⁴, Matthew T. Webster¹ & Leif Andersson^{1,2,5}

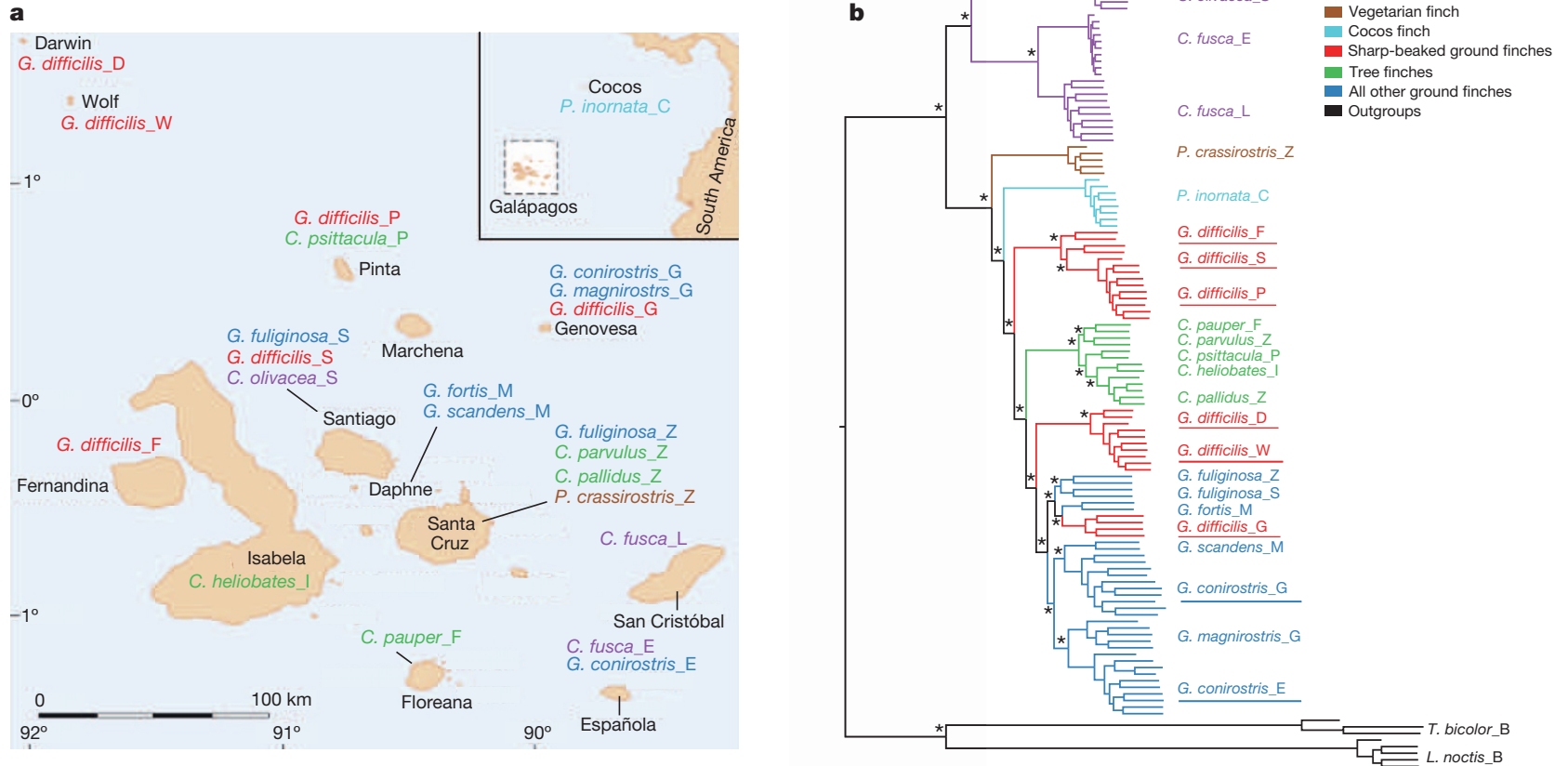


Figure 1 | Sample locations and phylogeny of Darwin's finches.

a, Geographical origin of samples; the letter after the species name is the abbreviation used for geographical origin. The map is modified from ref. 30.
b, Maximum-likelihood trees based on all autosomal sites; all nodes having full

local support on the basis of the Shimodaira–Hasegawa test are marked by asterisks. The colour code for groups of species applies to both panels. Taxa that showed deviations from classical taxonomy are underscored.

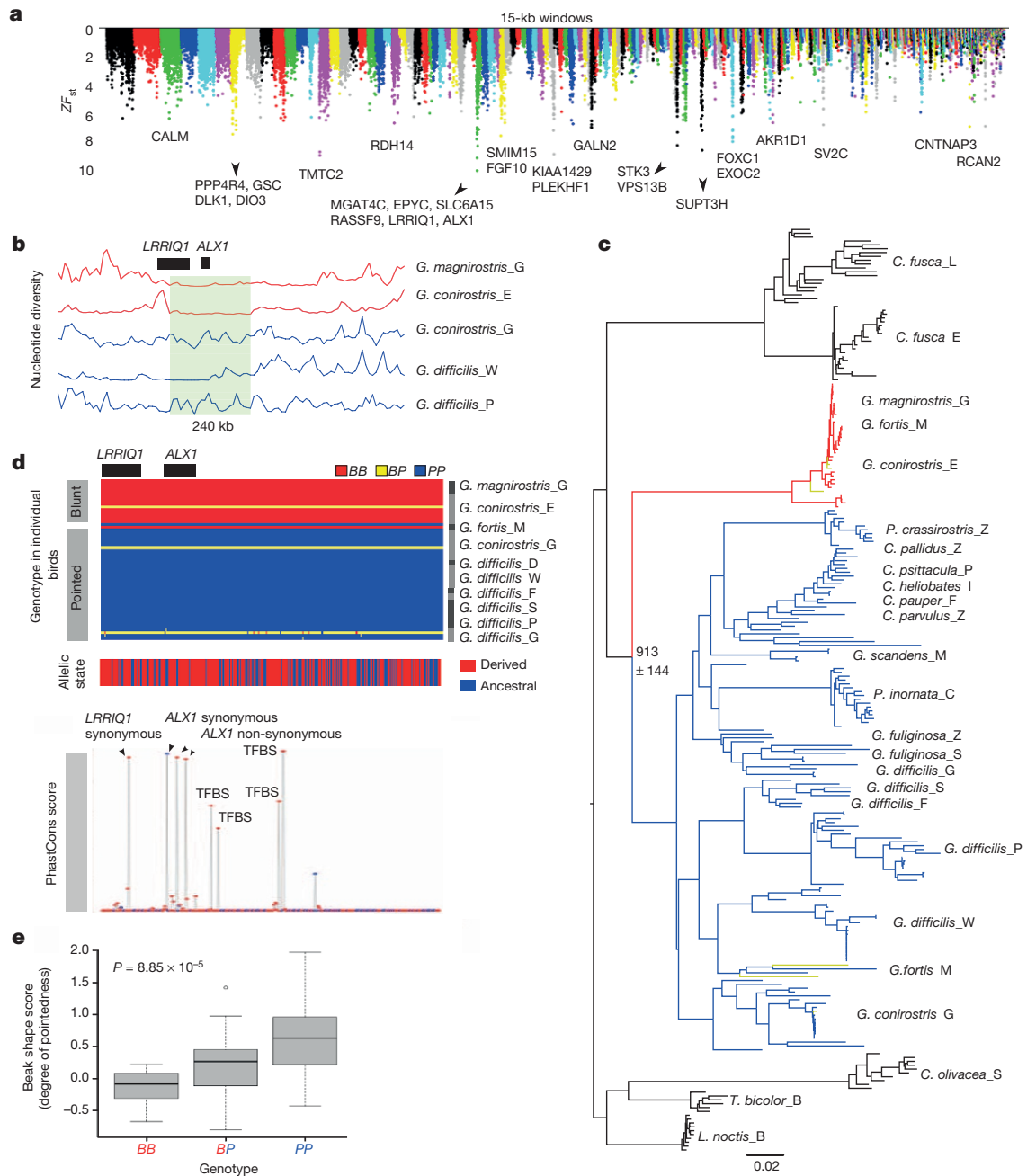


Figure 3 | A major locus controlling beak shape. **a**, Genome-wide F_{ST} screen comparing *G. magirostris* and *G. conirostris* (Española) having blunt beaks with *G. conirostris* (Genovesa) and *G. difficilis* (Wolf) having pointed beaks. The y axis represents ZF_{ST} values. **b**, Nucleotide diversities in the *ALX1* region. The 240-kb region showing high homozygosity in blunt-beaked species is highlighted. Red and blue colours in **b–d** refer to blunt and pointed beak haplotypes, respectively. **c**, Neighbour-joining haplotype tree of *ALX1* region. Haplotypes originating from heterozygous birds (see text) are indicated in yellow. Estimated time since divergence (\pm confidence interval) of blunt and pointed beak haplotypes are given in thousands of years. **d**, Upper panel: genotypes at 335 SNPs showing complete fixation between *ALX1* haplotypes associated with blunt (*B*) and pointed (*P*) beaks. **d**, Middle panel: classification of alleles associated with blunt beaks at the 335 SNPs as derived or ancestral on the basis of allelic state in the outgroup. **d**, Lower panel: PhastCons³⁵ scores (on the basis of human, mouse and finch alignments) for the 335 SNP sites. TFBS, transcription factor binding sites. **e**, Linear regression analysis of beak-shape scores among *G. fortis* individuals on Daphne Major Island classified according to *ALX1* genotype; distribution of pointedness in each class is shown as a boxplot; $n = 62$; $F = 17.7$, adjusted $R^2 = 0.22$. Differences in six individual body and beak size traits were not significant (all $P > 0.05$).

Aristaless-Like Homeobox protein 1 (ALX1) variant associated with craniofacial structure and frontonasal dysplasia in Burmese cats

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Michael J. Carter^{e,f}, Christopher R. Helps^g, Hasan Alhaddad^h, Barbara Gandolfi^{a,f}

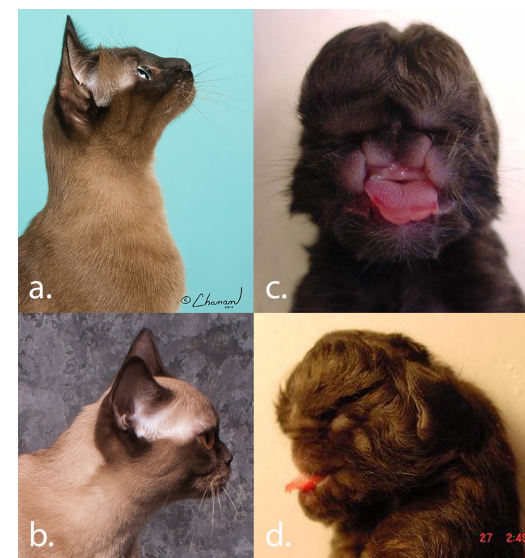
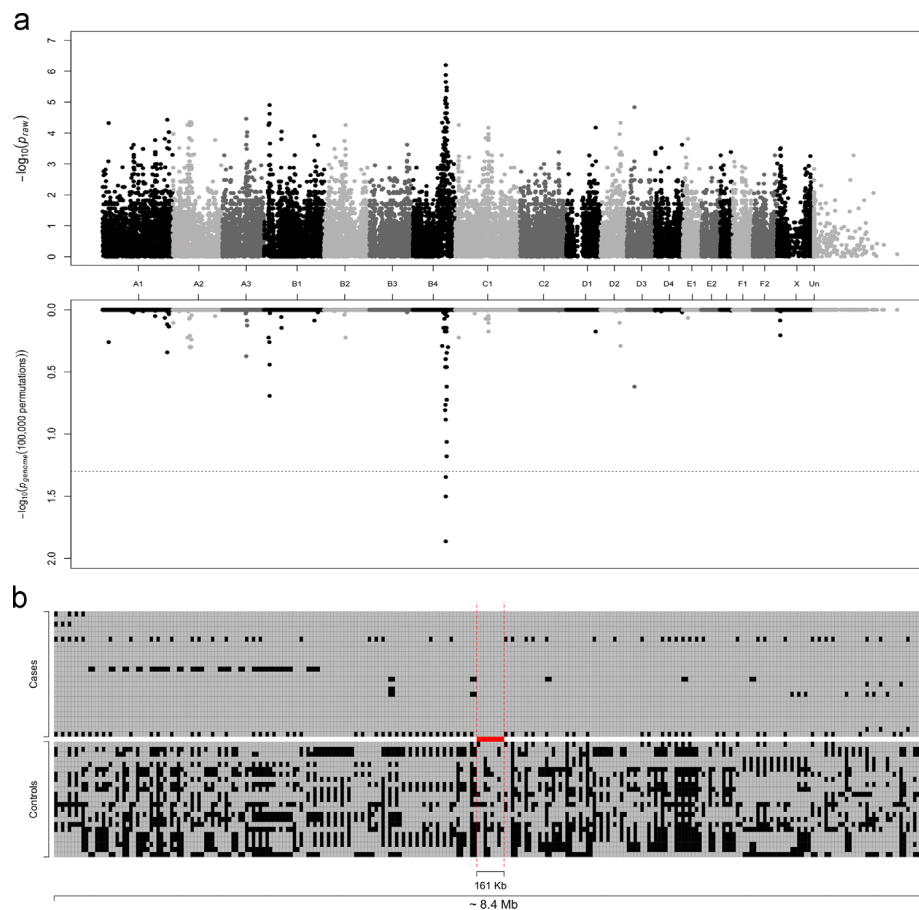


Fig. 2. Manhattan plot of the Burmese head deformity GWAS and SNPs genotypes within chromosome B4 haplotype. (a) The plot represents the P_{raw} (top) and P_{genome} (bottom) values of each SNP included in the case-control association study. The association study compared the affected Burmese and Bombay cats. A significant association with chromosome B4 was detected. (b) The area from SNP B4.121572441 (position 106,142,990) to SNP B4.114551707 (position 114,551,707) spans ~8.4 Mb. The two red vertical dashed lines represent the region of the single haplotype containing *ALX1*, from SNP B4.126353636 (position 110,094,604) to SNP B4.126530474 (position 110,255,914) spanning 161 Kb. Each SNP is represented by two squares where markers are on the x-axis and individuals on the y-axis. Gray boxes represent the major allele in the cases and black squares represent the minor.



Did Darwin answer where variation come from?

Did he know about heredity?

Did he know about genes/factors?

Did evolutionary biology stop and end with Darwin's theory?

Is natural selection the only force of evolution?

The field of evolutionary biology has itself evolved and evolutionary studies have gone way beyond Darwin



Modern evolutionary biology

Gregor Johann Mendel and the development of modern evolutionary biology

Nils Chr. Stenseth^{a,1}, Leif Andersson^{b,c}, and Hopi E. Hoekstra^{d,e,f,g}

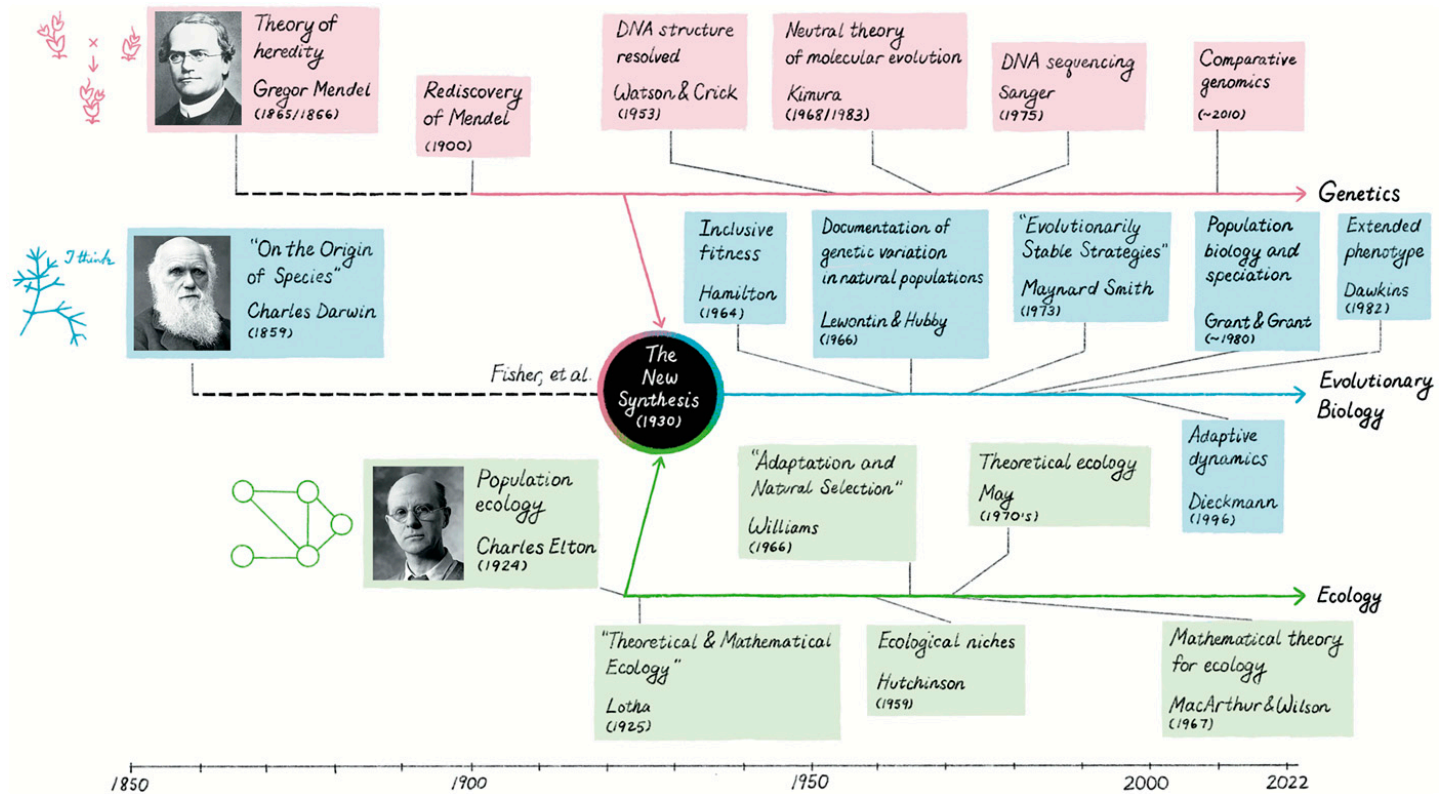


Fig. 4. Bringing genetics, ecology and the process of natural selection together into the field of evolutionary biology. The development of the field of genetics (the genetic strand) starting with Mendel (8), the field of ecology (the ecology strand) starting with Elton (61), and the combination of genetics and ecology in the field of evolutionary biology (the evolution strand) starting with Fisher’s (9) and others’ pioneering work.

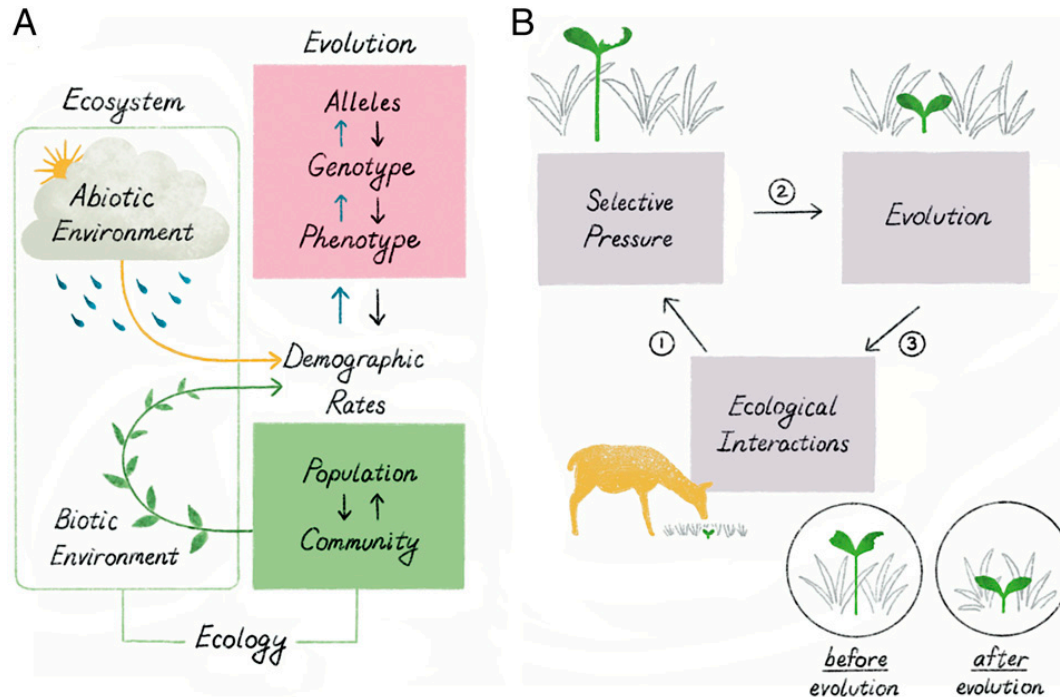


Fig. 5. Modern evolutionary biology. (A) The interaction between ecology (green) and evolution (blue arrows); the red box represents the genotype–phenotype mapping (corresponding to the genetic strand in Fig. 4). Evolution, typically inferred from phenotypic changes, represents the changes of allele frequencies in population across generations. The selective pressure is determined by the internal biotic interactions between individuals within and among species (green box and arrows) in combinations with external abiotic forces (yellow arrows) within the ecosystem (including both biotic [all living individuals within an area] and abiotic [including air, soil, water and climate] components). This ecologically determined selective pressure acts through the demographic rates of the genetically determined demographic rates (survival and reproduction). The ecological interactions refer to within population interaction, within community (the assembly of all coexisting species) interactions and the ecosystem level interactions (the combined biotic and abiotic interactions). [For similar, although more detailed figures, see Coulson et al. (96, 97)]. (B) The interaction between biotic and abiotic ecological interactions defining the evolutionary selective pressure (arrow #1) leading to evolutionary changes (arrow #2) in populations, which in turn feeds back to the ecological interactions (arrow #3).

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