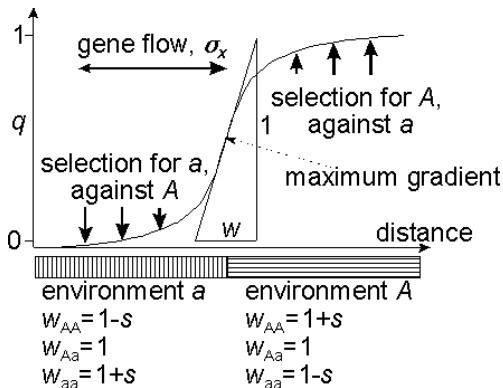


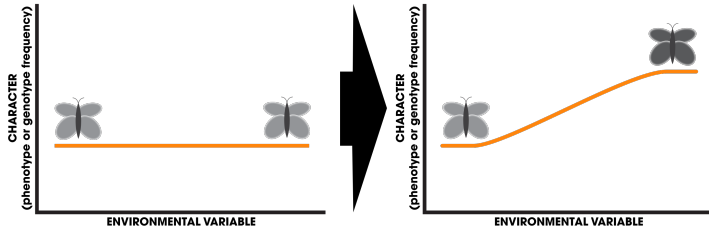
Intro to clines

Clines are gradients of traits or allele frequencies typically formed by the tension between gene flow (or sometimes drift) and selection



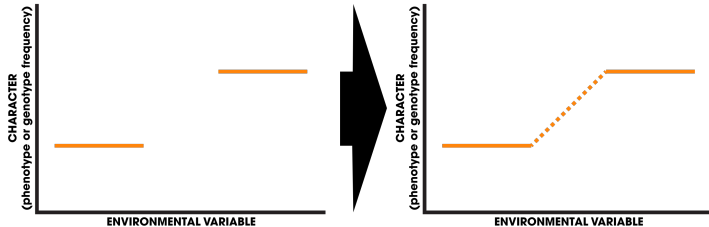
(UCL)

Clines from primary differentiation



(Wikipedia)

Clines from secondary contact



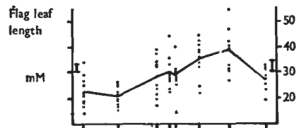
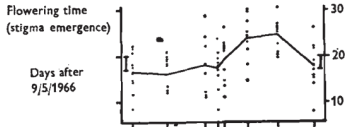
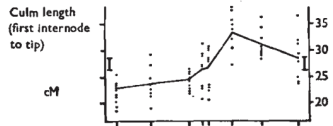
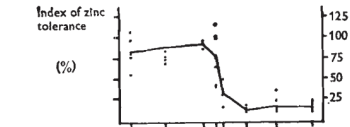
(Wikipedia)

Sweet Vernal Grass (*Anthoxanthum odoratum*)



(iNaturalist)

Sweet Vernal Grass (*Anthoxanthum odoratum*)



Antonovics & Bradshaw 1970

Blood Group Genes

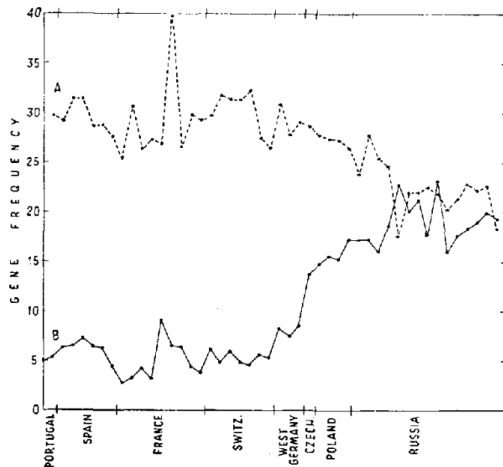


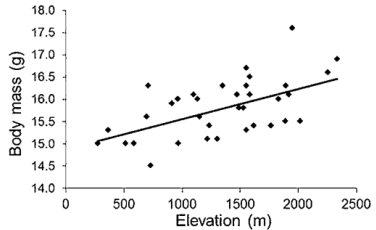
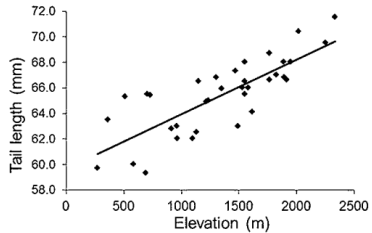
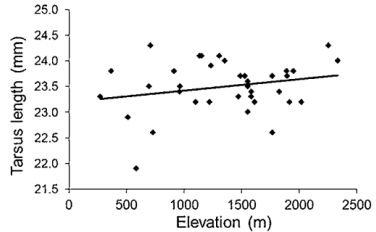
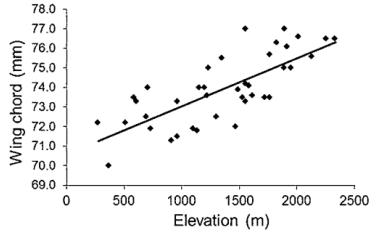
Fig. 1 The frequencies of the A(---) and the B(—) blood group genes on an approximately straight line from Lisbon to Molotov (Perm).

Elapaios



(eBird)

Elapaios



VanderWerf 2012

Rufous-collared Sparrow



(eBird)

Rufous-collared Sparrow



(eBird)

Cheviron & Brumfield 2009

- 1) What was their question?
- 2) What is the purpose of the “control transects”?
- 3) Why do they want to know if population genetic and environmental clines are congruent?
- 4) What do they infer from the width of the mitochondrial DNA cline?
- 5) What traits do they think selection is acting on?

Cheviron & Brumfield 2009

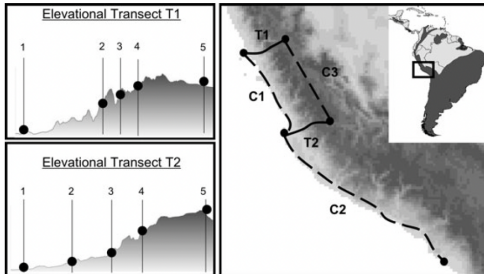
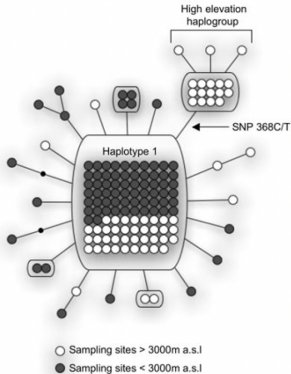


Figure 1. Sampling design. Elevational test transects are illustrated as solid lines, control transects as dashed lines, and the approximate locations of the sampling sites as black dots. Geographic coordinates and elevations of the sampling localities are listed in Table 2. Shading represents the Andes. Inset depicts the distribution of *Z. capensis* shaded in dark gray. Digital range map created by Ridgely et al. (2003) and downloaded from InfoNatura (2005).

Chevron & Brumfield 2009

A



B

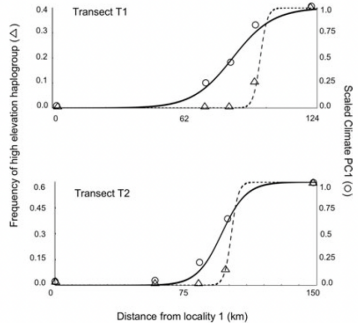


Figure 2. (A) Network of *Z. capensis* ND3 haplotypes. Each circle represents an individual, with white circles representing individuals collected above 3000 masl and gray circles representing individuals collected below 3000 masl. Smaller black circles represent unsampled hypothetical haplotypes. Individuals within boxes share a given haplotype. Branches represent a single nucleotide substitution. The substitution that defines the high elevation haplogroup (see text) is indicated with an arrow. Haplotypes that are referred to in the text are numbered. (B) Clines in haplogroup frequency (Δ) and climate PC1 scores ($\circ$) plotted against geographic distance along elevational transects. Dashed lines and solid lines are maximum-likelihood cline shapes for haplogroup frequency and climate PC1 score cline, respectively, estimated using the program Cline Fit (see Methods). Cline shape parameters are listed in Table 4.

Cheviron & Brumfield 2009

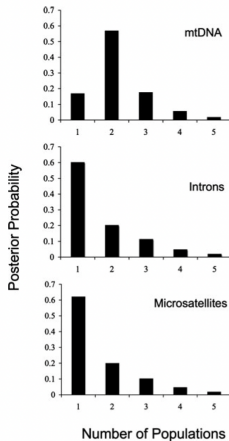


Figure 3. Results of Geneland analyses. For each dataset, the posterior probability of each value of K (number of populations) is presented. In each analysis, the total number of populations was allowed to vary from 1 to 11 (see text). Because values of $K \leq 5$ encompassed over 95% of the posterior probability distribution, the value of K is truncated at 5 for each marker class.