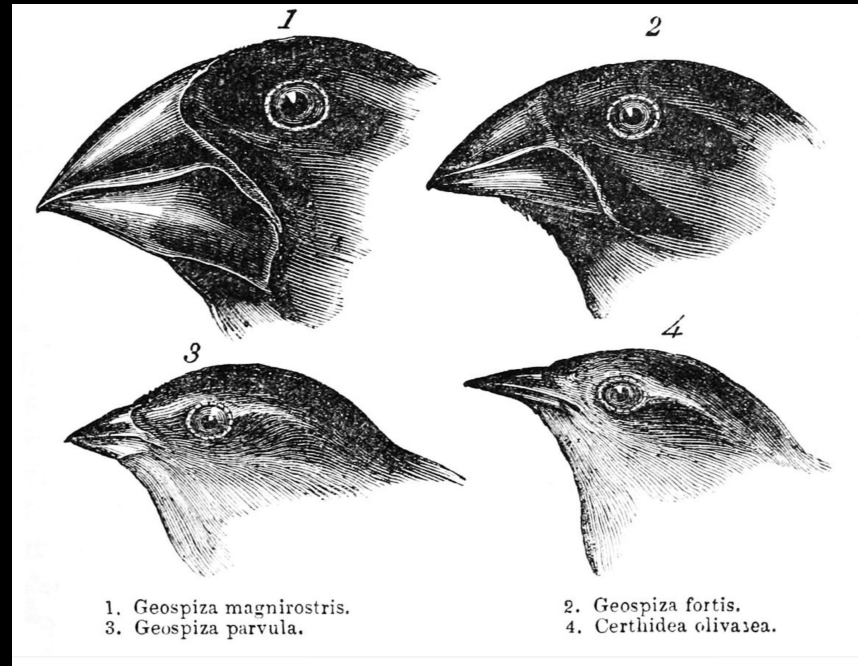


Update: Darwin and Finch Beaks

—

Chinmaya Joisa, Hannah Smith, Kelly Braden

Recall classic adaptive radiation



What is the
genetic/molecular
basis of the finch
adaptive radiation?

A beak size locus in Darwin's
finches
facilitated character displacement
during a drought

(Lamichhaney et al. 2016)

Introduction



Foundation of the Experiment

- Whole-genome sequencing of 60 Darwin finches (6 species) were used
- These included small, medium, and large ground and tree finches
- They were studied on the Daphne Major in the Galápagos Islands during a severe drought

Resource Competition

- Species may diverge in traits
- Beak sizes started to diverge during the drought
- The medium ground finch with the large beak had a disadvantage competing for food against the large ground finch

Beak Information

- Beak size and body size are strongly correlated ($r = .7$ to $.8$)
- Stronger association between survival and beak size ($S = -1.02$, $P < .0001$) than between survival and body size ($S = -.67$, $P < .05$)
- Beak dimensions and overall body size are highly heritable
- Regulatory gene, *ALX1*, was identified in regulating variation of beak shape

Summary of analyses

- Genome-wide screen for loci affecting beak size and body weight
 - Phylogenetic tree generation
 - Genome-wide differentiation and selection of candidate genes
 - Haplotype and fitness analysis of candidate HMG A2 gene in the population
-

Experiments & Results

—

Correlation of Morphological Differences

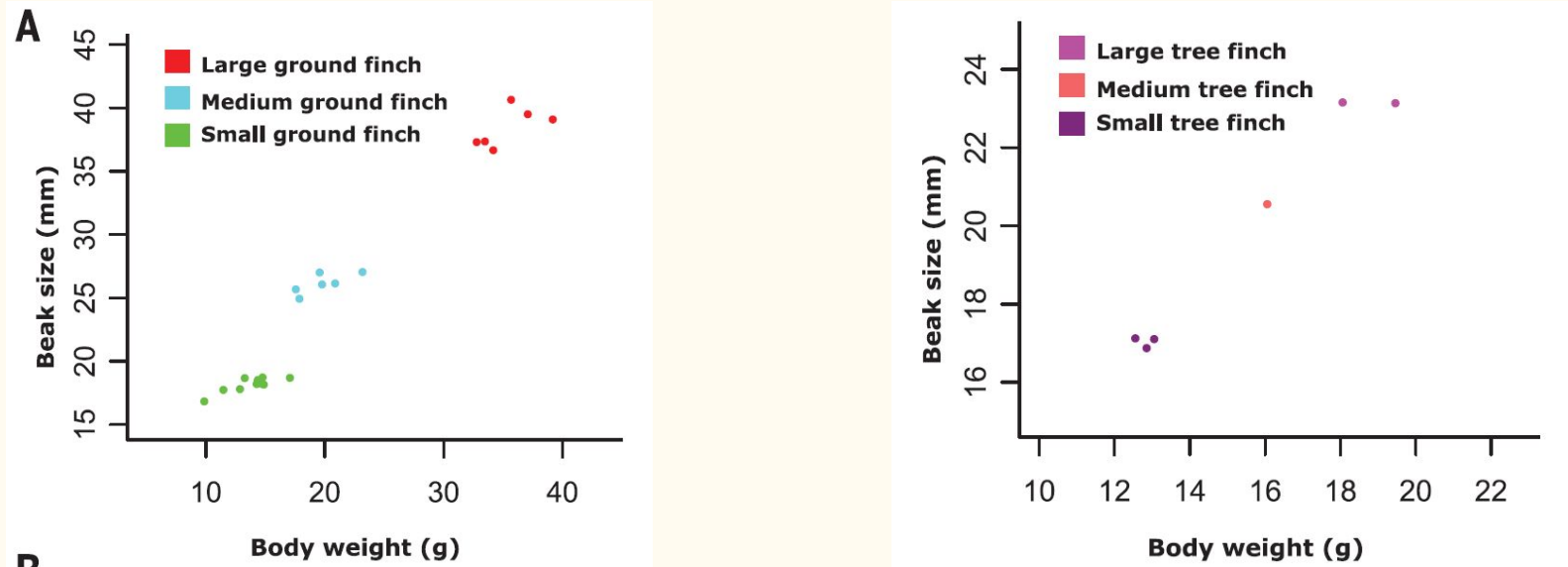


Fig. 1 A & B: Diversity in Population Means For Beak Size and Body Weight

Maximum Likelihood Phylogenetic Tree from sequence data

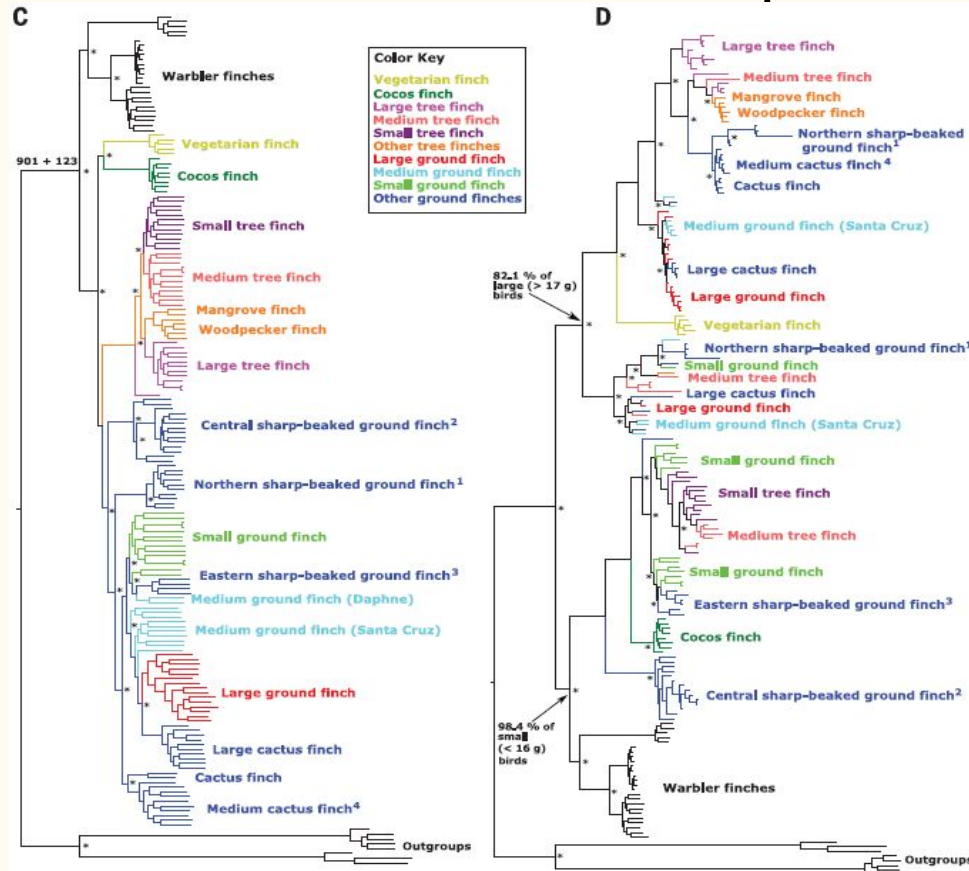
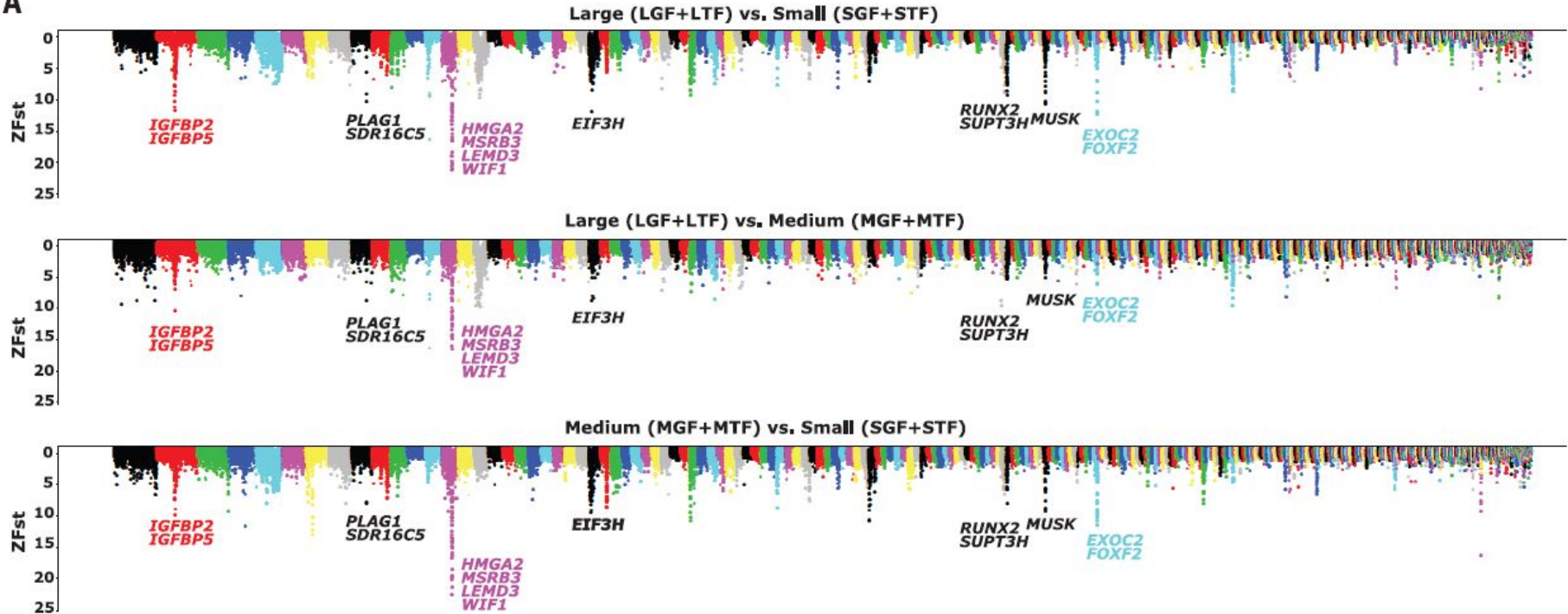


Fig 1 C&D: Computationally generated phylogenetic trees using all polymorphic autosomal loci (C) and 525-kb region around HGMA2 (D)

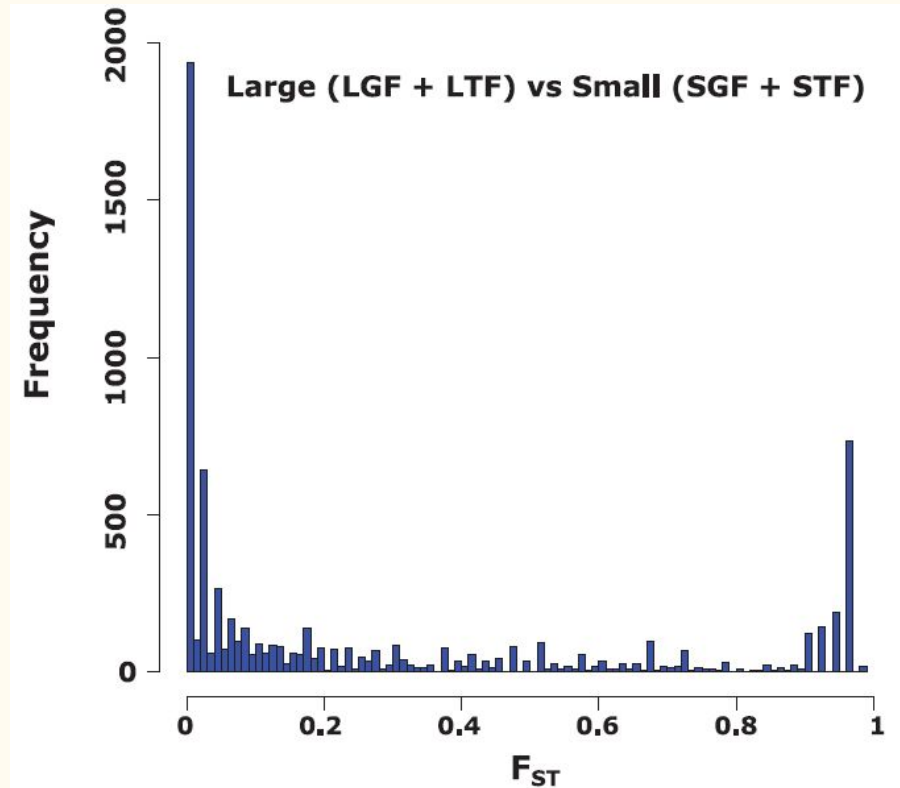
* indicates nodes in the phylogenetic tree confirmed by the Shimodaira-Hasegawa test for likelihood of statistically significant sequence alignment

Genome-wide Fixation Index (F-st) Test for Genetic Differences between Size Groups

A



Selection of significant SNPs and PhastCon analysis



Selection of significant SNPs and PhastCon analysis

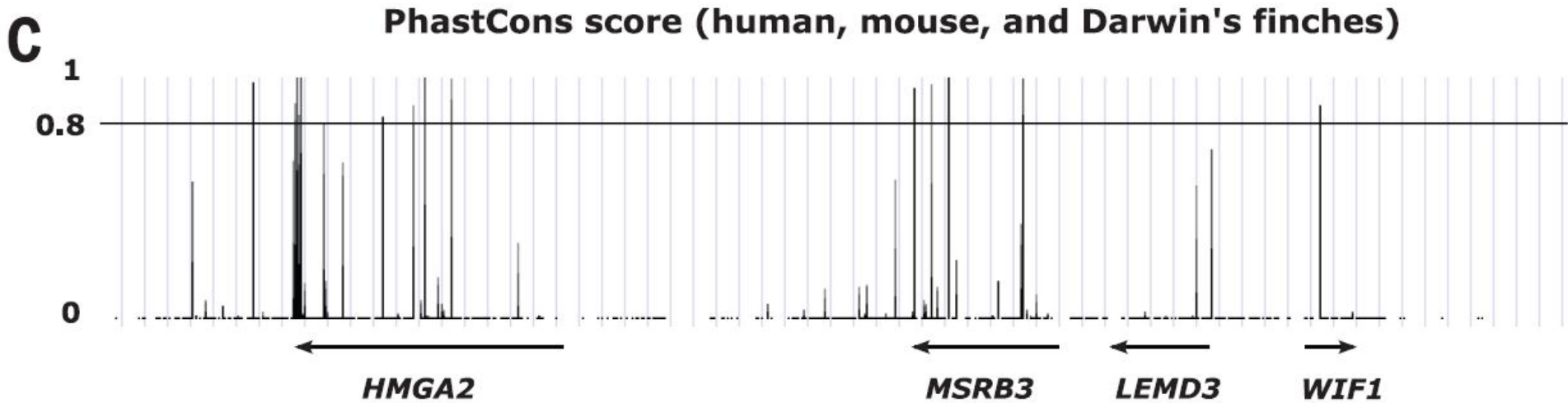


Fig 2C: Results of PhastCon analysis between finches and mammals

Genotypic analysis at selected SNPs in sampled groups

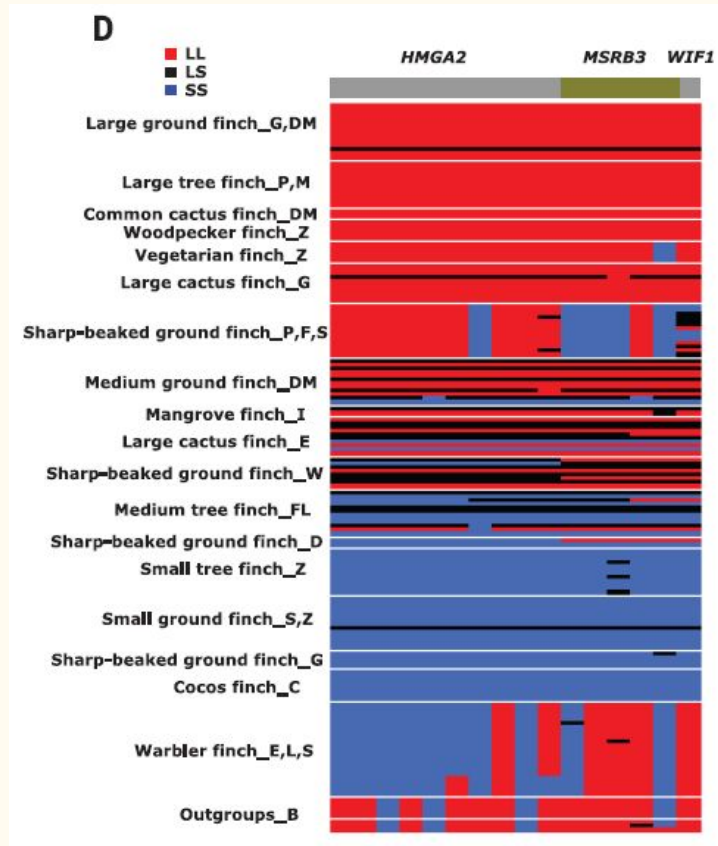
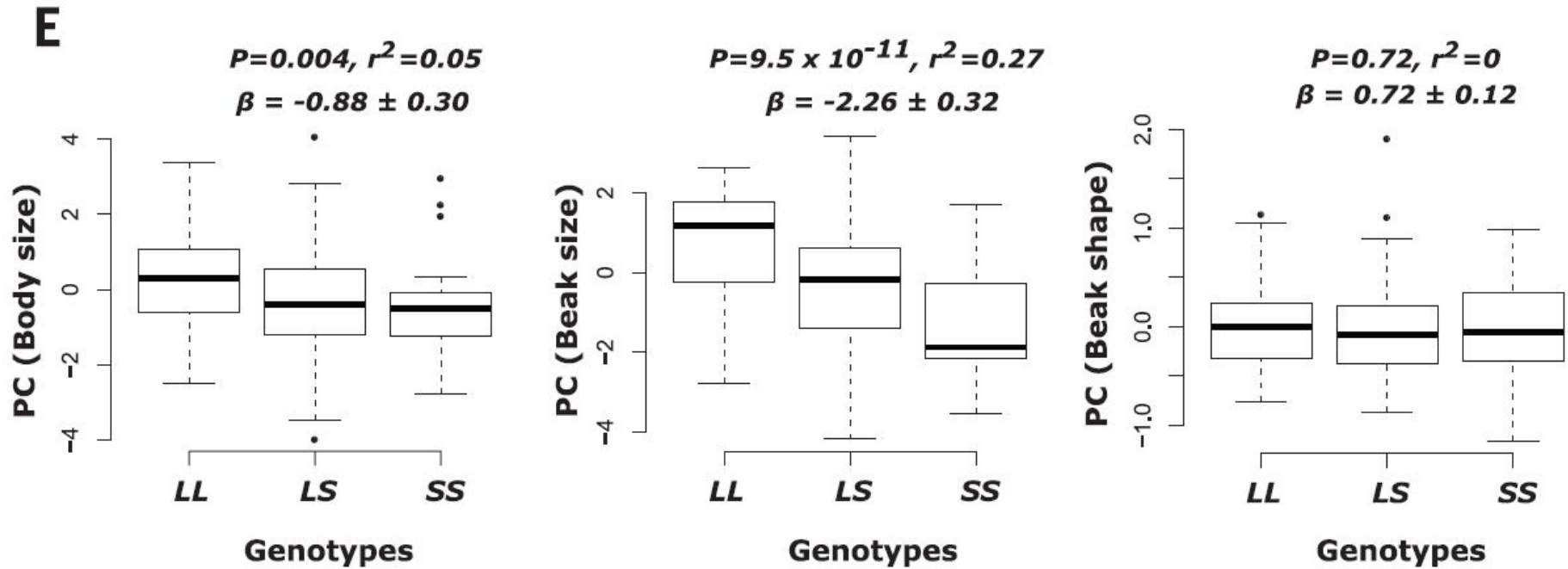


Fig 2D: Comparison of Homozygous Large (LL), Heterozygous Large/Small (LS) and Homozygous Small (SS) alleles in the 17 SNPs selected from F-st and PhastCon analysis

Regression Analysis of Genotypes vs size/shape characteristics



Survival Percentage According to HMG A2 Genotype of Medium Ground Finches

F

Genotype	Alive birds (n)	Dead birds (n)	Survival \pm SE (%)
<i>LL</i>	6	14	30.0 \pm 10.2
<i>LS</i>	17	15	53.1 \pm 8.8
<i>SS</i>	14	5	73.7 \pm 10.1

Conclusion

- HMG A2- Gene controlling beak size also in chickens and zebra finch
 - Additive effect of gene
 - ALX1- Beak shape
 - Also relevant in human heights and sizes of mice
- Single locus caused rapid diversification due to very high $.59 \pm 0.14$ selection coefficient
- **A single locus can have a very large effect in a population over a short amount of time**

Possible Future Research

- Sequence Darwin's finches to confirm location of HMGA2 gene
- Look at HMGA2 in chickens and analyze how it affects the size of the beak
 - Search for mechanism affecting beak shape and growth
- Observe how the fitness and phenotypic frequencies change if the environment changes again