

BIOL3110 Conservation & Ecological Genetics

LECTURE 7: GENETIC VARIATION & EVOLUTION



V_G and Evolution

IMPORTANCE OF QUANTITATIVE GENETICS

1. Quick review of key Quant Gen concepts
2. Importance for conservation
3. Case studies of evolution

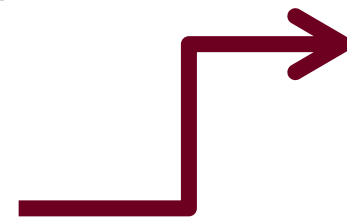


V_G and Evolution

QUANTITATIVE GENETICS

From studying phenotypes, we can partition:

- **Additive** genetic variation
- Non-additive genetic variation
- Environmental variation
(+ interactions/covariance – later)
- Total **Phenotypic** variation



$$\frac{V_A}{V_P} = h^2$$

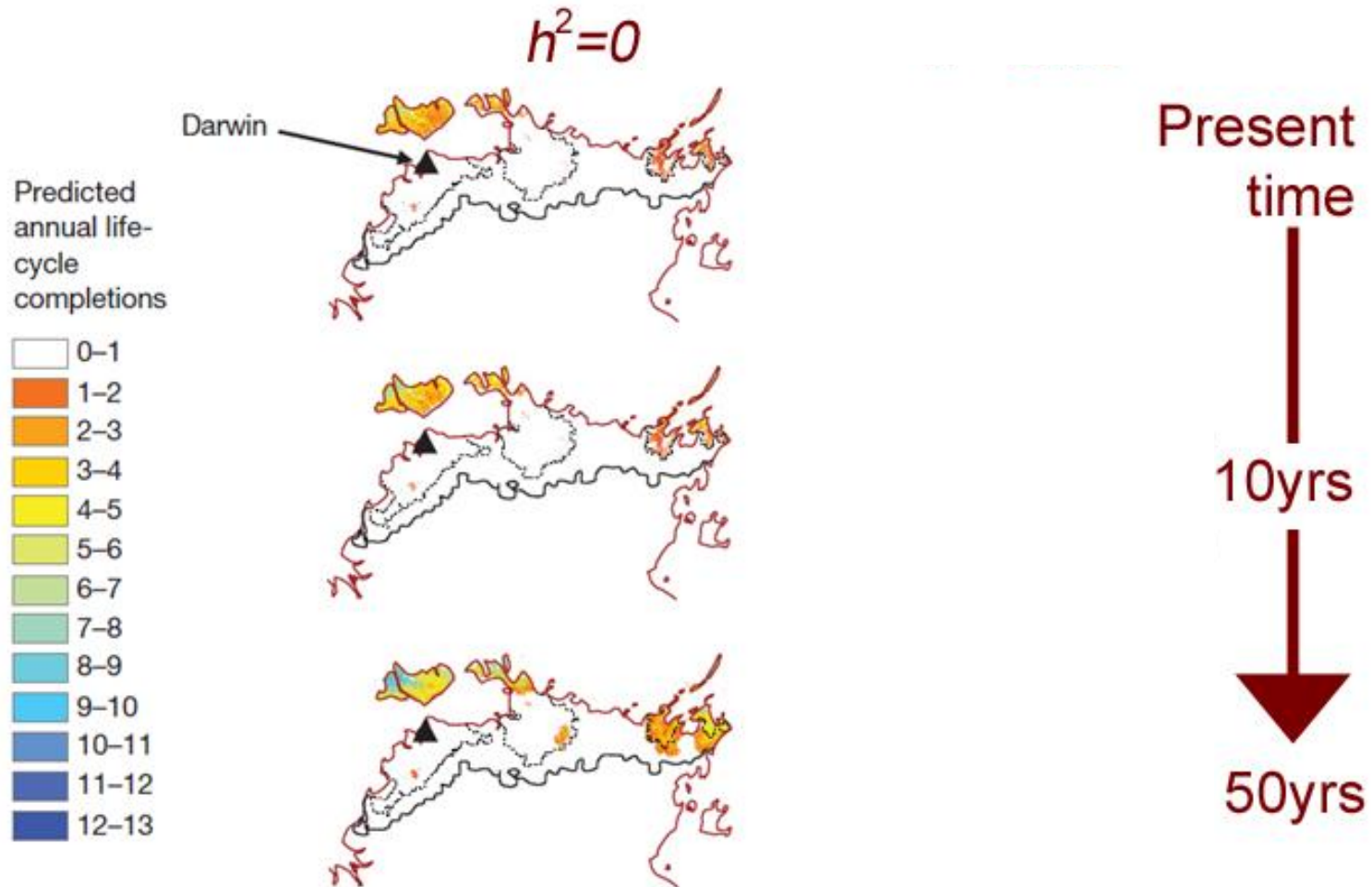
**Narrow-sense
heritability**

- Then, predict **Response to Selection**:
(via the “breeder’s equation”)

$$R = h^2 S$$

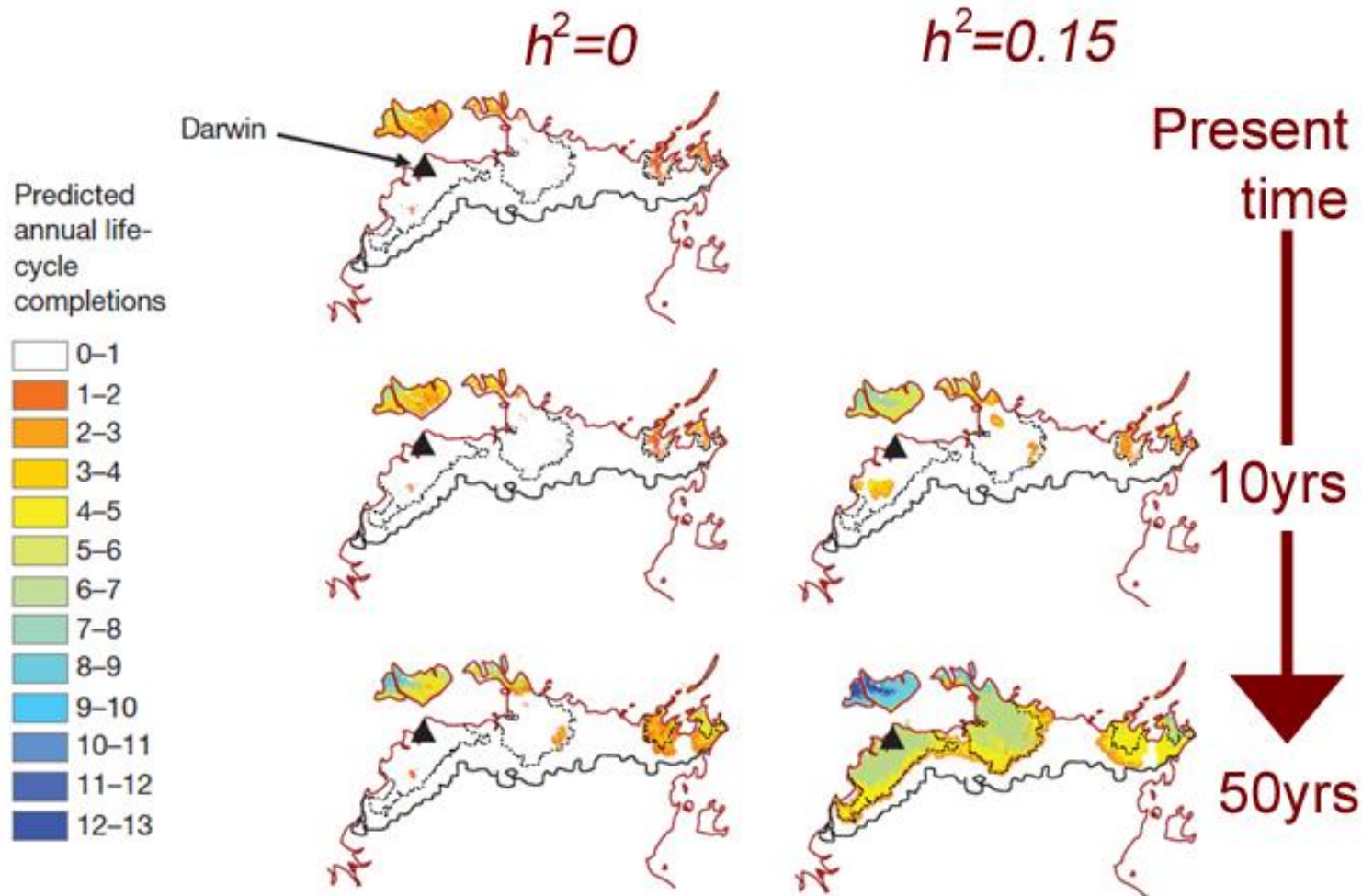
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IMPORTANCE OF QUANTITATIVE GENETICS



V_G and Evolution

IMPORTANCE OF QUANTITATIVE GENETICS

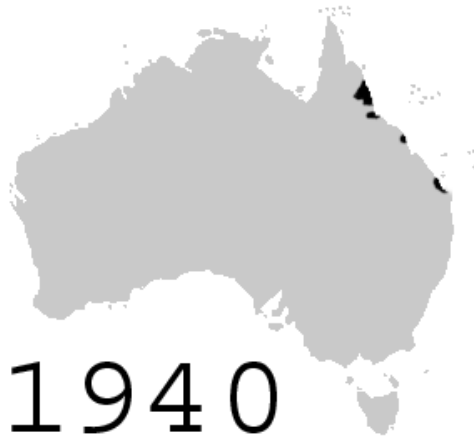


V_G and Evolution

Bufo marinus INVASION



Cane toad (*Bufo marinus*)



<http://www.cairnsunlimited.com>



Cane beetle (*Dermolepida albohirtum*)

V_G and Evolution

Bufo marinus INVASION



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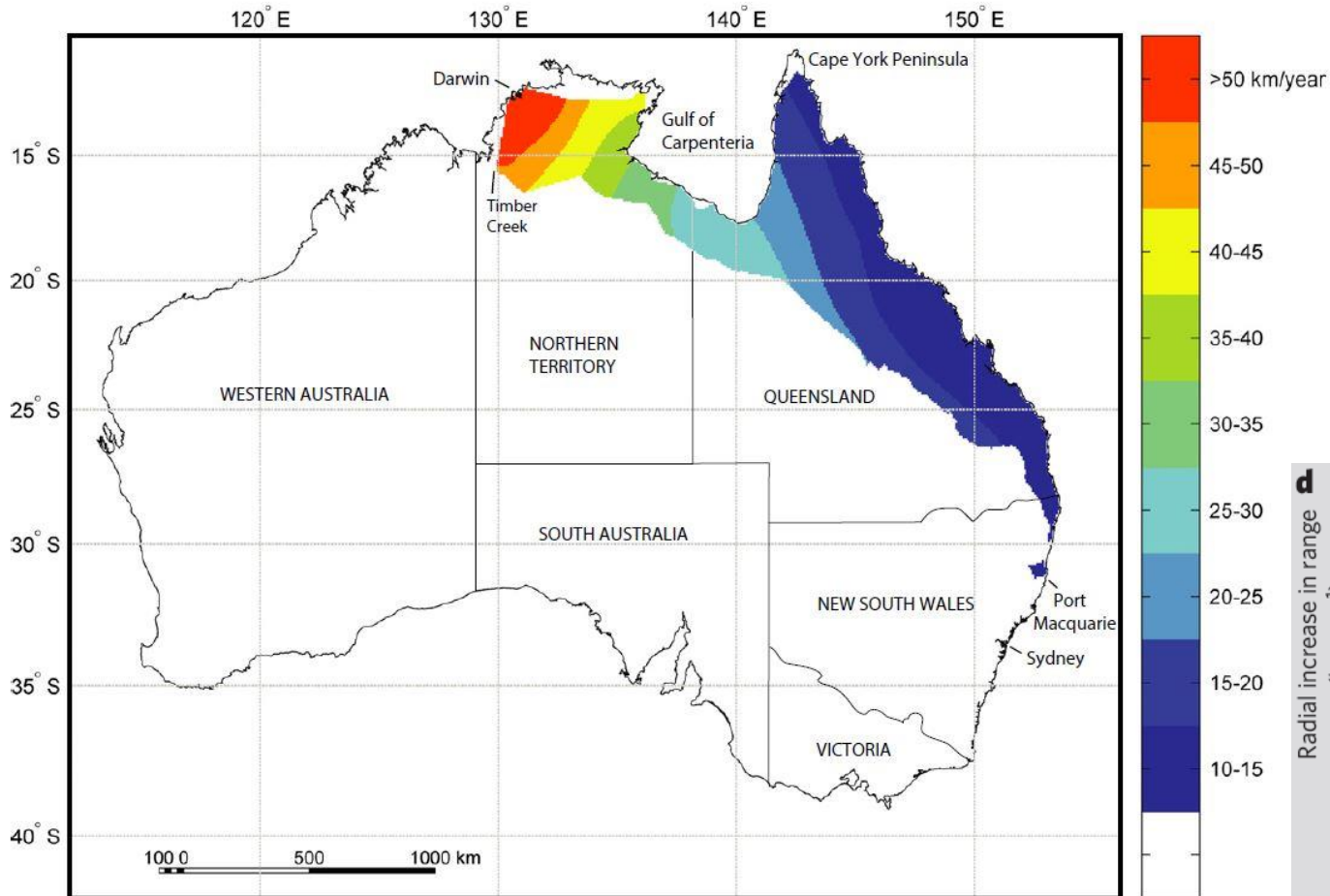
<http://www.frogwatch.org.au>

Biology

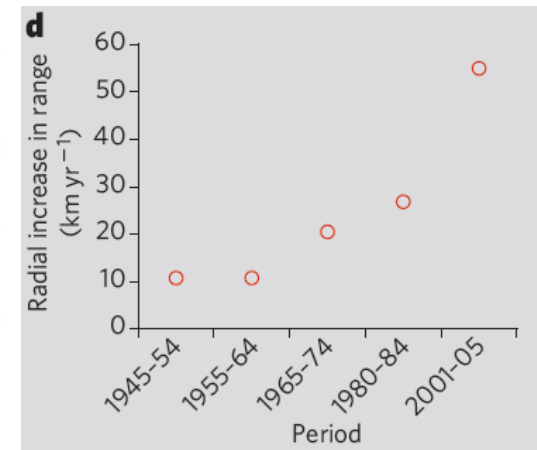
- Classic r-selected species
- **>30,000** eggs per clutch
- Metamorphosis **~12-days**
- Lifespan **10-15 years**
- Adults chemically protected by
bufotoxin (incl. bufotenin: a class 1 hallucinogen)

V_G and Evolution

Bufo marinus INVASION



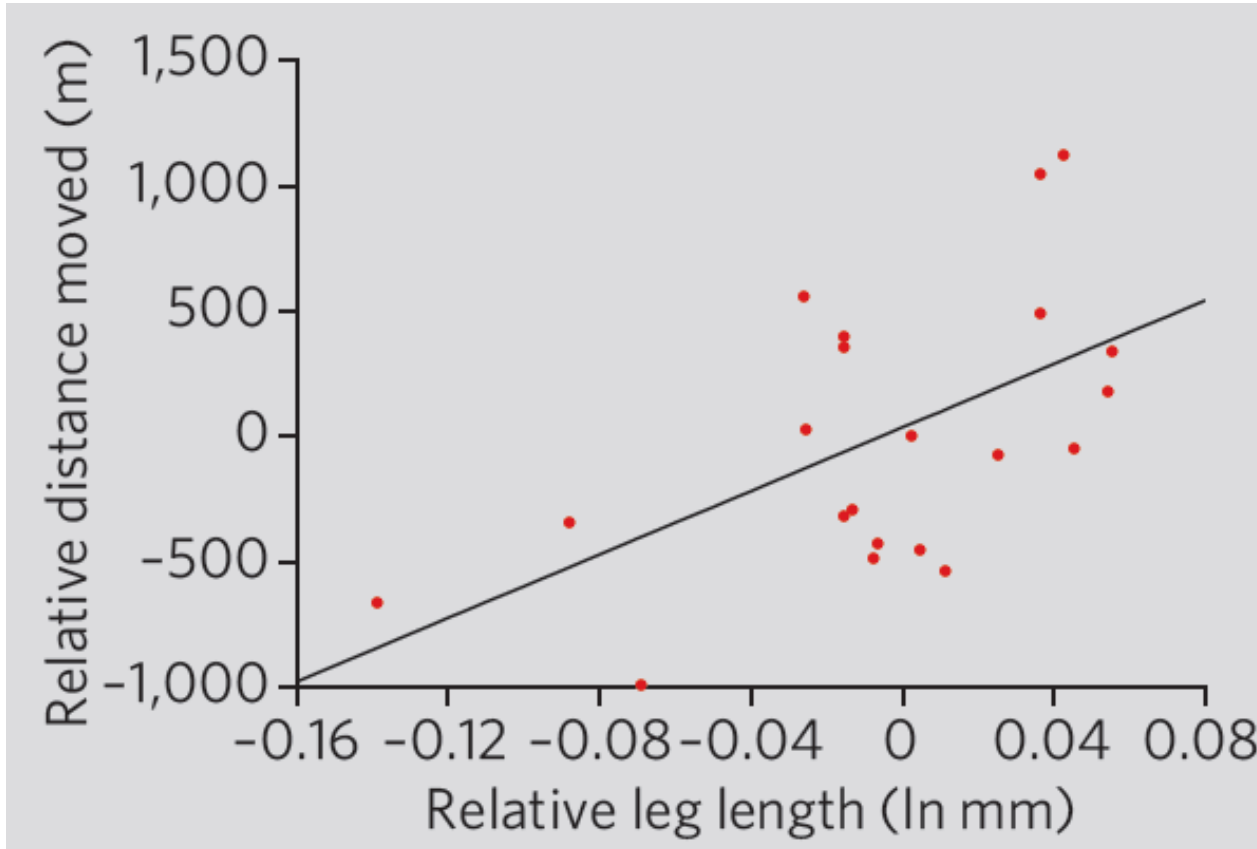
Rollins *et al.* 2015



Phillips *et al.* 2006

V_G and Evolution

Bufo marinus INVASION



Phillips *et al.* 2006

Longer-legged toads disperse more quickly

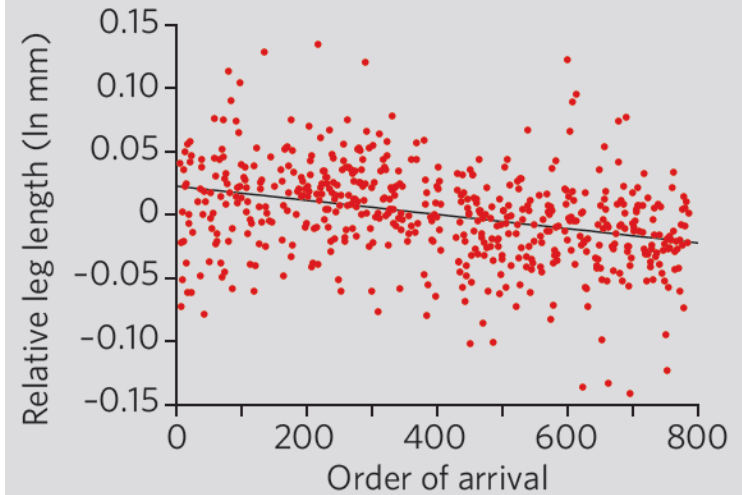
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Bufo marinus INVASION



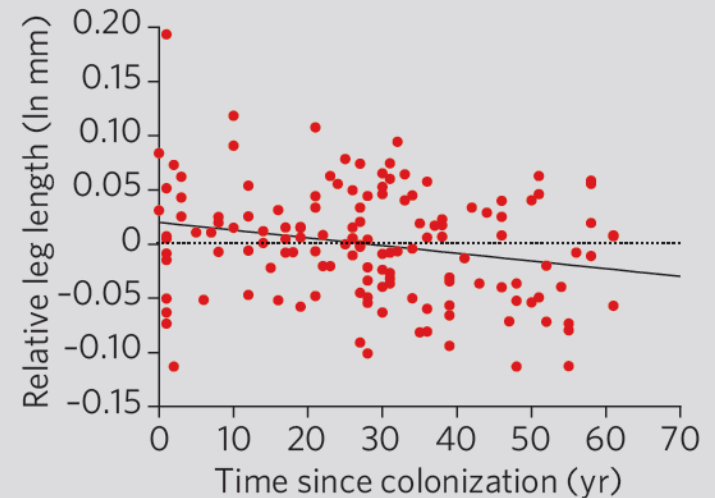
At the invasion FRONT:

- Long-legged toads arrive first
- Higher fitness
- Dispersal genes favoured at the front



After long establishment:

- Leg length declines
- Fitness 'target' shifts
- Dispersal genes disfavoured back from the front



Phillips *et al.* 2006

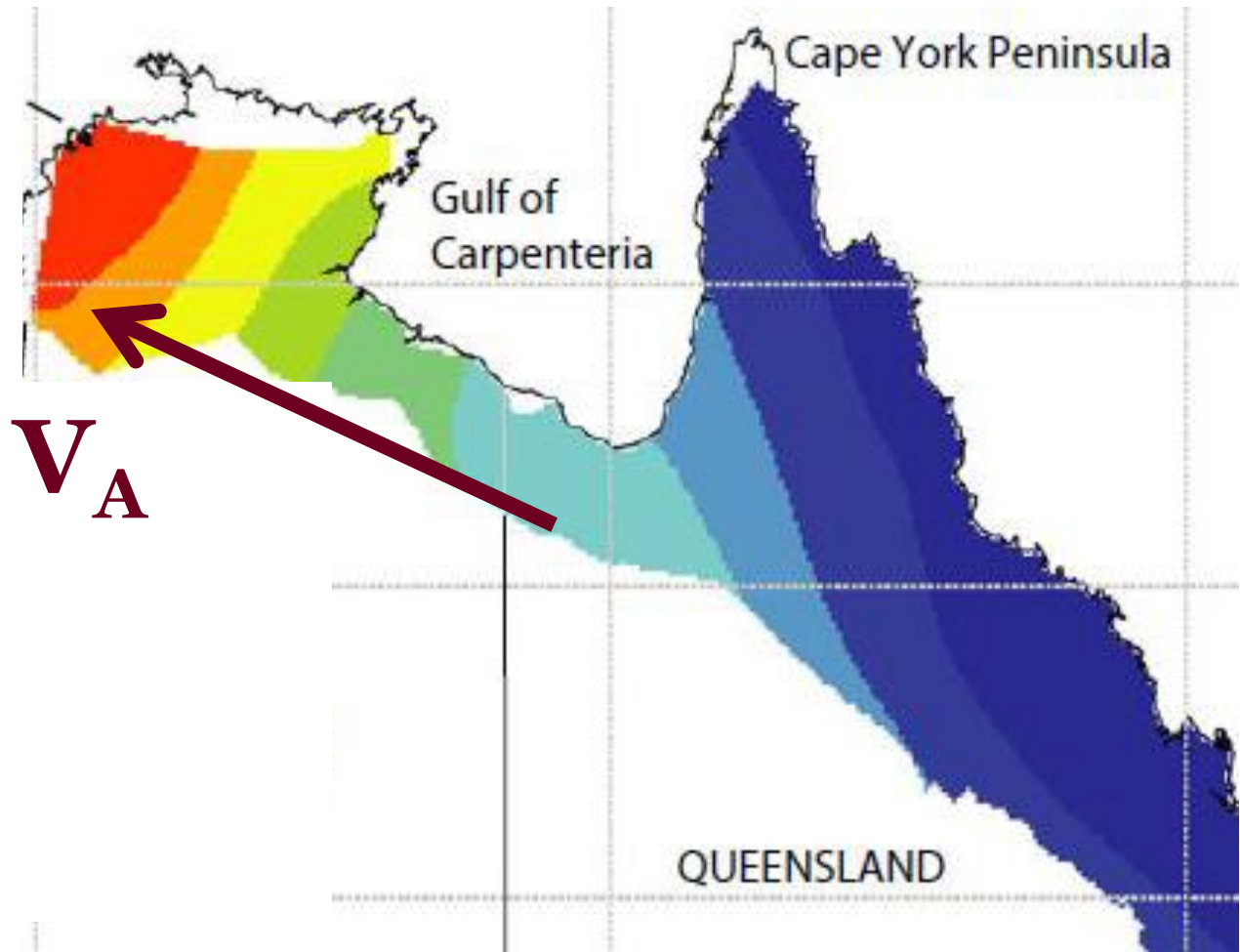
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“colocation”
of dispersal-
related
genes



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Red-bellied black snake (*Pseudechis porphyriacus*)



Freshwater crocodile
(*Crocodylus johnsoni*)



Red-cheeked dunnart
(*Sminthopsis virginiae*)



Corvis spp.)

V_G and Evolution

Bufo marinus INVASION

Under strong directional selection:

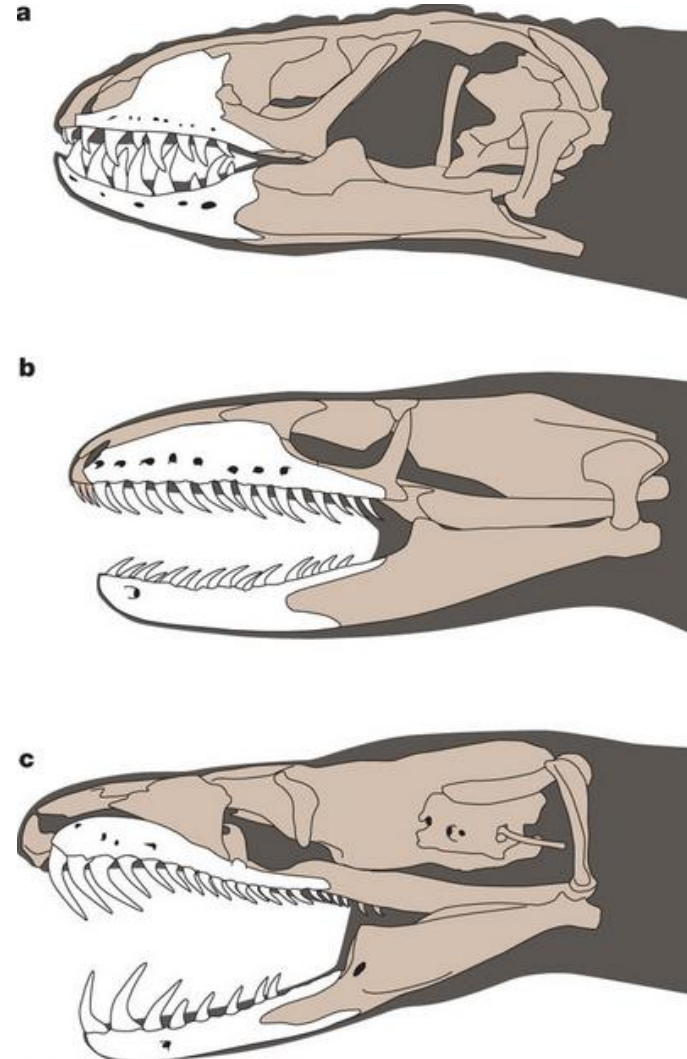
- Snakes avoid toads as prey (a **non-learned** behaviour)
- Morphological evolution.....?



Pseudechis porphyriacus



Dendrelaphis punctulatus



V_G and Evolution

Bufo marinus INVASION

Under strong directional selection:

- Snakes avoid toads as prey (a **non-learned** behaviour)
- Snake morphology has evolved in **~23 generations**



Pseudechis porphyriacus

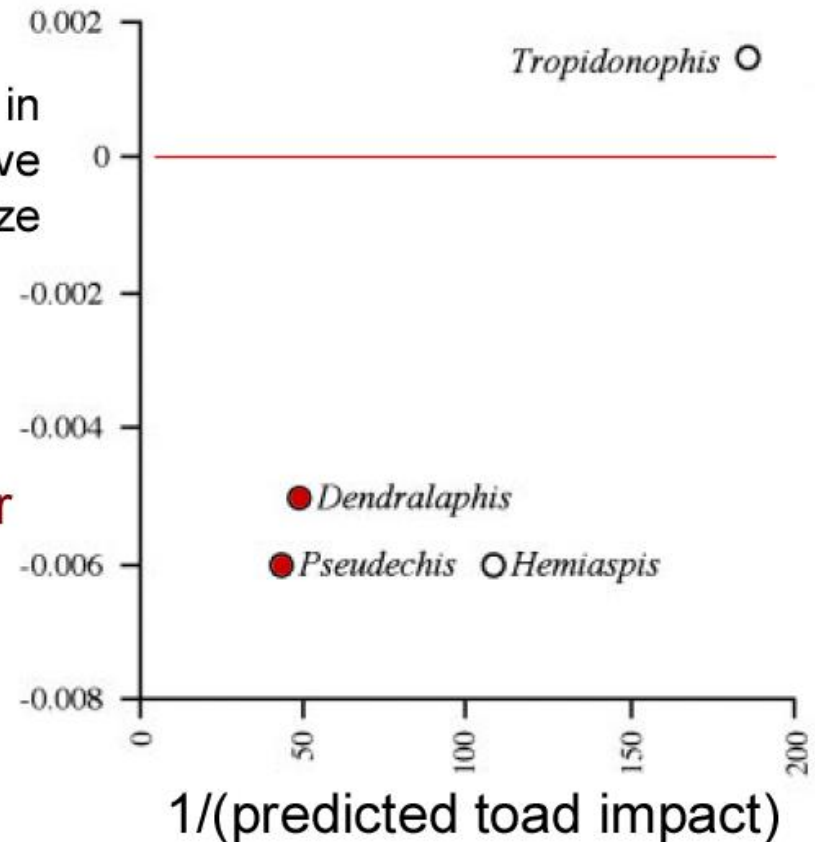


Dendrelaphis punctulatus



Change in
relative
head size

Smaller
gape



← Greater
risk

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Bufo marinus INVASION



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MOLECULAR ECOLOGY

Molecular Ecology (2015) 24, 2264–2276

doi: 10.1111/mec.13184

INVASION GENETICS: THE BAKER AND STEBBINS LEGACY

A genetic perspective on rapid evolution in cane toads (*Rhinella marina*)

LEE A. ROLLINS*, MARK F. RICHARDSON* and RICHARD SHINE†

*Centre for Integrative Ecology, School of Life & Environmental Sciences, Deakin University, Pausanias Drive, Geelong, Victoria 3217, Australia, †School of Biological Sciences A08, University of Sydney, Sydney, NSW 2006, Australia

Vol 439 | 16 February 2006

nature

BRIEF COMMUNICATIONS

Invasion and the evolution of speed in toads

Cane toads seem to have honed their dispersal ability to devastating effect over the generations.

Adapting to an invasive species: Toxic cane toads induce morphological change in Australian snakes

Ben L. Phillips* and Richard Shine

School of Biological Sciences A08, University of Sydney, New South Wales 2006, Australia

Edited by David B. Wake, University of California, Berkeley, CA, and approved October 27, 2004 (received for review August 31, 2004)

The arrival of invasive species can devastate natural ecosystems, but the long-term effects of invasion are less clear. If native organisms can adapt to the presence of the invader, the severity of impact will decline with time. In Australia, invasive cane toads

much less research has been conducted on counteradaptation by native species (17, 18).

Many species of Australian snake have been severely impacted by the invasion of highly toxic cane toads (*Bufo marinus*).

Evolving resistance and prey discrimination

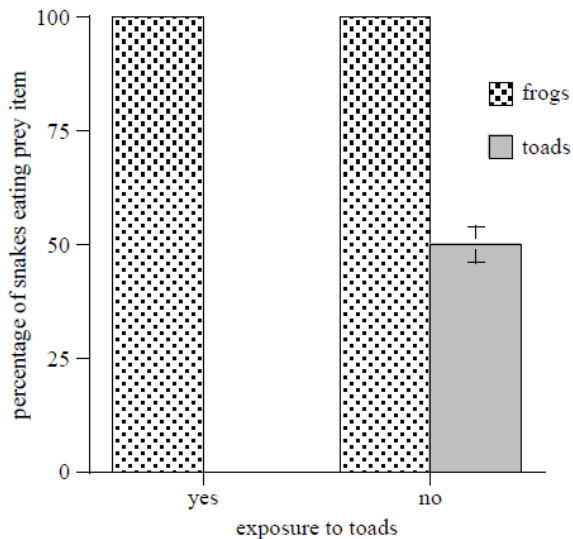


Figure 1. The percentage of black snakes from toad-exposed and toad-naive populations willing to eat a toad or a frog. No snake from a toad-exposed locality would consume a toad. Error bars represent a standard error.

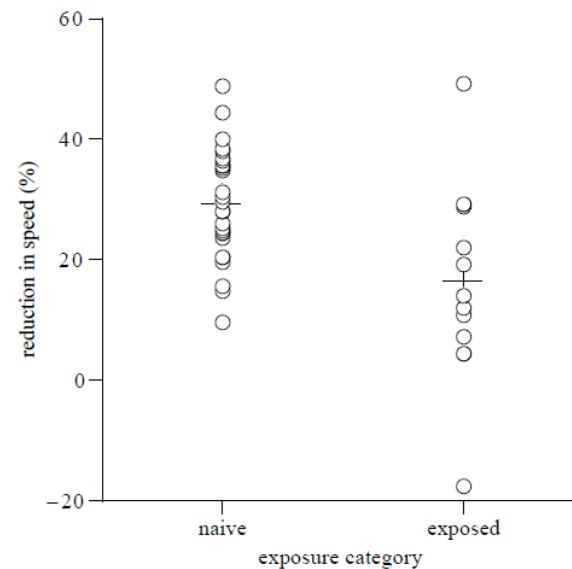


Figure 2. Resistance to toad toxin in toad-exposed and toad-naive populations. A large percentage reduction in speed indicates low resistance to toxin. Hence, snakes from toad-exposed populations exhibited higher resistance to toad toxin.

The standard equation used to estimate adaptive potential

The Breeder's equation, $R = h^2 S$

- applies only to conditions under which heritability was measured
- does not assess several major components of evolutionary genetic variation: dominance, epistasis, plasticity and epigenetics

Can we use genomics to estimate adaptive potential?



Using genomics to characterize evolutionary potential for conservation of wild populations

Katherine A. Harrison, Alexandra Pavlova, Marina Telonis-Scott and Paul Sunnucks

Evolutionary Applications

doi:10.1111/eva.12149

Given our current understanding of genomes - screening genome wide diversity will usually give a better estimate of evolutionary potential rather than trying to get estimates from particular components of the genome, eg focussing on genes of known function

Two distinct components of evolutionary potential

- **Genetic** (DNA-sequence-based)
- **Epigenetic** (non-DNA-sequence-based)

Molecular basis of evolutionary potential

Epigenetic

*Histone modification,
DNA methylation,
small non-coding RNAs
(microRNA, small
interfering RNA)*

Genetic (sequence-based)

*Distal/long-range transcription factor
binding sites (enhancers), splice
junctions, splicing enhancers,
synonymous mutations, silencers,
tandem repeats, non-coding variation of
unknown function*

*Non-synonymous
coding changes, known
transcription factor
binding sites
(enhancers/promoters)*

Unknown

small

LARGE

effect size on phenotype

effect size on phenotype



Integrative and Comparative Biology

Integrative and Comparative Biology, volume 53, number 2, pp. 351–358
doi:10.1093/ich/ict007

Society for Integrative and Comparative Biology

Patterns of DNA Methylation Throughout a Range Expansion of an Introduced Songbird

Andrea L. Liebl,^{1,*} Aaron W. Schrey,^{*,†} Christina L. Richards^{*} and Lynn B. Martin^{*}



Alvaro1984 18 -

- 1950s, house sparrow introduced into Kenya
- High levels of variation in DNA methylation (epigenetic marker)
- Epigenetics could be important part of phenotypic variability and adaptation

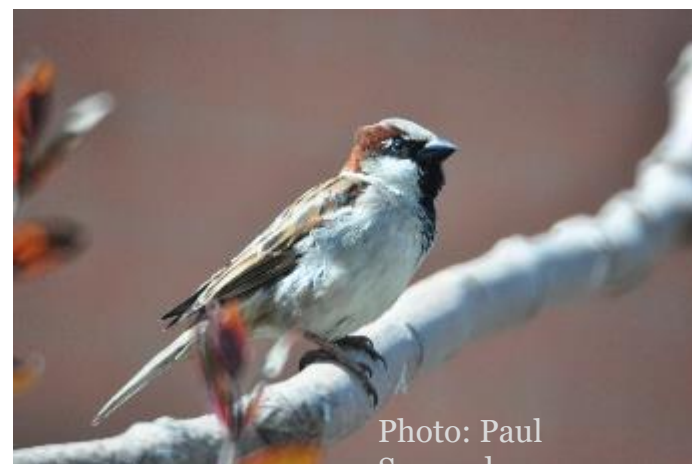
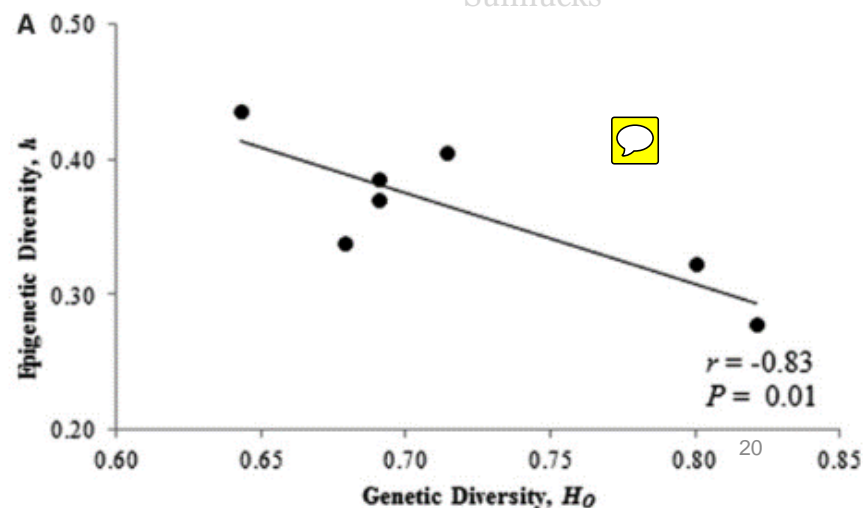
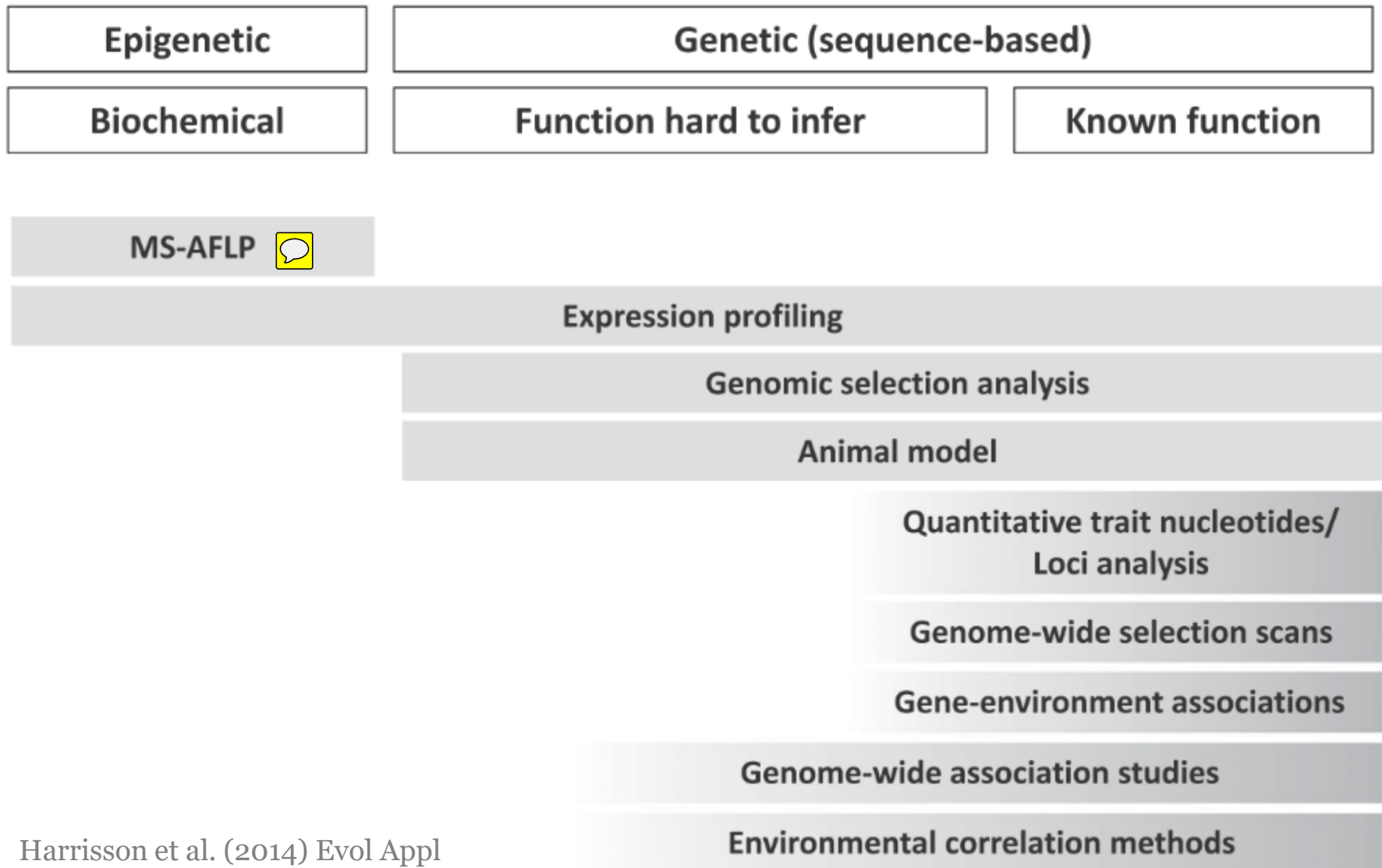


Photo: Paul Sunnucks

Epigenetic variation was greatest in the populations with the lowest genetic variation – may compensate for low genetic variation



Methods to infer selection are complex, numerous, emerging



Harrison et al. (2014) Evol Appl

Three main insights into evolutionary potential

summarized by Harrisson et al. 2014:

- (1) Rapid adaptive evolution is mainly from changes in gene expression
- (2) Most traits are polygenic (built by lots of genes of small effect)
- (3) Most recent adaptation is due to subtle shifts of allele frequencies

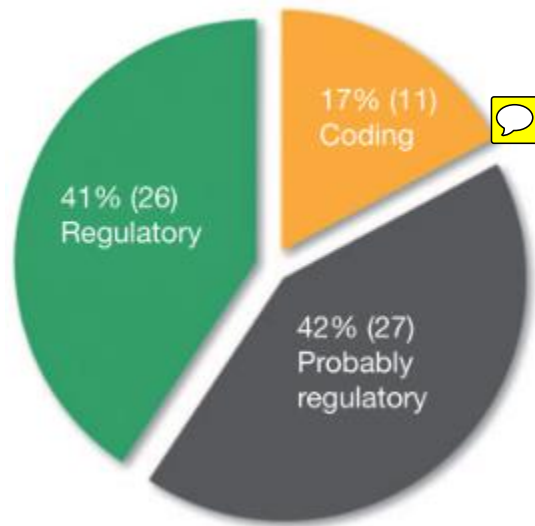
(1) Rapid adaptive evolution is driven predominantly by changes in gene expression

The genomic basis of adaptive evolution in threespine sticklebacks

5 APRIL 2012 | VOL 484 | NATURE | 55

Felicity C. Jones^{1*}, Manfred G. Grabherr^{2,3*}, Yingguang Frank Chan^{1†*}, Pamela Russell^{2*}, Evan Mauceli^{2†}, Jeremy Johnson², Ross Swofford², Mono Pirun^{2†}, Michael C. Zody², Simon White⁴, Ewan Birney⁵, Stephen Searle⁴, Jeremy Schmutz⁶, Jane Grimwood⁶, Mark C. Dickson⁶, Richard M. Myers⁶, Craig T. Miller^{1†}, Brian R. Summers¹, Anne K. Knecht¹, Shannon D. Brady¹, Haili Zhang¹, Alex A. Pollen¹, Timothy Howes¹, Chris Amemiya⁷, Broad Institute Genome Sequencing Platform & Whole Genome Assembly Team[‡], Eric S. Lander², Federica Di Palma², Kerstin Lindblad-Toh^{2,3} & David M. Kingsley^{1,8}

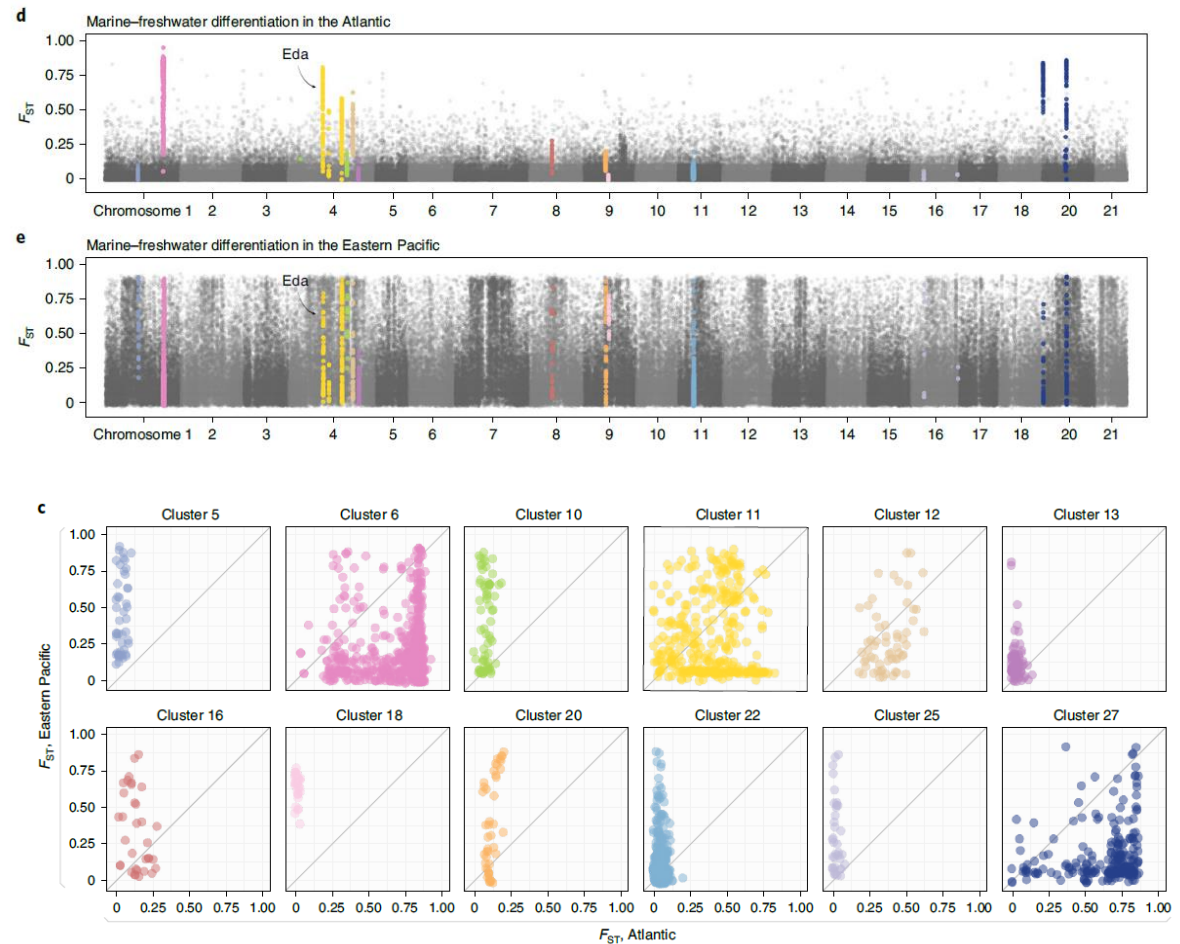
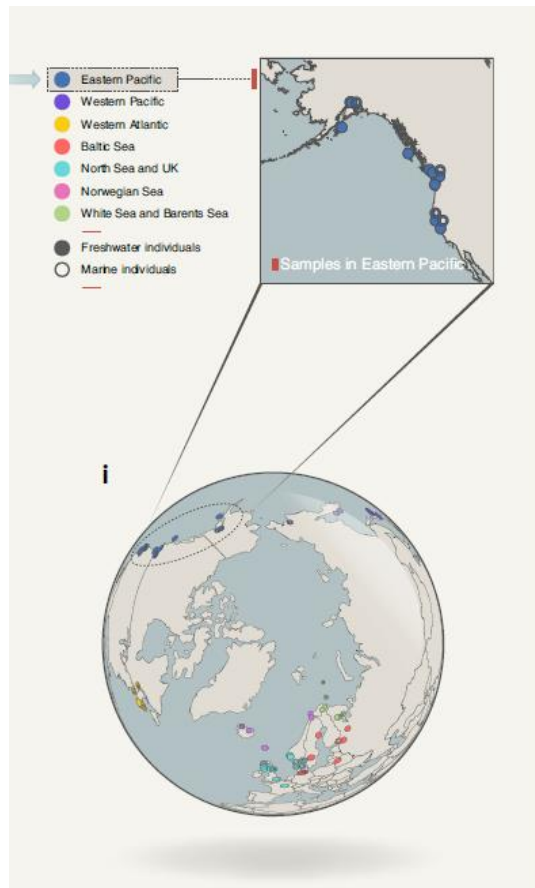
Found 64 strong candidate genes for evolutionary transitions between sea & freshwater.
Mostly regulatory



Freshwater
forms

Marine
forms

Ectodysplasin A (EDA) gene is known to be responsible for marine–freshwater differences in lateral armour plate development worldwide



(2) Most traits are polygenic

Genomic dissection of variation in clutch size and egg-mass in a wild great tit (*Parus major*) population

ANNA W. SANTURE,^{*1} ISABELLE DE CAUWER,^{*†1} MATTHEW R. ROBINSON,^{*}
JOCELYN POISSANT,^{*} BEN C. SHELDON[‡] and JON SLATE^{*}

MOLECULAR ECOLOGY

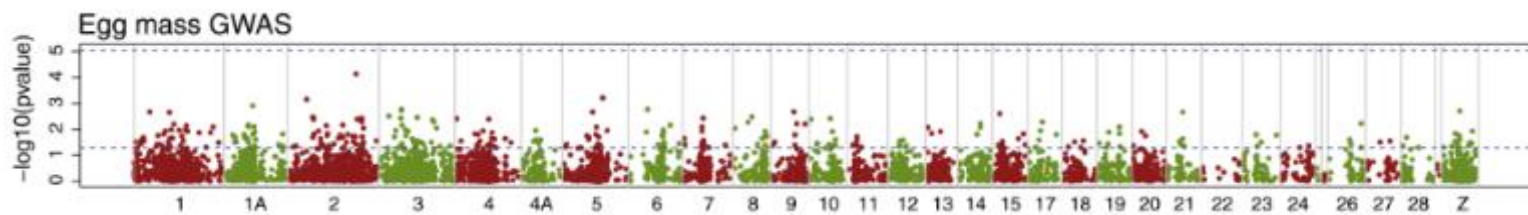
Molecular Ecology (2013) 22, 3949–3962



e.g. egg characteristics (number, mass) are predicted by variation at many genes – egg characteristics are polygenic

e.g. as done by genome-wide association studies (GWAS)

Probability
that each
marker is
associated
with egg mass



Position along the genome – chromosome number

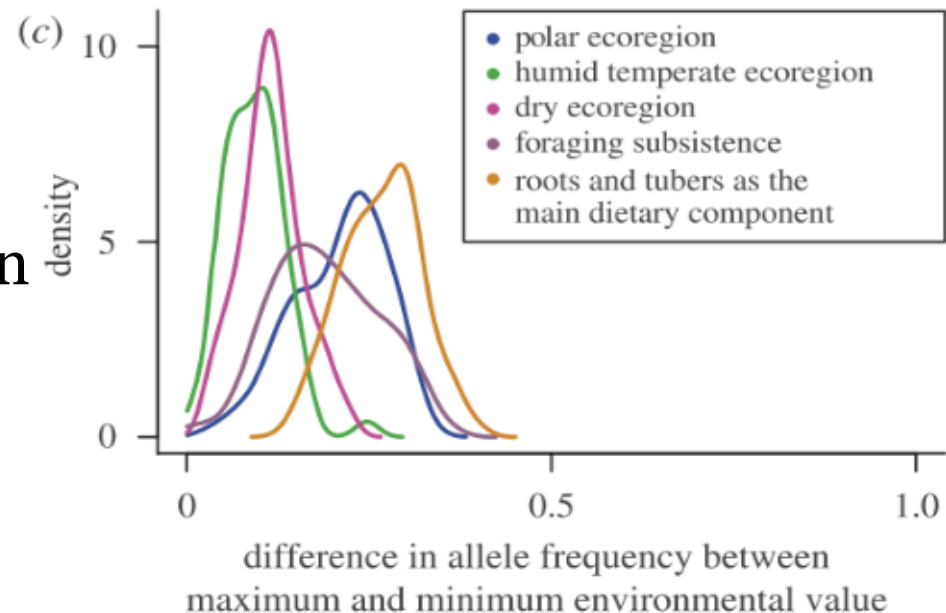
Can find specific candidate genes - the ones above the lower dotted blue line

(3) Most recent adaptation is due to subtle shifts of allele frequencies

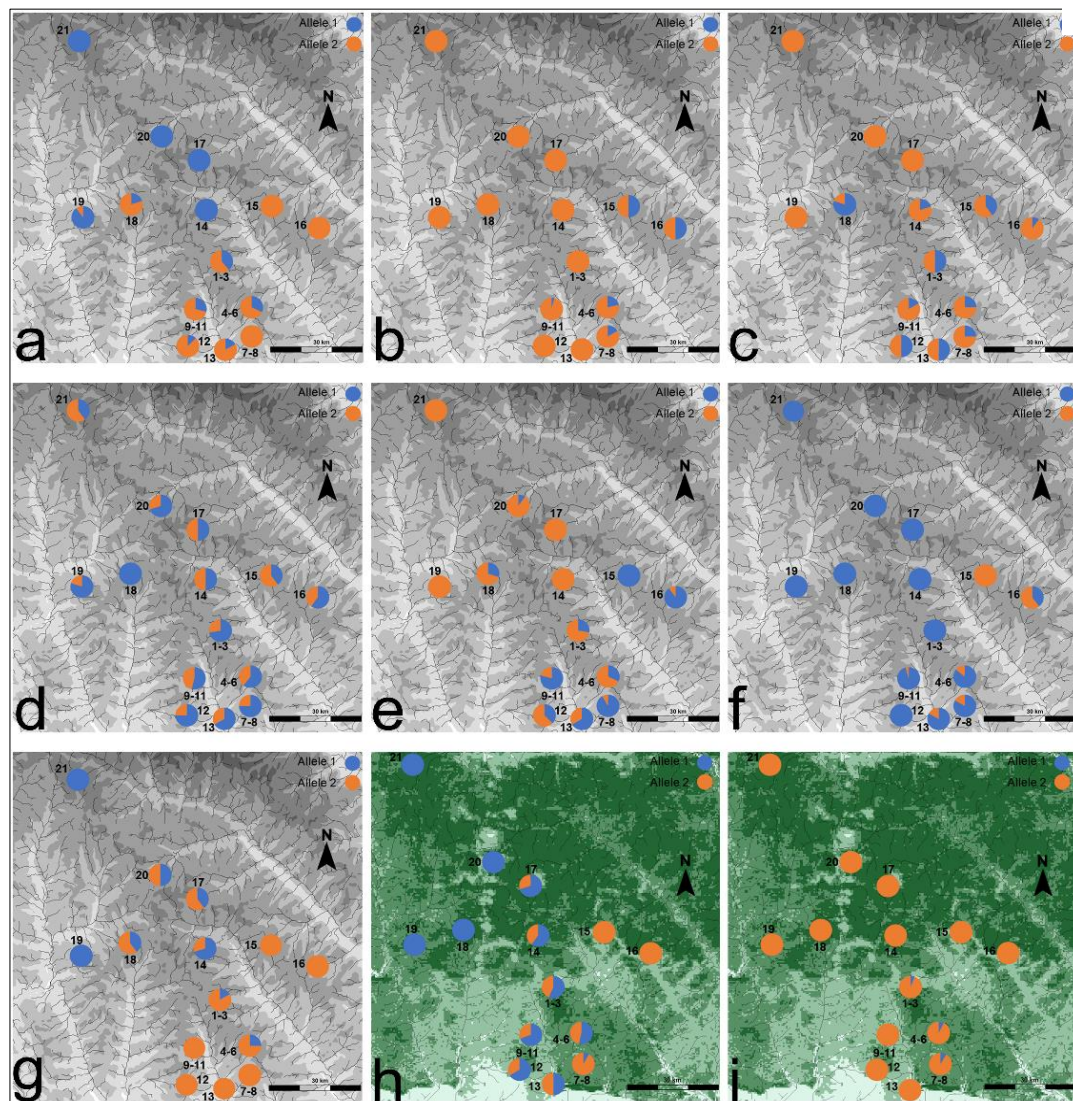
Subtle shifts in frequencies – need huge data sets, so many earlier studies are related to human health

E.g.

Adaptations to a diet rich in roots and tubers show association with changes in starch and sucrose metabolism and an ability to synthesize folic acid (tubers are low in this)



Hancock et al. (2010) *Phil Trans Roy Soc B* 365 2459-2468



Gray - altitude

functions for genes associated with forest biomass were annotated to blood, cell and chromatin functions, whereas genes with allele frequencies associated with altitude were annotated to the immune system, catabolic regulation, reproduction and functioning of sensorial organs (i.e., vision)

Green – forest density

Next:

Evolution part 2

