



Spring 2014: Mondays 10:15am – 12:05pm (Fox Hall, Room 204)

Instructor: D. Magdalena Sorger  
Website: [theantlife.com/teaching/bio295-islands-evolution](http://theantlife.com/teaching/bio295-islands-evolution)

## LECTURE 05

### Today:

Follow-up on minute papers

**Mutation**

**Genetic drift**

My research

Summary

## **FOLLOW-UP MINUTE PAPERS**



### **Follow-up on minute papers**

- Finding rules regarding nature and evolution
- Application of HWE
- More on orchids

# **MECHANISMS OF EVOLUTION**



## Mechanisms of evolution

**Gene flow (Migration)**

**Mutation**

**Natural selection**

**Non-random mating**

**Genetic drift**

## Mechanisms of evolution

Gene flow (Migration)

**Mutation**

Natural selection

Non-random mating

Genetic drift

## MUTATION

change of the nucleotide sequence of  
the genome of an organism

## Types of mutation

- Point mutation
- Chromosome inversion
- Gene duplication – replication slippage
- Genome duplication



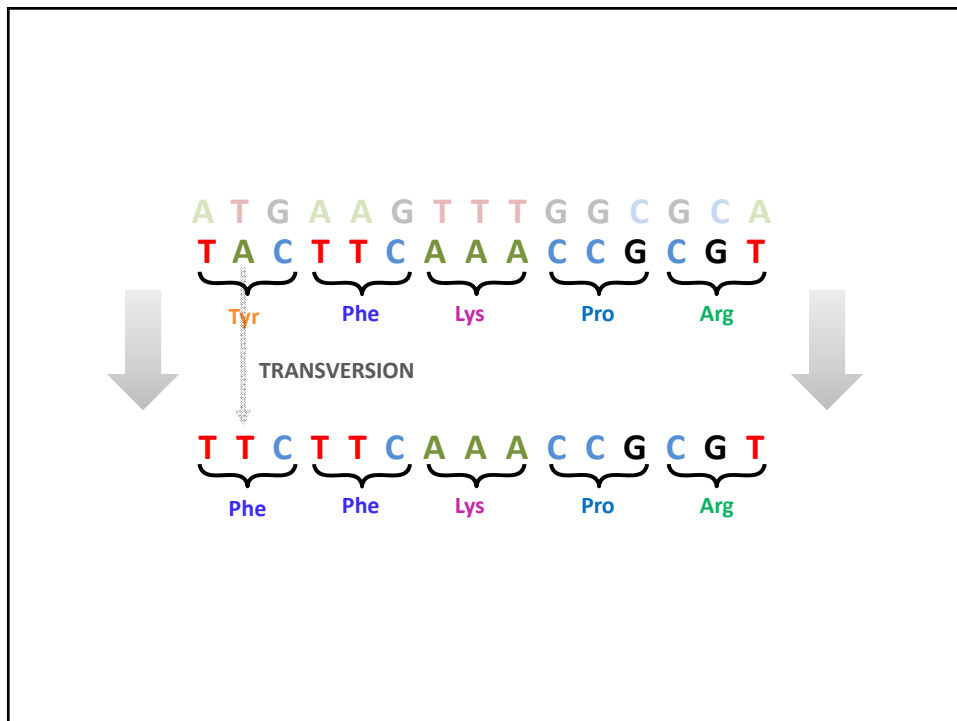
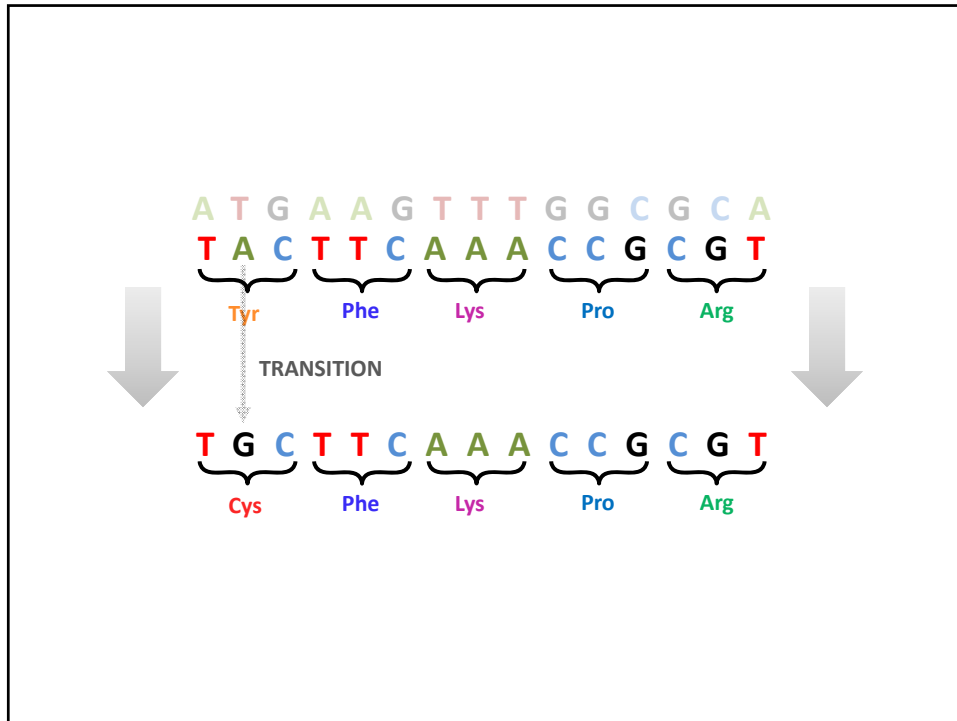
## Point mutation

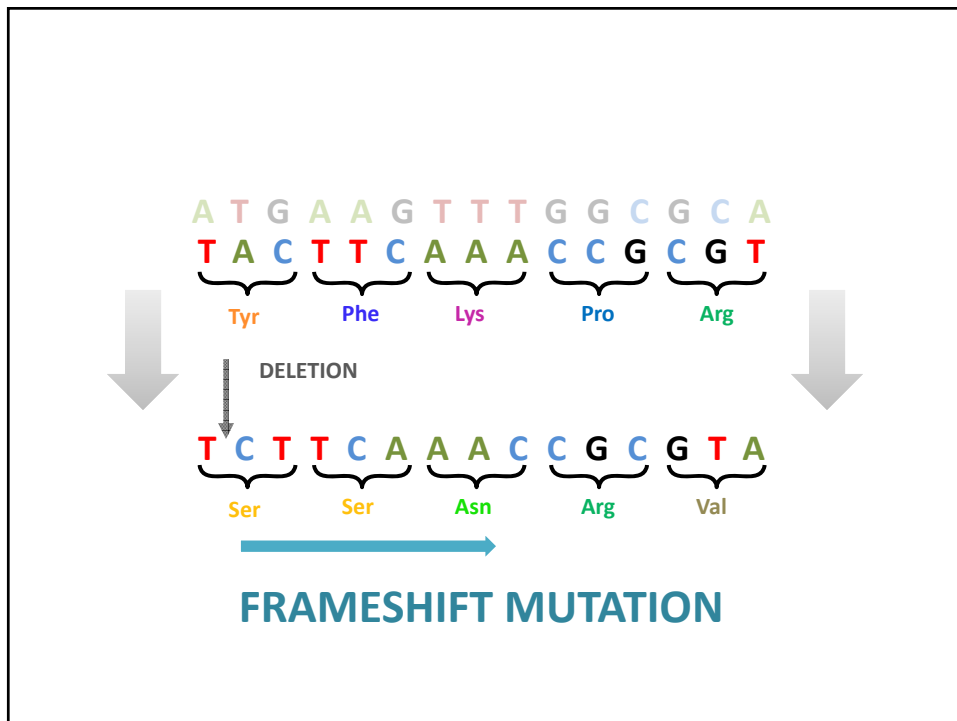
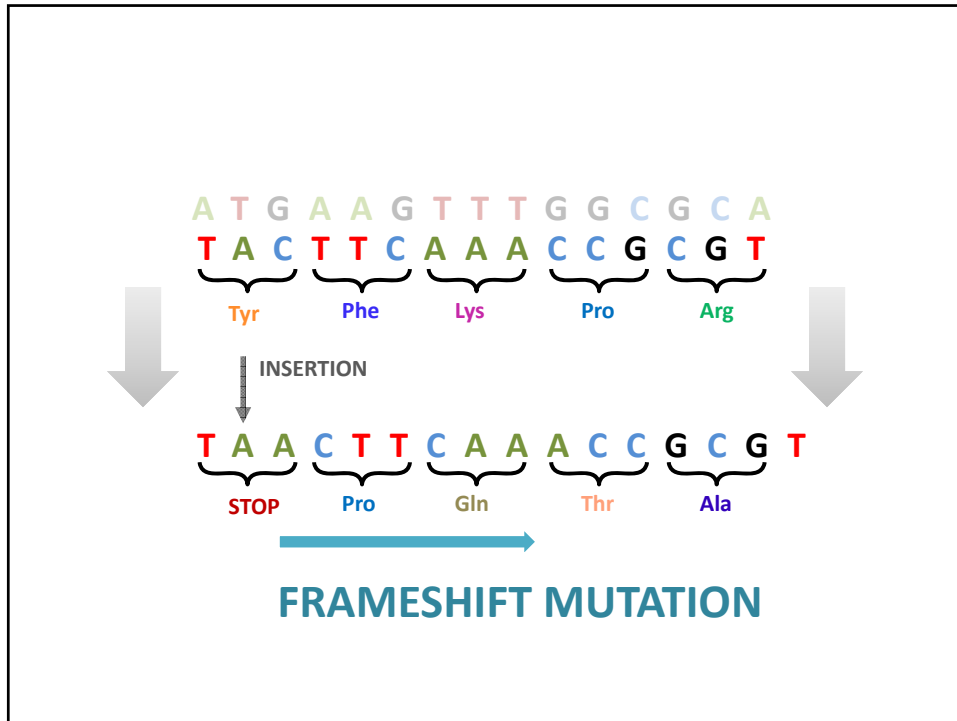
Result of

...errors made by DNA polymerase during DNA synthesis

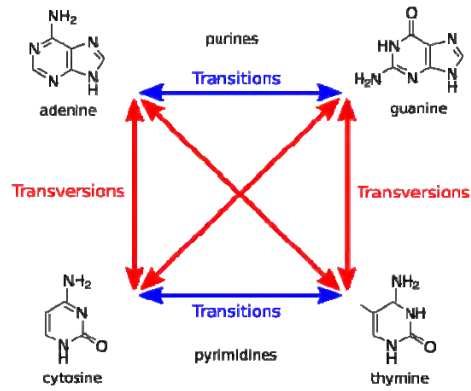
...errors made by DNA repair enzymes

**Not an adaptation!!**





## Point mutations



## TRANSITIONS

are **more common** than

**TRANSVERSIONS**



## Somatic mutations

- DNA under constant attack from mutagens
- e.g., radiation, free radicals
- majority of these errors gets repaired
- eventually if not repaired cause diseases, aging, and death

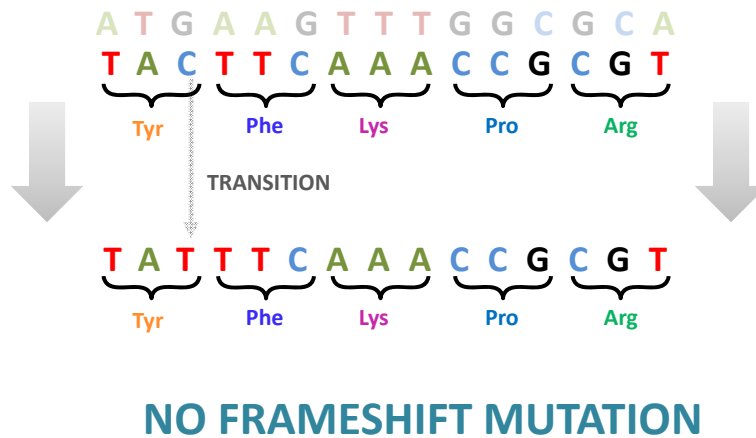
Little evolutionary importance!

## Germline mutations

- *Mutation occurs in single cell...*
- **if germ cell:** can give rise to gamete that carries mutation and could be inherited to offspring
- mutation can become fixed in a population because of selection or genetic drift

## SILENT MUTATIONS

- **Non-coding regions (introns)**
- **Change in a nucleotide that does not change the amino acid** (e.g., 3<sup>rd</sup> position change)



## Codon table

		second base in codon				
		T	C	A	G	
T	T	TTT Phe	TCI Ser	TAT Tyr	TGT Cys	T
	C	TTC Phe	TCC Ser	TAC Tyr	TGC Cys	C
	A	TTA Leu	TCA Ser	TAA stop	TGA stop	A
	G	TTG Leu	TCG Ser	TAG stop	TGG Trp	G
C	T	CTT Leu	CCT Pro	CAT His	CGT Arg	T
	C	CTC Leu	CCC Pro	CAC His	CGC Arg	C
	A	CTA Leu	CCA Pro	CAA Gln	CGA Arg	A
	G	CTG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	T	ATT Ile	ACT Thr	AAT Asn	AGT Ser	T
	C	ATC Ile	ACC Thr	AAC Asn	AGC Ser	C
	A	ATA Ile	ACA Thr	AAA Lys	AGA Arg	A
	G	ATG Met	ACG Thr	AAG Lys	AGG Arg	G
G	T	GTT Val	GCT Ala	GAT Asp	GGT Gly	T
	C	GTC Val	GCC Ala	GAC Asp	GGC Gly	C
	A	GTA Val	GCA Ala	GAA Glu	GGA Gly	A
	G	GTG Val	GCG Ala	GAG Glu	GGG Gly	G

## Replication slippage

- alters the number of short repeats in microsatellites
- growing (3') end of DNA strand becomes dissociated from template strand and forms a **loop**
- next repeat copied is one that has already been copied
- **extra repeats** formed in growing strand

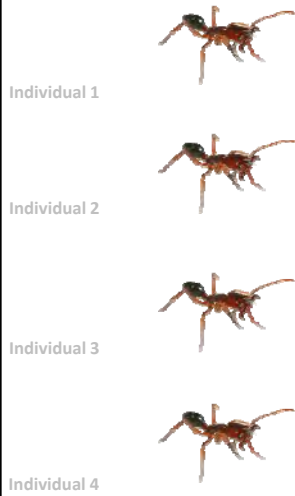
## Microsatellites

- “Short Tandem Repeats”
- repetitive sequences of 2-6 base pairs
- in non-coding regions (introns)
- Highly polymorphic
- Higher rate of mutation (slippage)

## Microsatellite locus



## Microsatellite locus



## Microsatellite locus



## Microsatellite locus

T A C T T C A C A C A C A C A C A C A C A C A A A C C G C G T

Individual 1

T A C T T C A C A C A C A C A C A A A C C G C G T

Individual 2



T A C T T C A C A C A C A C A C A A A C C G C G T

Individual 3

T A C T T C A C A C A A A C C G C G T

Individual 4

## SNP (Single Nucleotide Polymorphism)

Individual 1



Individual 2



Individual 3



Individual 4



## SNP (Single Nucleotide Polymorphism)

Individual 1  
 T A C T T C **C** C C G C G T **C** T A **G** T C T A A **T** A C A G G T

Individual 2  
 T **T** C T **A** C A C C G C G T T **C** A C T C T A A G A C A G G T

Individual 3  
 T A C T T C **C** C C G C G T **C** T A **G** T C T A A **T** A C A G **C** T

Individual 4  
 T A C T T C **T** C C G C G **G** T T A C T C T A A G A C A G G T

## SNP (Single Nucleotide Polymorphism)

Individual 1  
 T A C T T C **C** C C G C G T **C** T A **G** T C T A A **T** A C A G G T

Individual 2  
 T **T** C T **A** C A C C G C G T T **C** A C T C T A A G A C A G G T

Individual 3  
 T A C T T C **C** C C G C G T **C** T A **G** T C T A A **T** A C A G **C** T

Individual 4  
 T A C T T C **T** C C G C G **G** T T A C T C T A A G A C A G G T

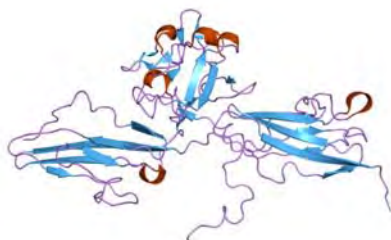
## How to estimate rates of mutation?

Count # of offspring that have observable mutant phenotypes

Knock-out / Loss-of-function **mutations**

## Achondroplasia

- Dwarfism
- Mutation in Fibroblast growth factor receptor 3 (FGFR3)





## Hemophilia A

- Impaired blood-clotting
- Mutation in clotting factor VIII
- 30 % of cases caused by new mutations



- Loss-of-function mutations inactivate genes
- Underestimate of actual mutation rate
- Silent mutations & replacement substitutions: more subtle effects
- Not detected when assessing phenotypes!!

How to estimate rates of mutation?

## Pattern discovered

- mutation rates scaled for generation time
- per-genome basis
- bacteria, archaea, fungi, plants, animals
- ...all roughly the same mutation rates
- mutation rate per cell division approx. equal

**Hypothesis:** Natural selection led to a single, common mutation rate.



ROUNDWORM *C. ELEGANS*

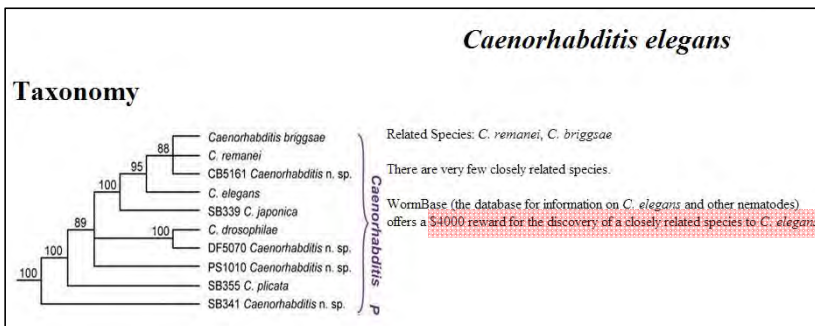
# CASE STUDY

## Biology of *Caenorhabditis elegans*

- nematode
- approx. 1 mm in length
- female & male gonads: self-fertilize
- live in temperate soil environments
- first multicellular organisms to have full genome sequenced

ROUNDWORM *C. ELEGANS*

## *Caenorhabditis elegans*



ROUNDWORM *C. ELEGANS*

<http://www.easternct.edu/~adams/C.eleganstaxonomy.html>

## Methods

- Denver et al. challenged hypothesis
- Started work with single individual
- Established many independent lines from single individual
- Each line maintained at optimal conditions
- **Minimize** impact of **natural selection**
- **Maximize** probability that every **mutation** is passed on regardless of fitness impact
- Sequenced DNA from starting individual and from individuals from over 50 family lines

ROUNDWORM C. ELEGANS

## Results: *nuclear genome*

- 30 mutations
- more than ½ indels (small numbers of bases inserted/deleted from genome)
- $2.1 \times 10^{-8}$  mutations per site per generation
- every worm carries average of 2.1 new mutations
- This is a LOT!
- Supports notion that mutation introduces a lot of genetic variation into population each generation

ROUNDWORM C. ELEGANS

## Results: *mitochondria*

- 26 mutations
- 16 base mutations: 13 transitions, 3 transversions
- 10 indels
- $1.5 \times 10^{-7}$  mutations per site per generation
- order of magnitude higher than for nuclear genome
- fewer errors repaired: mitochondria lack DNA repair enzymes (found in nucleus)

ROUNDWORM C. ELEGANS

**Hypothesis:** Natural selection led to a single, common mutation rate.

## What you should know about mutation

- Mutation rates vary **among genes**, even regions **within genes**
- Mutation rates can be **affected by environmental factors** (mutagens)
- Mutation in master control genes → regulate expression of other genes in developmental pathway
- Most mutations are pleiotropic → affect more than one character

## What you should know about mutation

- Mutation is **not evolution**
- Mutation alone does not cause character states to evolve from one state to another → **rate is too low**
- Mutation may alter one or more phenotypic characters that affect survival and/or reproduction → **fitness**

## What you should know about mutation

- Evolution would not occur unless some mutations were **advantageous**
- Mutations with phenotypic effects alter developmental processes but cannot alter developmental **foundations** that don't exist
- The supply of rare mutations might **limit** capacity of a species for adaptation

**Mutation** is the **ultimate source of variation.**

But usually too slow to cause evolution by itself.



EVOLUTION IN A BIG CITY

CASE STUDY

## Mechanisms of evolution

**Gene flow (Migration)**

**Mutation**

**Natural selection**

**Non-random mating**

**Genetic drift**



## Mechanisms of evolution

Gene flow (Migration)

Mutation

Natural selection

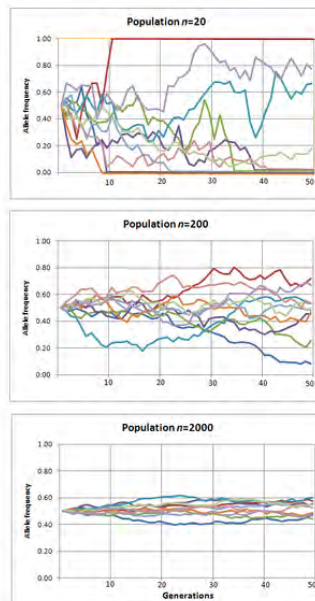
Non-random mating

**Genetic drift**

## GENETIC DRIFT

random fluctuations in allele frequencies

## Genetic drift



## Genetic drift

- Genetic drift and inbreeding are related

- ***Inbreeding:***

homozygotes



heterozygotes



## Heterozygosity

- As an allele approaches 1.0
- frequency of heterozygotes declines
- **rate of decline of heterozygosity** often used as measurement of genetic drift in population
- **expected vs. observed heterozygosity**

**All individuals in a population are**  
breeding adults.

**= census size**

All individuals in a population are

**breeding adults.**

**= effective population size**

**effective population size  $<$  census size**

- Variation in number of progeny
- Sex ratio
- Natural selection
- Overlapping generations
- Fluctuations in population size

## Northern elephant seals (*Mirounga angustirostris*)

- Large males compete for smaller females
- Only a few successful: harems (30-100 females)



## Founder effect

- bottleneck population needs to pass through
- new colonists established by single pair (or more)
- if population persists and grows large, new mutations will eventually restore higher heterozygosity levels
- but in beginning allele frequencies similar to source population

## Northern elephant seals: **bottleneck**

- harvested for oil
- down to 20-100 individuals in 19<sup>th</sup> century (Guadalupe)
- current population = 175,000
- no allelic variation in 24 genes



©Alex Wild

ARGENTINE ANTS

# CASE STUDY

## Biology

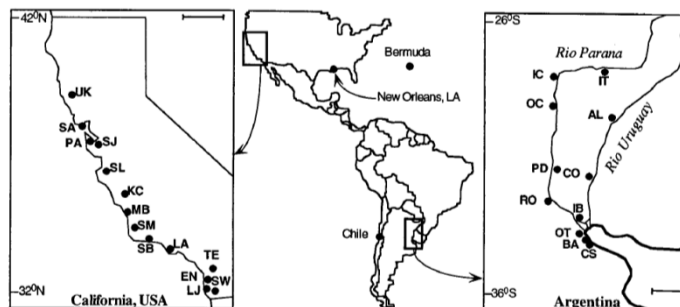
- *Linepithema humile*
- small: ca. 3 mm
- smells like blue cheese
- tend to aphids and scale insects
- native to northern Argentina
- invasive almost worldwide
- form supercolonies



ARGENTINE ANTS

## Methods

- Collected samples from native and introduced range



Tsutsui et al. 2000

ARGENTINE ANTS

## Methods

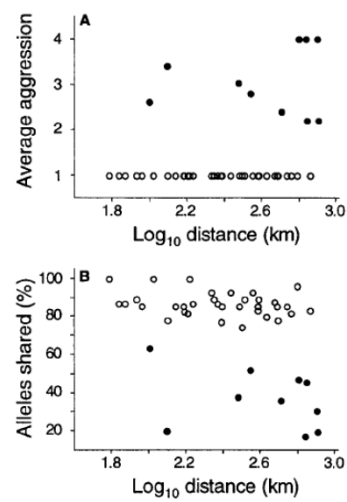
- Conducted aggression assays
- DNA sequencing: 4 microsatellite loci



Tsutsui et al. 2000, Photo by A. Wild

ARGENTINE ANTS

## Results



Tsutsui et al. 2000

ARGENTINE ANTS



## Results

Table 1. The expected heterozygosity ( $H_{exp}$ ) and number of alleles at seven microsatellite loci for native (Argentina) and introduced (California) populations

Locus	Argentina ( $n = 255$ )		California ( $n = 460$ )	
	$H_{exp}$	No. of alleles	$H_{exp}$	No. of alleles
Lhum-11/11B	0.851	15	0.726	11
Lhum-14	0.430	3	0.058	3
Lhum-33	0.611	9	0.093	3
Lihu C1.1	0.654	5	0.121	2
Lihu M1	0.642	8	0.073	3
Lihu S3	0.465	6	0.160	3
Lihu T1	0.821	13	0.199	5
Mean (SE)	0.639 (0.060)	59	0.204 (0.089)	30

Tsutsui et al. 2000

ARGENTINE ANTS

## Results

- genetic bottleneck during introduction to CA
- # of alleles in introduced range is half of that in native range
- average expected heterozygosity in CA decreased by 68 % relative to native range

Tsutsui et al. 2000

ARGENTINE ANTS

## Supercolony in Europe



ARGENTINE ANTS

## What you should know about genetic drift

- Genetic drift is a **major** factor in evolution
- Rate of **decline in heterozygosity** often used as measure of genetic drift
- Allele just arisen by mutation is more likely to be **fixed** in **small** than in large population
- Evolution by genetic drift proceeds **faster** in **small** than in large populations

## SUMMARY



1. What was the most important thing you learned during this class?
2. What important question regarding what you learned remains unanswered for you? (What would you like to know about next?)

# SUMMARY

NAME & DATE  
2/10/2014

For next week:

*The Beak of the Finch*: Read Chapter 7 & 8

**Read paper (will be posted)**

*Homework due Feb-14 (Fri) 5pm*