

### The use and implications of genetics in border security and invasive ant management



Phil Lester

School of Biological Sciences  
Victoria University of Wellington



### Ant genetics

- Talk aims:
  - Convince you that ant population genetics is a useful tool for biosecurity or invasive ant management.
  - Give you some examples of from my laboratory group & that of others.
- Working up from the ground floor (I'm assuming varying knowledge).



### DNA (Deoxyribonucleic acid)

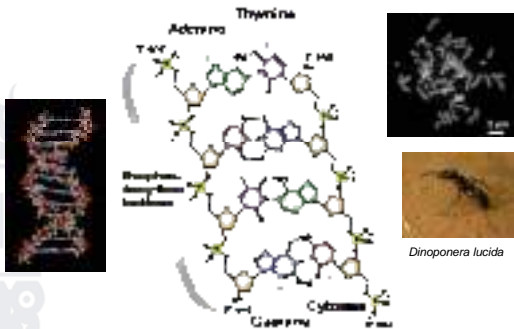
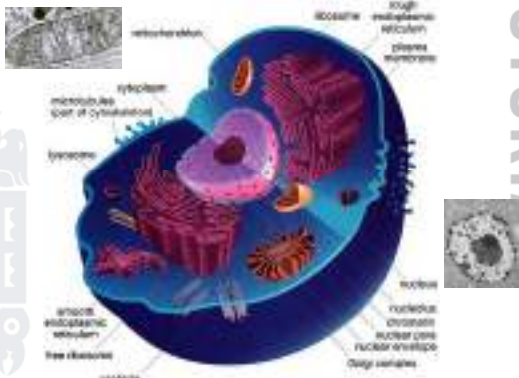


FIG. 1—Ergatanidromorph of *Myrmecia galiois*. Notice the large left worker mandible and the remains of male wings on the right. Length about 2 cm. (Photo by D. P. Masland)

From Crosland et al. 1988 (J Aus Ent Soc 27: 305)

### Cells have two sources of DNA



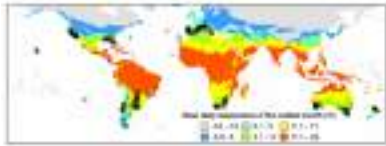
### Determining the origin of invasive species



Argentine ants (*Linepithema humile*)

Case study: How did Argentine ants get to NZ?

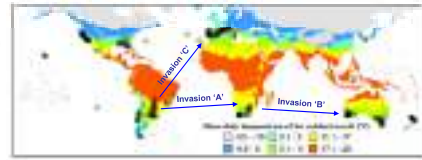
- Argentine ants have a world wide distribution.
- Known to show variation in the mitochondrial DNA gene, cytochrome b.
  - Mitochondrial analyses are especially useful for inferring "commonality by descent".



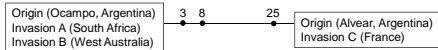
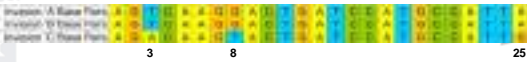
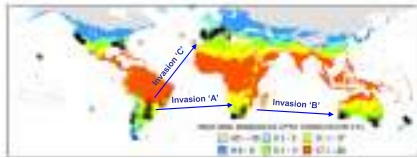
Hartley, Harris & Lester 2006. Ecology Letters 9: 1086

Multiple invasions out of South America

- Because Argentine ants are known to have moved out of their wide South American range on multiple occasions....
  - We can start to reconstruct invasion pathways.



Multiple invasions out of South America



TCS analysis

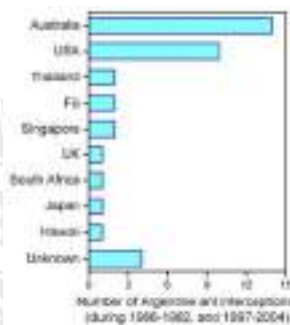
Network analysis

- TCS collapses identical haplotypes and calculates the probability of parsimony.
- Minimum connections are made in TCS using a 95% confidence assessment.
- Australia a likely origin.



Corin, Lester, Abbott & Ritchie (2007) Diversity & Distributions 13: 510-518

The NZ interception record



- **Management implications:**
  - It is all Australia's fault!!!
  - This method could define entry pathways prior to pest establishment.

Determining if multiple invasions have occurred

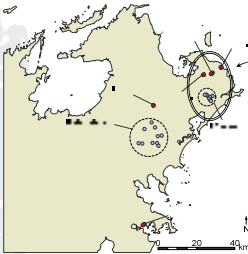


The yellow crazy ant (*Anoplolepis gracilipes*)



### Pairwise $F_{ST}$ : structure varies in north and south

- Fixation index ( $F_{ST}$ ) is a measure of population differentiation. Compares the genetic variability within and between populations.



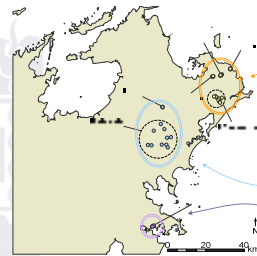
Pairwise  $F_{ST}$  values ranged from 0.0 to 0.1

Northern colonies: no significant differences except Yirrkala – Dhupuma ( $P < 0.05$ )

All other pairwise comparisons significantly different ( $P < 0.001$ )

### BAPS mixture: three genetic clusters

- BAPS: implements a stochastic optimization algorithm to infer the genetic structure.

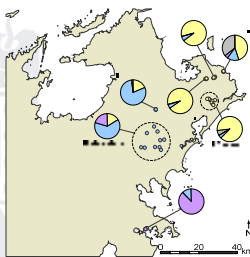


Mixture analysis grouped populations into clusters:

1. Yirrkala, Airfield, Powerline, Dhupuma,
2. Mainroad, Balkbalkpuy,
3. Gurrkawuy.

### BAPS admixture: three genetic clusters

- Admixture analysis reveals ancestral sources of alleles.



Potentially one invasion with genotypes spreading North and South, (idea supported by mitochondrial DNA).

**Biosecurity implications...**

Microsatellites might help find patterns better than mitochondrial DNA.

### ECOLOGICAL QUESTIONS WE CAN ASK WITH GENETICS & MICROSATELLITES

**Which population did these individuals originate from?  
How many populations are there?**

**Did the population expand or contract in the recent past?**  
Do populations differ in past and present size?

**What are the genetic relationships of individuals?**  
Which individuals have moved? (i.e. mark/recapture natural tags)  
Which individuals are clones?

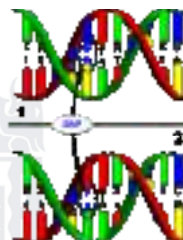
**What is the average dispersal distance of offspring (or gametes)?**  
What are the source–sink relationships among populations?  
How do landscape features impact population structure and migration?  
What are the extinction/recolonization dynamics of the metapopulation?  
**Did the population structure or connectivity change in the recent past?**

### New techniques: SNP data and next generation sequencing



Green tree ant (*Oecophylla smaragdina*)

### Identifying genes under selection



- Next generation sequencers & SNPs (single-nucleotide polymorphisms).
  - variations in DNA sequence that can show major impacts on how animals respond to disease, environmental factors, toxins, and chemicals, etc.
  - We can use SNPs to examine for genes under selection and evolution in a population.



### Identifying genes under selection

- For example: Guppies in Trinidad
  - Evidence that predation is driving selection on genetic markers associated with ornamental traits.

Willing et al. (2010) *Molecular Ecology* 19: 968



- For example: Sunflower downy mildew
  - Evidence for 14 different introduction events, providing raw material for new races.

Delmotte et al. (2008) *Infection, Genetics and Evolution* 8: 534



### Collaborators...

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