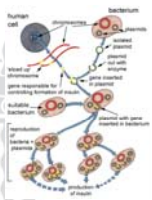
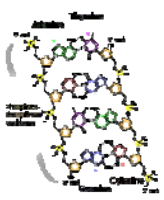
The use and implications of genetics in border security and invasive ant management



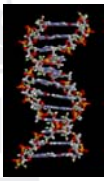
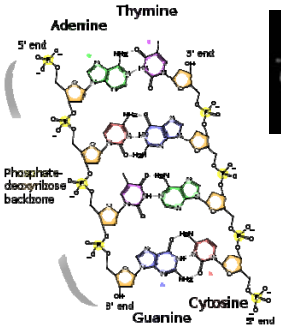


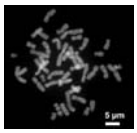
Phil Lester
School of Biological Sciences
Victoria University of Wellington

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)




Dinoponera lucida

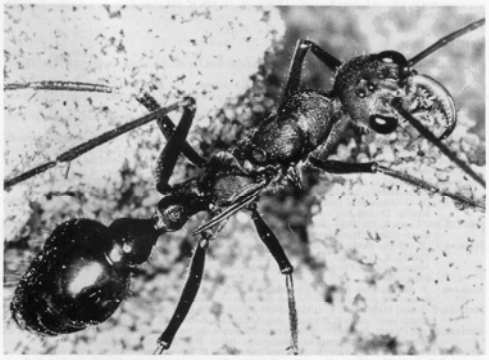
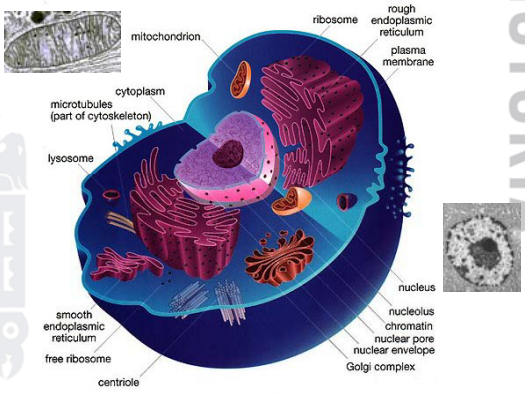


FIG. 1—Ergatandromorph of *Myrmecia gulosa* Notice the large left worker mandible and the remains of male wings on the right Length about 2 cm (Photo by D P Maitland)

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

Cells have two sources of DNA

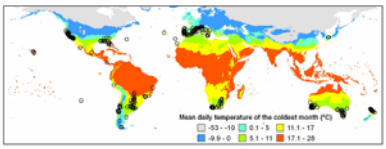


Determining the origin of invasive species

Argentine ants (*Linepithema humile*)

Case study: How did Argentine ants get to NZ?

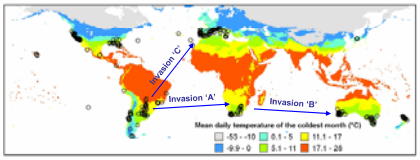
- Argentine ants have a world wide distribution.
- Known to show variation in the mitochondrial DNA gene, cytochrome b.
  - Mitochondrial analyses are especially useful for inferring “commonality by descent”.



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

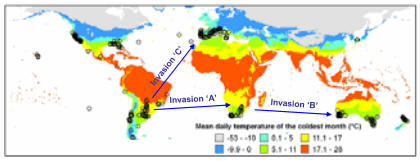
Multiple invasions out of South America

- 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.



Invasion 'A' Base Pairs	A	G	T	C	A	A	G	G	A	C	T	G	A	T	C	C	A	T	G	C	C	A	T	T	A
Invasion 'B' Base Pairs	A	G	T	C	A	A	G	G	A	C	T	G	A	T	C	C	A	T	G	C	C	A	T	T	A
Invasion 'C' Base Pairs	A	G	A	C	A	A	G	T	A	C	T	G	A	T	C	C	A	T	G	C	C	A	T	T	G

Multiple invasions out of South America



Invasion 'A' Base Pairs	A	G	T	C	A	A	G	G	A	C	T	G	A	T	C	C	A	T	G	C	C	A	T	T	A
Invasion 'B' Base Pairs	A	G	T	C	A	A	G	G	A	C	T	G	A	T	C	C	A	T	G	C	C	A	T	T	A
Invasion 'C' Base Pairs	A	G	A	C	A	A	G	T	A	C	T	G	A	T	C	C	A	T	G	C	C	A	T	T	G
			3					8																	25

Origin (Ocampo, Argentina)
Invasion A (South Africa)
Invasion B (West Australia)

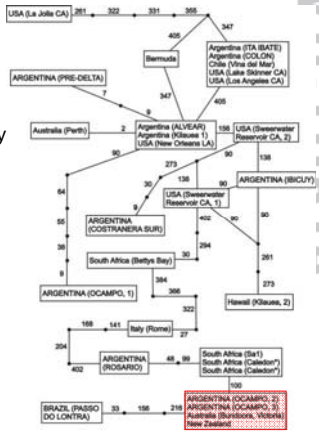
3 8 25

Origin (Alvear, Argentina)
Invasion C (France)

TCS analysis

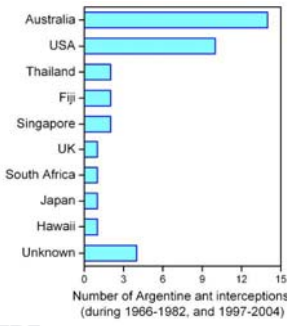
Network analysis

- 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

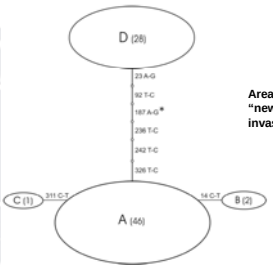
The yellow crazy ant (*Anoplolepis gracilipes*)

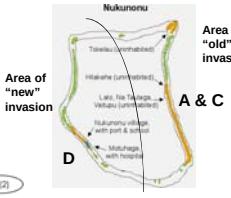
Case study: Multiple invasions of yellow crazy ants, with haplotype specific effects?

- Sudden, massive populations of yellow crazy ants on Tokelau... why?

Two major distinct haplotypes [~ mitochondrial genotypes] identified

- Population genetics examined using 460 bp of the mitochondrial locus cytochrome b.





Abbott, Greaves, Ritchie & Lester (2007) Biol. Invasions 9: 453-463.

Haplotype effects & management implications

- **Haplotype effects:**
  - Islands with the "old" haplotype had 15 co-occurring species & a yellow crazy density of ~35 per trap.
  - Islands with the "new" haplotype had 7 co-occurring species & a yellow crazy density of ~243 per trap.

Haplotype effects & management implications

- **Haplotype effects:**
  - Islands with the "old" haplotype had 15 co-occurring species & a yellow crazy density of ~35 per trap.
  - Islands with the "new" haplotype had 7 co-occurring species & a yellow crazy density of ~243 per trap.
- **Management implications**
  - Different haplotypes of the same species might have different effects?
  - Even if you have a pest, keep other genes of the same pest out!

Determining if multiple invasions have occurred & the role of genetic diversity

The yellow crazy ant (*Anoplolepis gracilipes*)

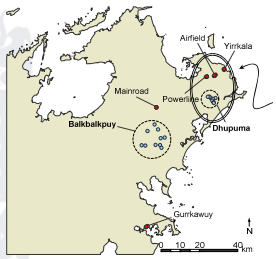
Case study: Using Nuclear DNA micosatellites to infer invasion history & population structure

- Yellow crazy ants occur in high-densities & low-densities.
  - No mitochondrial variation.
  - Is there reduced genetic diversity within aggregated colonies?
- What does population structuring reveal about invasion history?

Several microsatellites are used in any one study

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.



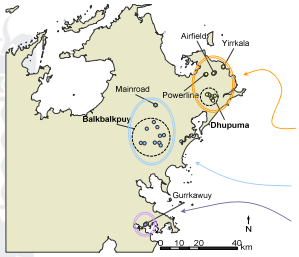
Pairwise F_{ST} values ranged from 0.0 to 0.1

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.

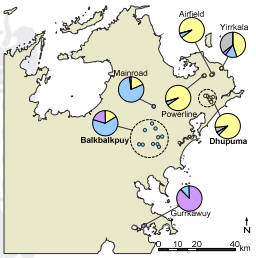


Mixture analysis grouped populations into clusters:

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

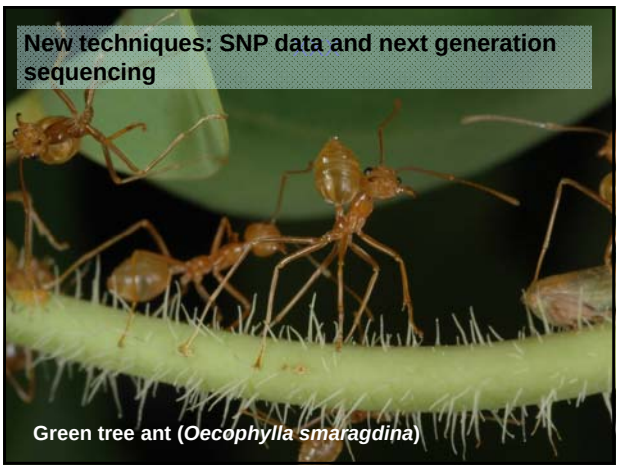
Which population did these individuals originate from?
How many populations are there?

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?

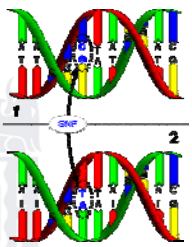
What is the average dispersal distance of offspring (or gametes)?
What are the source–sink relationships among populations?
How do landscape features impact population structure and migration?
What are the extinction/recolonization dynamics of the metapopulation?
Did the population structure or connectivity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