

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



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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)

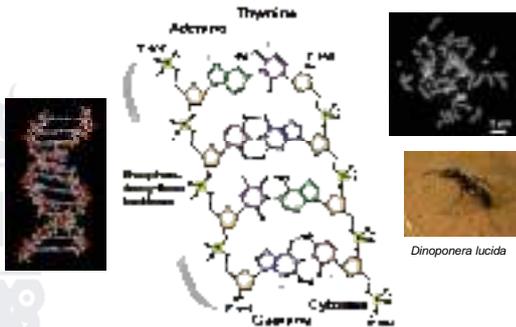
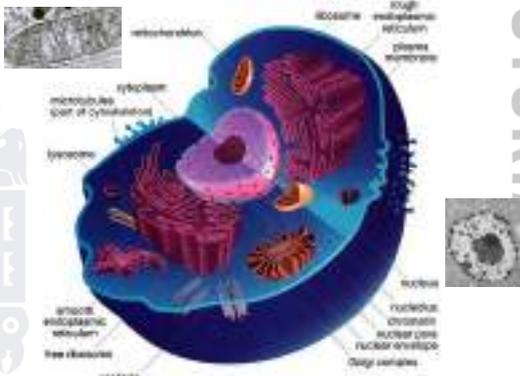


FIG. 1—Ergatanid morph of *Myrmecia gulosa*. Notice the large left worker mandible and the remains of male wings on the right. Length about 2 cm. (Photo by D. P. Maistland)

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

Cells have two sources of DNA



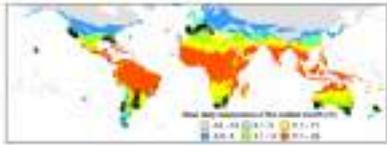
Determining the origin of invasive species



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”.



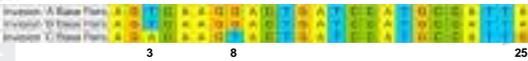
Hartley, Harris & Lester 2006. Ecology Letters 9: 1086

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.



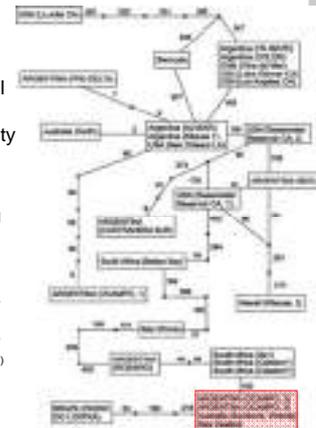
Multiple invasions out of South America



TCS analysis

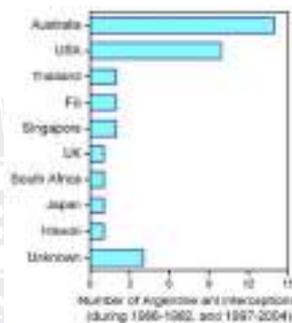
Network analysis

- 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.

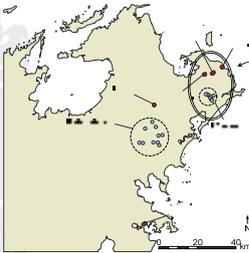
Determining if multiple invasions have occurred



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.



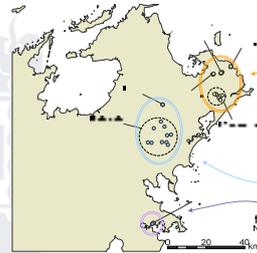
Pairwise F_{ST} values ranged from 0.0 to 0.1

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.

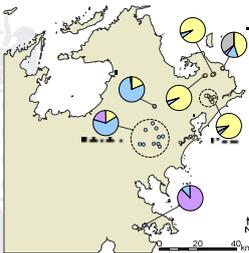


Mixture analysis grouped populations into clusters:

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?

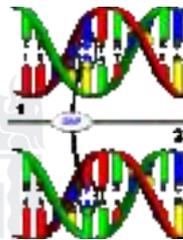
What is the average dispersal distance of offspring (or gametes)?
What are the source-sink relationships among populations?
How do landscape features impact population structure and migration?
What are the extinction/recolonization dynamics of the metapopulation?
Did the population structure or connectivity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

Kirsti Abbott, Ben Hoffman, Monica Gruber, Steph Chapple, Alice McNatty, Megan Sarty, Peter Ritchie, Alapati Tavite & many others.



Funding...

Royal Society of NZ Marsden Fund, Pacific Development and Conservation Trust, National Geographic, Conservation International, Victoria University of Wellington.

