

Assessing the potential of microsatellite markers
to infer origin and movements of locust swarms:
the case studies of *L. migratoria* in Madagascar
and *C. terminifera* in Australia

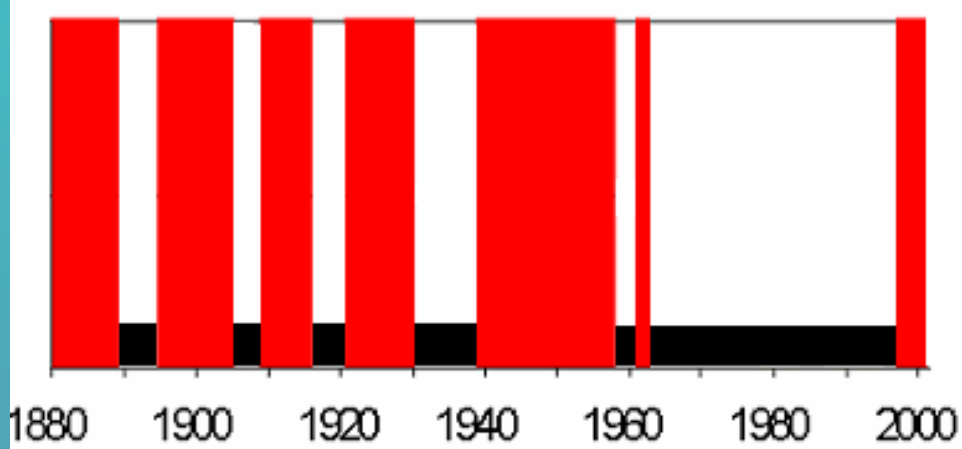
Chapuis MP, Loiseau A, Popple JA, Michalakakis Y, Lecoq M, Franc A,
McCulloch L, Simpson S, Estoup AE, Sword G



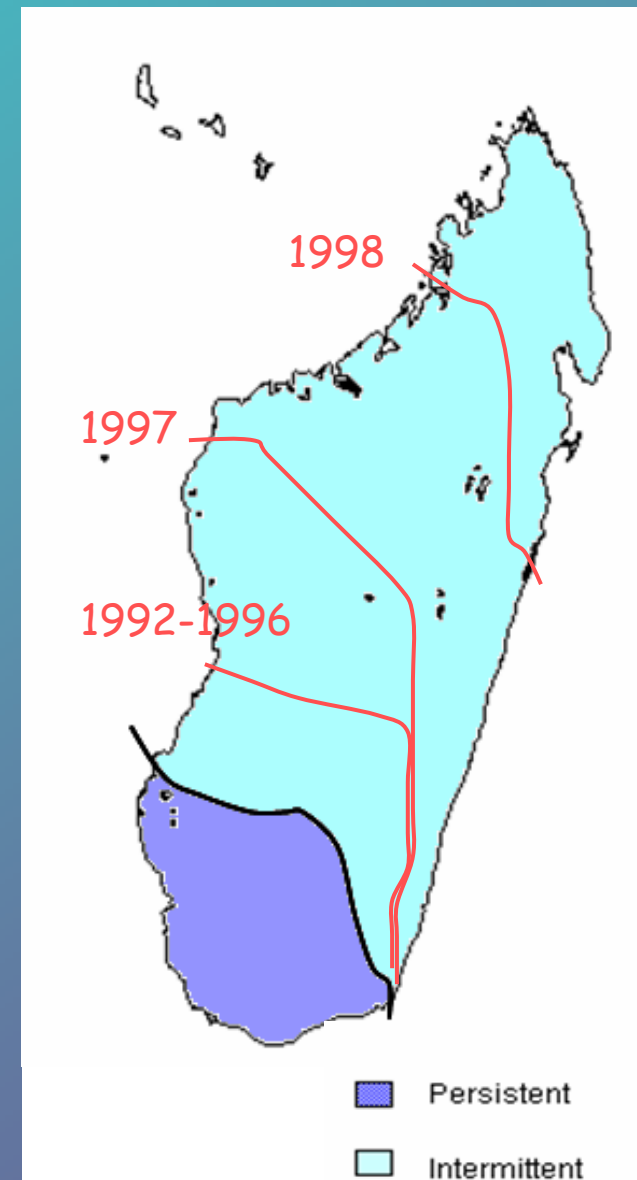
The University of Sydney



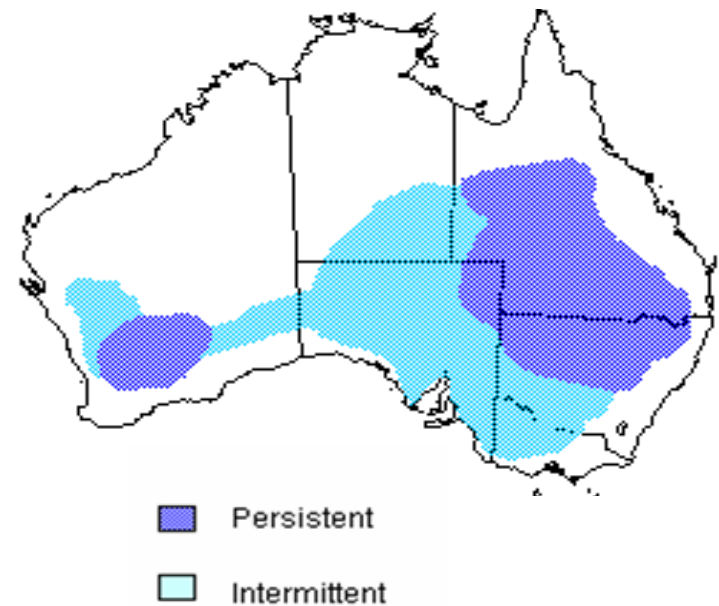
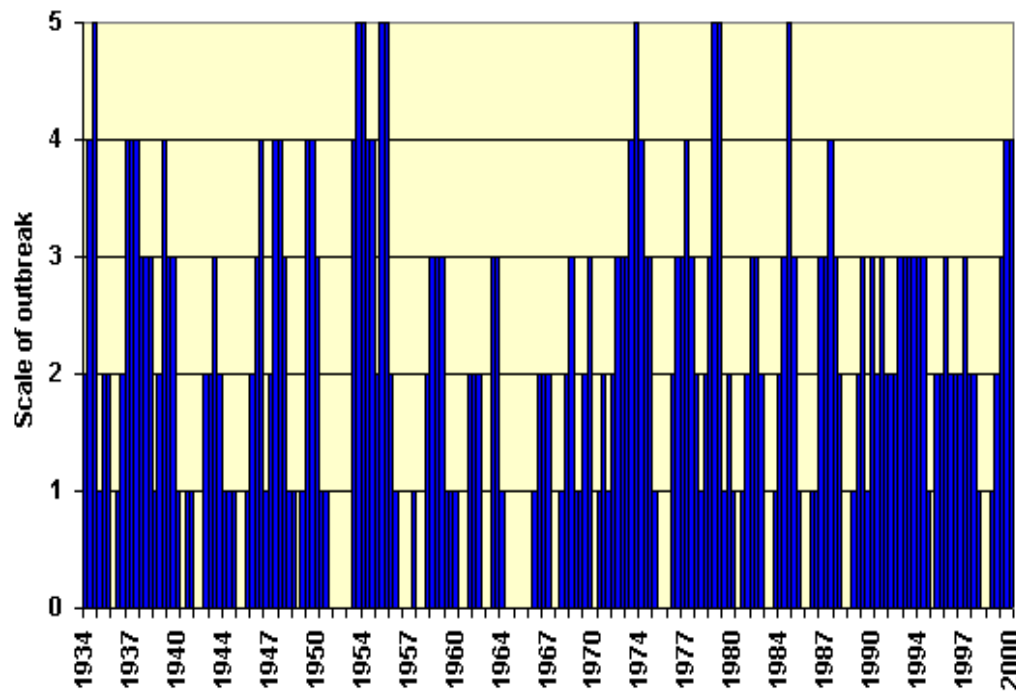
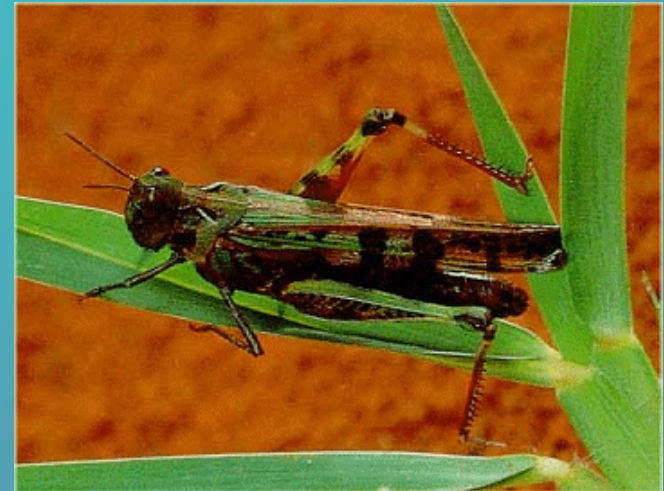
Locusta migratoria in Madagascar



Remissions : 1-100 individuals/hectare



Chortoicetes terminifera in Australia



Preventative control strategy

Malagasy National Anti-Locust Center (CNA)

Australian Plague Locust Commission (APLC)

- monitoring locust populations (locust surveys and light trap information)
- forecasting (meteorological, habitat, and density data)
- early controls (chemical and biological)
- research

Need for a better understanding of the spatial population dynamics in the early outbreak stage

- limits of direct ecological approaches because of the great dispersal ability of locusts
- population genetics may be an useful alternative

WHAT IS THE POTENTIAL OF APPLICATION OF POPULATION GENETICS TO THE MANAGEMENT OF SWARMING LOCUSTS?

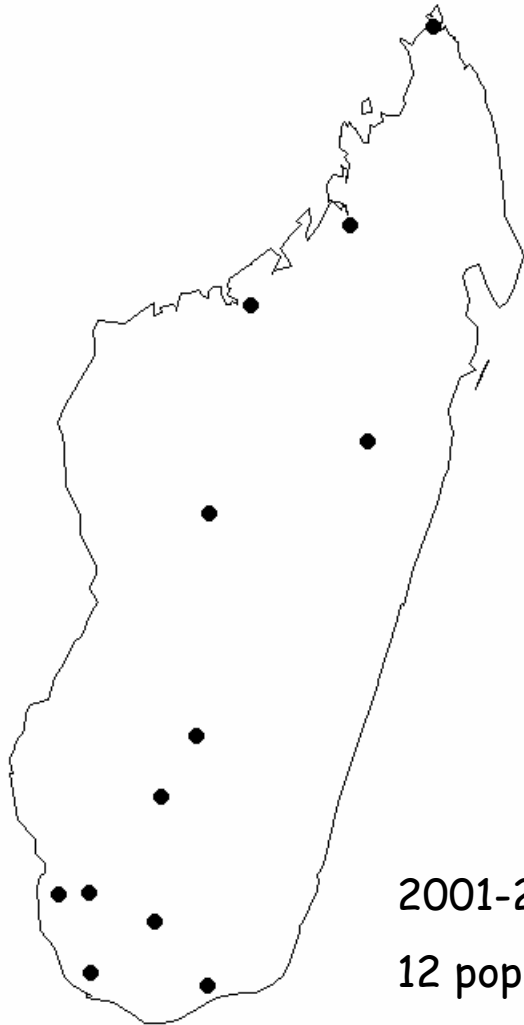
The genetic approaches might lack resolution for low genetic differentiation among populations

- **Demographic effect** = outbreeding populations experience demographic flushes

- large number of effective migrants

- **Behavioural effect** = outbreeding insects travel together in migratory bands of nymphs and fly large distances in swarms of adults

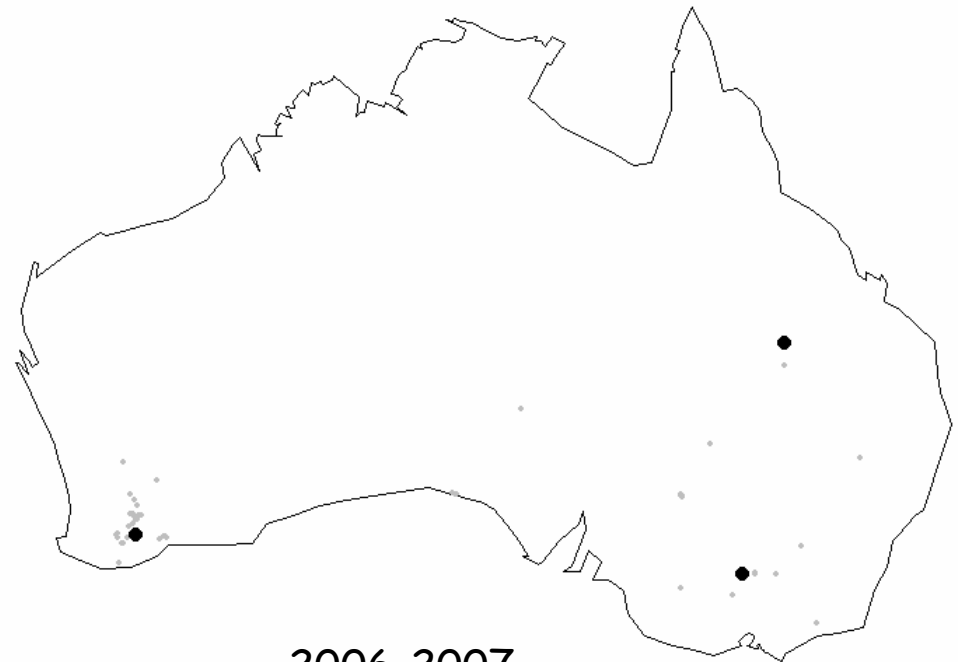
- large effective migration rate and distance

L. migratoria in Madagascar

2001-2004

12 populations

14 loci

C. terminifera in Australia

2006-2007

> 50 populations

10 loci

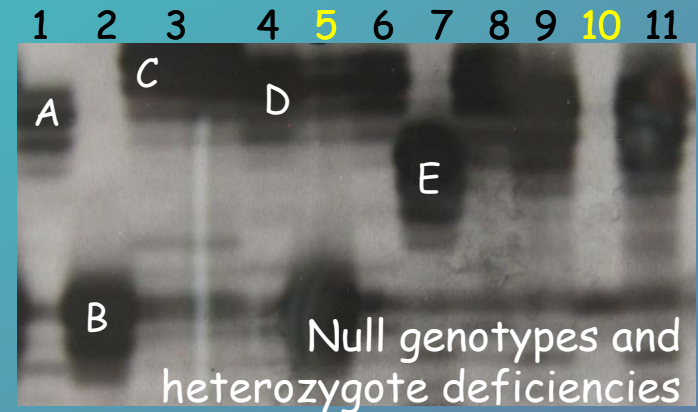
Presence of null alleles

L. migratoria in Madagascar →

from 32 loci, 47% excluded by pre-testing
from 14 remaining loci, 13% of null alleles

C. terminifera in Australia →

from 33 loci, 59% excluded by pre-testing
from 10 remaining loci, 22% of null alleles



binding site 1

Repeat region

binding site 2

5'TGTAAACGACGGCCAGTGAT...(GT)_n... AATGTAGGAGGATTTAGCCT3'

← X || |||||

3'TTTCATCCTCCTAAATCGGA5'

Allele not amplified (null)

primer

Presence of null alleles - HOW DO I ANALYSE DATA?

- Null alleles bias
- Efficiency of the method for correcting genotype datasets

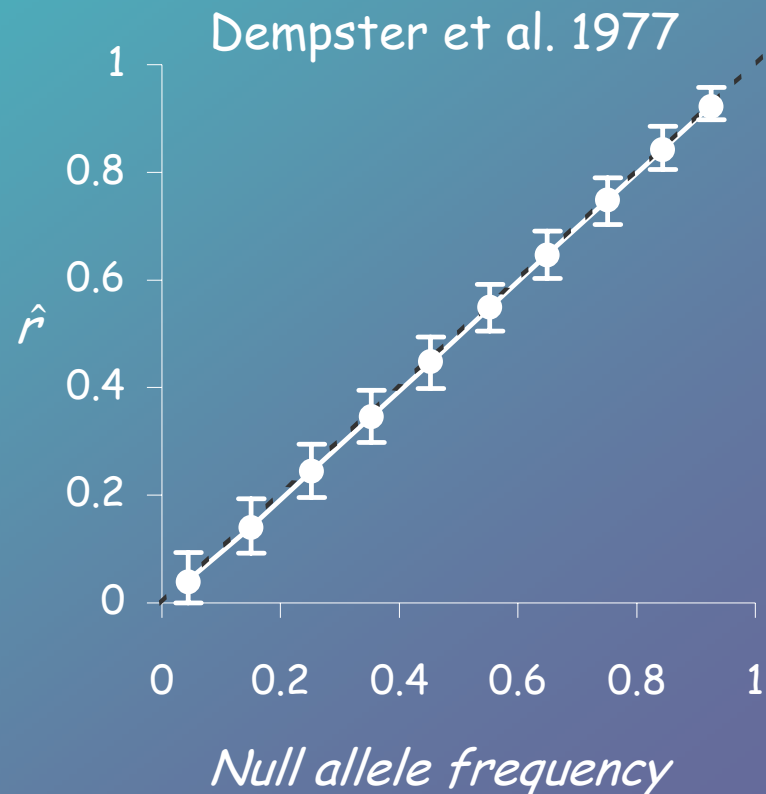
INA correction →

Estimating null allele
frequency \hat{r}



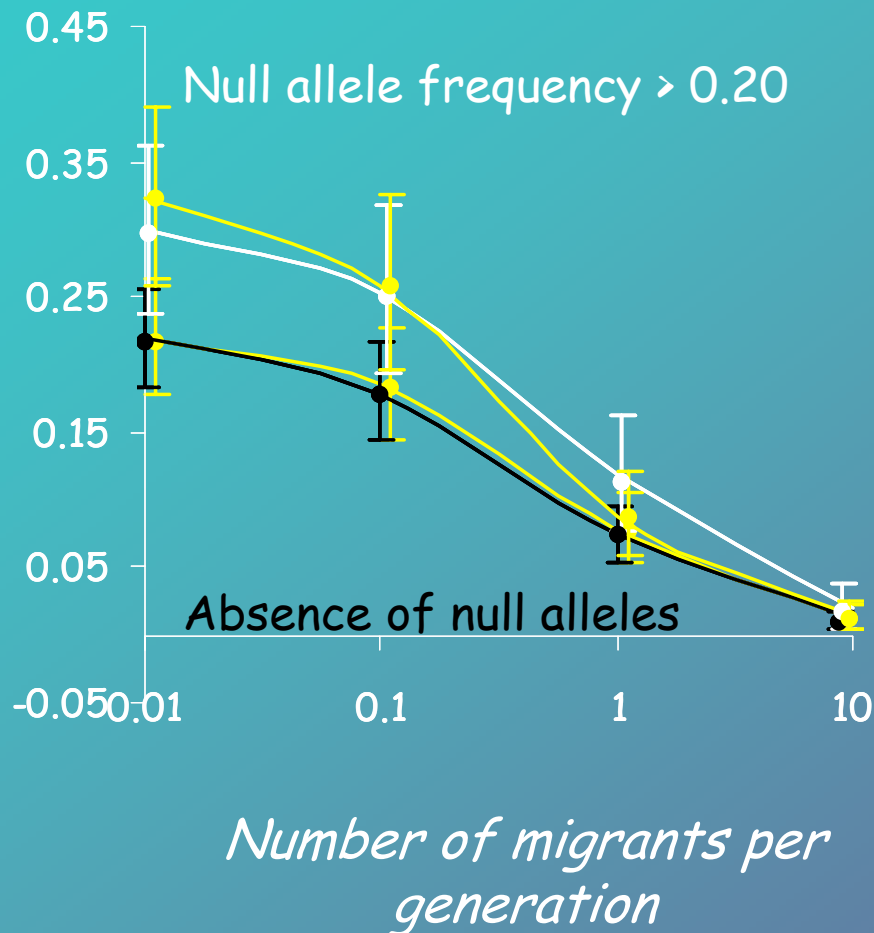
Allocating a single new allele
state common to all
genotyped populations

Adjusting allele and genotype
frequencies based on \hat{r}



Presence of null alleles

Traditionally used estimator of genetic variation among populations

 F_{ST} (Weir 1996)

INA correction

ENA correction

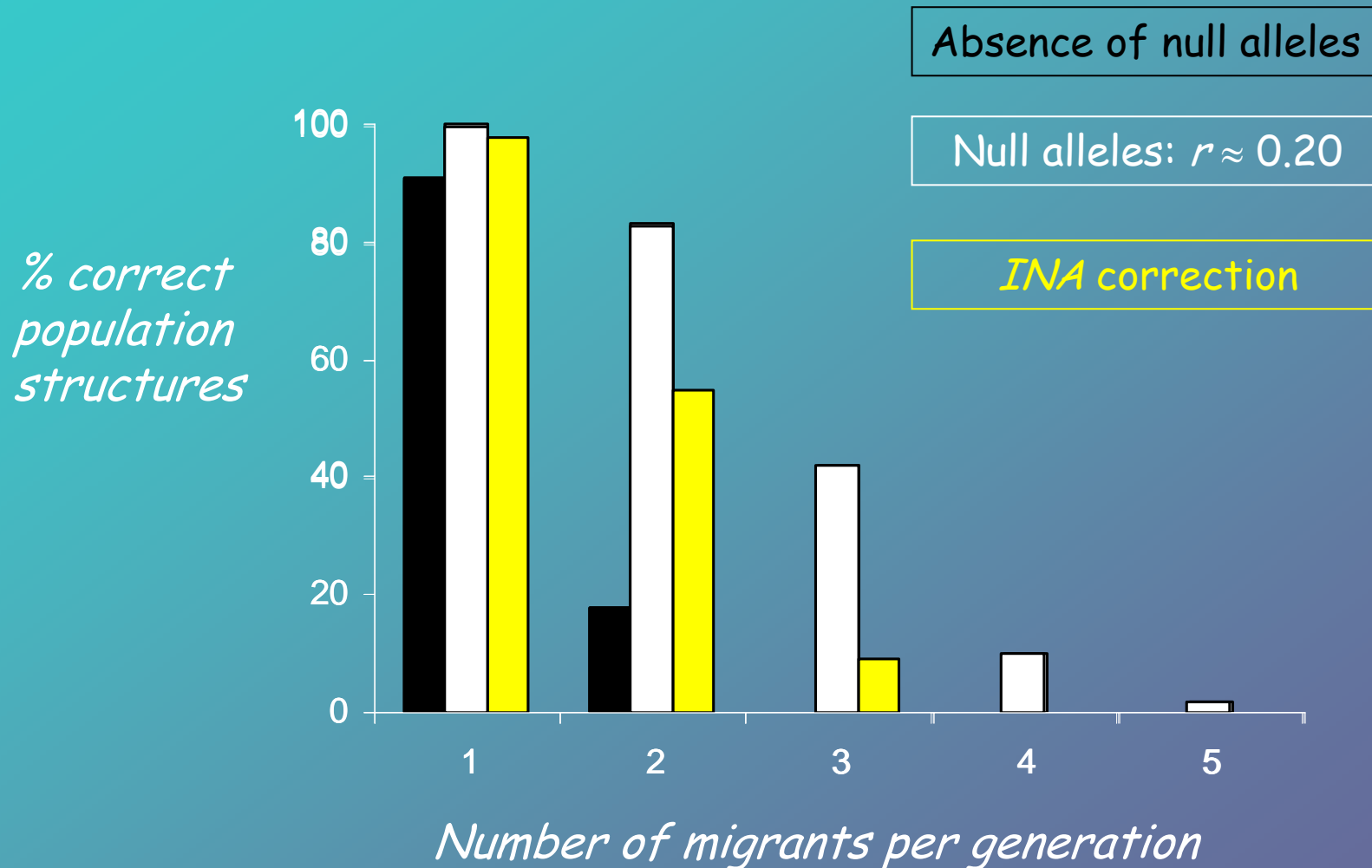
Estimating F_{ST} by excluding null allele state

→ FreeNA software

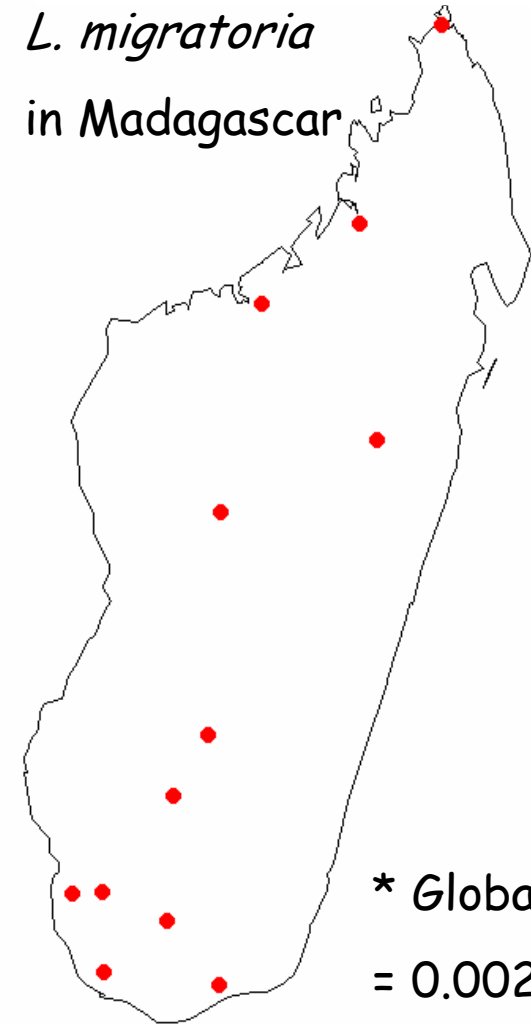
<http://www.montpellier.inra.fr/URLB/>

Presence of null alleles

Delineating clusters of population samples: *BAPS* (Corander *et al.* 2003)



L. migratoria
in Madagascar

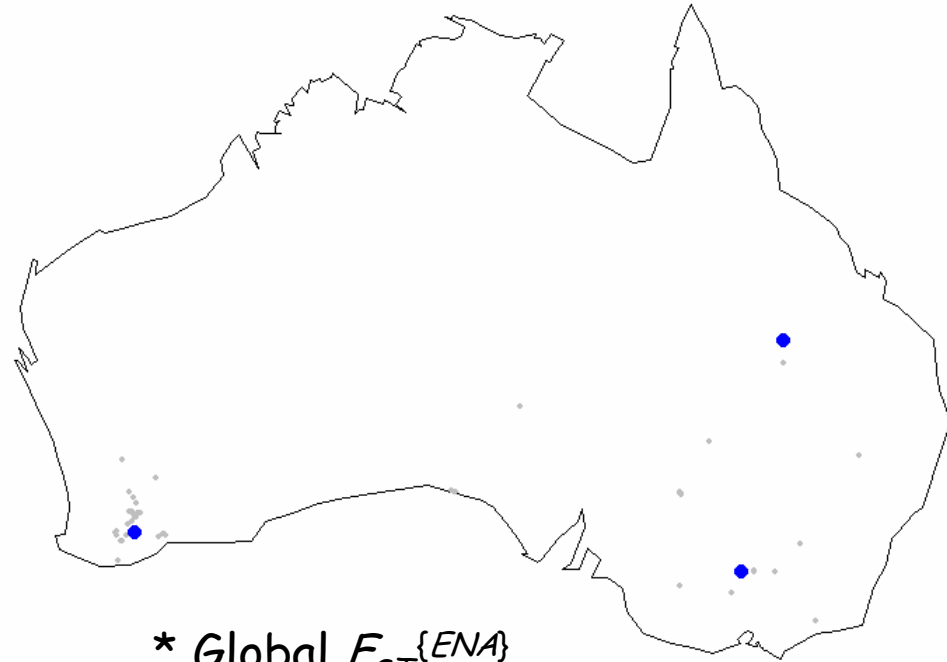


* Global $F_{ST}^{\{ENA\}}$
= 0.002 [0.000 - 0.004]

* A single genetic cluster of populations

* Global and pairwise tests of genotypic differentiation all non significant

C. terminifera in Australia

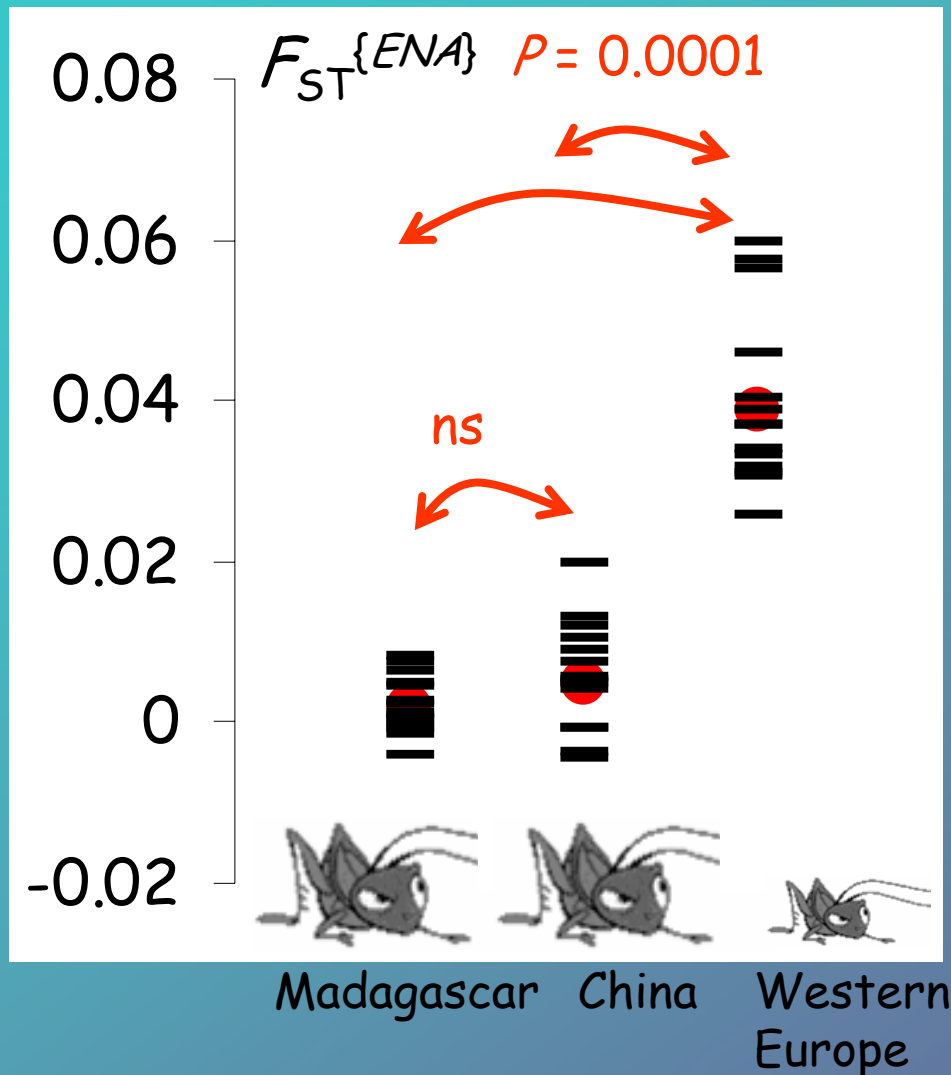


* Global $F_{ST}^{\{ENA\}}$
= 0.001 [-0.002 - 0.004]

* A single genetic cluster of populations

Comparative study in *L. migratoria*

→ absence or low levels of genetic differentiation are partly associated with outbreaks



Homogenizing effect of outbreaks at a wide scale

→ Lack of resolution to detect migrants and infer their origin

Perspectives

→ integrating other type of data, such as demographic, behavioural, or environmental data

→ use of genetic linkage disequilibrium information
(e.g. Bayesian methods of Gaggiotti et al. 2002, 2004)

Thank you for your attention