

# Otters & Genetics

- *Taxonomy*
- *DNA typing from spraints*

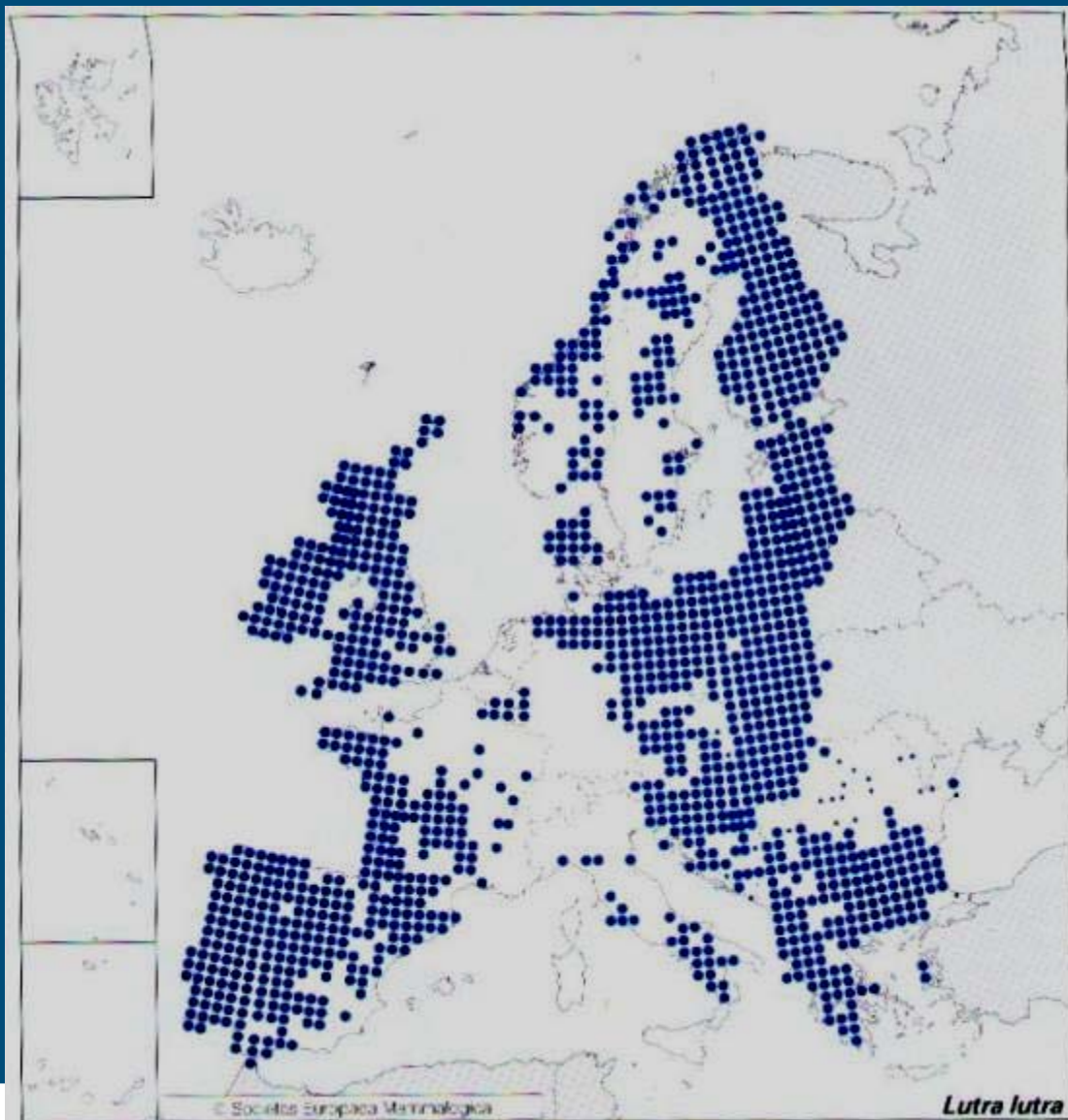


*Alterra, Centre for Ecosystems*

Hugh Jansman

Hans Peter Koelewijn

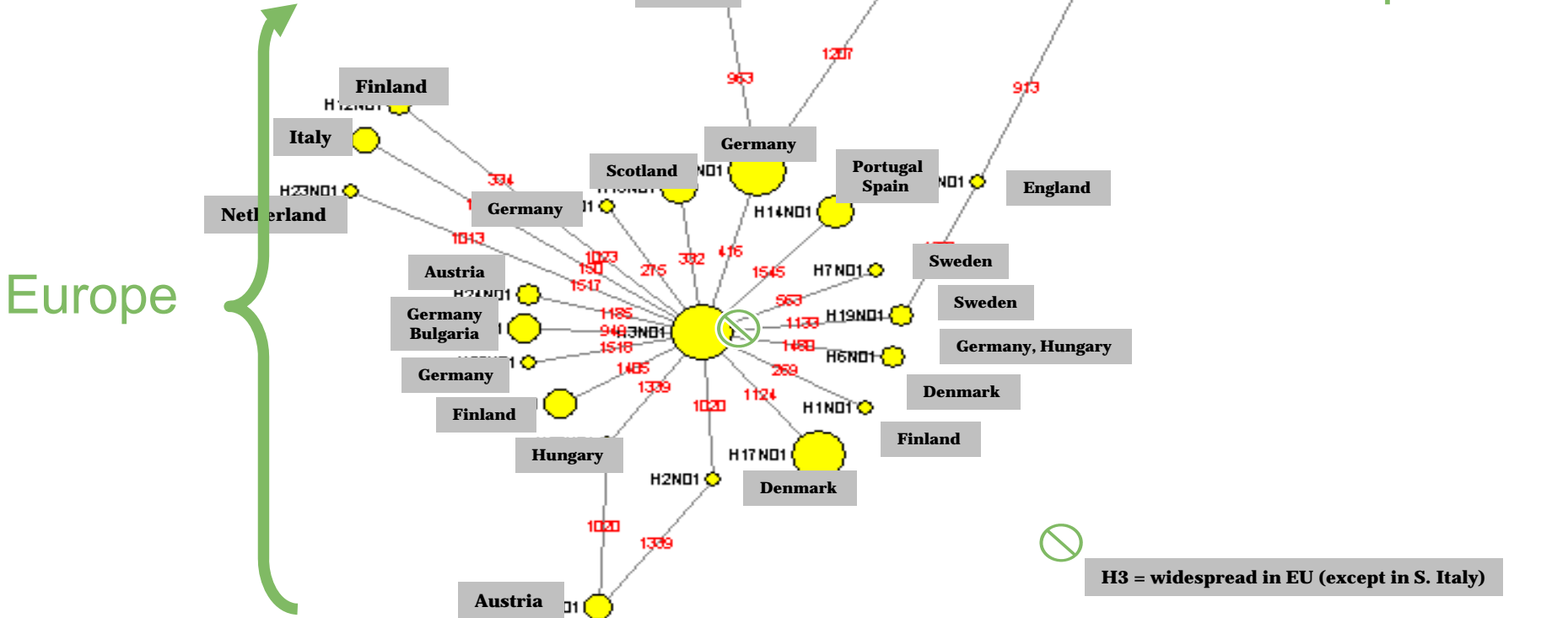
# Distribution otters



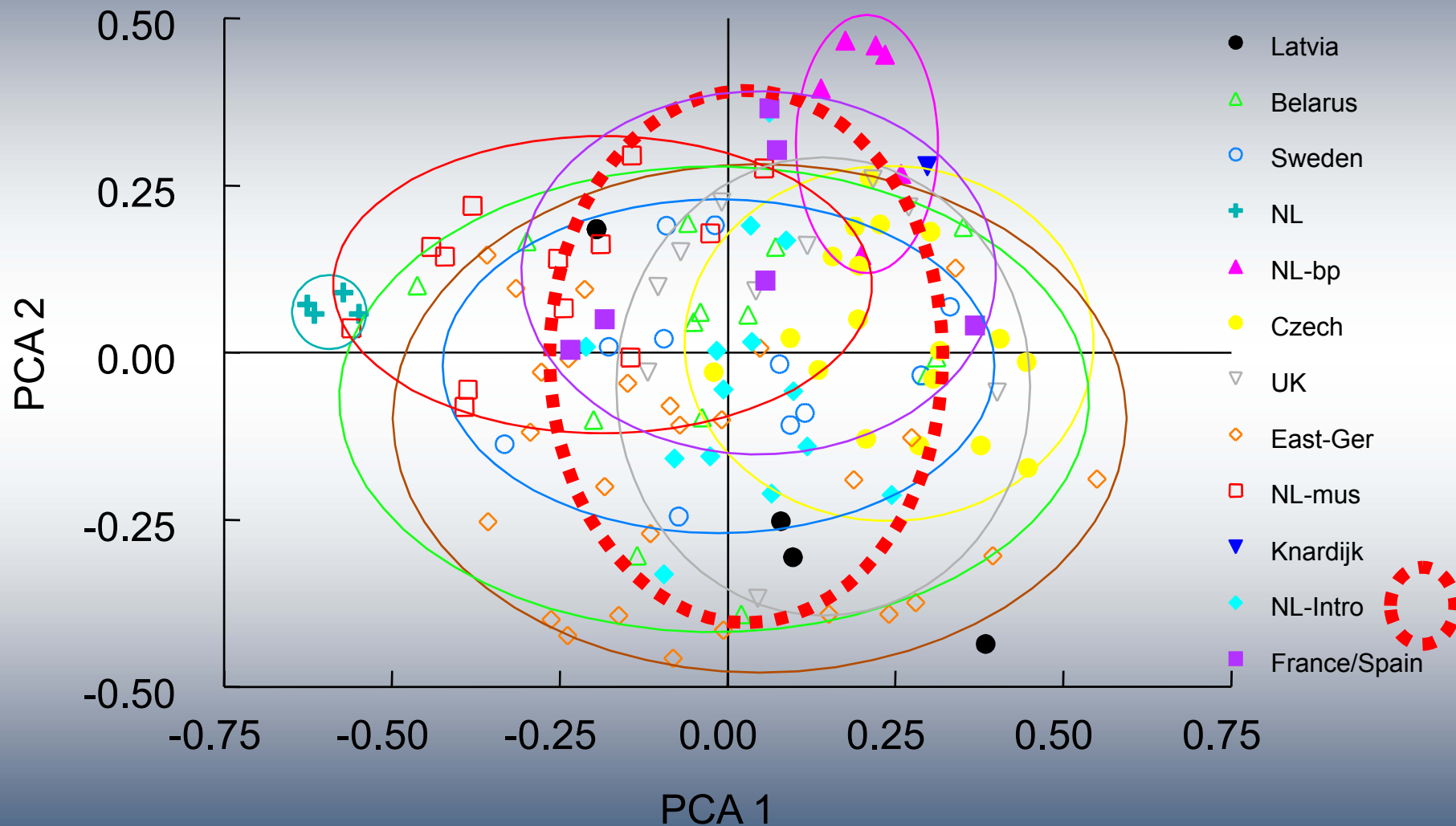
- Ecosystems
- Geographic barriers
- Local adaptation & differentiation

**\* mtDNA in captive-reproduced otters in:**  
**UH (Otter Trust)**  
**Italy (from Otter Trust)**  
**France (from Norfolk Wildlife Park)**

Source: E Randi, Italië

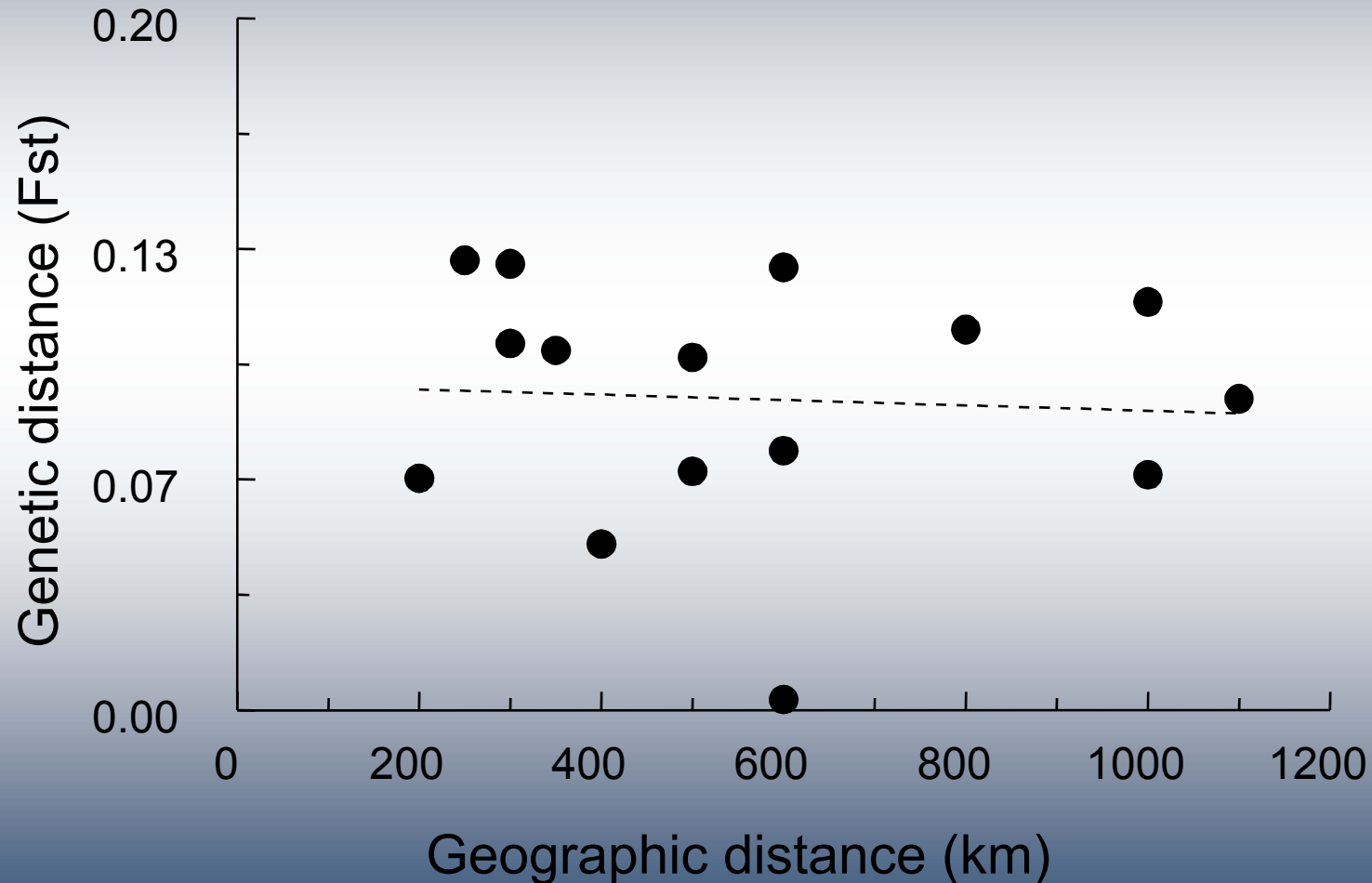


# Microsatellite analyses



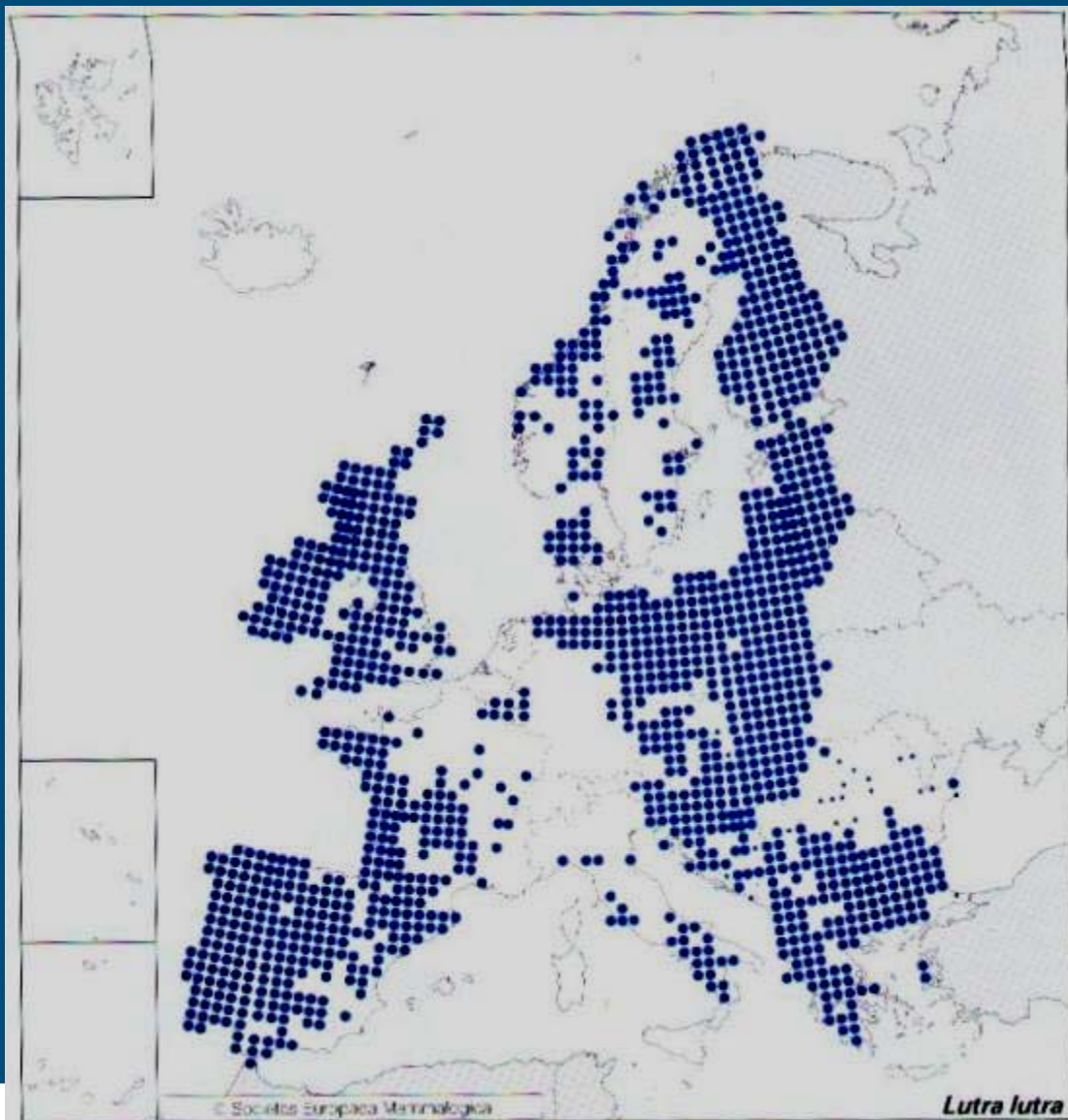
# Isolation by Distance (IBD)

Otter - Population structure





# Distribution otters



Clusters:

- Continental
- Coastal
- Mediterranean

## Research Strategy

## Monitoring

- Traditional
  - Field tracks
  - Telemetry - but, transmitters last  $< 1$  year
- Non-invasive genetics by taking DNA out of spraints
  - Promising new technique
    - + many years
    - + newborn
    - + abundance estimates
    - - technical issues (dropouts, false alleles, specific protocols)
    - - startup and development costs

# Non-invasive genetics



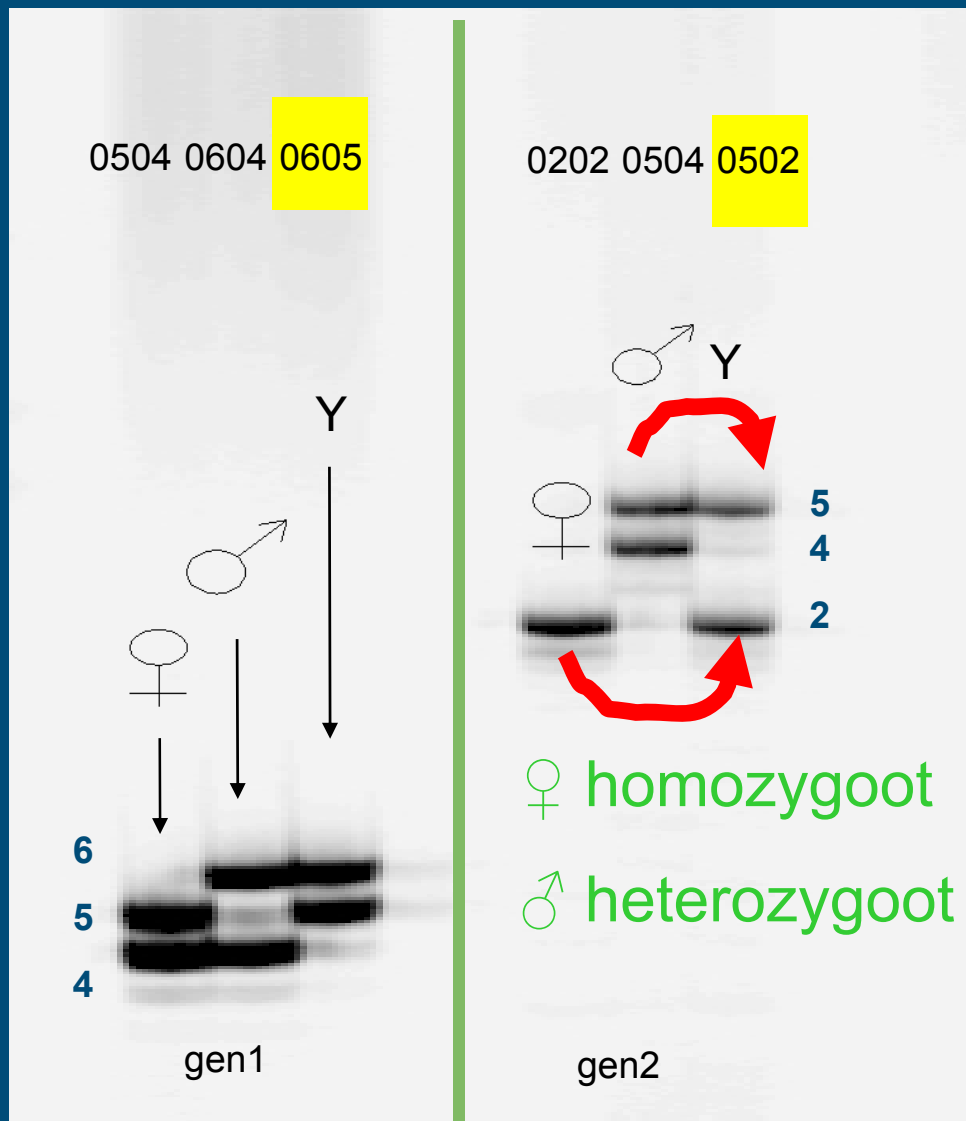
- **Other**
  - Food
  - Pollution
  - Parasites



# Spraints

- **DNA**
  - Individual
  - Sex
  - Kinship
  - Abundance
  - Population structure
- **Hormones**
  - Reproductive biology



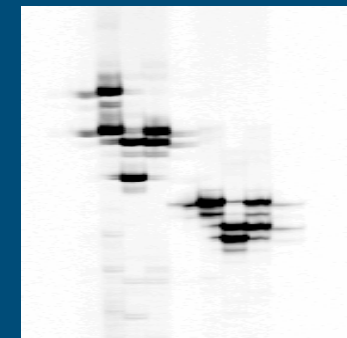


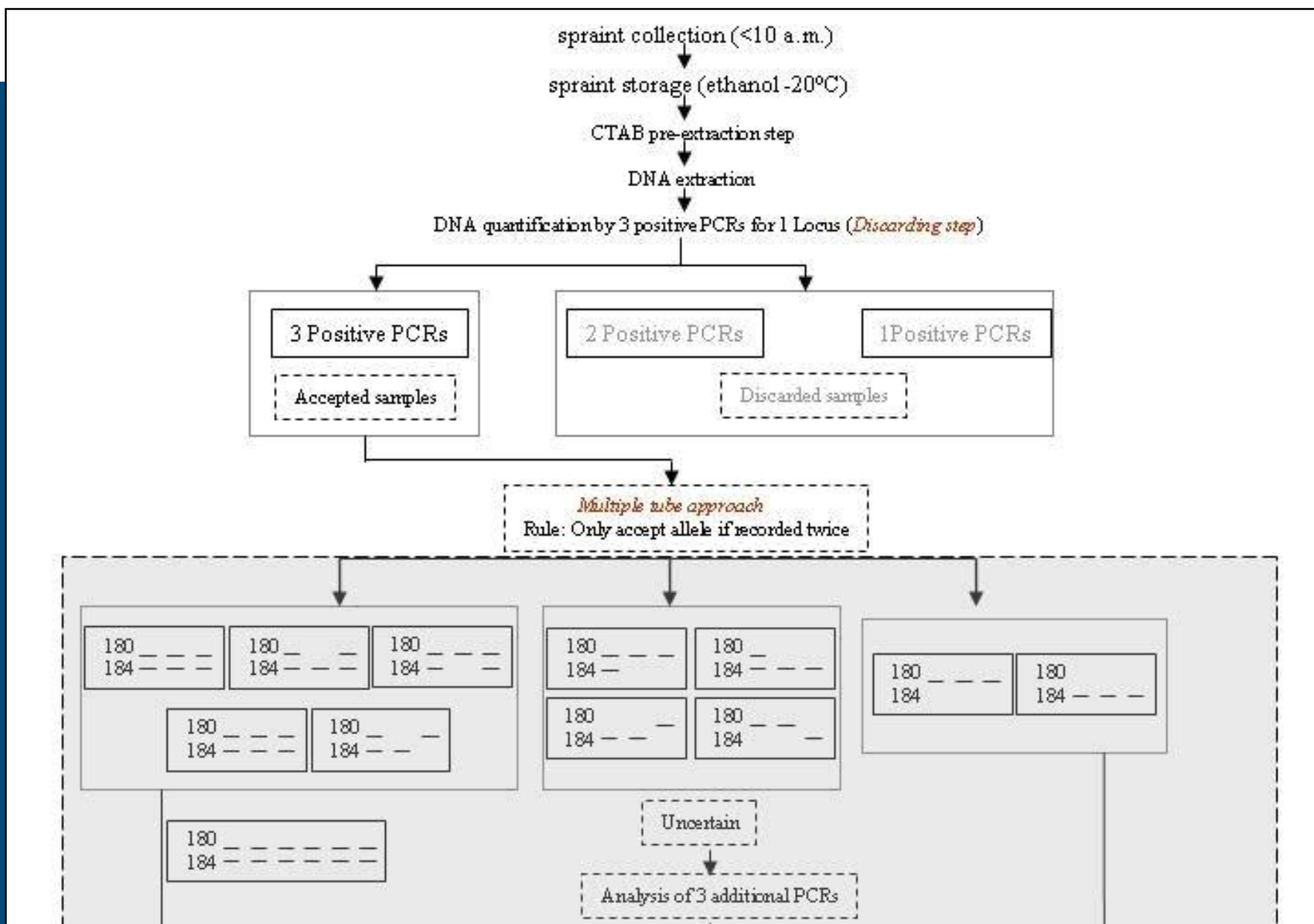
# Microsatellite analysis

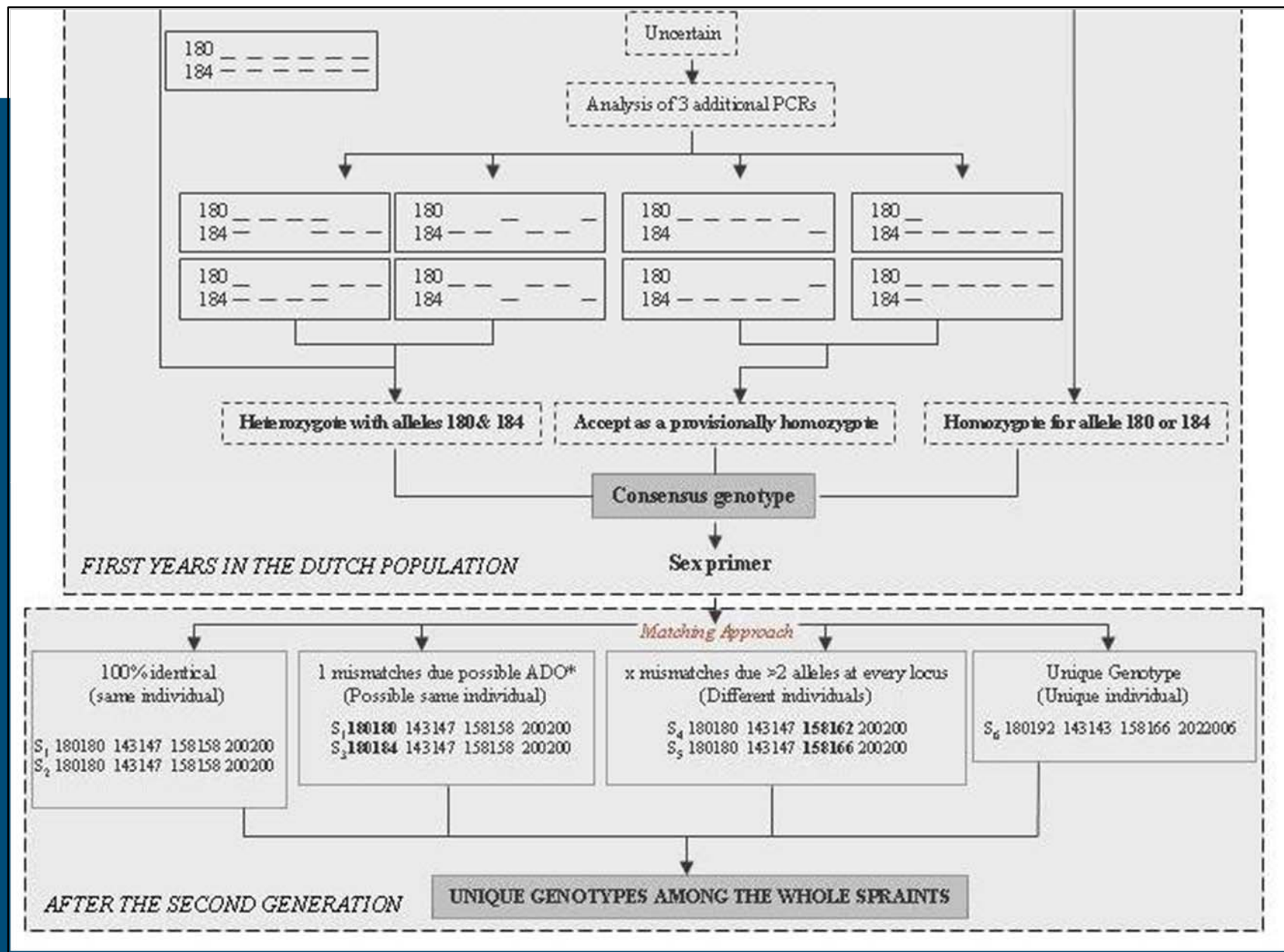


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1. Field collection (as fresh as possible)
  - Storage in 99% Ethanol
2. CTAB cleaning
  - Remove polysaccharides
  - Laborious
  - Increase in success rate from 32% to 41%
3. DNA extraction (tissue kit)
4. Pre-screening with standard SSR primer
  - Multiple tube – 3 replicates
  - Continue with those samples that gave 3 positive PCRs
5. Run selected samples with 5 - 15 SSR primers
  - Multiple tube (at least 3 replicates)
  - Trade-off quality/quantity of SSRs
6. Sex primer
7. Data processing
  - Consensus genotypes
  - Compare with known individuals



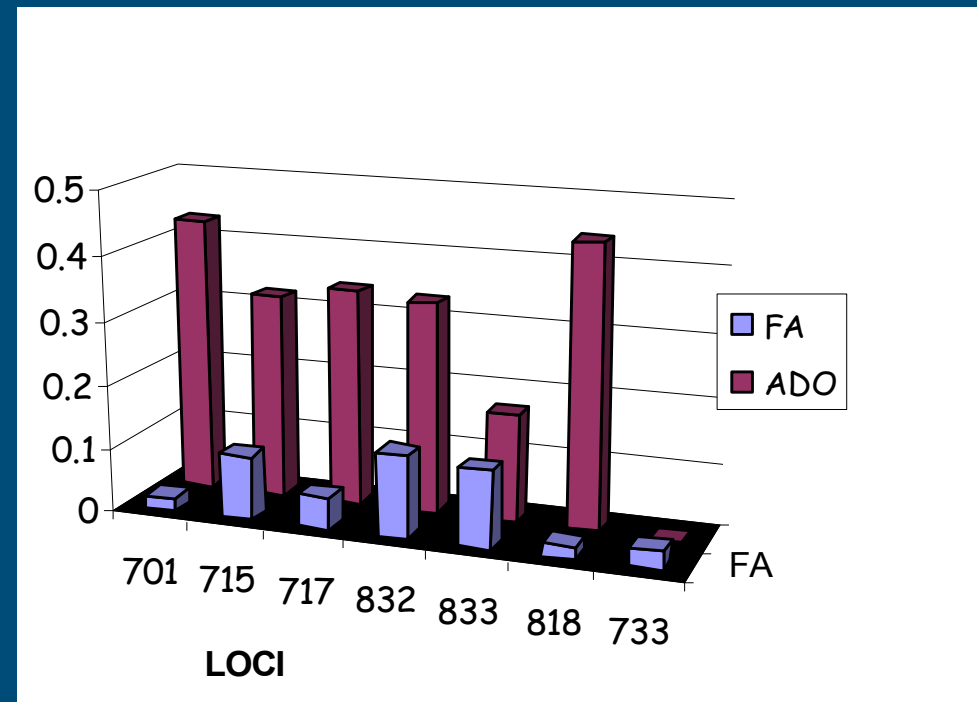




174 spraints gathered  
117 contain DNA (=70%)

Remaining 117:  
Rate of success >40%  
ADO 31%  
FA 7%

Error rate varies among loci





# Dutch Population Results

Relatively higher succesrate because:

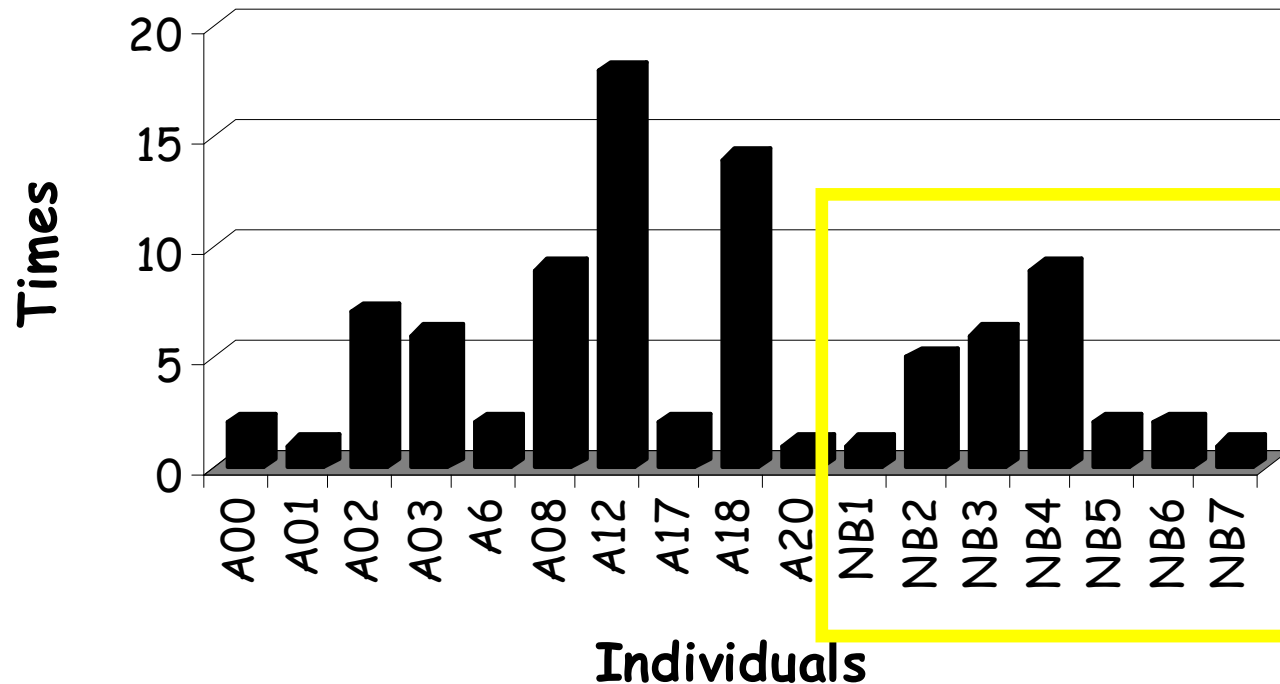
DNA passport of all released otters >

incomplete fingerprint + other data as location  
and unique alleles => Identification!

10 % additional succesrate (>50%)



## Resampled Genotypes



### Newborn

NB1 ♂

NB2 ♀

NB3 ♂

NB4 ♀

NB5 ?

NB6 ?

NB7 ♀

### Parentals

(A01\*A05)

(A03\*A12)

(A03\*A12)

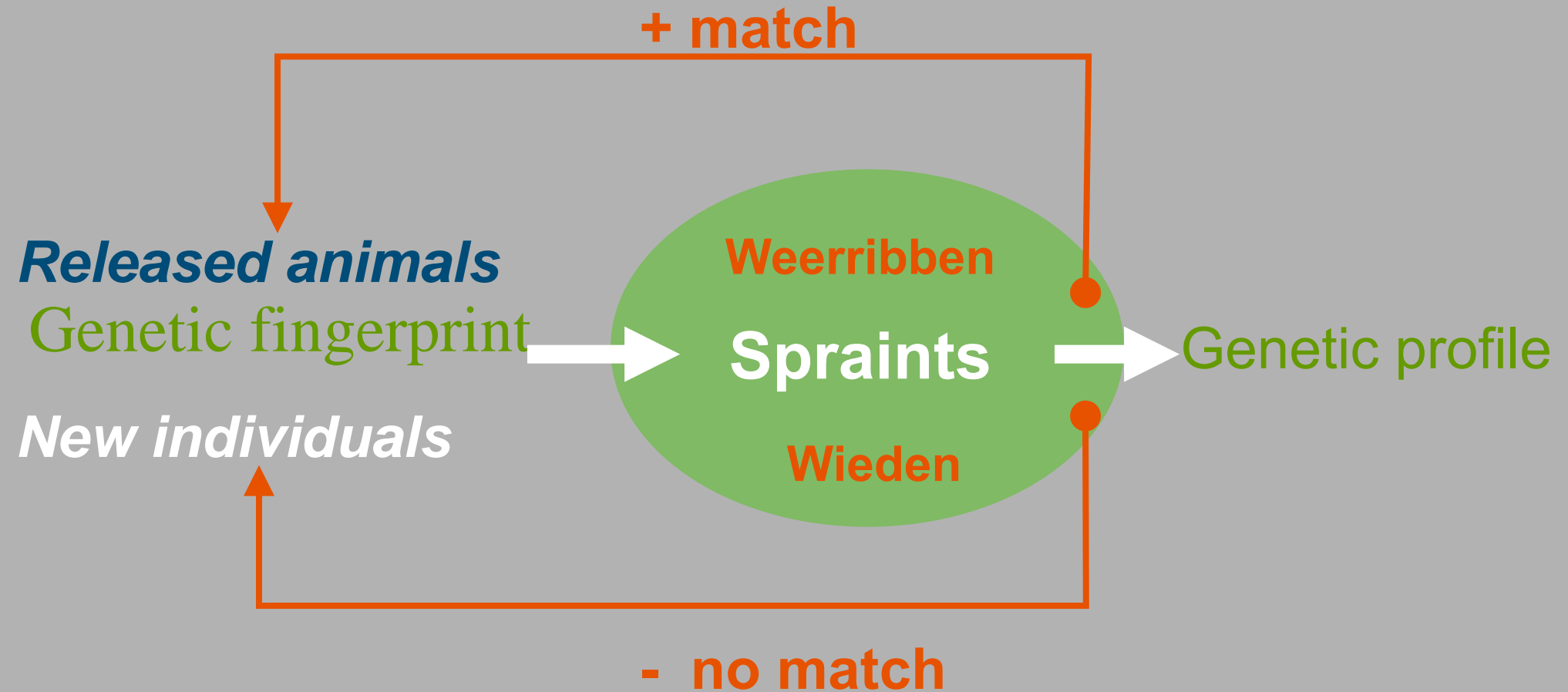
(A02\*A06)

(A00\*A04)

(A00\*A04)

(A03\*A12)

# Closed population – using genetic fingerprints



## Conclusions - Non-invasive genetic monitoring

- improved our knowledge of the life of otters
  - Distribution and territory size (habitat use)
  - Mating structure (paternity, multiple spouses)
  - Sex biased dispersal
  - Population development (density)
  - Effective population size
- is worth the effort of initial investment (costs) and, with proper protocols, can be done cost efficiently
- turned out to be indispensable for proper management advise (genetic diversity)
- long term monitoring tool

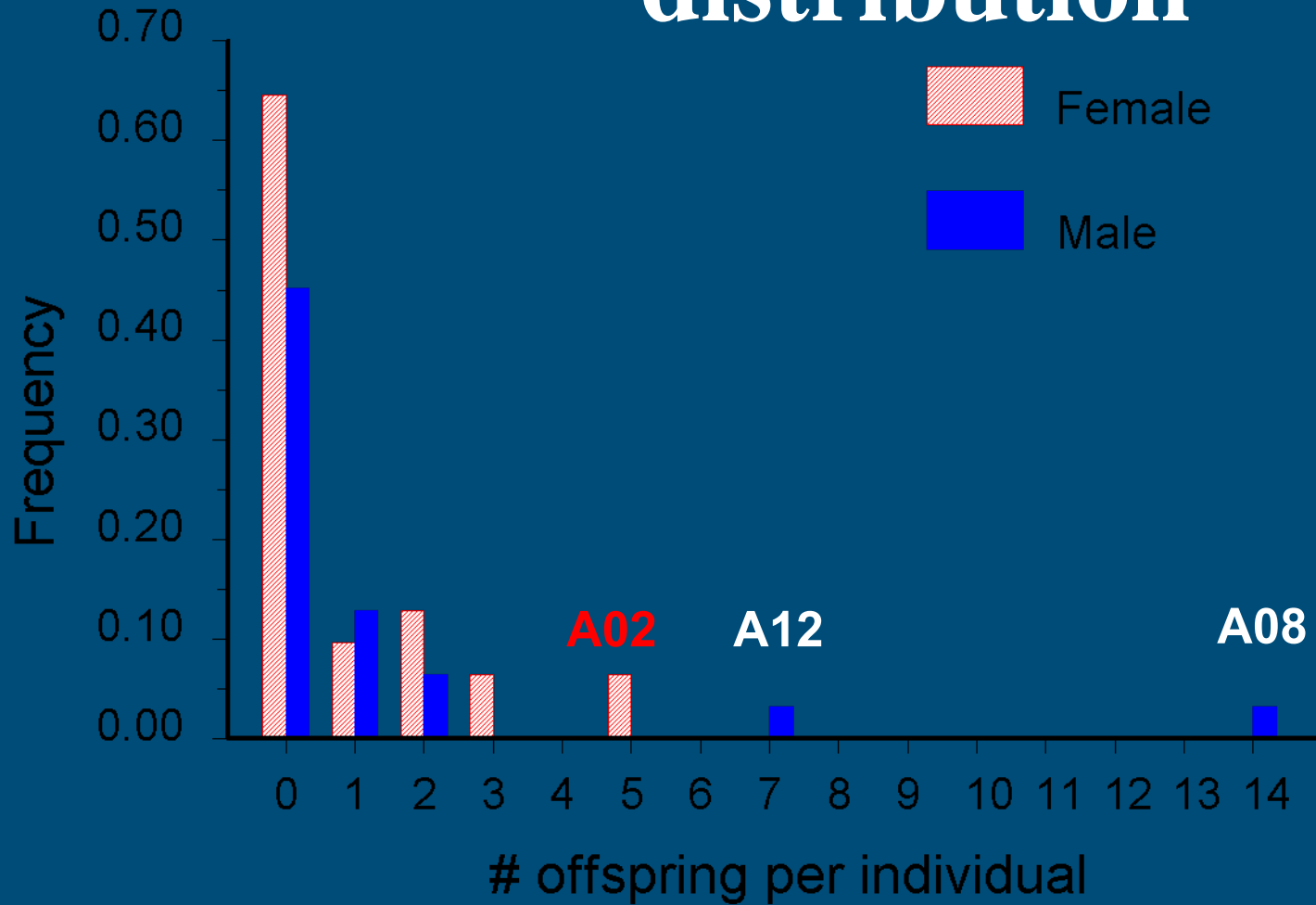




# Mating structure

# Skewed

## distribution



Variance:

Female - 2.0

Male - 10.4

**A02**

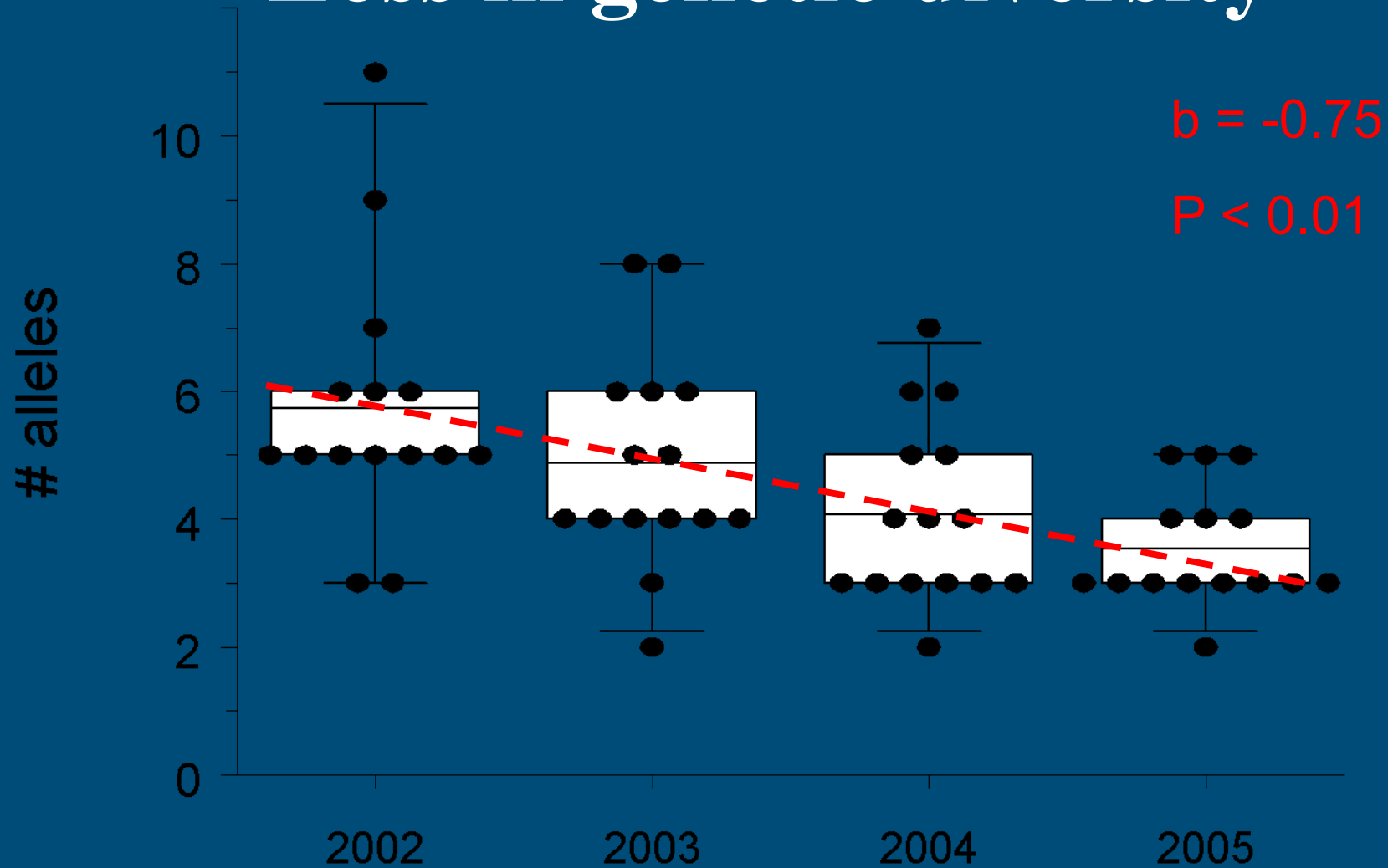
**A12**

**A08**

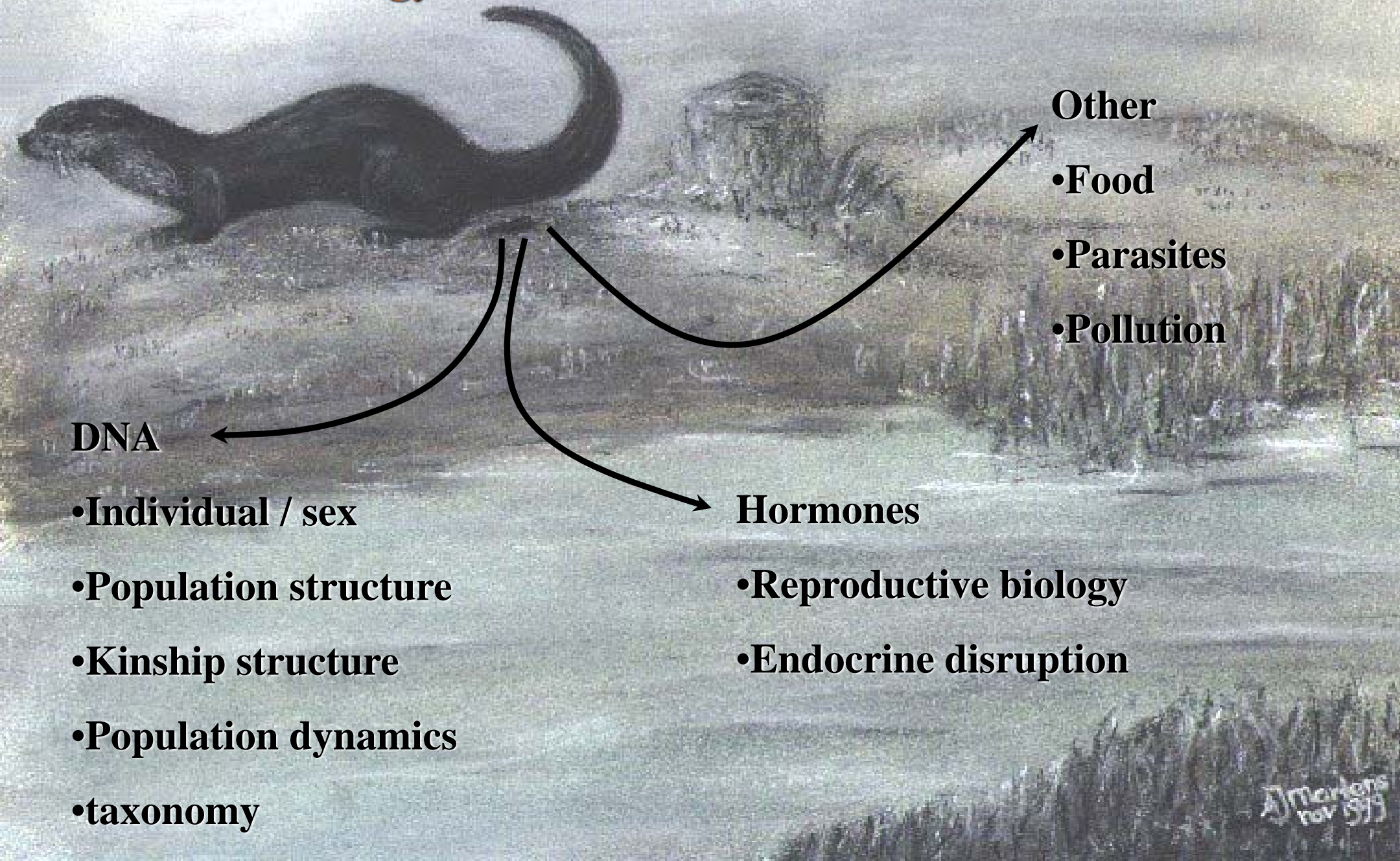
# Effective population size ( $N_e$ )

- Average density (2002-2006): **22**
  - Unequal numbers (time): 21
  - Sex ratio: 19
  - Juvenile - Adult: 11
  - Non-random family size: **5**
- 
- **$N_e$  is only about  $0.25 * N$**

# Loss in genetic diversity




# **Molecular Scatology**



# Effective population size ( $N_e$ )

$$N_e \approx \frac{8N}{V_f + V_m + 4}$$

  
2.0      10.4

$$N_e \approx \frac{8}{16} N \approx 0.5 N$$

- Difficult to control  $V_m$ 
  - Mating system – one male with several females
  - Dominant territorial behaviour



# Genetic diversity and composition in fragmented populations

