



**Emvt**  
France



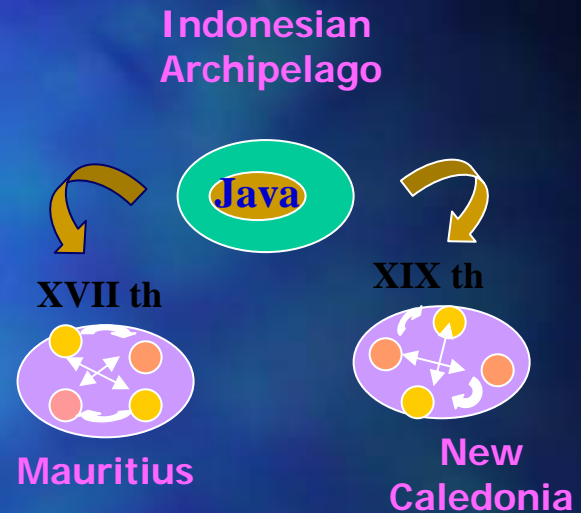
**Genetic analysis  
of insular Rusa deer (*Cervus timorensis russa*) populations  
in Mauritius and New Caledonia**

**Maillard J.C.**  
**De Garine-Wichatitsky M.**  
*et al.*

# Context and Introduction

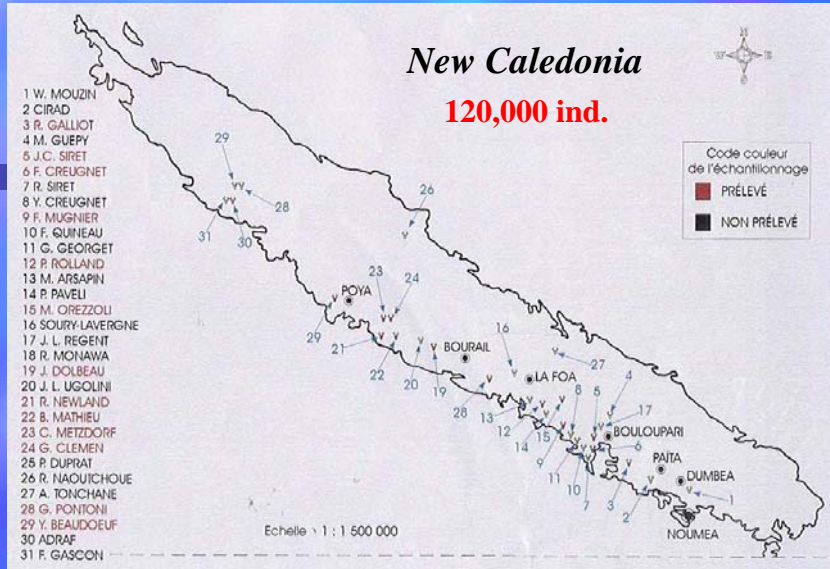
## ➤ Exotic species introduced

- from Java
- to Mauritius
- and to New-Caledonia



- Different populations radiated rapidly from the founding animals
- Differentiation driven by environmental pressures and by genetic drive
- Animals were hunted or domesticated for meat and horn velvet

# Animal material and sampling

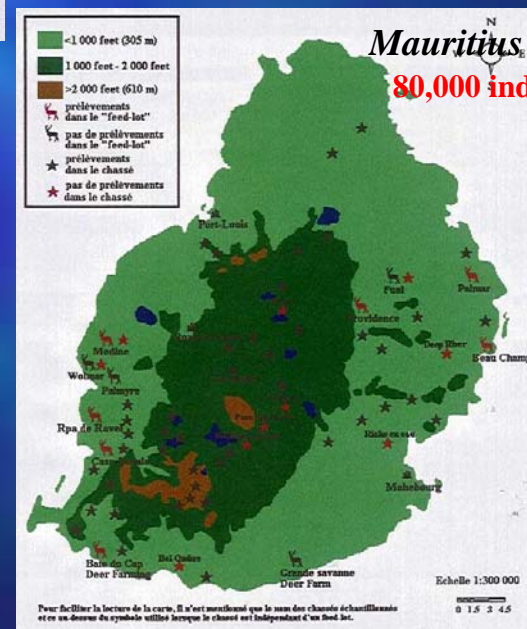


## 130 individuals selected

- ☞ both sexes
- ☞ from 13 domestic herds
- ☞ + 26 wild animals in 2 locations
- ☞ blood / hair samples taken

## 86 individuals selected

- ☞ both sexes
- ☞ from 7 domestic herds
- ☞ blood samples taken



# Genotyping by microsatellite fluorescence multiplexing

convenient grouping of allelic size ranges

3 different fluorescent labels (*FAM* / *JOE* / *NED*) for PCR primers

Multiplexed loci	Ranges of allelic sizes	Fluorescence groups
TGLA 57 INRA 121 IDVGA 55 BMC 1009	70-110 120-170 180-240 250-330	<b>FAM</b>
VH 110 BM 757 BL 42	90-150 160-220 230-280	<b>JOE</b>
BM 203	210-240	<b>NED</b>

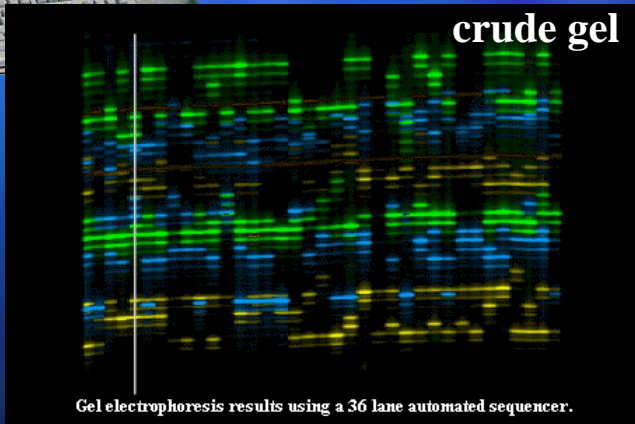


1 electrophoresis lane / individual

36 individuals / gel

crude gel

genescan



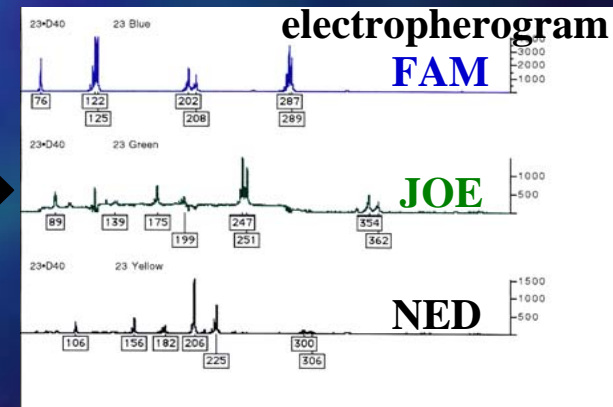
Gel electrophoresis results using a 36 lane automated sequencer.

8  $\mu$ sat / individual



16 alleles / individual

genotyper



# Population Genetic Analysis Software

Derive general population structure...

...and assign individuals to groups

F stat:  $H$  /  $F_{is}$  /  $F_{st}$  /  $F_{it}$  (*Wright / Weir & Cockerham*)

☞ **Genepop & Genetix**

Genetic distances (*Cavalli-Sforza & Edwards / DAS*)

☞ **Tree Maker**

Assignment

☞ **GeneClass II**

# Results (1)

Populations well differentiated between islands

## Cladogram for individuals

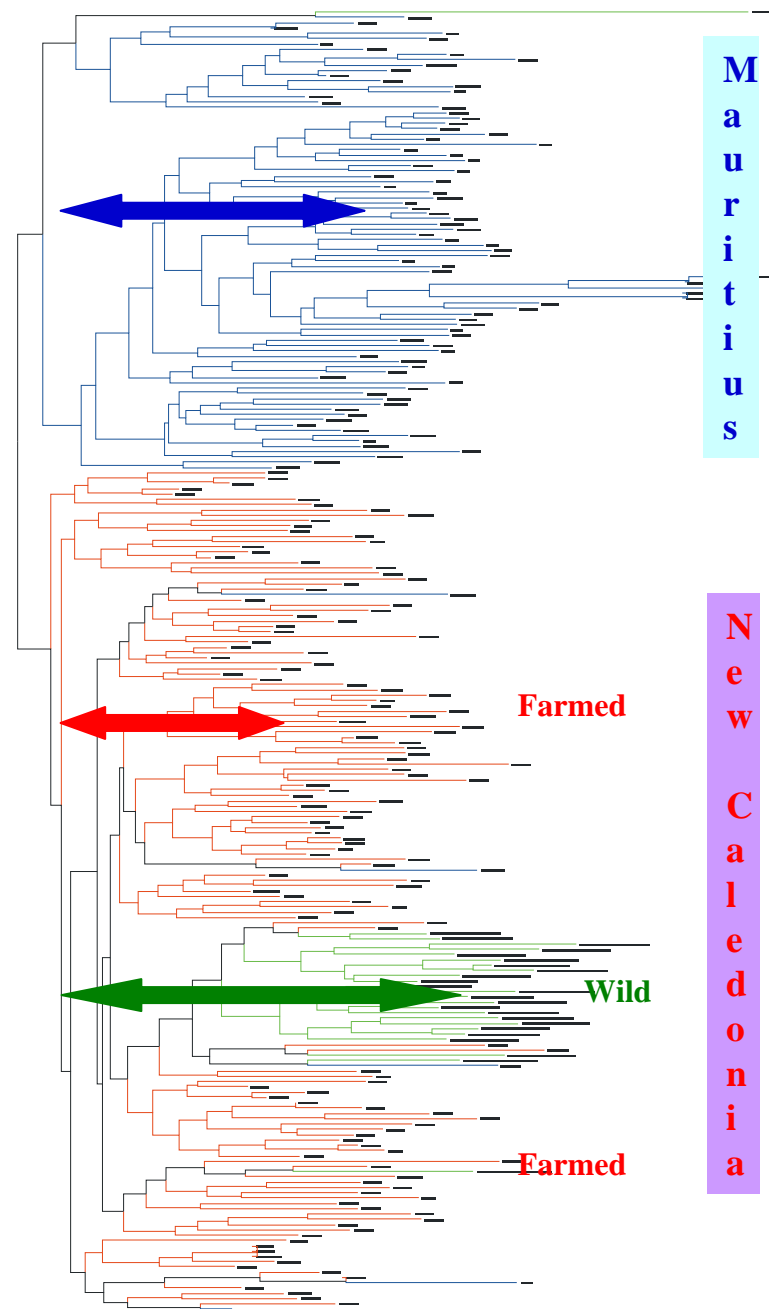
Mean genetic distances from root:

Greatest – **Wildlife pop**

Median – **Mauritius farm pop**

Smallest – **New Caledonia farm pop**

Genetic divergence is proportional to the time elapsed from founding population(s)



# Results (2)

## 👉 Genetic diversity

	AANL	H. expect.	H. observ.	Fis	Fst	Fit
New Caledonia N=130	7,5	0,63 ±0,16	0,59 ±0,15	0,07 (***)	-	-
Mauritius N=86	6,4	0,54 ±0,18	0,49 ±0,17	0,08 (***)	-	-
Total population N=216	-	-	-	0,08 ±0,02 (***)	0,25 ±0,07 (***)	0,30 ±0,07 (***)

AANL: allelic average number per locus

H: heterozygosity

N : sample size

\*\*\* =  $p < 0.001$

## AANL

👉 High variability

👉  $NC > M$

## Heterozygosity

👉 In normal mammalian range

👉  $Ho < He$

👉  $Ho_{NC} > Ho_M$

= NC founder effect >

= intro wild animals

## Fis

👉 positive Fis ( $P < 0,001$ )

= genetic sub-structure

# Results (3)

## Assignment and Traceability using TreeMaker

### *New Caledonia*

**1 trait per individual**  
**1 colour per herd**



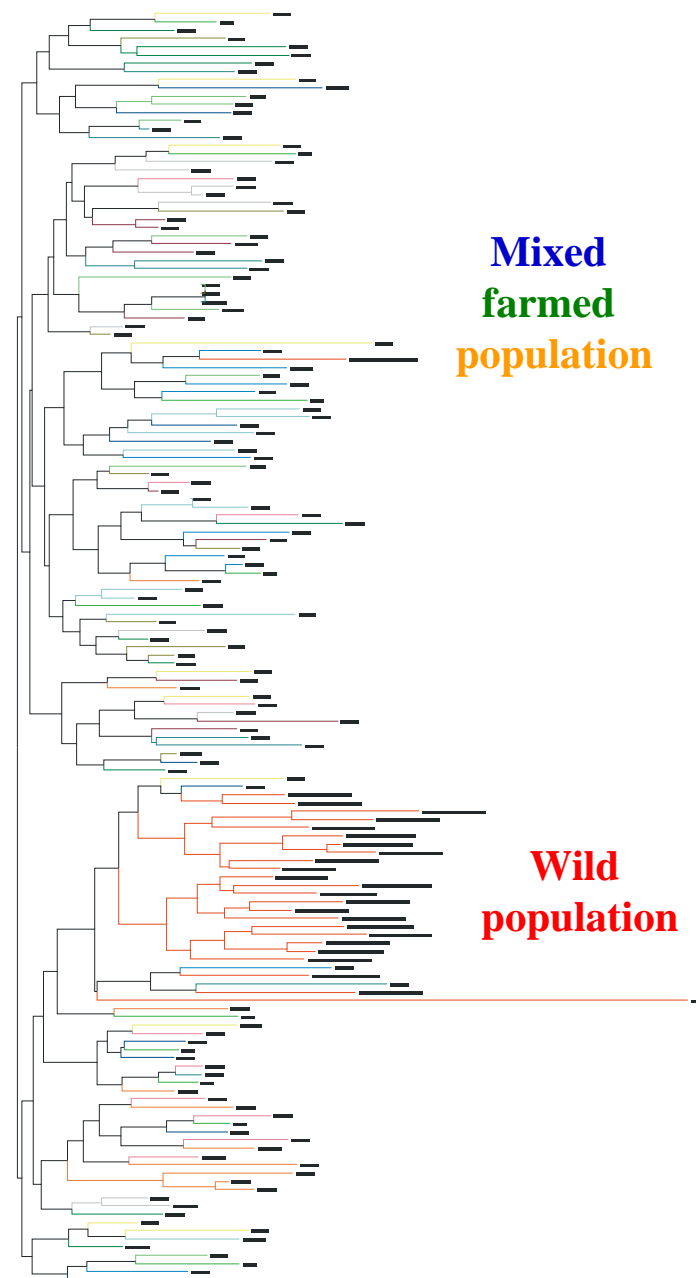
#### **Farmed population**

General mixing: not useable as a reference population for « herd » assignation



#### **Wild population**

Compact clade: useable as a reference population for « wild » assignation





# Results (3)

## ➡️ Assigination and Traceability using *Gene Class II*

- 2 reference populations: domestic (DP) vs wild (WP)
- Classification by range of affiliation probability

➡️ All animals are of domestic origin

➡️ Some wild animals were captured in certain farmed herds

➡️ F1 hybrid animals

➡️ F2 hybrid animal

Creugnot herd					
<i>individual</i>	<i>rank 1</i>	<i>score (%)</i>	<i>rank 2</i>	<i>score (%)</i>	<i>assignation</i>
CR1	DP	50,80	WP	49,20	hybride 1/2
CR2	WP	51,50	DP	48,50	hybride 1/2
CR3	DP	74,50	WP	25,50	hybride 1/4
CR4	DP	100			domestic
CR5	WP	96,20	DP	3,80	capt. wild
CR6	DP	82,10	WP	17,90	hybride 1/8
CR7	DP	91,70	WP	8,30	hybride 1/6
CR8	DP	99,80	WP	0,20	domestic
CR9	WP	97,90	DP	2,10	capt. wild
CR10	DP	80	WP	20	hybride 1/5

## Discussion / Conclusion

- Well differentiated populations with high founding effects with different divergence time and genetic drift depending of different environmental pressure selections
- Mauritius population is better structured as New Caledonia herds
- High genetic diversity in New Caledonia due to exchange of animals, short breeding cycles and weak but constant wild life introduction
- Microsatellite multiplex kit and analysis software are efficient tools for population genetic analysis and traceability
- Need well structured populations for reference groups to assign

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