

Using the information collected for genetic evaluation to assess the French ruminant and equine breeds' genetic variability

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INTERBULL 2013

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Do we *really* need genetic variability in livestock breeding?

$$\Delta G = \frac{i \rho \sigma_A}{t}$$

ΔG , genetic progress

- i selection intensity
- ρ accuracy of selection
- σ_A genetic variability of the given trait
- t generation interval

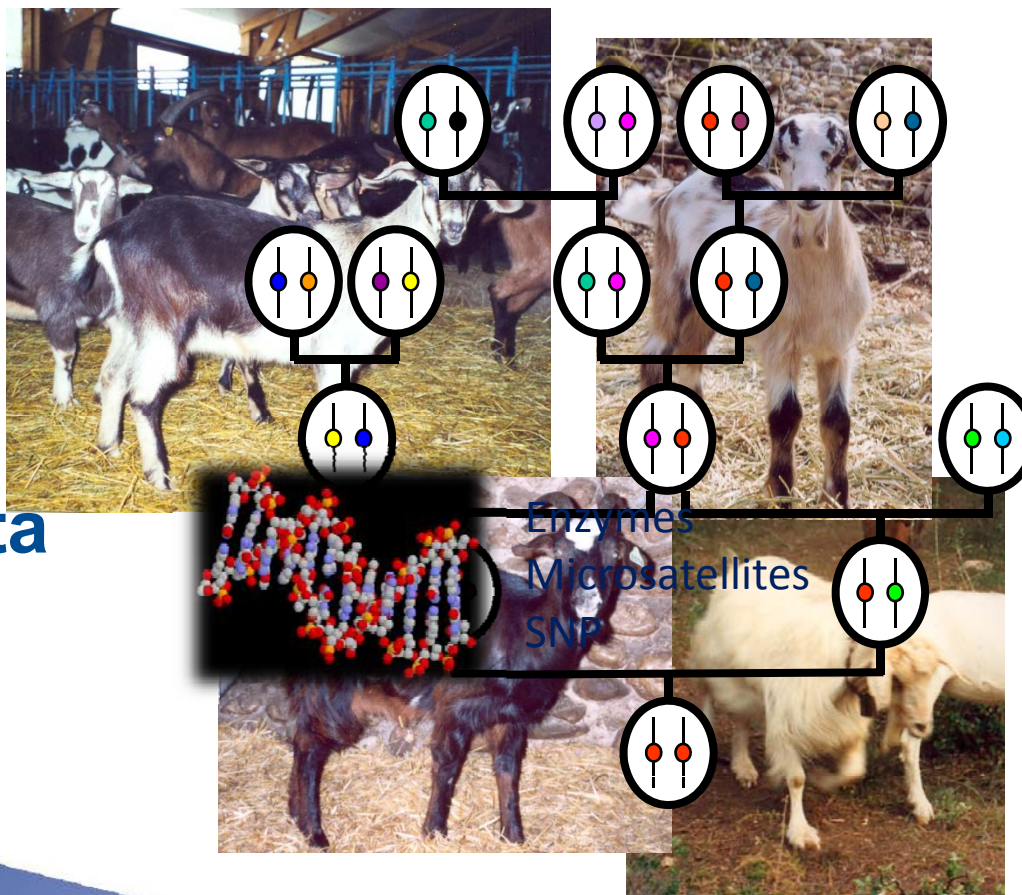
***Without genetic variability, no
genetic progress can be achieved !***



Various data sources to monitor genetic variability



- Phenotypes
- Pedigrees
- Molecular data



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The VARUME project

Aim: monitoring the within-population genetic variability of the Ruminants and Equids breeds selected in France

- ▶ **Species involved:** dairy and beef cattle, dairy and meat sheep, goat, horses and donkeys
- ▶ **Generation of indicators of genetic variability**
 - Based on Pedigree Data already available in selection database (Ruminants: CTI, INRA; Equids: SIRE, IFCE)
 - Based on already existing genotypes (produced for genomic selection) => feasibility study
- ▶ **In order to inform the breeds managers on a regular basis of their breeds' "health"**



Indicators based on pedigree data

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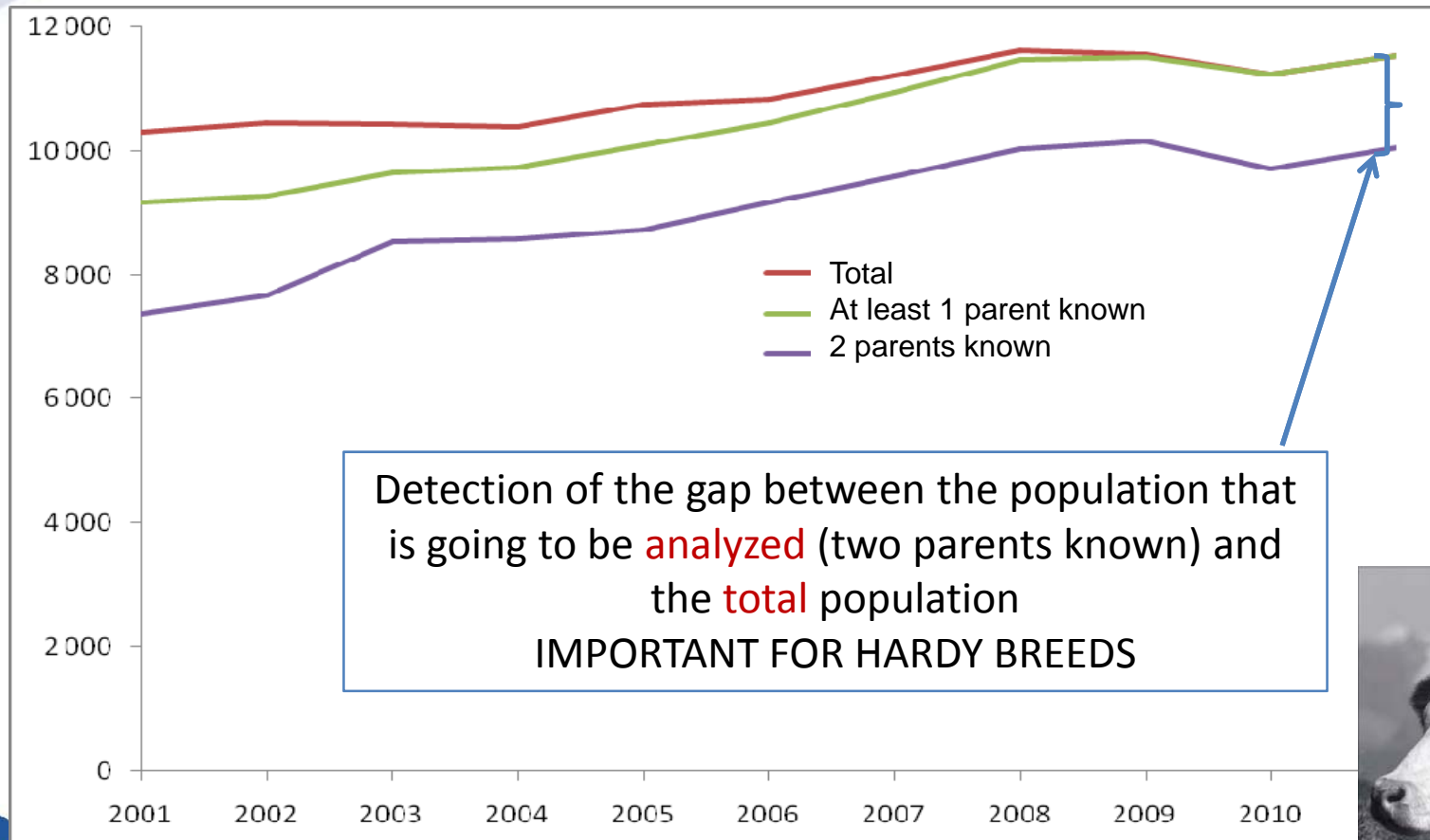
Main principles of a pedigree analysis

- Mendelian gene transmission
- **Probabilistic** approach for a given locus, assuming a neutral polymorphism and without mutation
- Strong assumption: two individuals without pedigrees (= founders) are considered as **unrelated**



Example of demographic indicators

Evolution of the number of birth per year in the Abondance breed



Detection of the gap between the population that is going to be **analyzed** (two parents known) and the **total** population
IMPORTANT FOR HARDY BREEDS



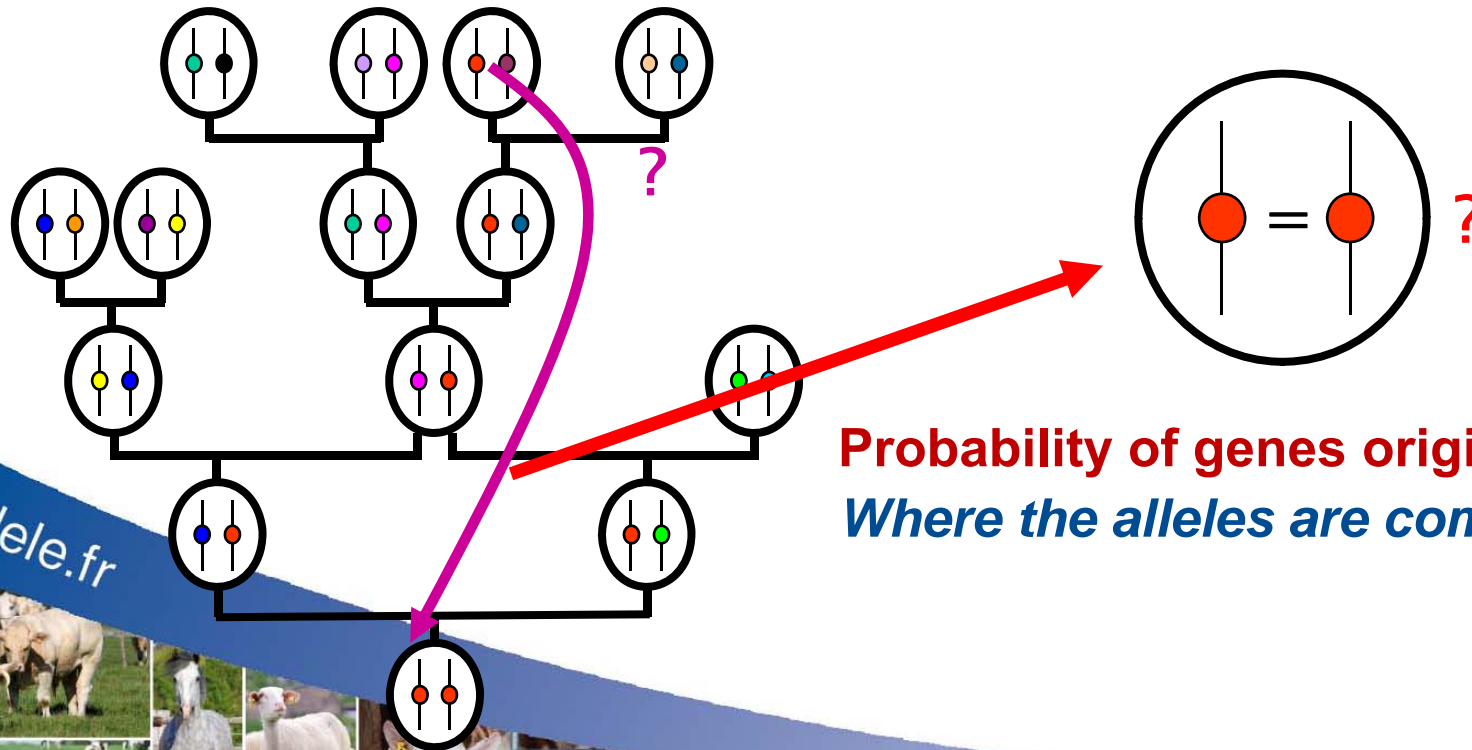
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Indicators based on two types of probabilities



Probability of identity

For a given animal, are two alleles identical?



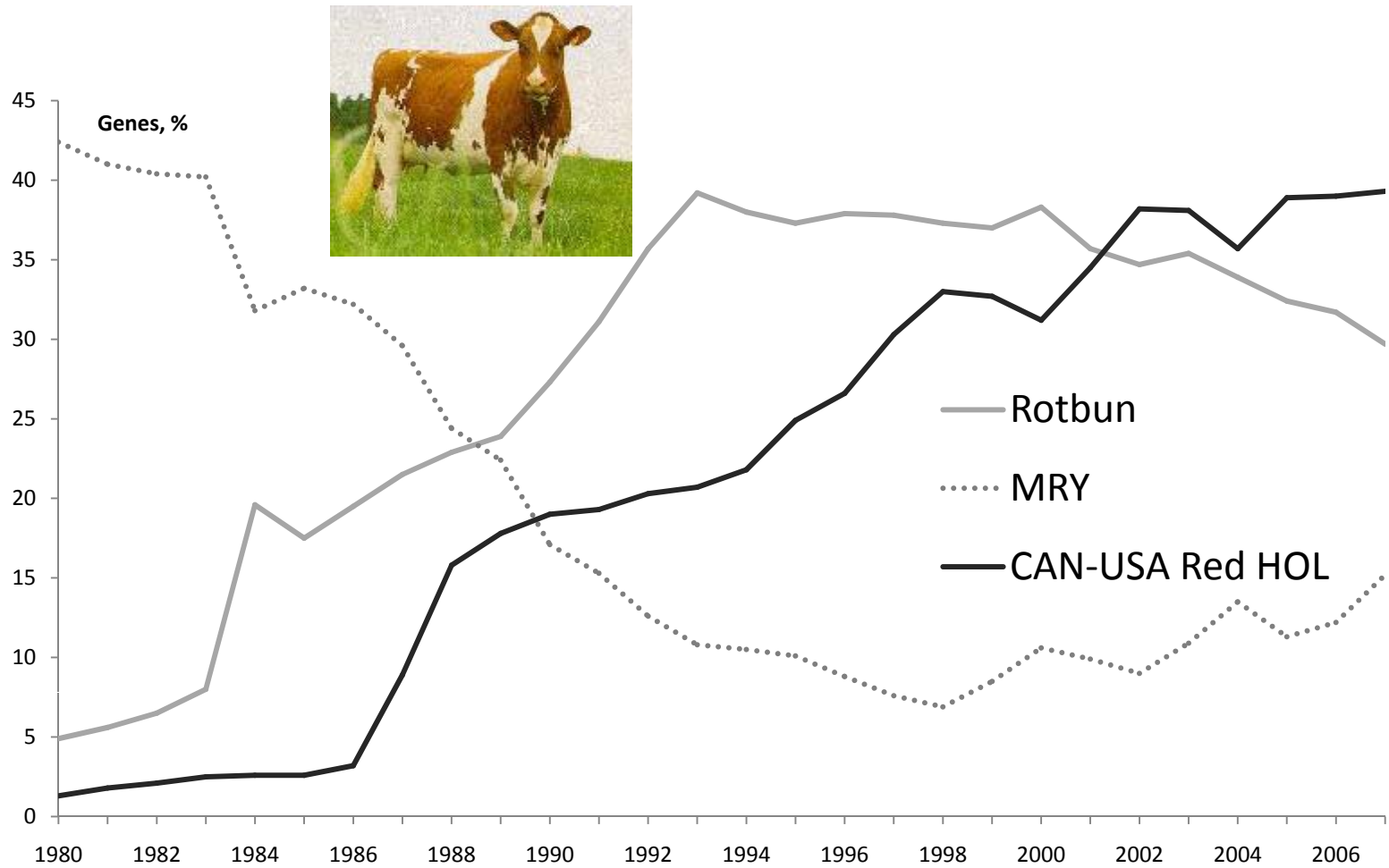
Probability of genes origin

Where the alleles are coming from ?

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Example of a Probability of Genes Indicator: Evolution of the % foreign genes in the « Pie Rouge des Plaines » breed

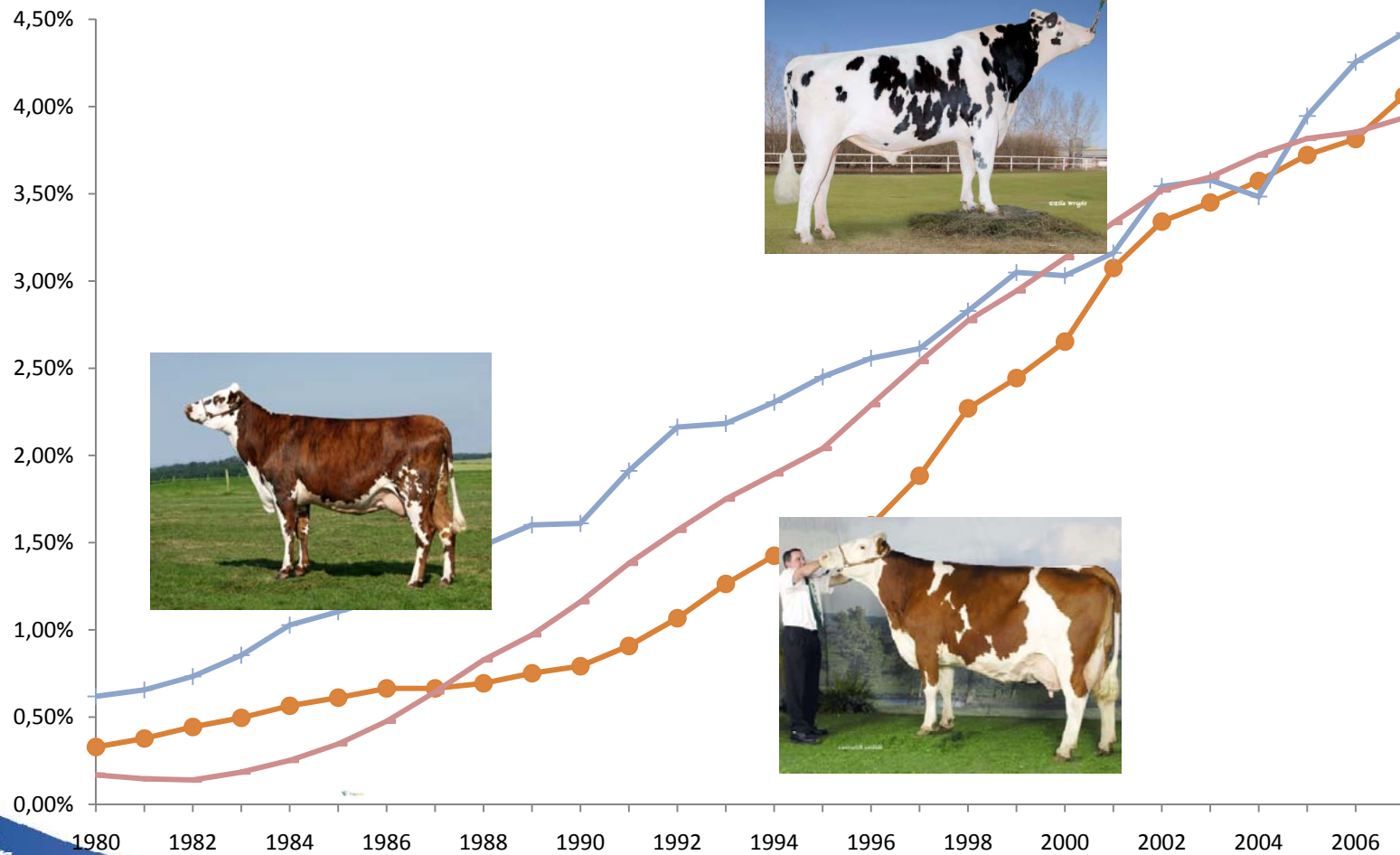


Danchin-Burge et al., 2011





Example of a Probability of Identity Indicator: Evolution of inbreeding



Danchin-Burge et al., 2011

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What is the reliability of our indicators ?

Quality control based on a **pedigree depth** analysis

For instance: a breed with an average of 2 generations known is likely to have less inbreeding than a breed with an average of 10 generations known

=> Comparison between breeds must be done for a given pedigree depth

Pedigree indicators: Pros / Cons

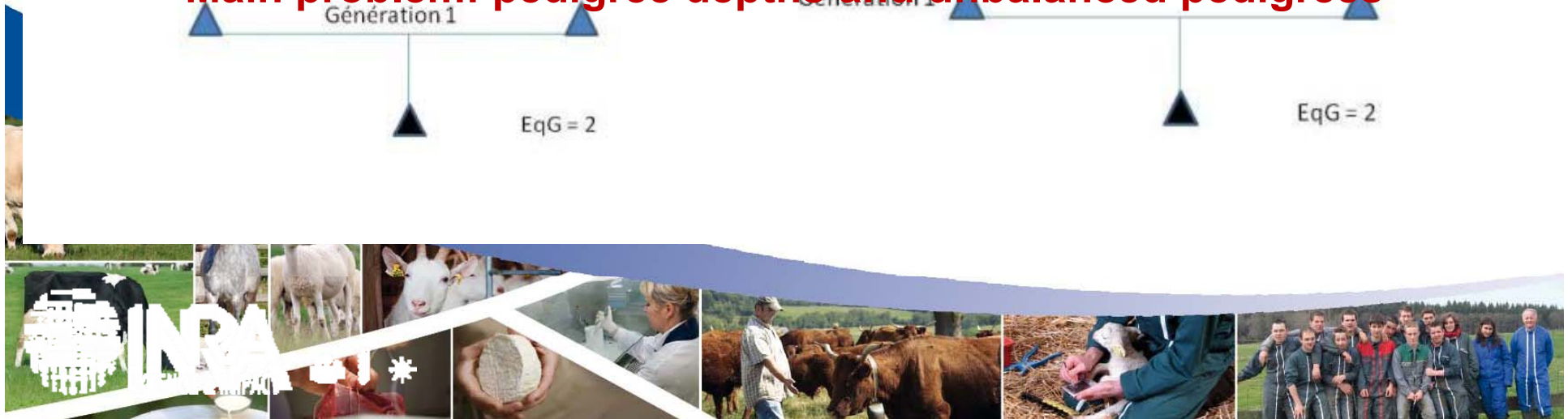
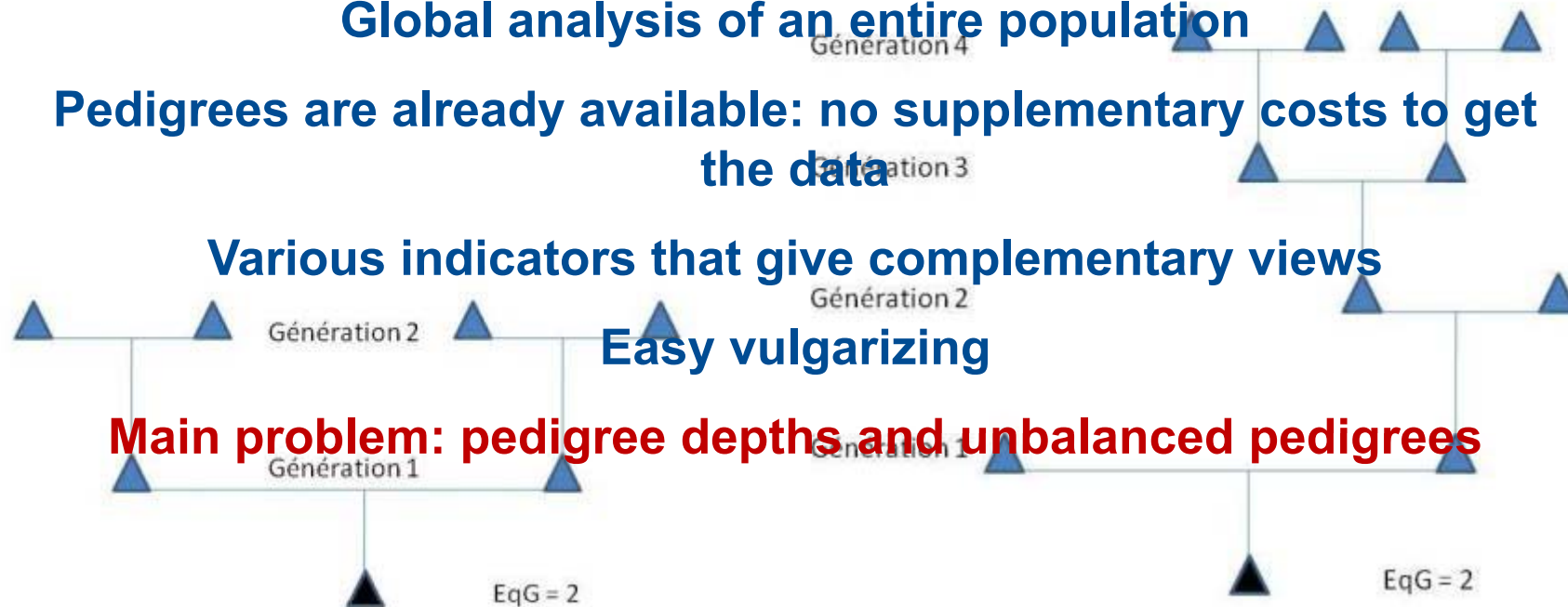
Global analysis of an entire population

Pedigrees are already available: no supplementary costs to get the data

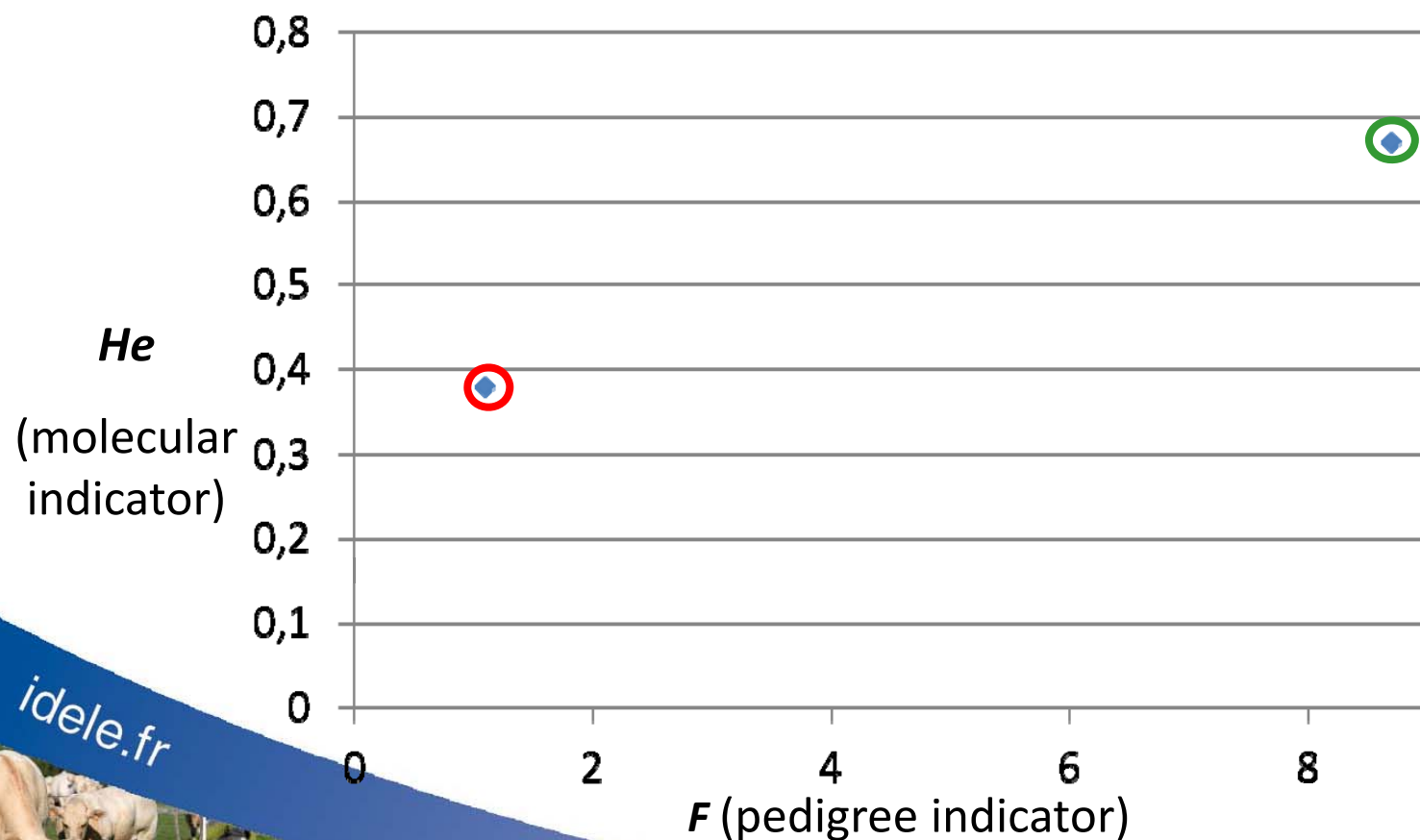
Various indicators that give complementary views

Easy vulgarizing

Main problem: pedigree depths and unbalanced pedigrees



Pedigree and molecular data: a different kind of information



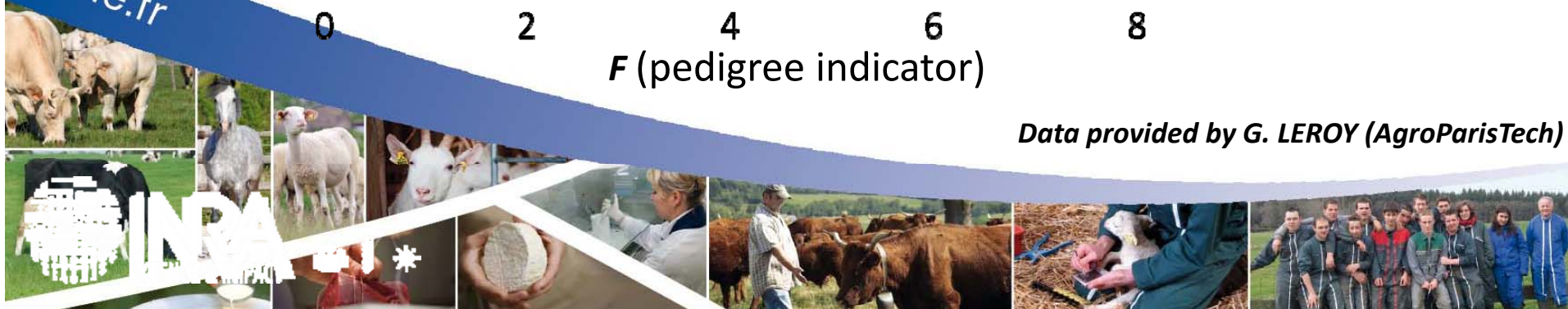
Berger des
Pyrénées



Bull terrier

Data provided by G. LEROY (AgroParisTech)

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Indicators based on SNP data

Feasibility study

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A new paradigm for indicators based on molecular data ?



- ✓ Indicators with a lot of benefits

Indicators based directly on the genome

Various possible studies (genetic diversity, inter breed genetic comparison, history of the breeds...)

- ✓ But some major problems

Genotyping costs

Sampling problems: number of markers, number of individuals

... Not anymore with **SNP data** and **genomic selection** !



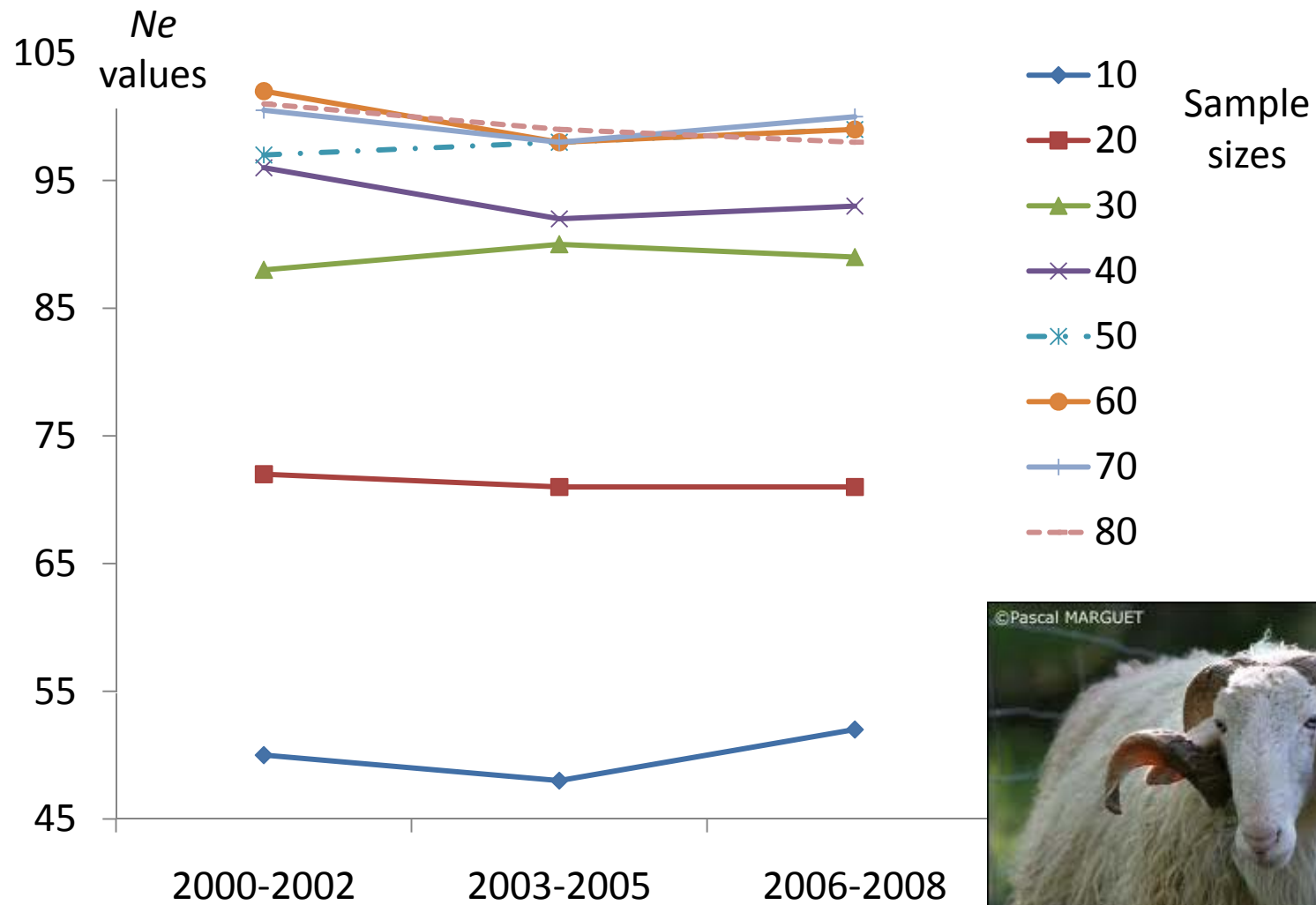
Concept: Effective population size (N_e)

- ▶ In a breed, all the animals don't breed and among the reproducing animals, the progeny sizes vary greatly
- ▶ N_e is equal to the number of individuals needed, in a *panmixia* situation, that would have an equivalent genetic variability than the breed under analysis.
- ▶ Three different methods used in our study based on **dairy sheep** genotypes :

1. Linkage Disequilibrium - N_e LD (SNP data)
2. Inbreeding - N_e F (Pedigree data)
3. Kinship – N_e K (Pedigree data)

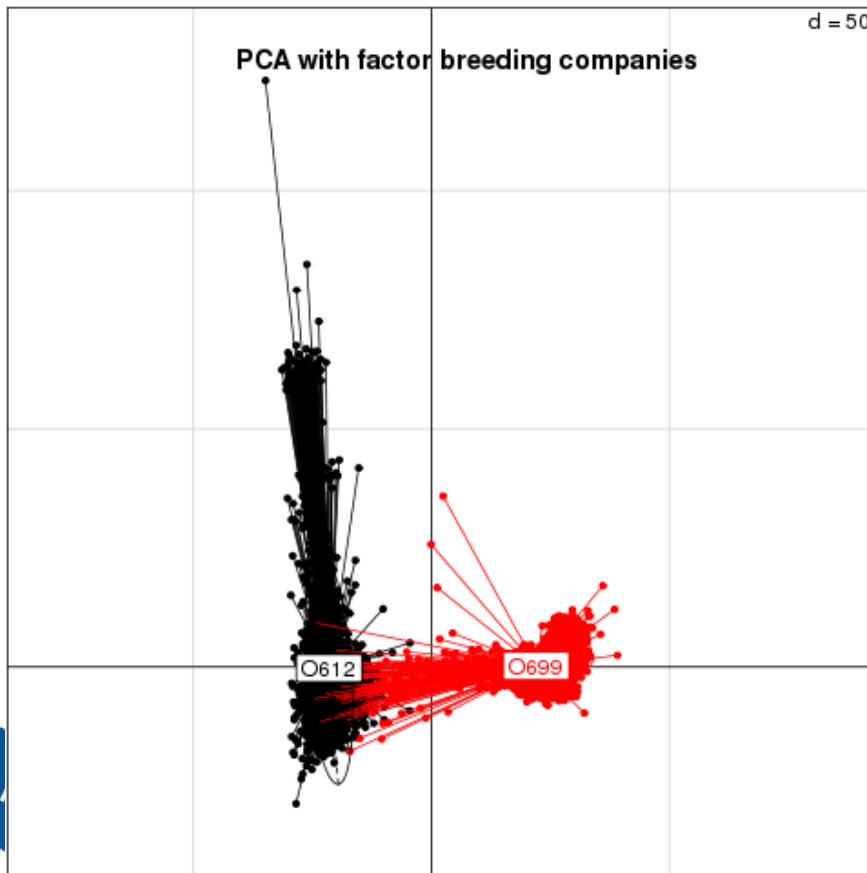


Effects of sample size on N_e

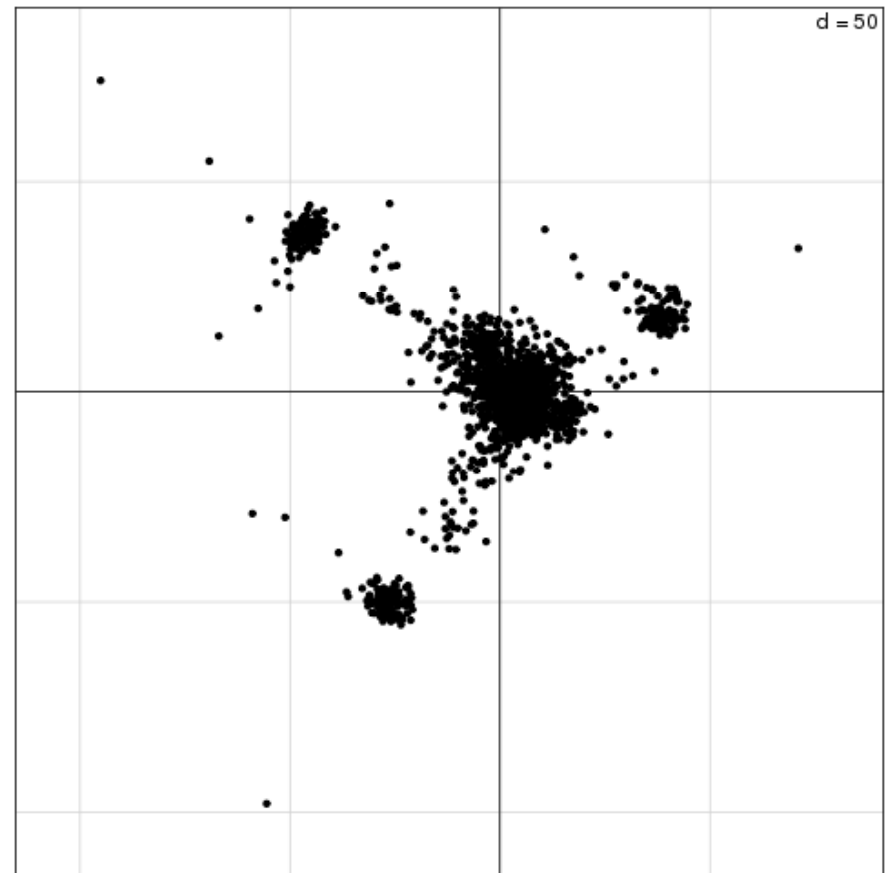


Problem: presence of substructure in 2 breeds

Lacaune



Manech Tête Rousse



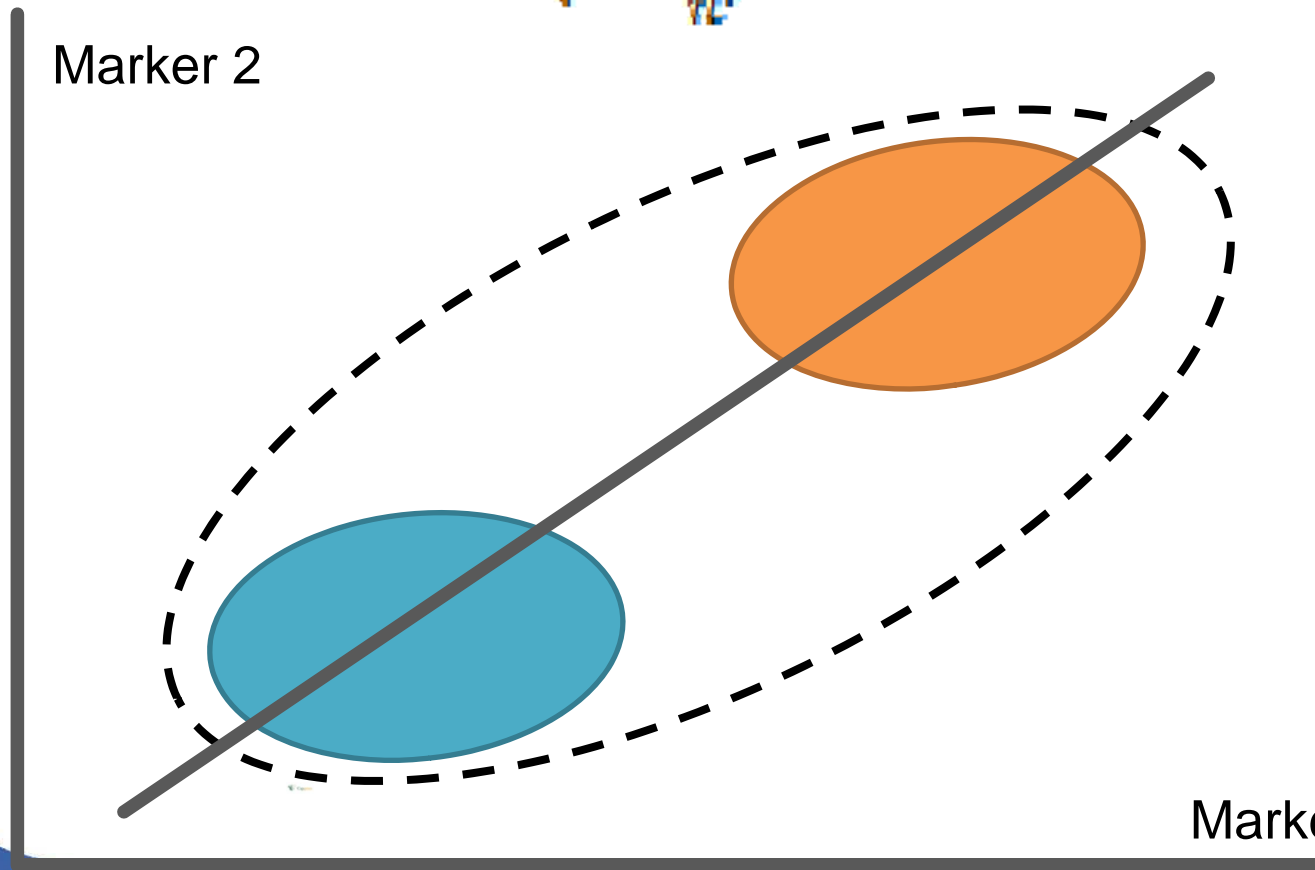
Account for substructure (1)

$$N_e = \frac{1}{3(r^2 - \frac{1}{n})}$$

r^2 = allelic correlation

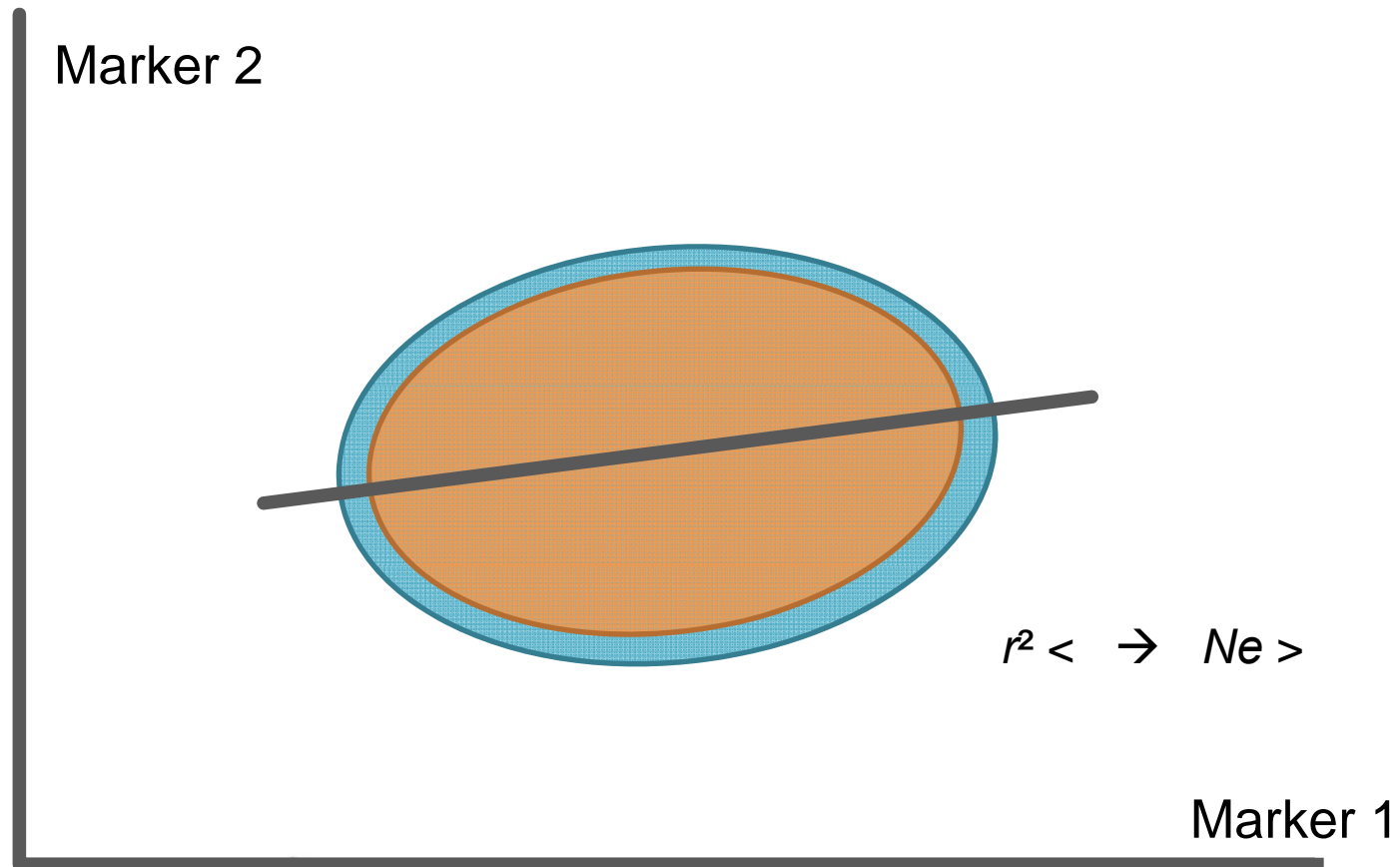
$r^2 \gg \frac{1}{n} \rightarrow N_e \ll$

Marker 2







Marker 1

Account for substructure



Ne results for four dairy sheep breeds (across 4 generations)

Breed	N_e (LD)	N_e (LD struct.)	N_e (F)	N_e (Φ)
	195	303	223	312
	118	145	153	148
	98	/	108	91
	92	/	82	82

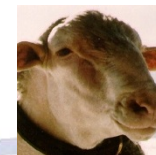
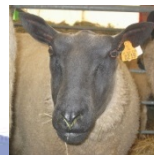
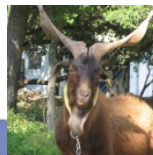
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In the end, what could be accomplished by 2015 ?

- **Regular monitoring of the genetic variability of all ruminant and Equids breeds thanks to an Observatory based on pedigree data:**
 - ✓ All indicators are freely available, by breed, through a web site (? Equids ??)
 - ✓ All indicators are regularly updated
- **Setting up of an Observatory based on genotypes for the breeds using genomic selection**

... if it is feasible and there is true add up value / Pedigrees

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GENOMIA

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Thank you for your attention



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