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Scientific contribution of INRA to pig Genetics

Jean Pierre Bidanel

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Jean Pierre Bidanel. Scientific contribution of INRA to pig Genetics. Rencontre France - Corée, Jun 2003, Paris, France. hal-03364914

HAL Id: hal-03364914

<https://hal.inrae.fr/hal-03364914>

Submitted on 5 Oct 2021

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Session d'information en France «Génétique Porcine»
CORÉE DU SUD

Paris, UBI France, 30 juin - 4 juillet 2003

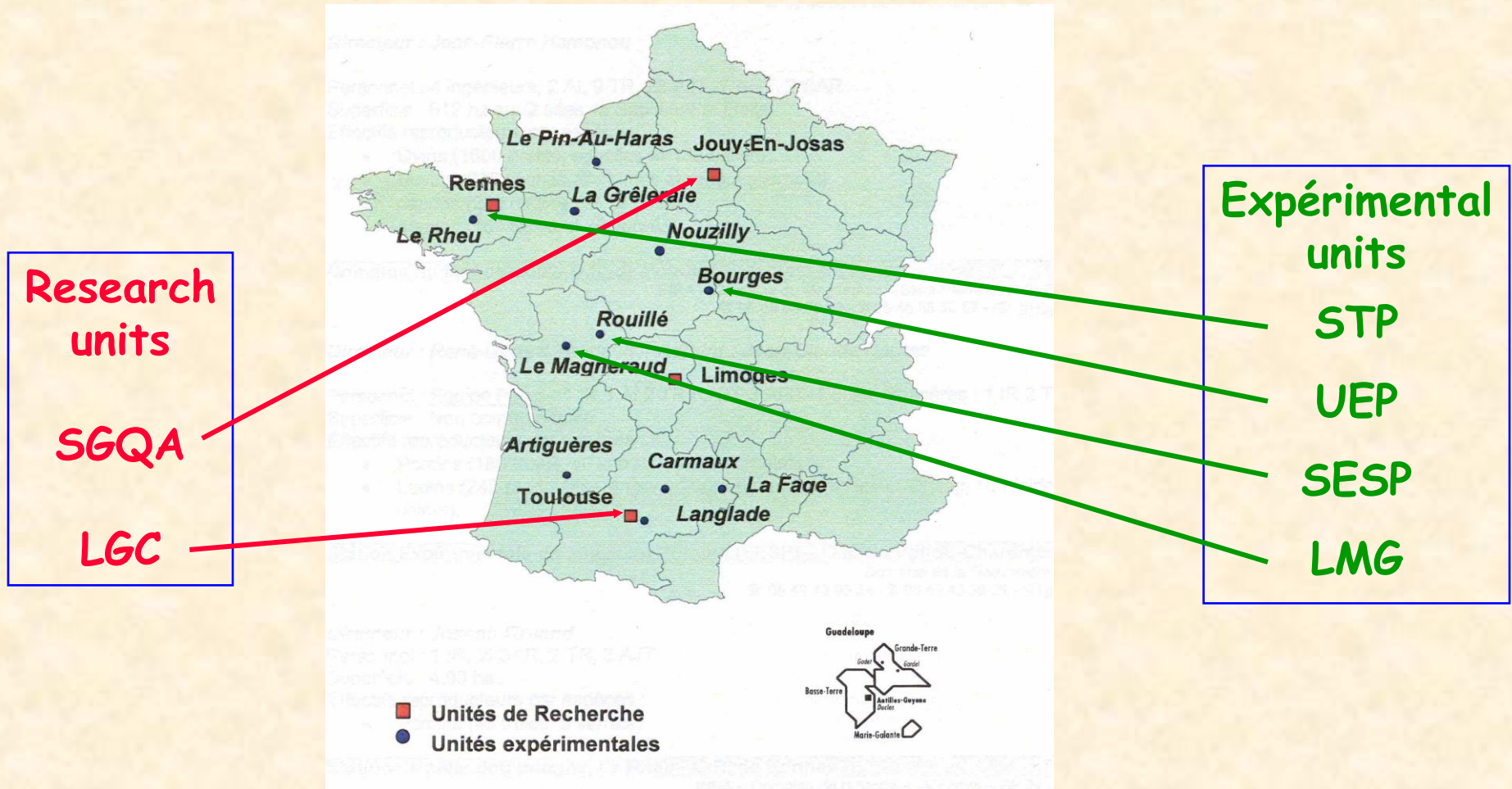
*Scientific contribution of INRA to pig
genetics*

J.P. Bidanel

I.N.R.A.

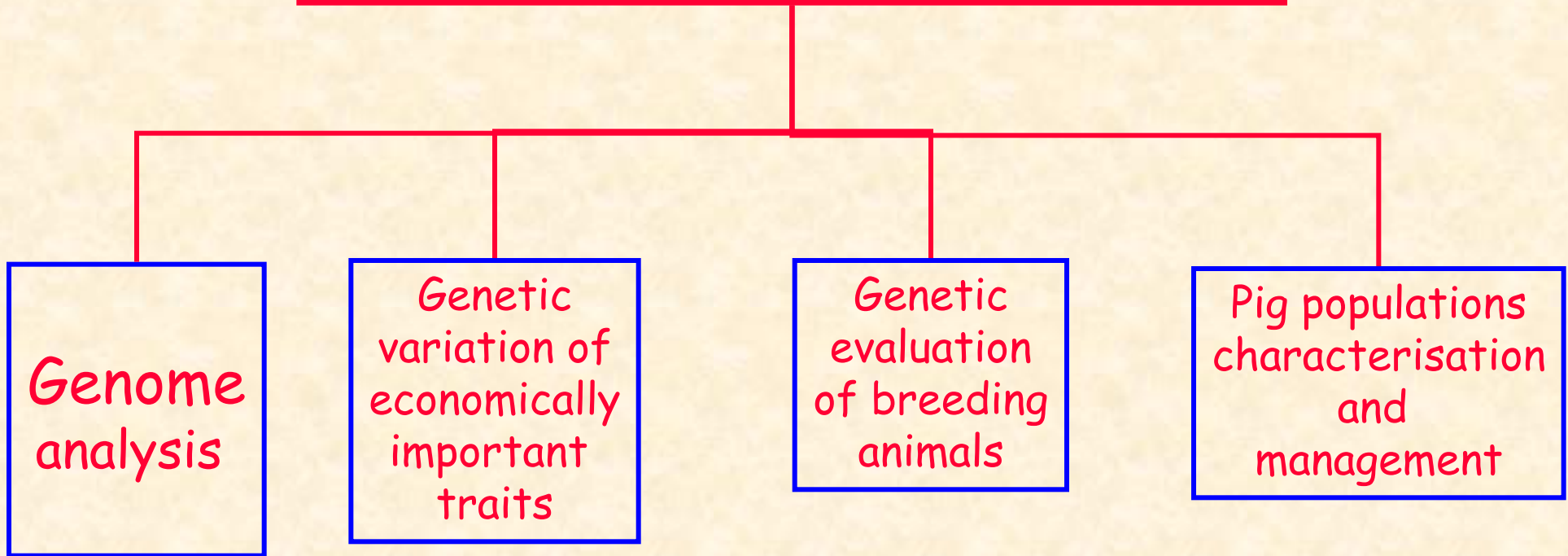
Station de Génétique quantitative et appliquée
78352 Jouy-en-Josas France

Pig genetics at INRA

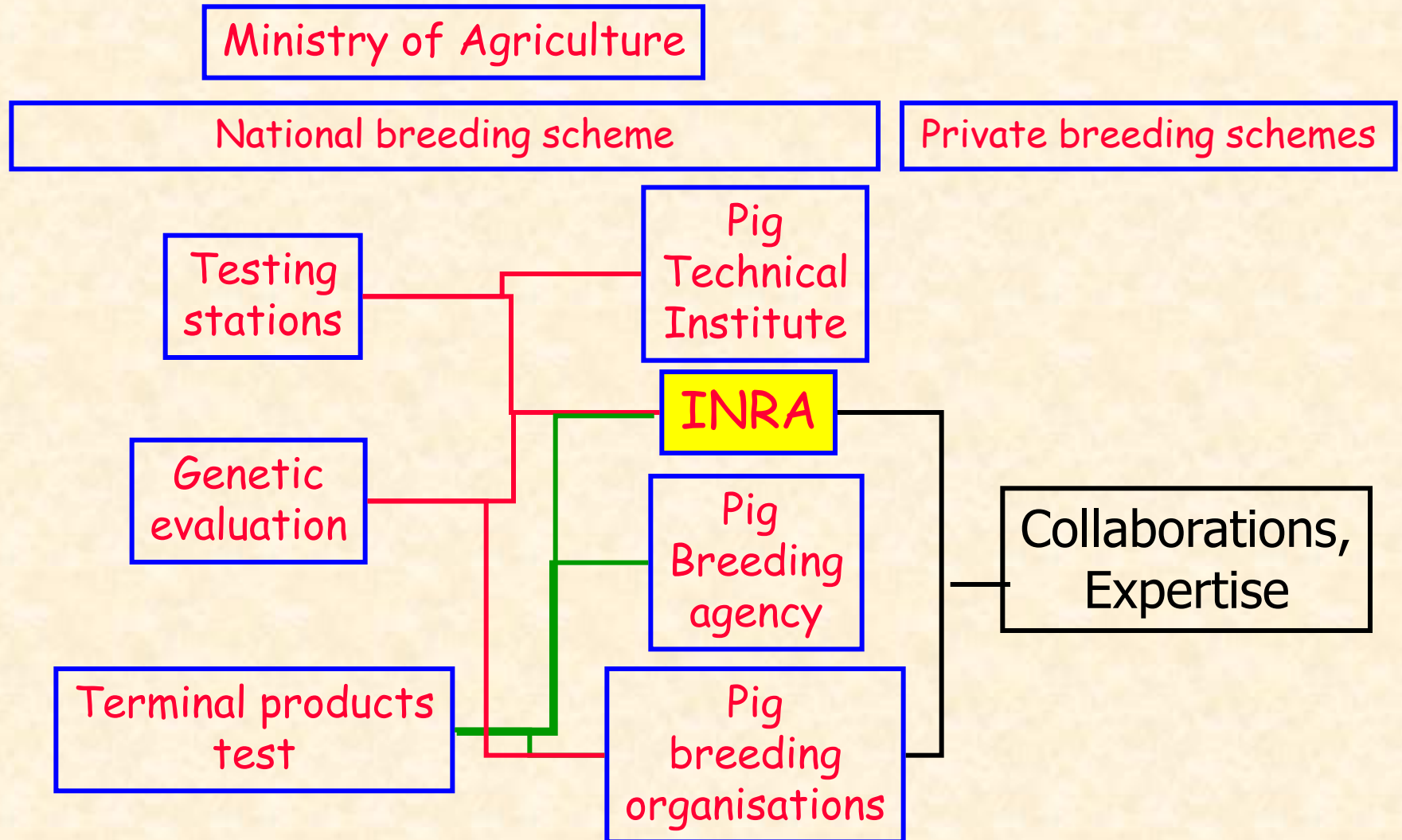


Pig genetics

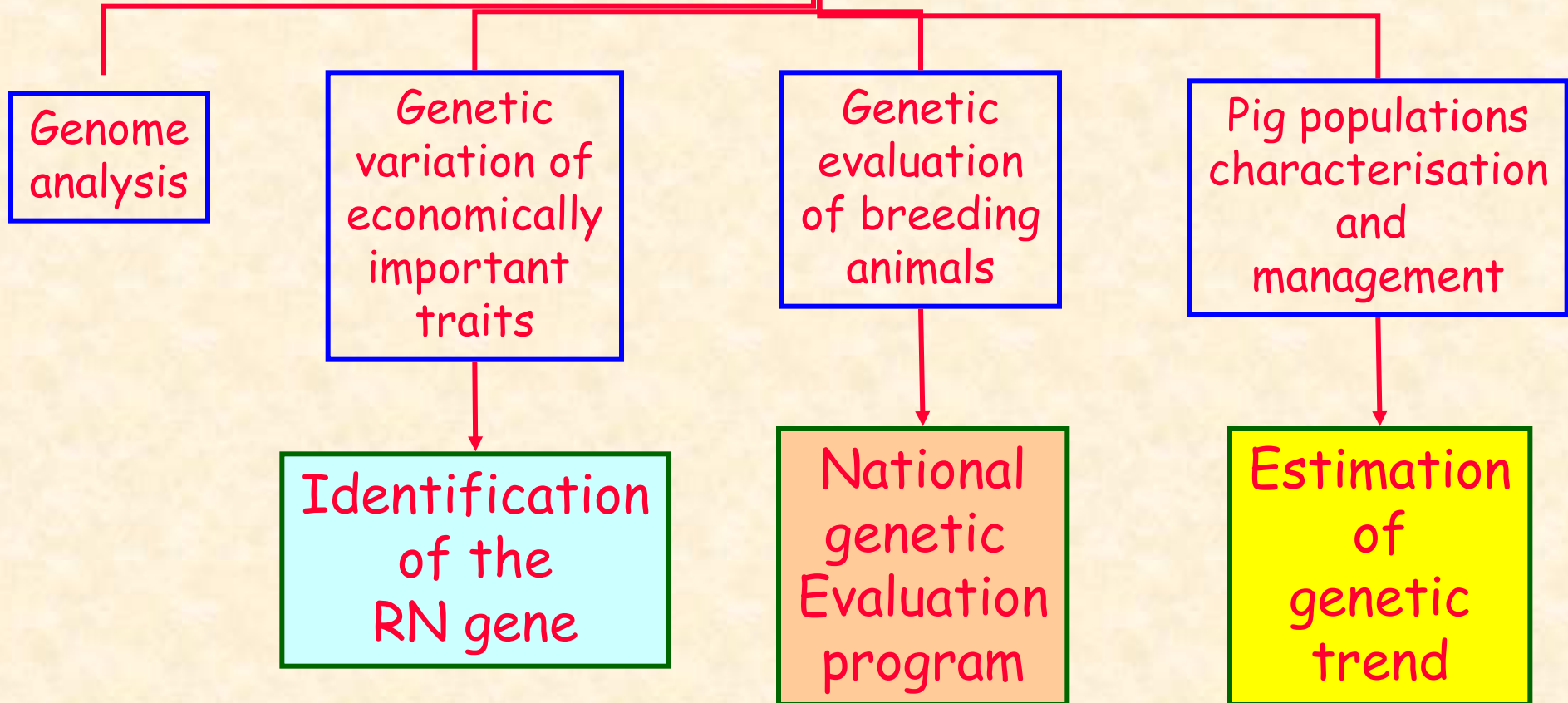
Main research themes



Relationships between INRA and breeding organisations



Research projects - some examples



The RN gene

First results

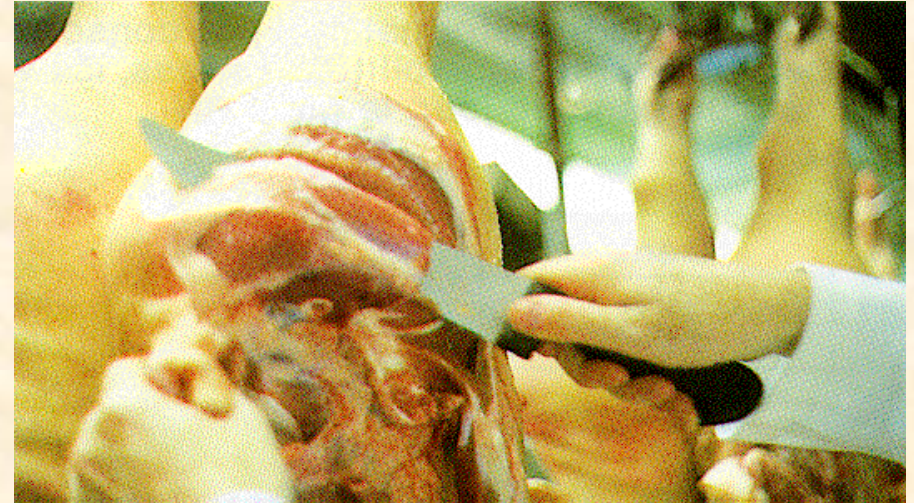
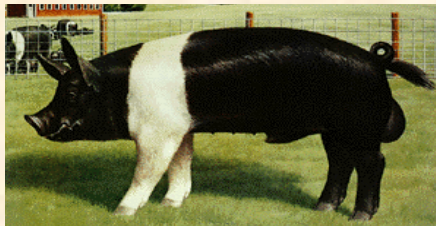
Laconie sire line

Piétrain



Large White

Hampshire

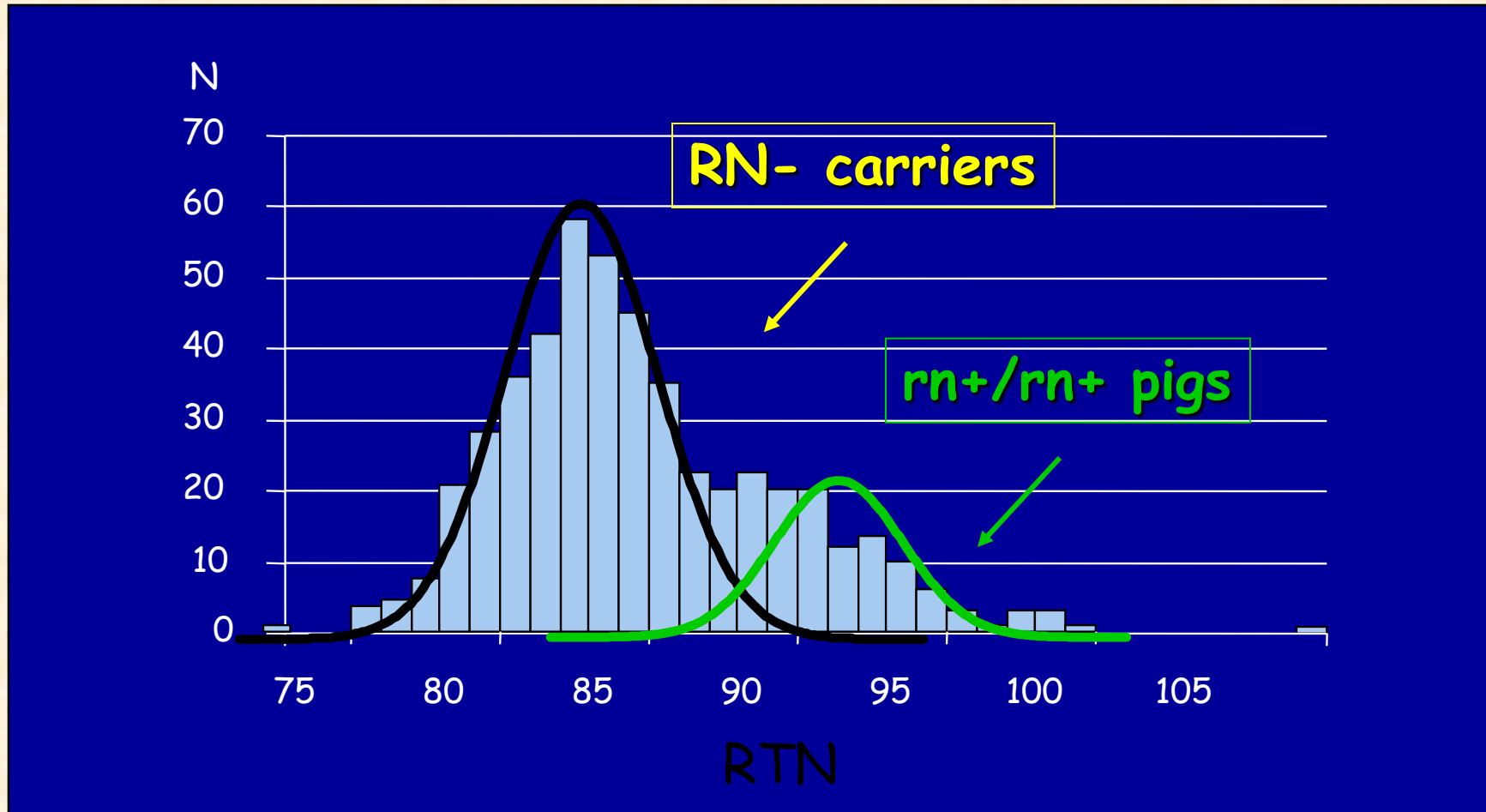


$$\text{RTN} = \frac{\text{Cooked weight}}{\text{Fresh weight}}$$

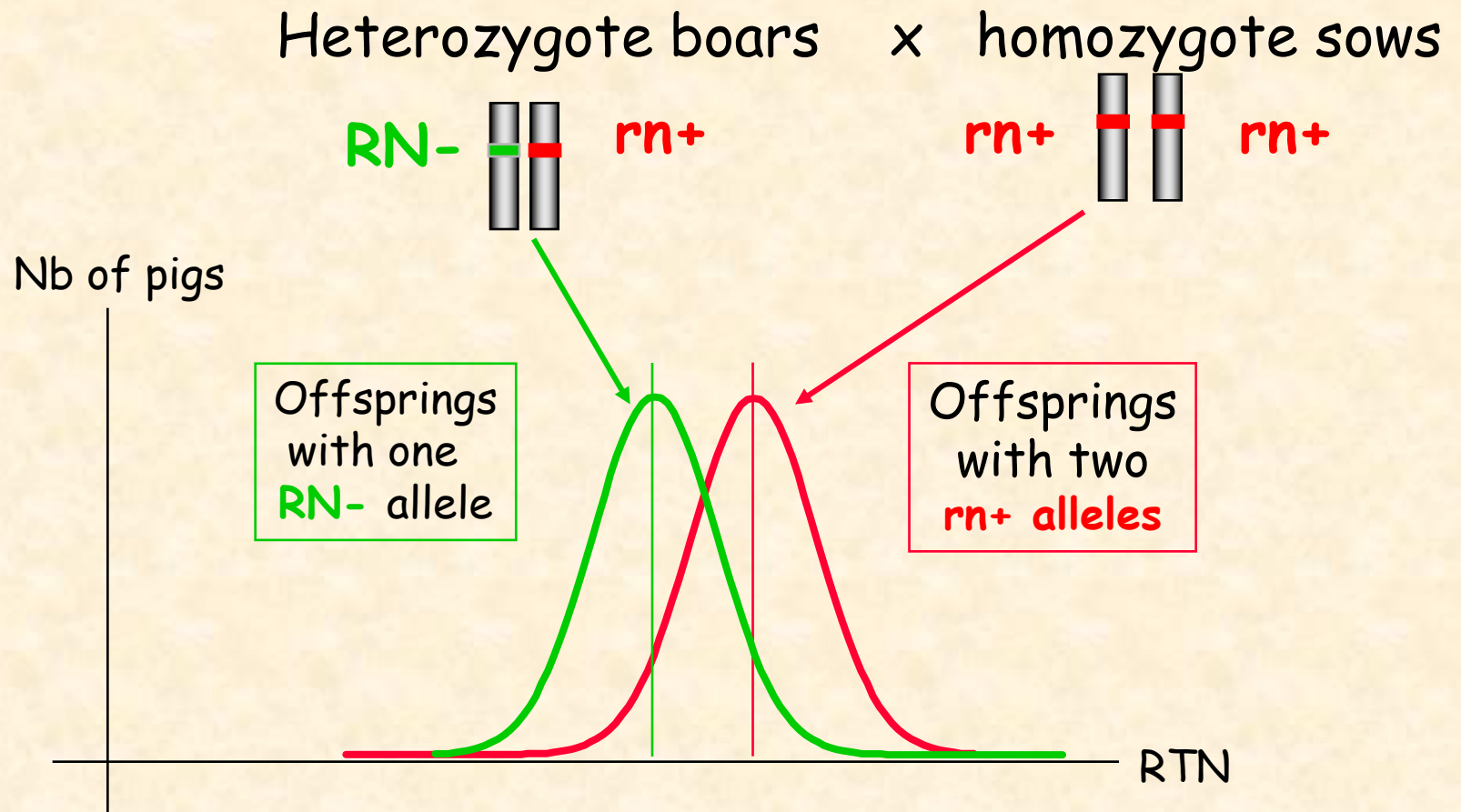
« Paris ham » cooking yield

Distribution of RTN in the Laconie line

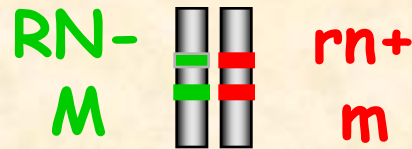
Segregation analysis



Experimental confirmation of RN gene segregation



Looking for a linked genetic marker

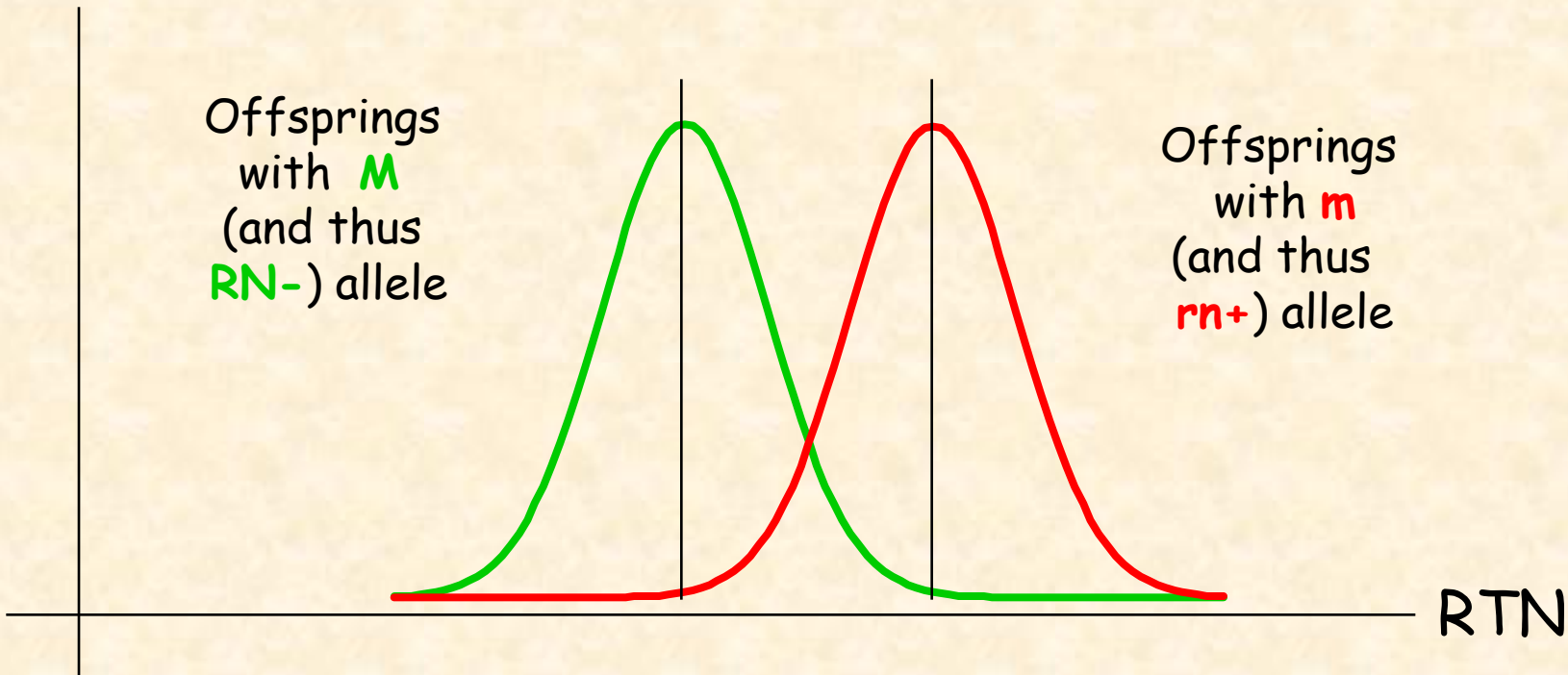


Heterozygote sire
 $RN-M / rn+ m$

Nb of pigs

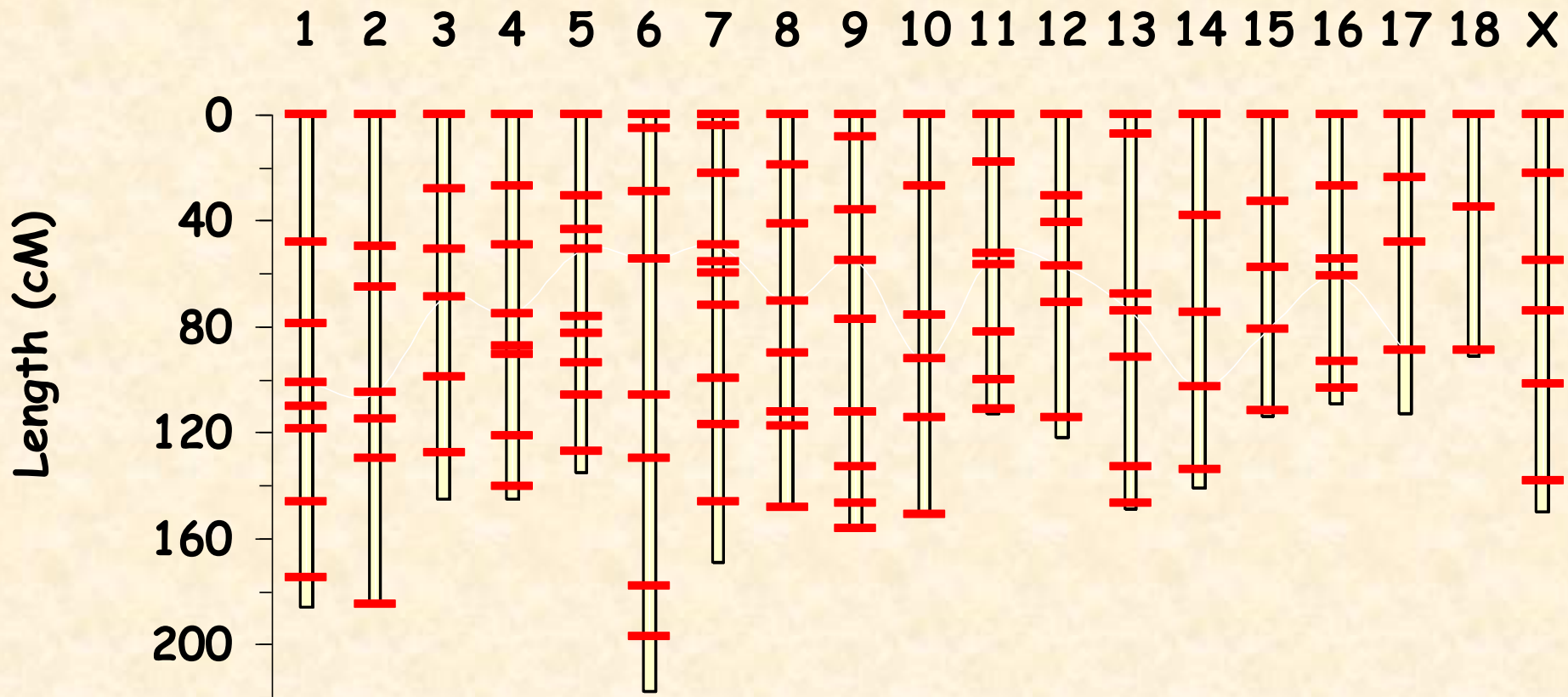
Offsprings
with M
(and thus
 $RN-$) allele

Offsprings
with m
(and thus
 $rn+$) allele



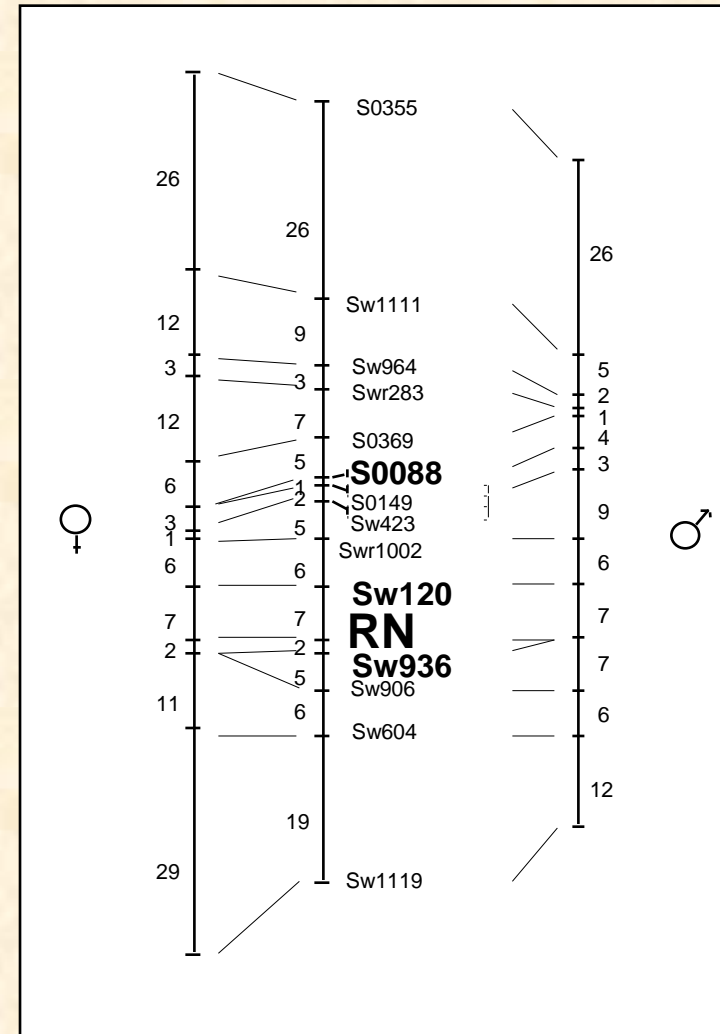
Panel of genetic markers

Chromosome



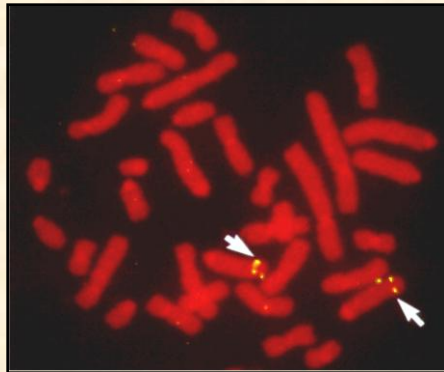
Genetic mapping of the RN gene

- Production of experimental families
- Analysis of **microsatellite** markers
- RN is mapped on chromosome **15** between Sw120 and Sw936 at **2cM** from **Sw936**

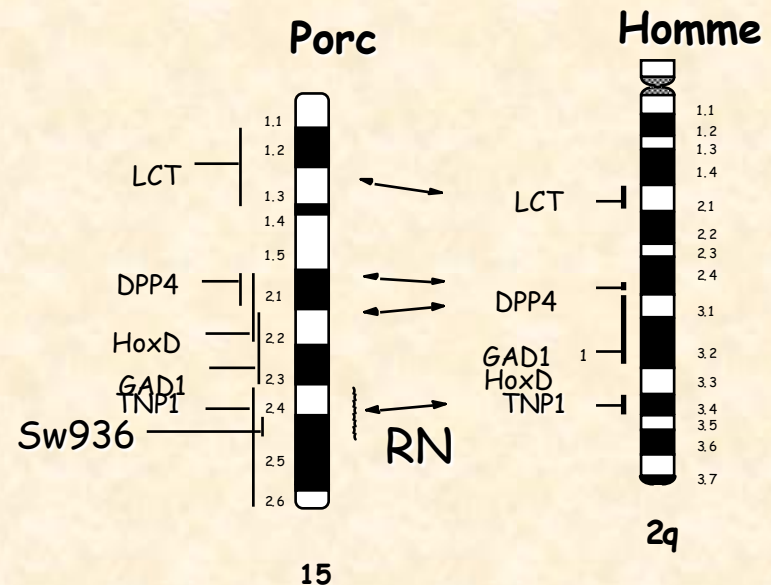


Positional cloning of RN gene (1996-2000)

- ➡ Physical assignment of RN gene in pigs
- ➡ Comparative mapping (with human genome)

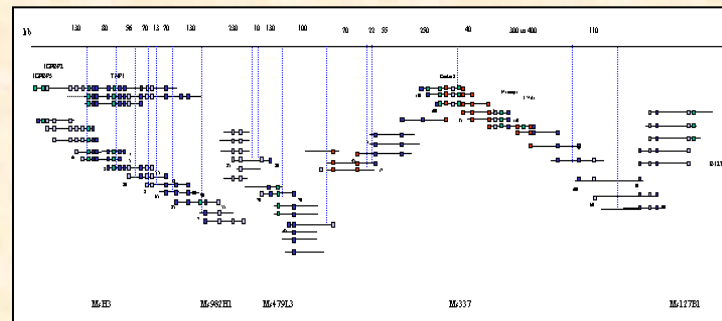


15 q2.5



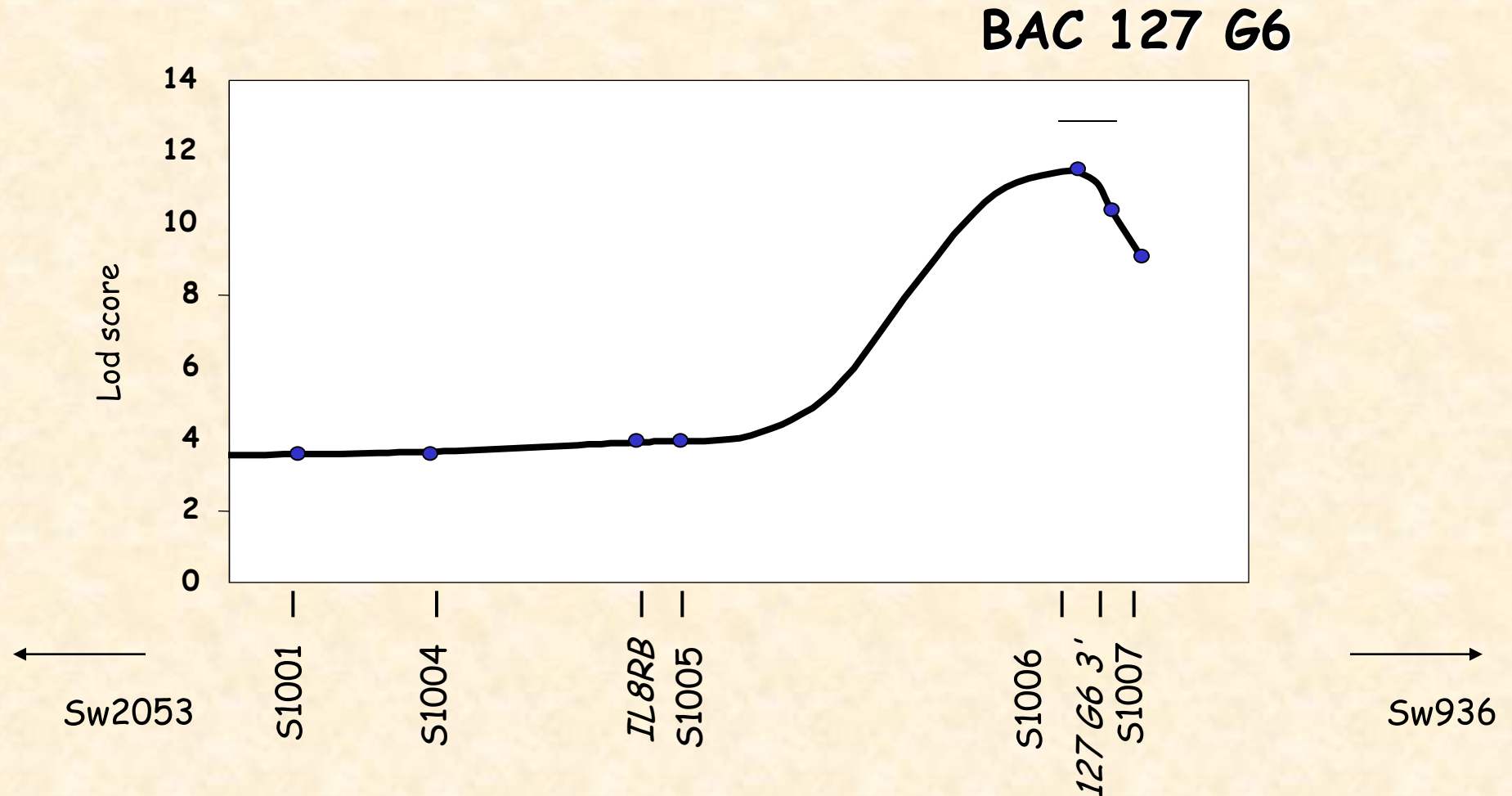
Positional cloning of RN gene (1996-2000)

👉 **physical map** of the RN chromosomal région (contig of **BAC clones**)



Cloning of 2.4 billions letters

Linkage disequilibrium mapping



Séquencing of BAC 127 G6 clone

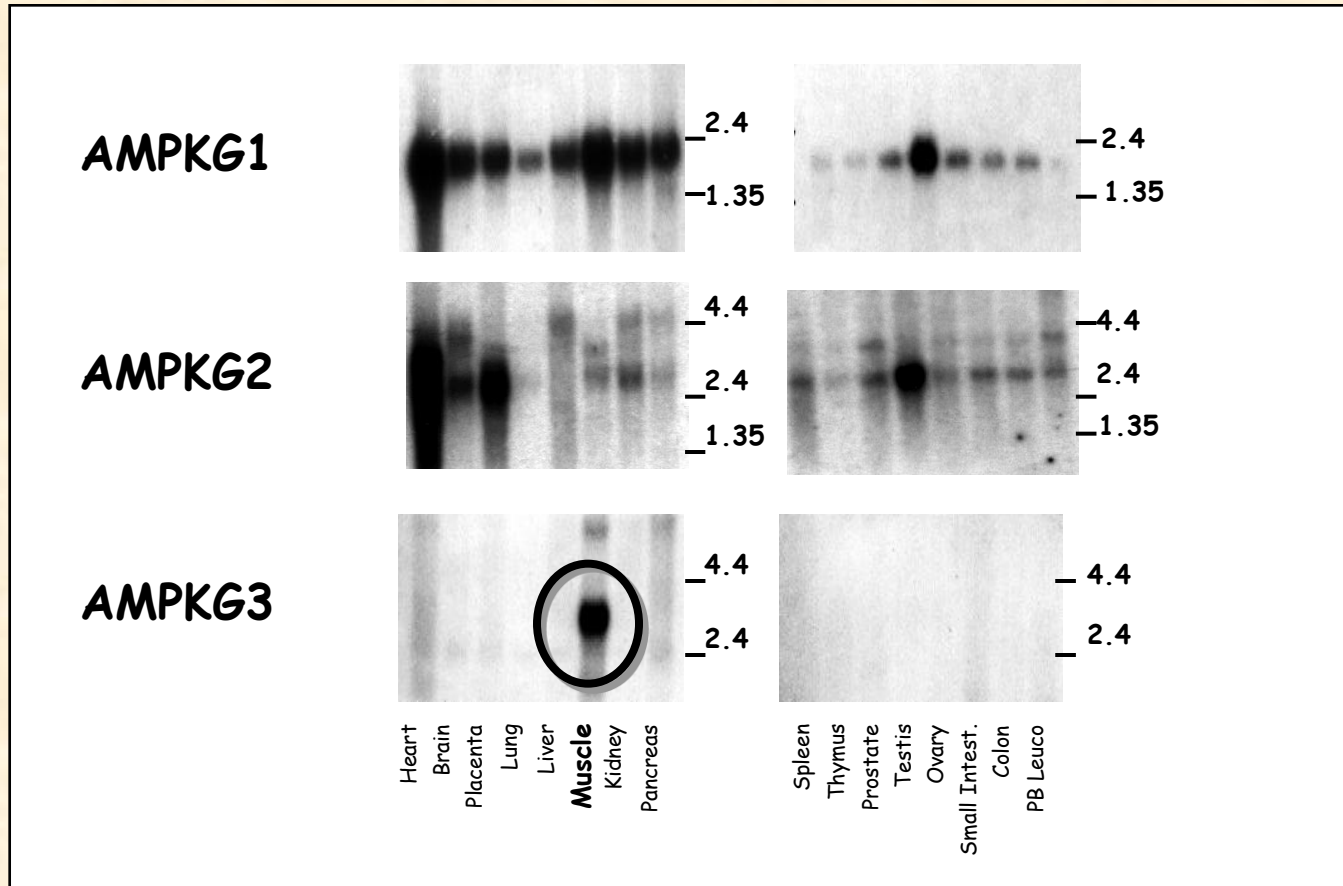
- ☞ The sequence (130.000 lettres) of the **BAC clone** containing the nearest markers has been determined
- ☞ The sequences of 3 genes have been identified

~~CYP27A1~~

~~KIAA0173~~

AMPKG

AMPKG3 is specifically expressed in muscle



Northern blot with human ARNm

Identification of a candidate mutation

- Séquencing of the gene on: $rn+/rn+$ pigs
 $RN-/RN-$
- Identification of a candidate mutation

R 200 Q

The R200Q mutation is associated with RN-

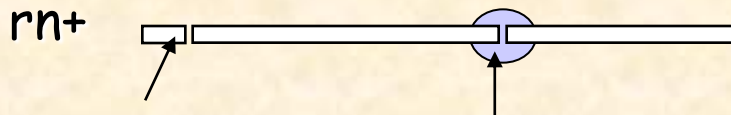
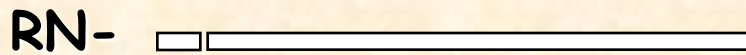
Breed	no	RN	AMPKG3
Hampshire (Sweden)	60	++	R - R
Hampshire (Sweden)	87	[-]	R - Q
Hampshire (Sweden)	40	[-]	Q - Q
Hampshire synthetic line	103	++	R - R
Hampshire synthetic line	91	[-]	R - Q
Hampshire synthetic line	18	[-]	Q - Q
Piértrain	75	++	R - R
Duroc & synthetic lines	160	++	R - R
Large White	72	++	R - R
Landrace	83	++	R - R
Meishan	8	++	R - R
Wild boar	8	++	R - R
Other breeds	70	++	R - R

Development of a diagnostic test

PCR amplification

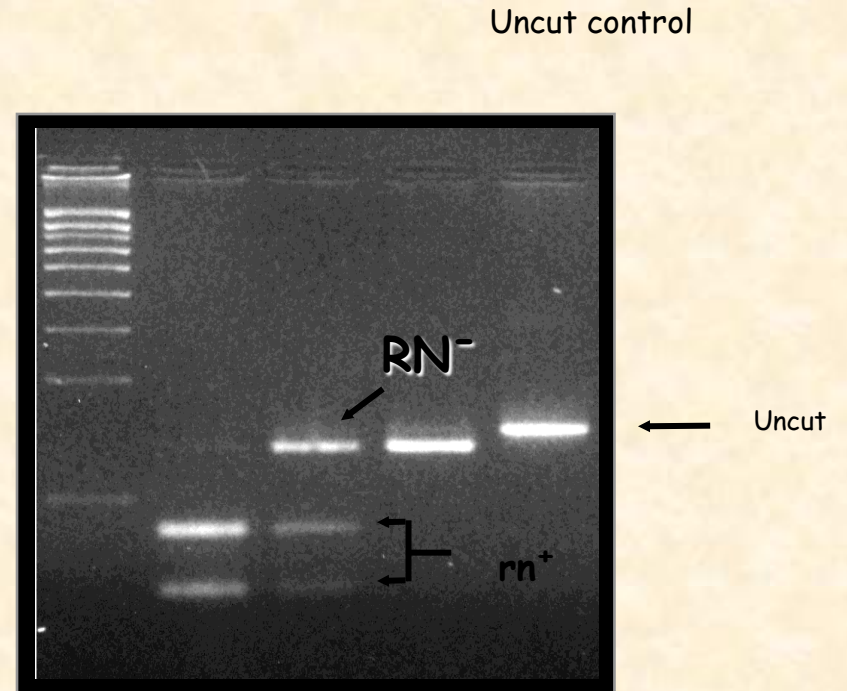


Enzyme digestion



Primer control site

Diagnostic site



rn⁺ RN⁻ RN⁻
rn⁺ rn⁺ RN⁻

Genetic evaluation of pigs

Genetic evaluation of pigs

« BLUP - animal model » genetic evaluation

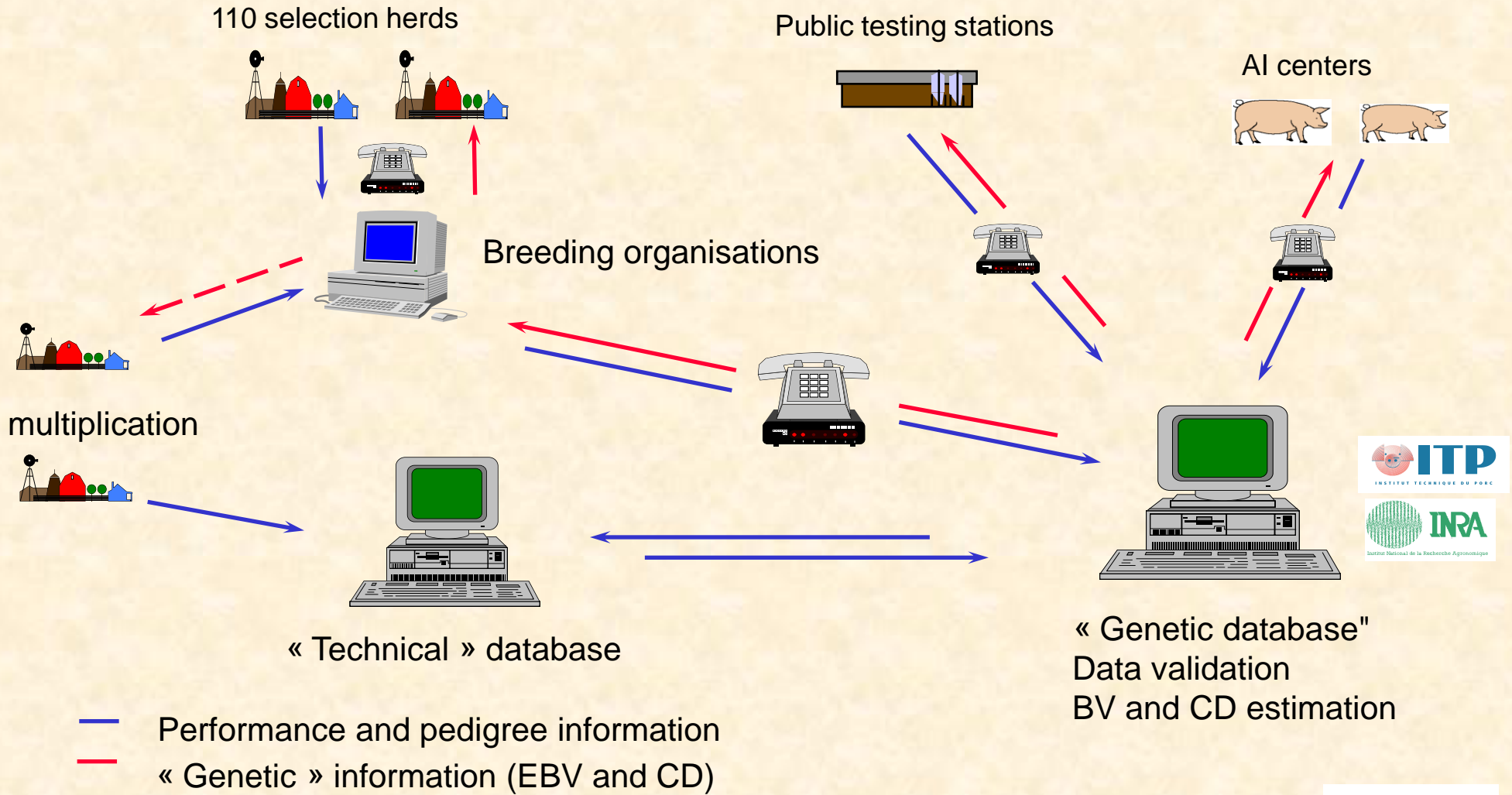
- ☛ - performances have to be centralised
- pedigrees

☛ Information has to be transmitted quickly

☛ High frequency of genetic evaluations

- National genetic evaluation every month
- Within - herd evaluation

Genetic information flow

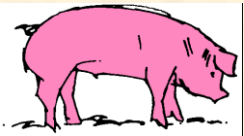


Genetic evaluation

Production traits

On-farm test

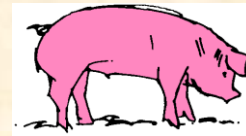
Male and female candidates to selection



Age at 100 kg (A100)
Backfat thickness at 100 kg (BF100)
(Loin depth)
(Meat quality)

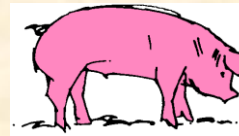
Station test

Young candidate boars (until 1996)

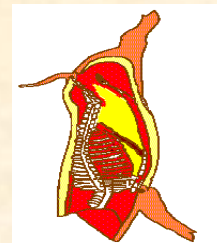


Average daily gain (ADG)
Backfat thickness (ABF)
Food conversion ratio (FCR)

Slaughtered sibs (since 1997)



Average daily gain
Food conversion ratio



Dressing % (DP)
Muscle content (MC)
Meat quality index (MQI)

Genetic parameters

Large White

	ADG1	ABF	FCR	ADG2	DP	MC	MQI	A100	BF100
ADG 1	0.30	0.27	0.02	0.89	-0.25	-0.22	0.11	-0.65	0.22
ABF	0.25	0.73	0.74	-0.11	0.20	-0.79	0.23	0.05	0.85
FCR	0.01	0.40	0.41	-0.36	0.07	-0.78	0.22	0.16	0.55
ADG 2	0.27	-0.05	-0.41	0.30	-0.31	0.12	0.07	-0.80	-0.06
DP	-0.09	0.11	0.10	-0.09	0.40	-0.02	-0.10	0.30	-0.03
MC	-0.10	-0.54	-0.47	-0.03	0.02	0.63	-0.22	0.01	-0.85
MQI	0.03	0.09	0.08	0.00	-0.04	-0.07	0.21	0.00	0.13
A100								0.19	-0.09
BF100									0.42

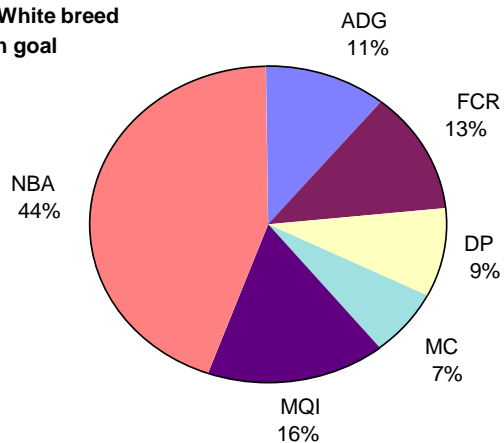
On the diagonal : heritabilities

Above diagonal : genetic correlations

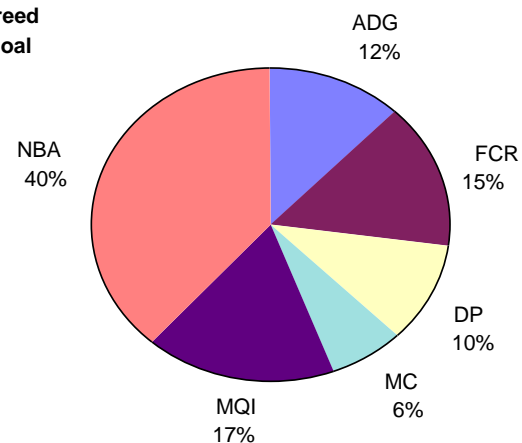
Below diagonal : phenotypic correlations

Selection goals (until 2002)

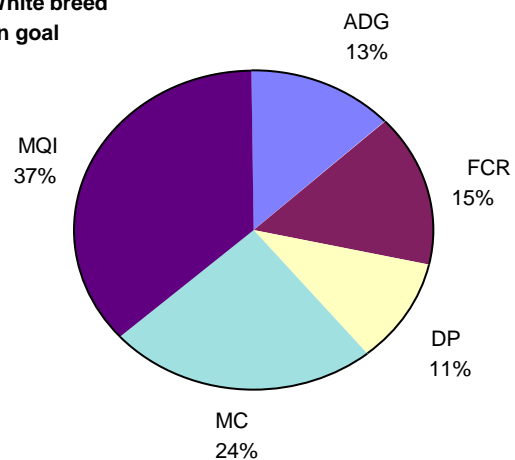
**Female Large White breed
Selection goal**



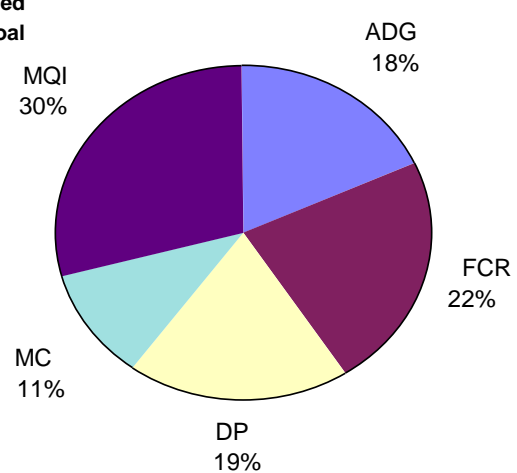
**Landrace breed
Selection goal**



**Male Large White breed
Selection goal**

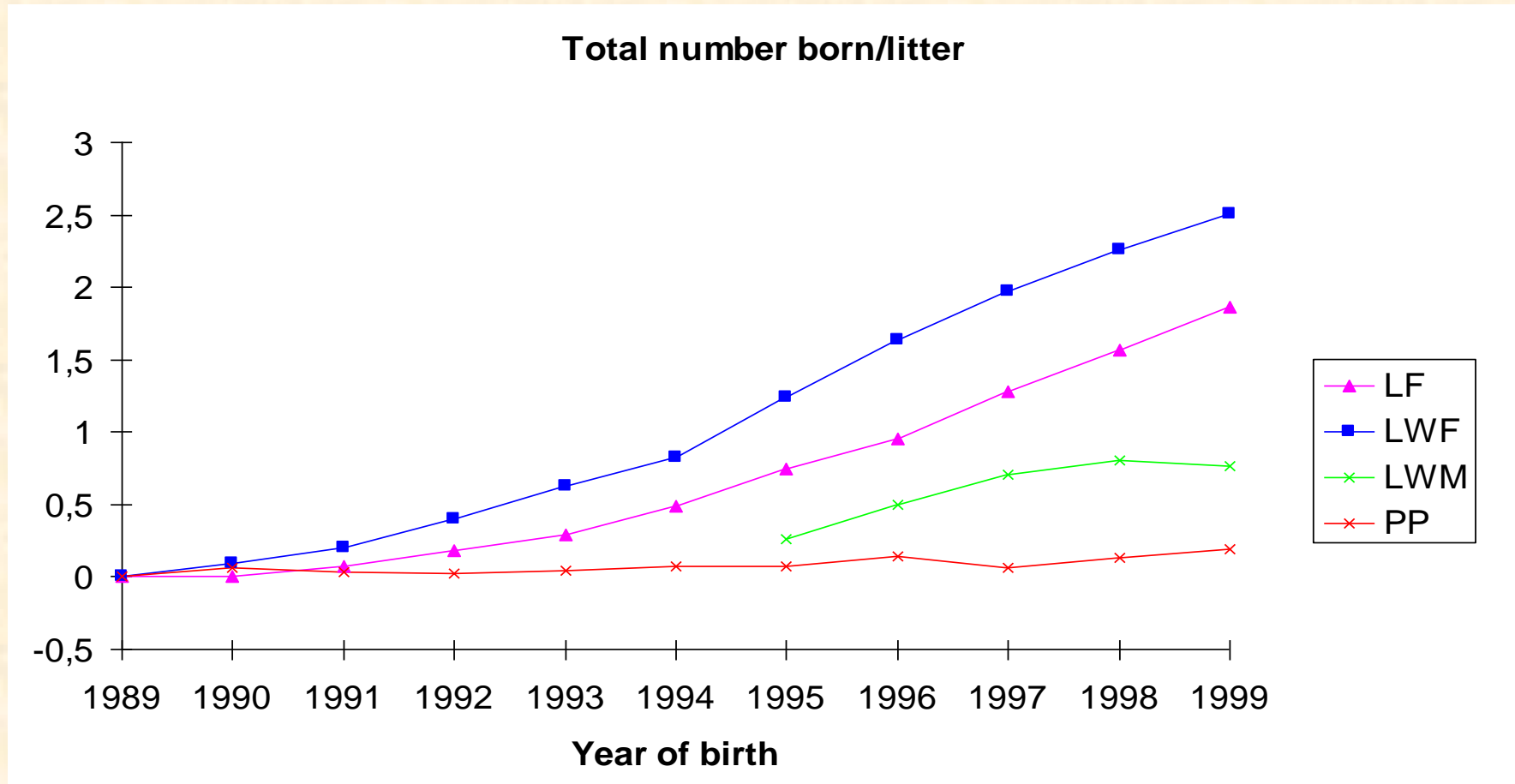


**Piétrain breed
Selection goal**



Estimating genetic trend from genetic evaluation results

Estimated genetic trends : main French breeds



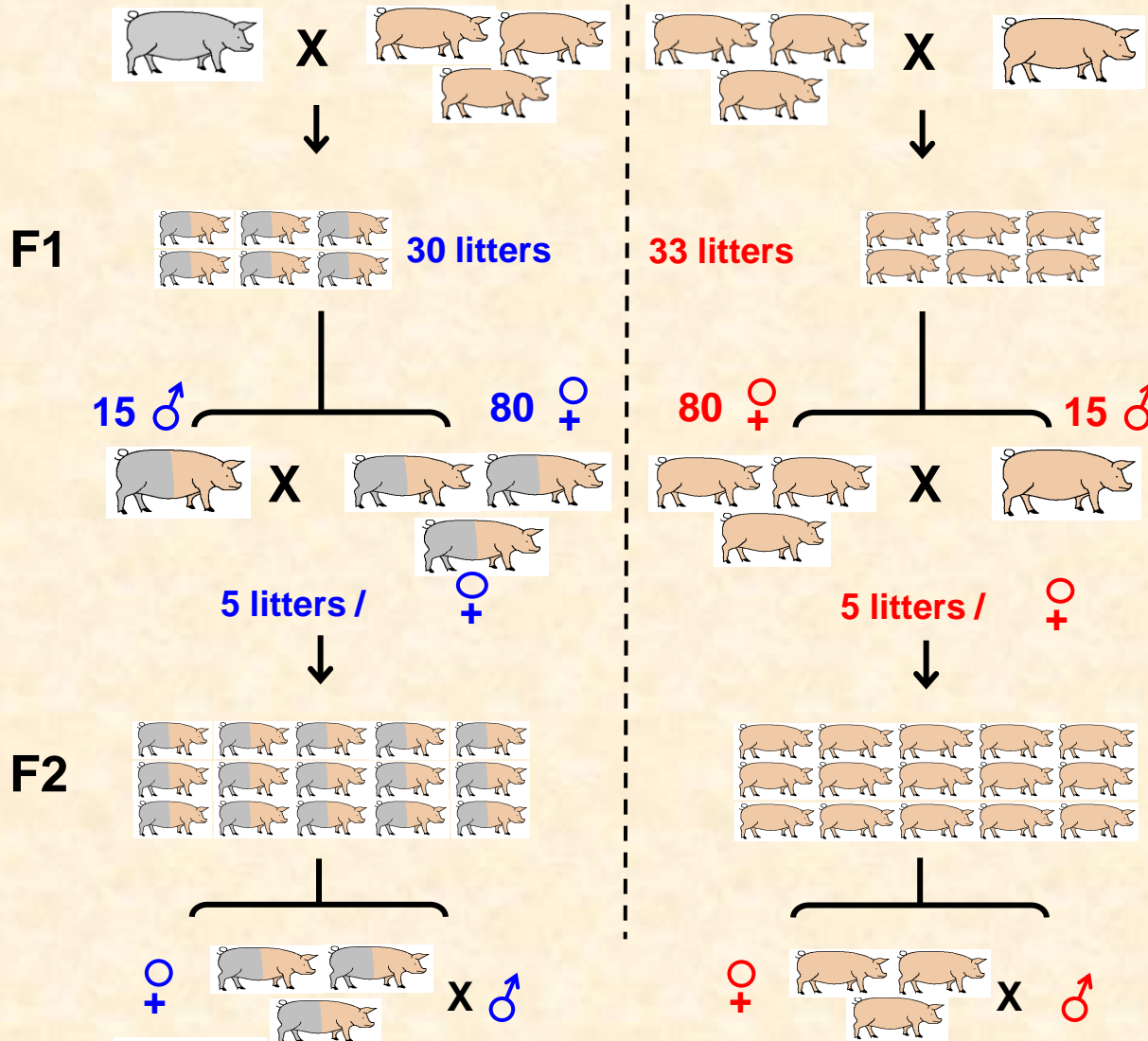
Estimation of realised genetic trend using frozen semen

Experimental design

17 AI boars born in 1977

LW females

23 AI boars born in 1998



- growth, backfat thickness
- puberty ♀, intensity of oestrus
- Sexual development ♂
- Semen production

- Ovulation rate
- Litter size at birth and at weaning
- Piglet weight at birth & weaning
- colostrum & milk composition
- Milk production, ...

- Growth & carcass traits
- Tissue characteristics & quality
- Teat number
- Disease resistance
- Piglet maturity
- Leg and bone quality

- Maternal behaviour

Estimated genetic trends - reproduction (1)

Trait	Estimated genetic trend
Age at puberty (d)	-9,2 ns
Ovulation rate	4,0 **
Prenatal survival (%)	5,3 ns
Total number born	2,9 **
Number born alive	2,1 *
Number of stillborn	0,7 *
0-21 d survival rate	-4,2 ns

Ns =not significant; * $P < 0.05$; ** $P < 0.01$

Estimated genetic trends - reproduction (2)

Trait	Estimated genetic trend
Birth weight (g)	74 ns
Adjusted (T NB) birth weight (g)	182 **
Standard deviation(birth weight) (g)	76 ***
ADG 0-21 d /piglet genotype (g)	-10 ns
ADG 0-21 d /sow genotype (g)	-22 *
Total teat number	0,4 *
Functional teats	1,8 ***

Ns =not significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$

Estimated genetic trends - production (1)

Trait	Estimated genetic trend	
	Large White	Landrace
ADG from 10 to 22 wk	206 ***	130 **
Food conversion ratio	-0,44 ***	-0,10 ns
Daily feed intake (kg/d)	0,18 ns	0,22 ns
Estimated lean content	7,1 ***	5,1 ***
Dressing %	-3,1 *	-0,9 ns

Estimated genetic trends- production (2)

trait	Estimated genetic trend	
	Large White	Landrace
pH 30 mn	0,02 ns	0,12 ***
pH (DM) 24 h	-0,26 **	0,0 ns
Water retention (%)	5,6 ***	-3,3
Water losses	1,0 ns	-4,4 **

Conclusion

- Animal breeding in France
- Close relationships between research, development and breeding organisations
 - Innovations are quickly used in practise
- Participation of the ministry of agriculture
- Strong concurrency
- Objective comparisons (terminal products)