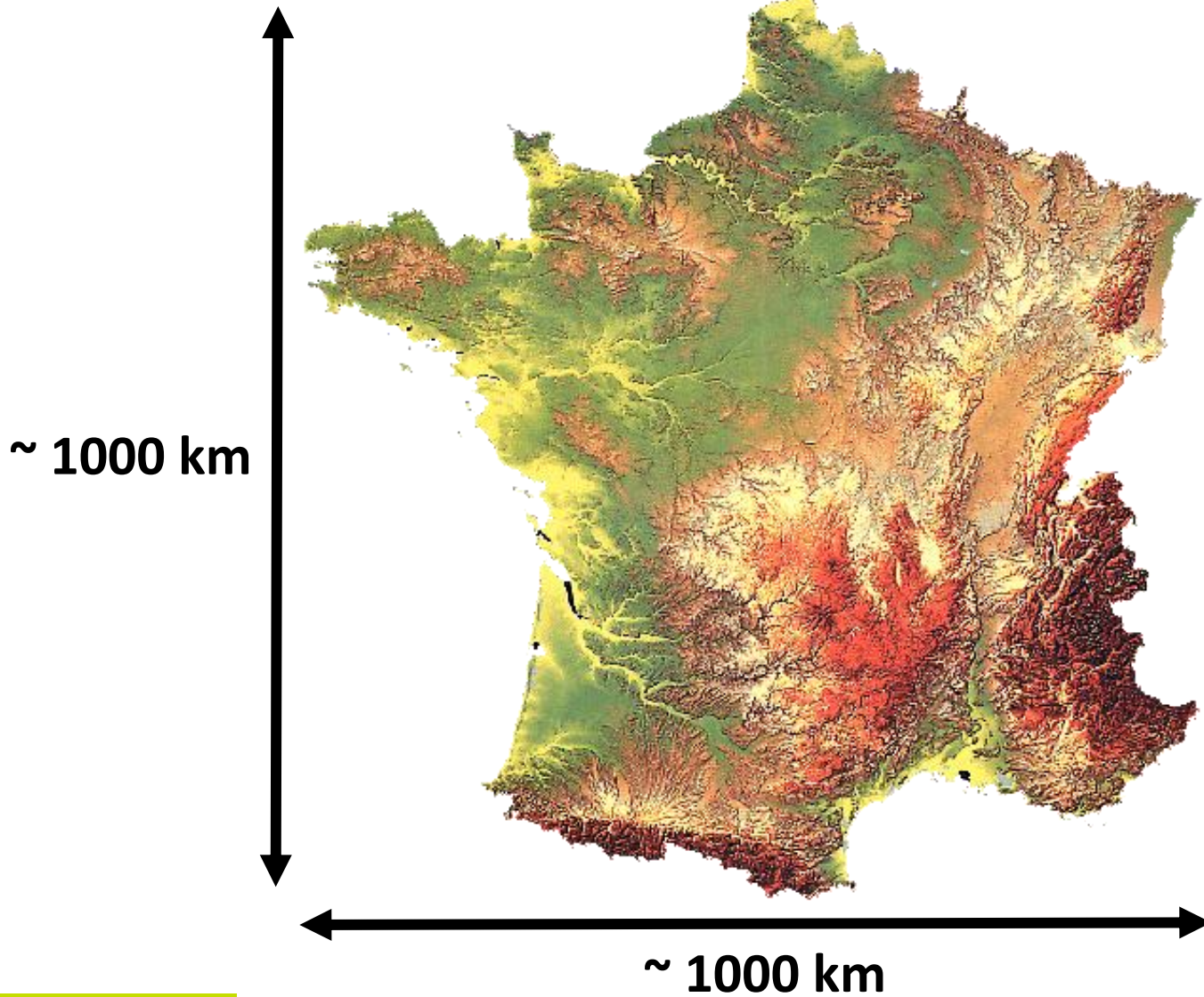# French genomic experience: genomic for all ruminant species

E. Venot[1], D. Boichard[1], V. Ducrocq[1], P. Croiseau[1], S. Fritz[3], A. Baur[3], R. Saintilan[3], T. Tribout[1], .M-P Sanchez[1], P. Boulesteix[2], JM. Astruc[2], A. Legarra[1], C. Robert-Granié[1], C. Carillier[1], I. Palhière[1], F. Tortereau[1], R.Rupp[1], H. Larroque[1], V. Loywyck[2], S. Mattalia[2]

[1] INRA, [2] IDELE, [3] ALLICE

French specificities

~ 1000 km

~ 1000 km

Source: www.CartesFrance.fr

**French genomic experience:
genomics for all ruminant species
27th October 2016**

French specificities

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Large number of breeds

French Bovine Breeds

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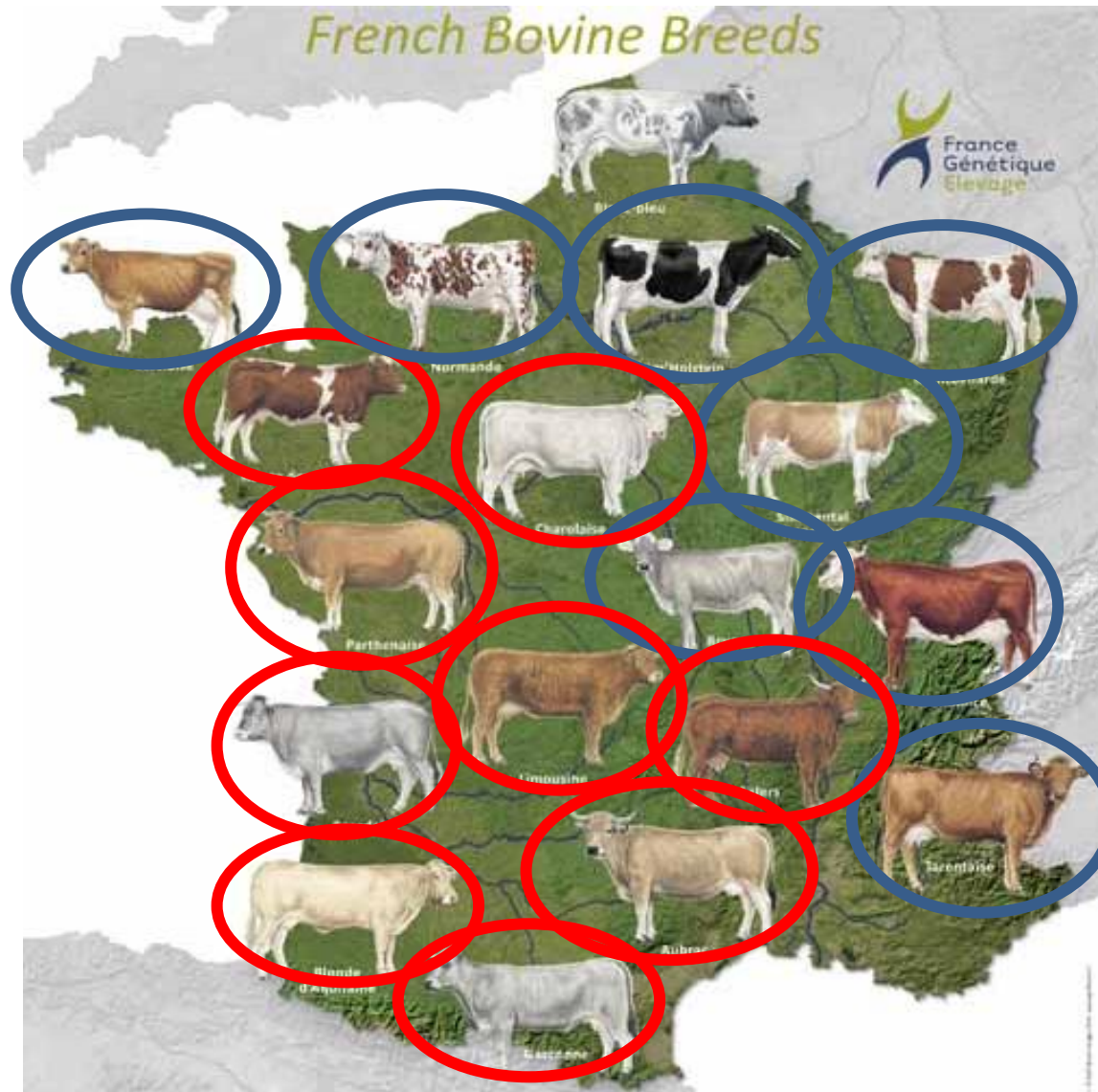
Small ruminant breeds

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French national and collective organization

▶ **Inter-professional association for genetic improvement of all ruminants**

▶ **Common management quality system for all on-field organizations**

▶ **Centralized national database**

▶ **Close relationship between Industry partners and R & D**

➡ **Win – Win situation**

▶ **Share of R & D between species**

▶ **Example with the share of tools:**

   ○ **in 2016 a common pipeline to impute & phase Dairy & Beef genomic information from different chips**

   ○ **implementation of dairy sheep in the same pipeline in progress**

French genomic developments led by Dairy cattle pioneers

IDEAL SITUATION

► **large number of tested bulls and large use of AI**

► **large generation interval**

► **high cost of progeny testing**

► **small genetic size populations**

► **relative small genotyping cost / breeding animal price**

► **international breeds (Interbull evaluation and possible consortia)**

ALL TOOLS TO IMPROVE:

$$\Delta G = \frac{i.R.\sigma_g}{T}$$

Reference population size & Accuracy (R)

Reference population per breed and reliabilty expected for candidates

Breed	Nb Bulls	Nb Dams	Young candidate REL
HOLSTEIN	33000	-	[0.55-0.70]
BROWN	6000	-	[0.45-0.70]
MONTBELIARDE	2800	31000	[0.55-0.70]
NORMANDE	2400	16000	[0.50-0.65]

December 2015

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Reference population size & Accuracy (R)

Reference population per breed and reliabilty expected for candidates

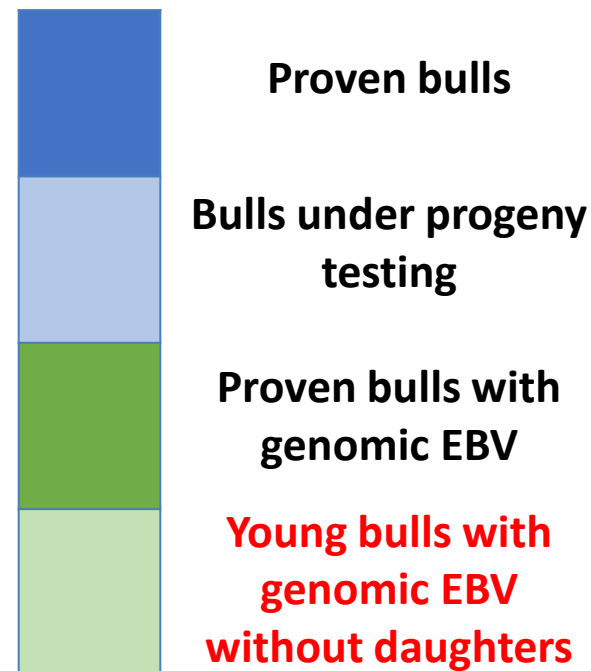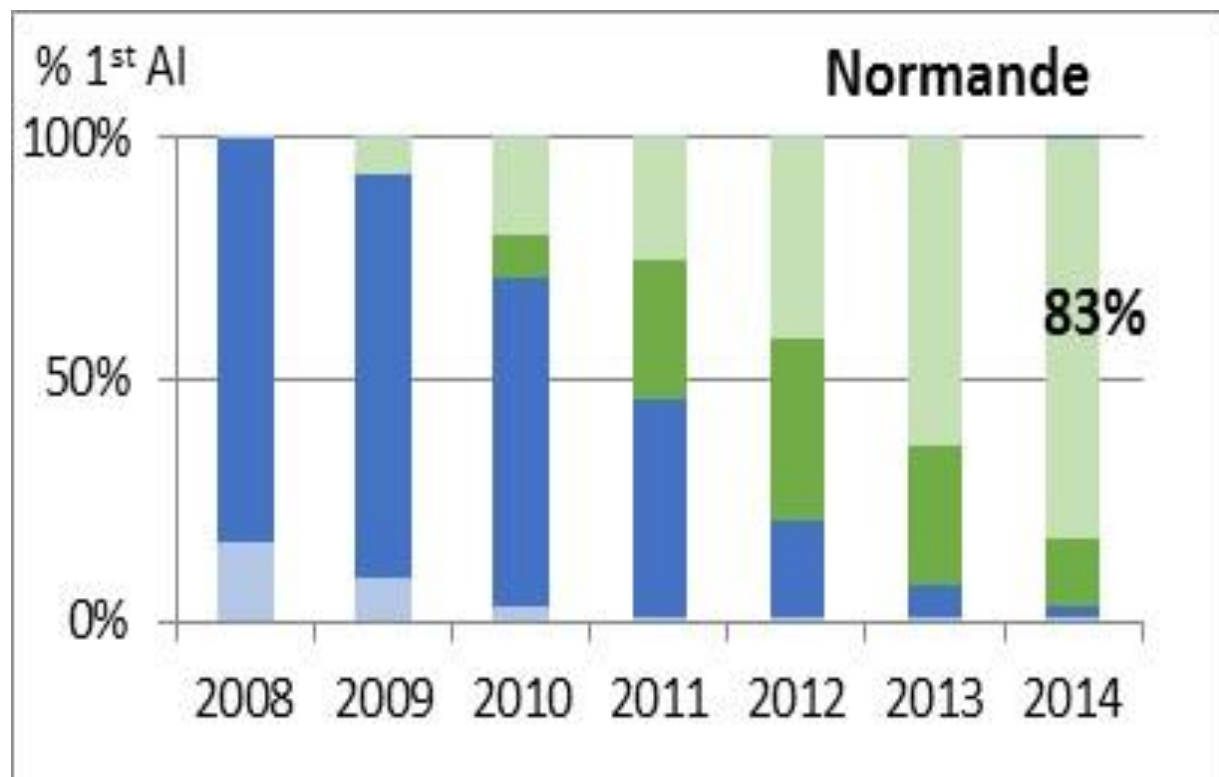| Breed	Nb Bulls	Nb Dams	Young candidate REL
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December 2015

Genomic selection started in 2009 (QTL-GS)

6 times / year with QTL and marker effects estimation

+

Weekly (without QTL effect estimation)

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Reduction of generation interval and more efficient selection on functional traits

Milk yield REL	0.30			0.75	0.95
Fertility REL	0.20			0.45	0.95

Before GS — Birth

Pedigree index → EBV based on progeny results

18 months
Few AI

6 years
1st daughters in production

6-8 years
Most AI

After GS

Pedigree index → Genomic breeding value → EBV based on progeny results

3 months
Genotyping + GEBV computation

Most/all AI

Milk yield REL	0.70	0.95	
Fertility REL	0.60	0.95	

=> T shortened by 3-4 years
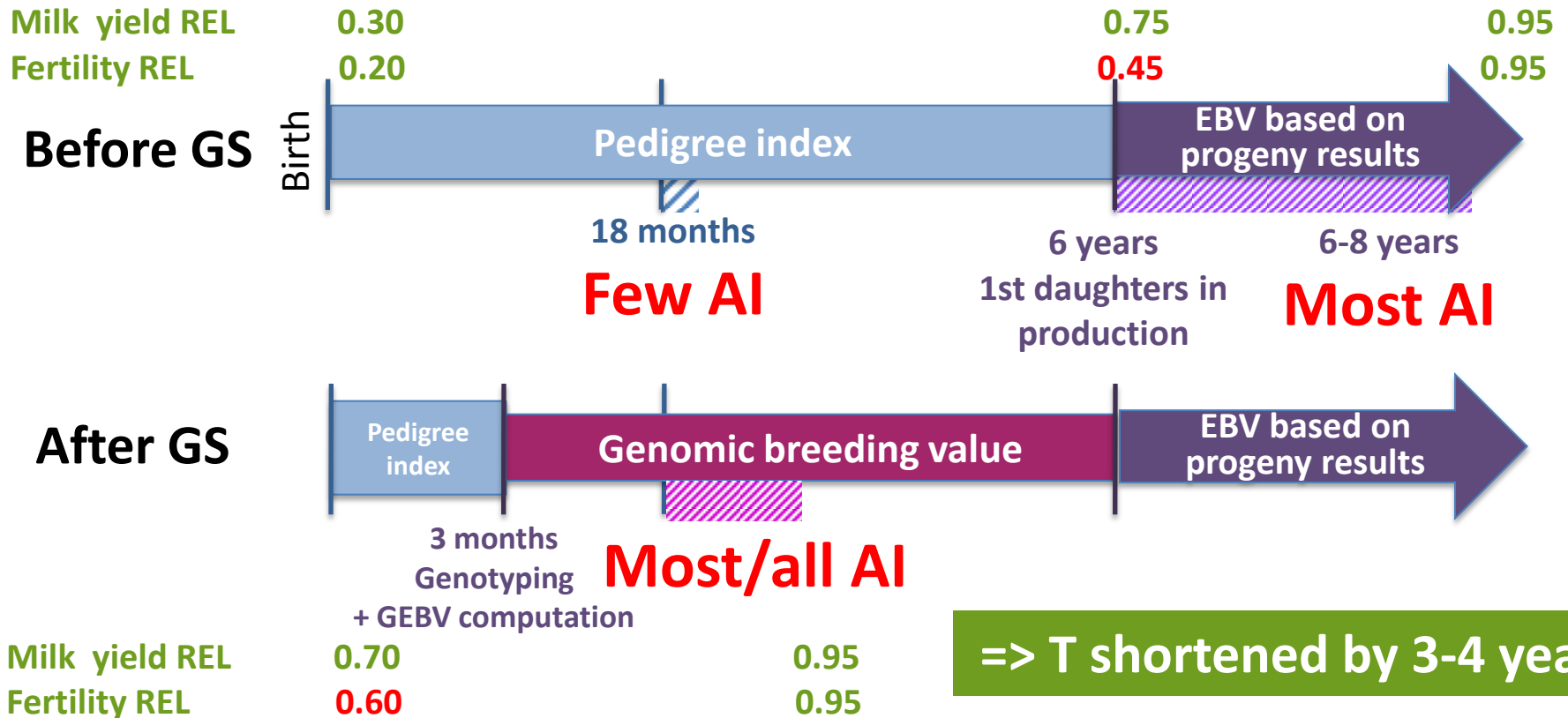
Quick adoption of GS by breeders: use of young genomic bulls

AI % in France

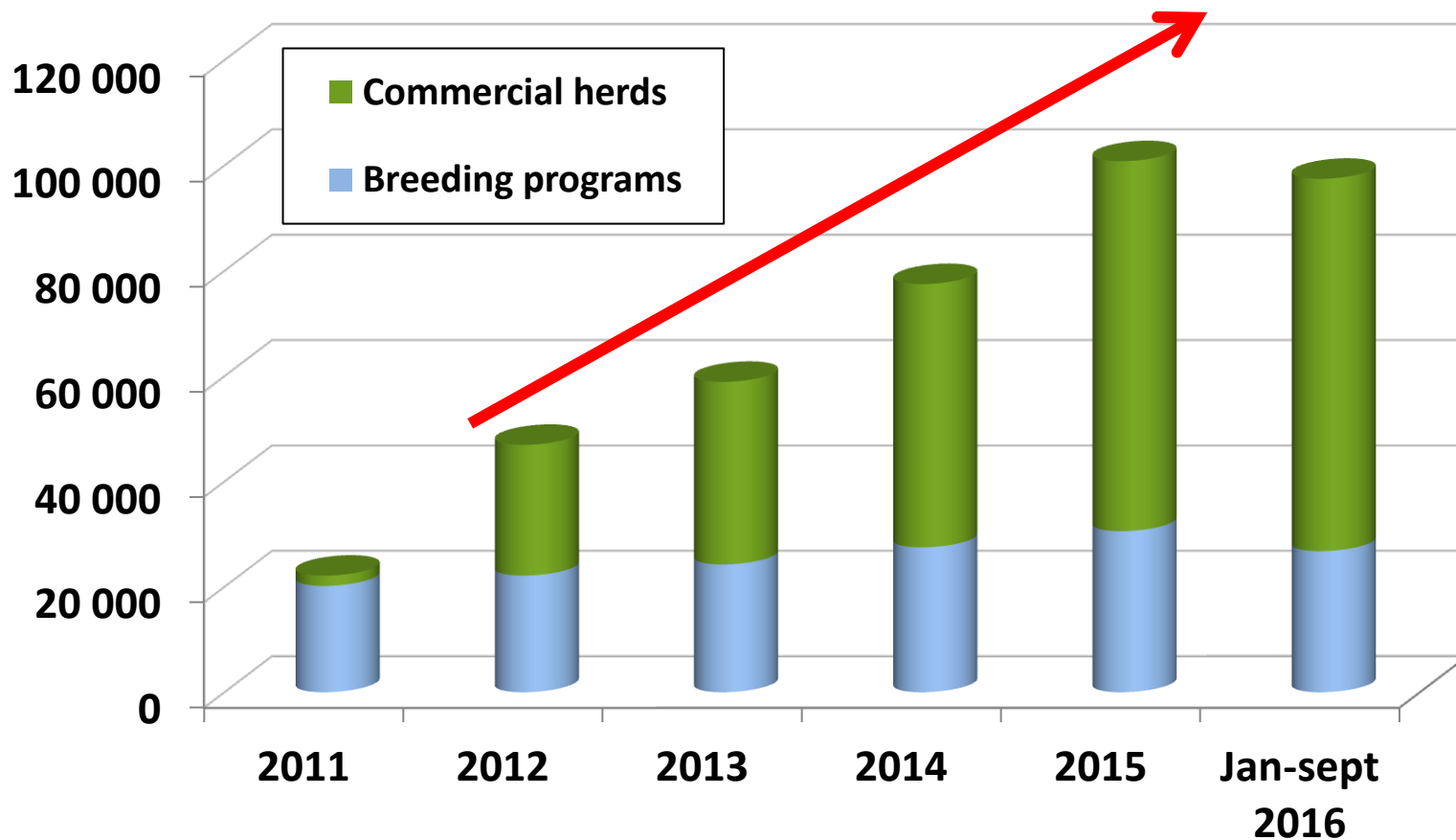**French genomic experience:
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Quick adoption of GS by breeders: more balanced selection

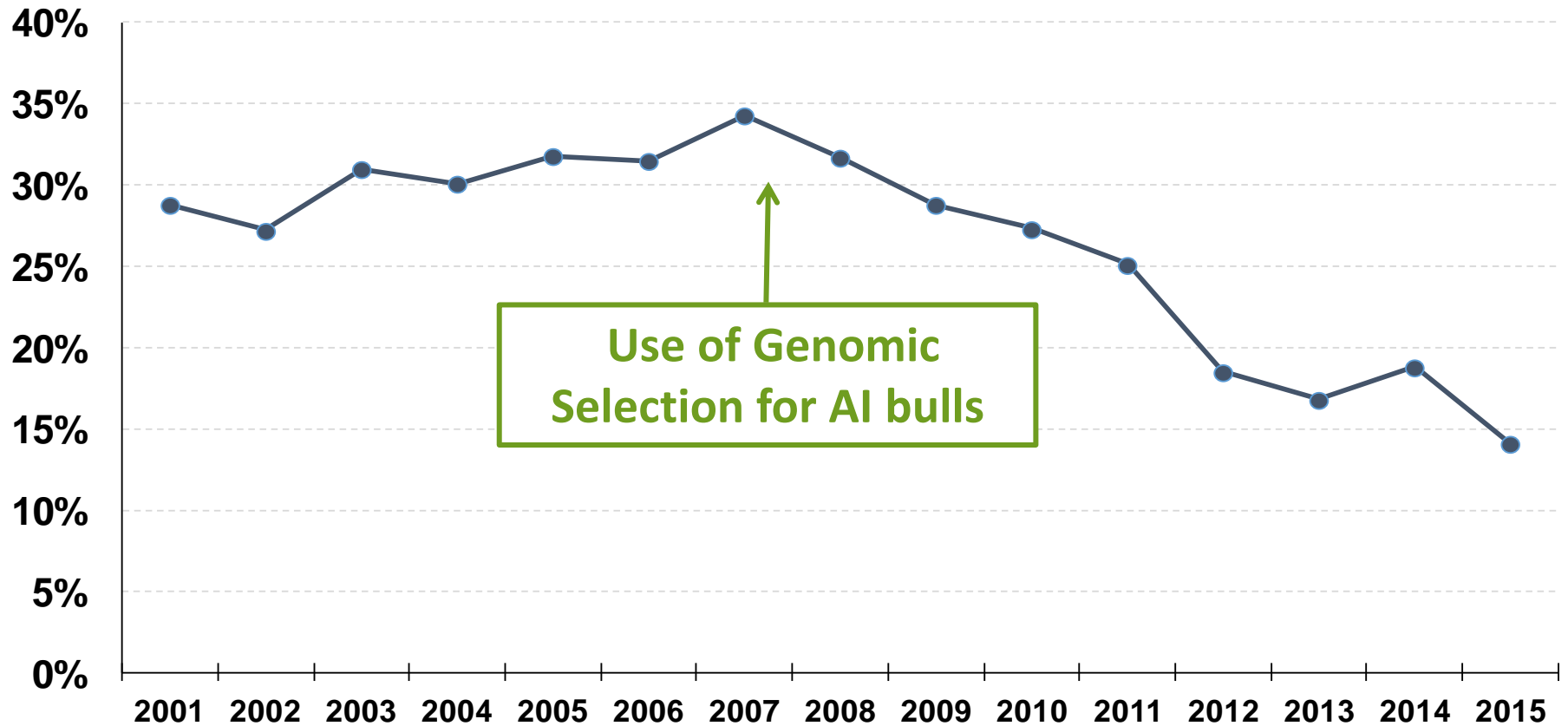Genetic profile of the AI bulls used /year
Prim Holstein breed

Genomic selection
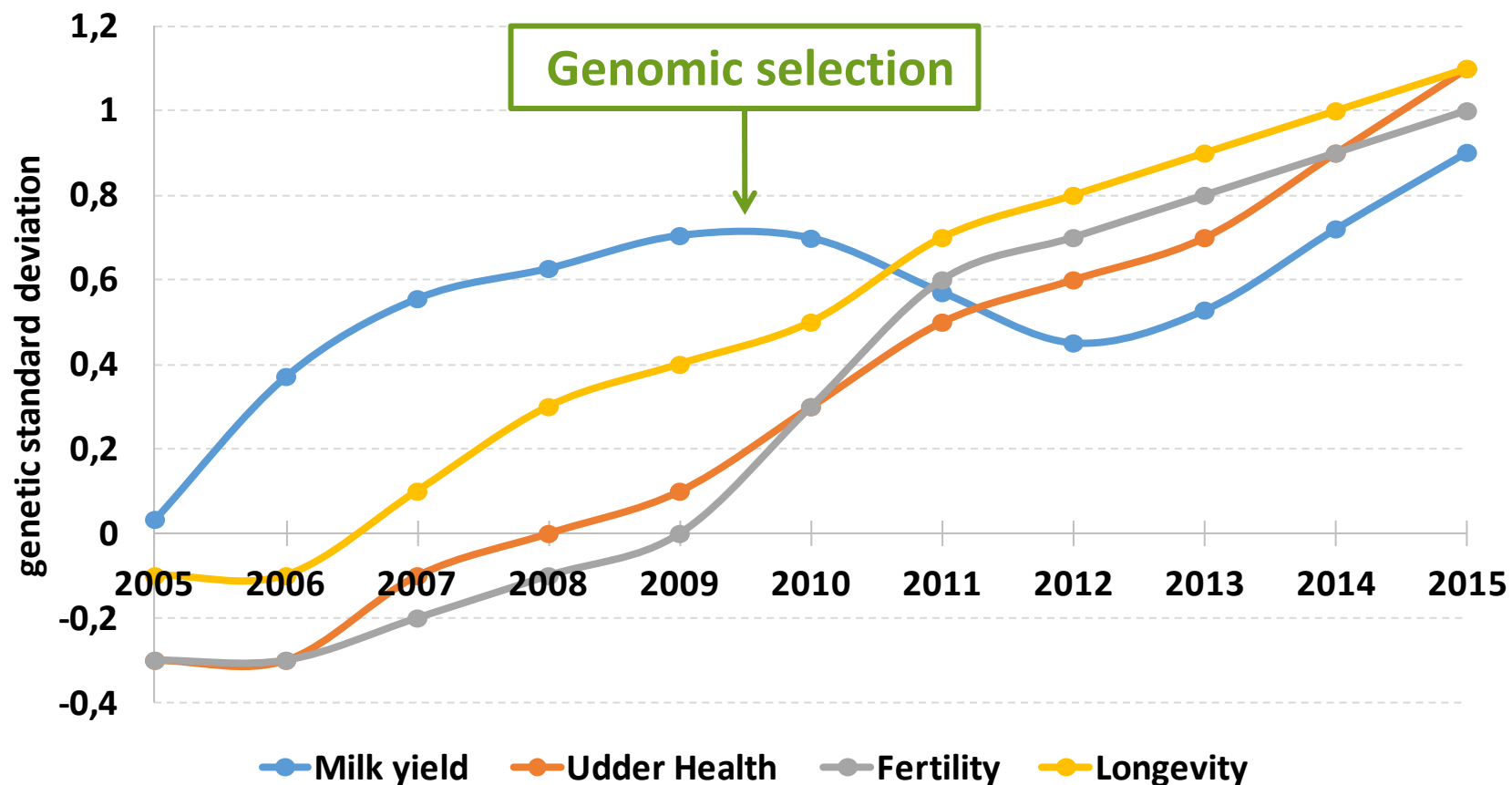
Large increase of genotyping

Larger panel of bulls used

% of AI done with the 5 most used bulls each year Montbéliarde breed

Use of Genomic Selection for AI bulls

Implementation in other breeds and species?

► **Less favorable situation for Beef cattle breeds**
and Dairy regional breeds

o **genetic population size larger**

o **reference population more difficult to generate**

• **smaller population size**

• **less AI for beef breeds**

• **phenotype less precise / DYD**

Multi-breed option?

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Multi-breed genomic evaluation for cattle?

HD genotyping of bulls from 18 cattle breeds in selection in France

Unsuccessful

=> very few common QTL found between breeds

=> no multi-breed genomic evaluation possible

**Good basis
to develop genomic selection for several breeds**

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Genomic selection for regional dairy cattle breeds

Reference population per breed and reliabilty expected for candidates

Breed	Nb Bulls	Nb Dams	Young candidate REL
ABONDANCE	350	1900	[0.35-0.55]
TARENTAISE	300	1300	[0.30-0.50]
SIMMENTAL	300	200	[0.20-0.50]
VOSGIENNE	60	1100	[0.20-0.50]

December 2015

Official in 2015

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Reference population for beef cattle breeds

		Charolais	Limousine	Blonde
Direct genetic effect	**Birth**	15 000 / 1800	6 600 / 2 700	5 600 / 1 200
	Weaning	12 500 / 2400	5 600 / 2 400	3 900 / 1 000
	Carcass	2 400 / 600	1 750 / 400	720 / 300
Maternal genetic effect	**Birth**	5 200 / 500	3 300 / 200	3 000 / 200
	Weaning	4 500 / 450	2 400 / 500	2 100 / 200

Maternal effects

➡ **Blending of polygenic and genomic results (VanRaden et al., 2009)**

Example of reliability gain for young Charolais calf

EBV	Reliability gain
Birth	+ 0.10
Growth Total Merit Index	+ 0.06
Maternal Total Merit Index	+ 0.09

INRA SCIENCE & IMPACT — Allice — INSTITUT DE L'ELEVAGE — ICAR Chile 2016

Reference population for beef cattle breeds

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Maternal genetic effect	Birth	5 200 / 500	3 300 / 200	3 000 / 200
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Blending of polygenic and genomic results (VanRaden et al., 2009)

Official since end 2015 for BLA, CHA and LIM

2 national runs / year

+

Weekly computation for new candidates
(without re-estimation of marker effects)

What about **Small ruminants?**

► **Less favorable situation for small ruminants**

- o **cost of genotyping relatively high**
- o **already short generation interval**
- o **use of fresh semen for AI in sheep**
- o **AI demand highly concentrated in time**

► **Different cases:**

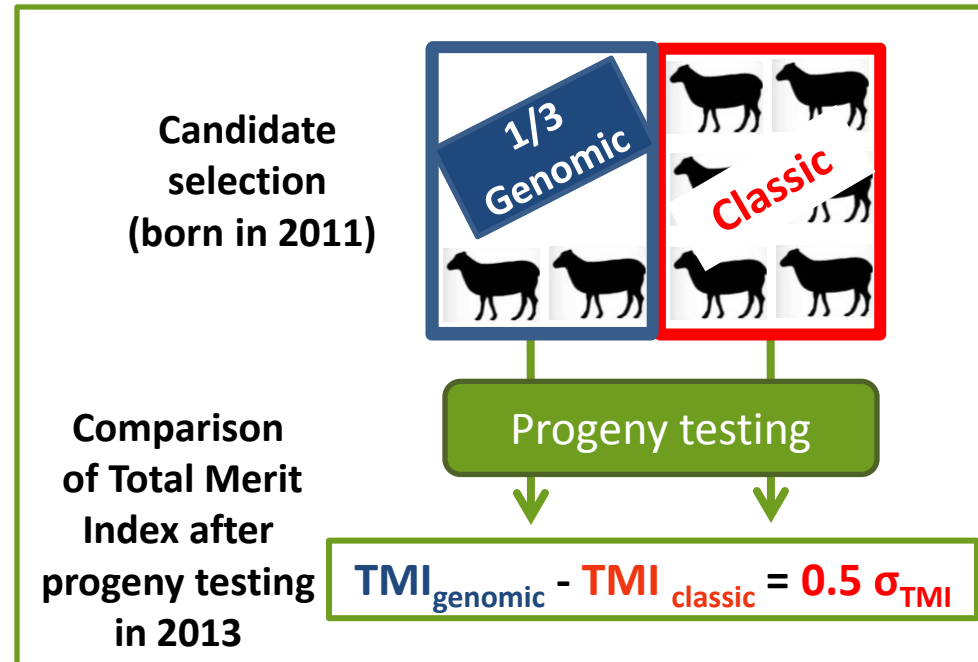|	Number of milk recorded ewes	Genotyped rams with daughters
Lacaune	**156 491**	**4 716**
Manech TR	**66 020**	**1 879**
Basco-Béarnaise	**21 620**	**562**
Manech TN	**9 302**	**475**
Corse	**14 028**	**197**

(2015)

Results for **dairy sheep**

▶ **QTL detection studies: no big QTL found (limited power detection)**

▶ **ssGBLUP with phantom group**

   => **reliability gain: [0.13 ; 0.20]**

▶ **Lacaune experimental study:**

▶ **different genomic selection pressures on young rams modelized**

Candidate selection (born in 2011)

1/3 Genomic

Classic

Comparison of Total Merit Index after progeny testing in 2013

Progeny testing

$TMI_{genomic}$ - $TMI_{classic}$ = 0.5 σ_{TMI}

=> **with 1/3 selection pressure, + 15 % genetic gain without extra cost**

=> **cost of genotyping balanced by reduction of number of rams in AI Center.**

   ➡ **GS started in 2015 (7 GS /year) + end of progeny testing**

Meat sheep

► **limited or no progeny testing and limited AI => No GS planned**

► **Genotyping first for parentage verification and assignation**

► **Research to include major gene in genetic evaluation (prolificacy…)**

Goats

► **Goat chip available in 2010**

► **Research in progress on:**

  o **combination of the 2 breeds (Alpine and Saanen)**

  o **international collaboration**

  o **major gene inclusion in genetic evaluation**

➡ **Goal: start of Genomic Selection in 2017**

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CONCLUSION

► **It has been a real genomic revolution these last years**

► **large impact on selection scheme organization**
  => early use of breeding animals for higher genetic gain on all traits

► **thanks to the French collective and efficient organization with Industry partners closely linked to R & D, genomic selection have been adapted to the different specificities of ruminant species and breeds**

Genomic evaluation in place in 14 cattle and 1 sheep breeds.

In the very next future for 4 sheep and 2 goat breeds

► **several challenges to come:**

o **Organizational reforms**

o **Reference population maintenance**

o **Competition for new phenotypes**

o **Integration of sequence information**

   …

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REFERENCES

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► **http://www.jouy.inra.fr/gabi_eng**

eric.venot@inra.fr

English version !

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