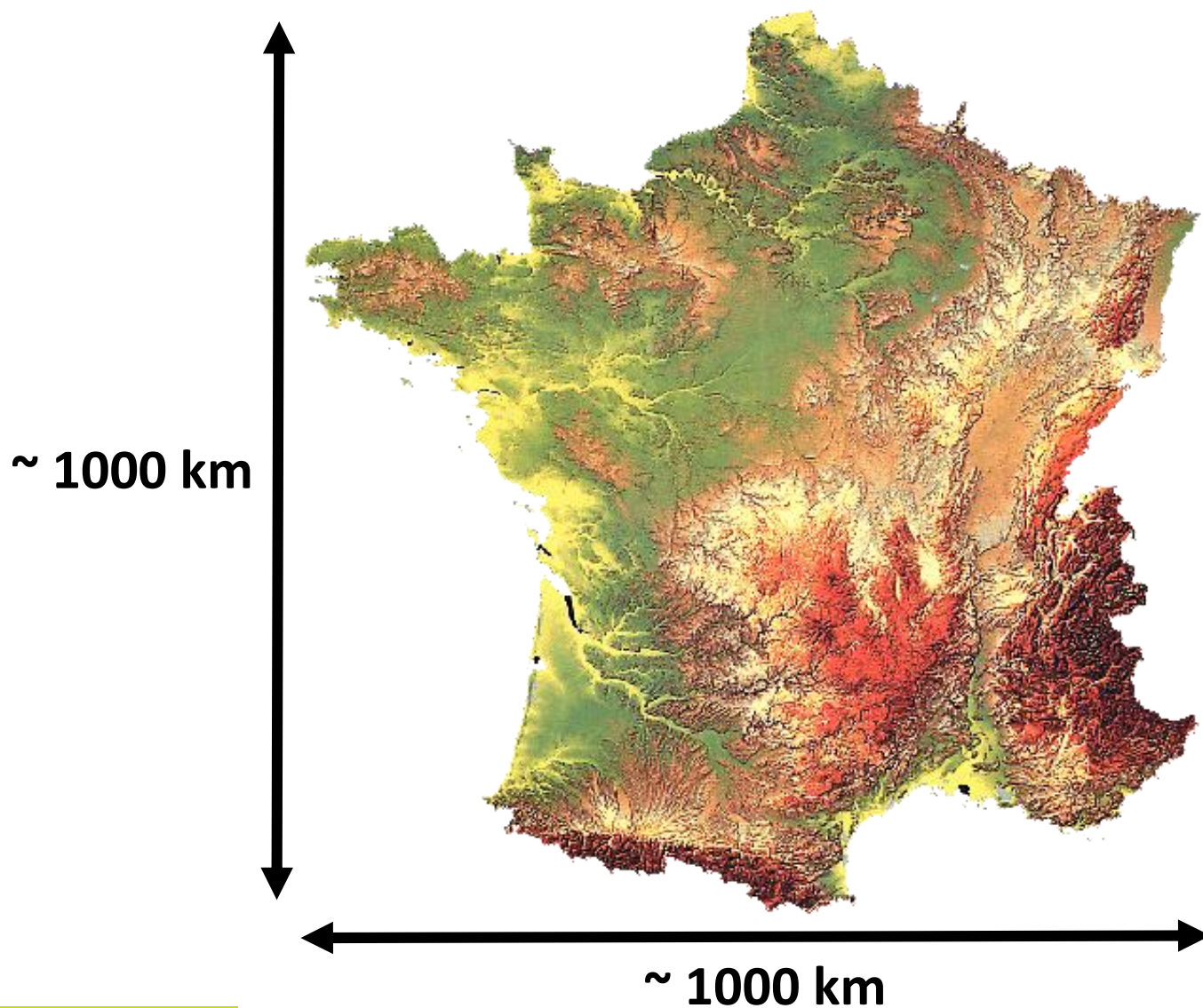# French genomic experience: genomic for all ruminant species

E. Venot[1], D. Boichard[1], A. Legarra[1], S. Fritz[3], H. Larroque[1],
C. Robert-Granié[1], V. Ducrocq[1], A. Vinet [1], JM. Astruc[2], M. Barbat[3],
A. Baur[3], P. Boulesteix[2], C. Carillier[1], MN. Fouilloux[2], P. Croiseau[1],
A. Gion[2], C. Hoze[3], A. Launay[2], F. Tortereau[1], R. Lefebvre[1],
V. Loywyck[2], I. Palhière[1], F. Phocas[1], J. Promp[2], R.Rupp[1],
R. Saintilan[3], T. Tribout[1], A. Barbat[1], M-P Sanchez[1], S. Mattalia[2]

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French specificities

~ 1000 km (vertical)

~ 1000 km (horizontal)

Source: www.CartesFrance.fr

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genomics for all ruminant species
27th October 2016**

French specificities

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Large number of breeds

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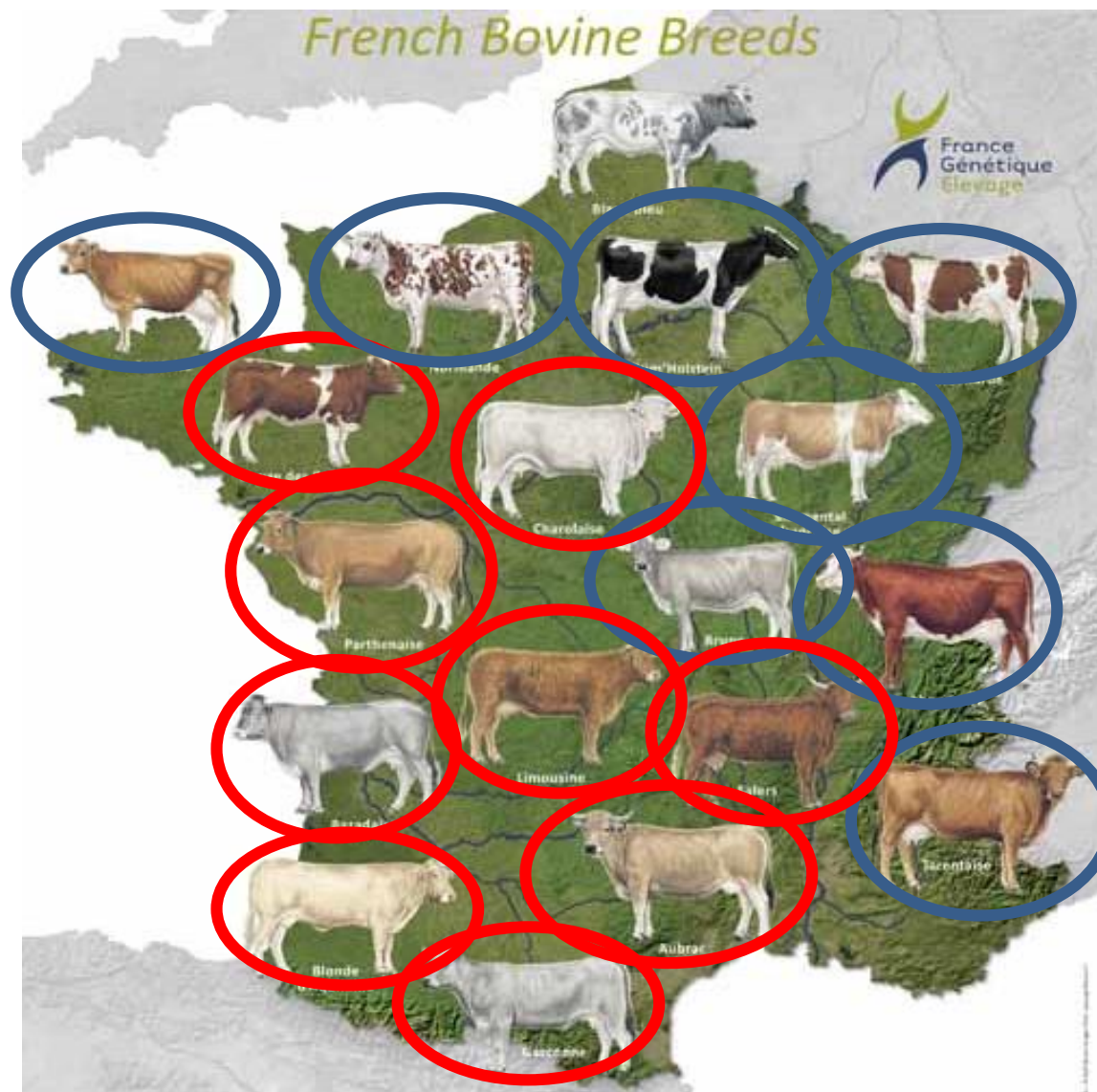
Small ruminant breeds

A constructive and efficient French 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:**

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

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

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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:**

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

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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
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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December 2015

Genomic selection started in 2009 (QTL-GS)

6 times / year with QTL and marker effects estimation

+

Weekly (without QTL effect estimation)

Reduction of generation interval and more efficient selection on functional traits

Milk production 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

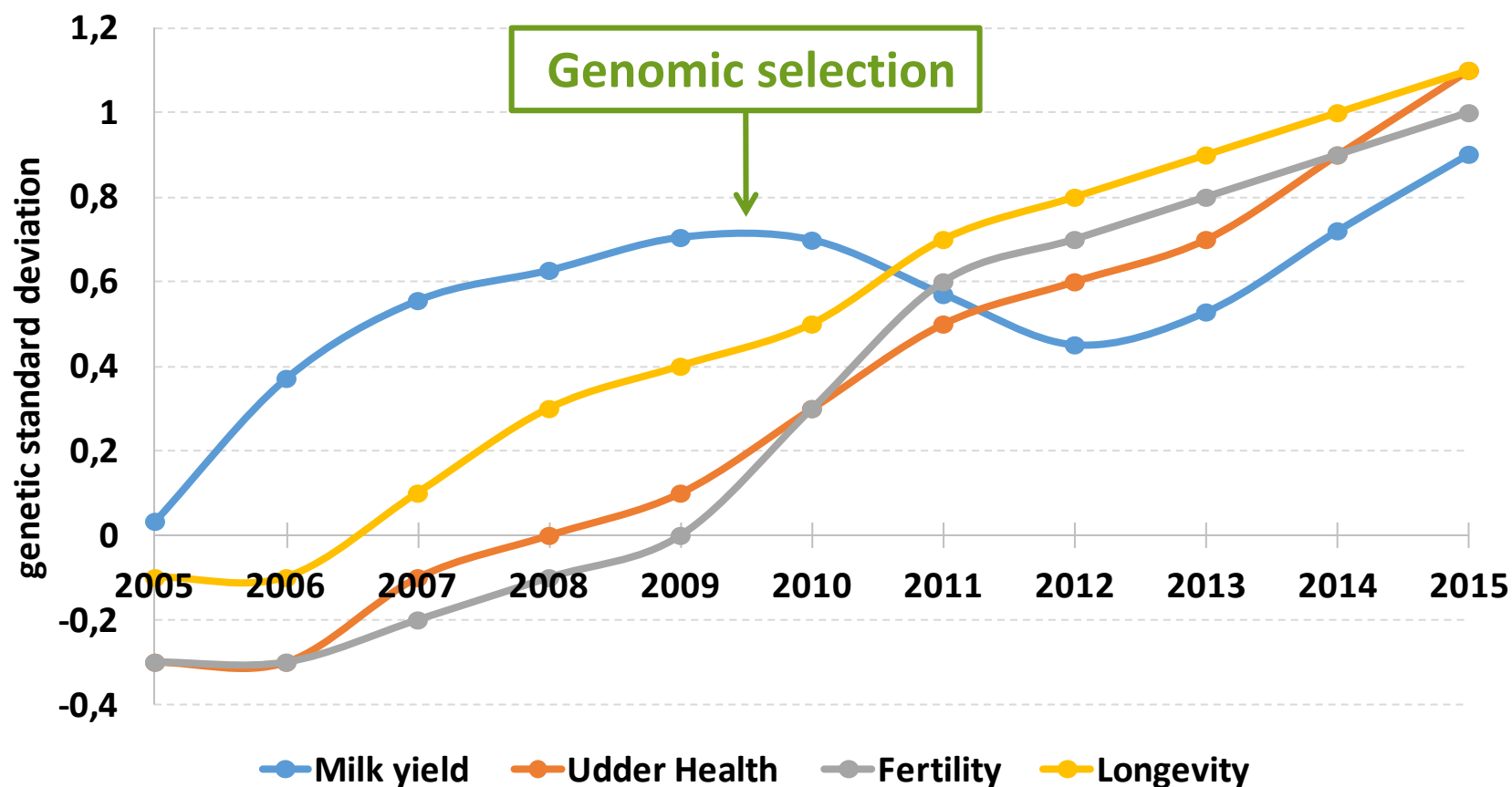Milk production REL 0.70   0.95

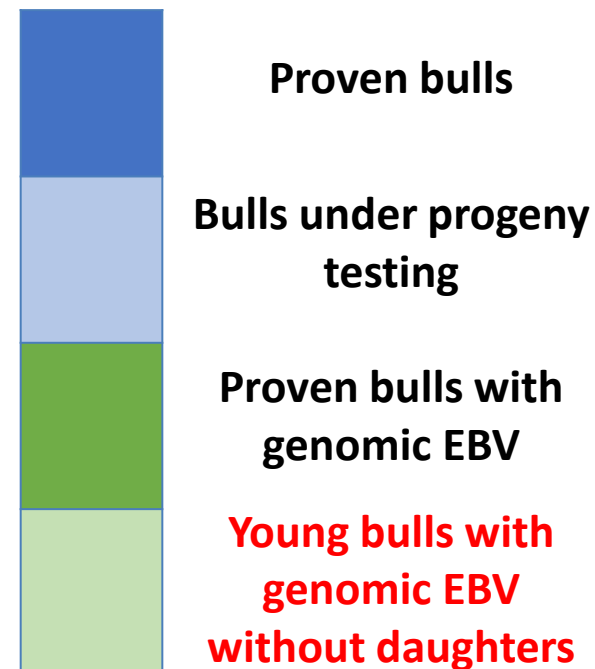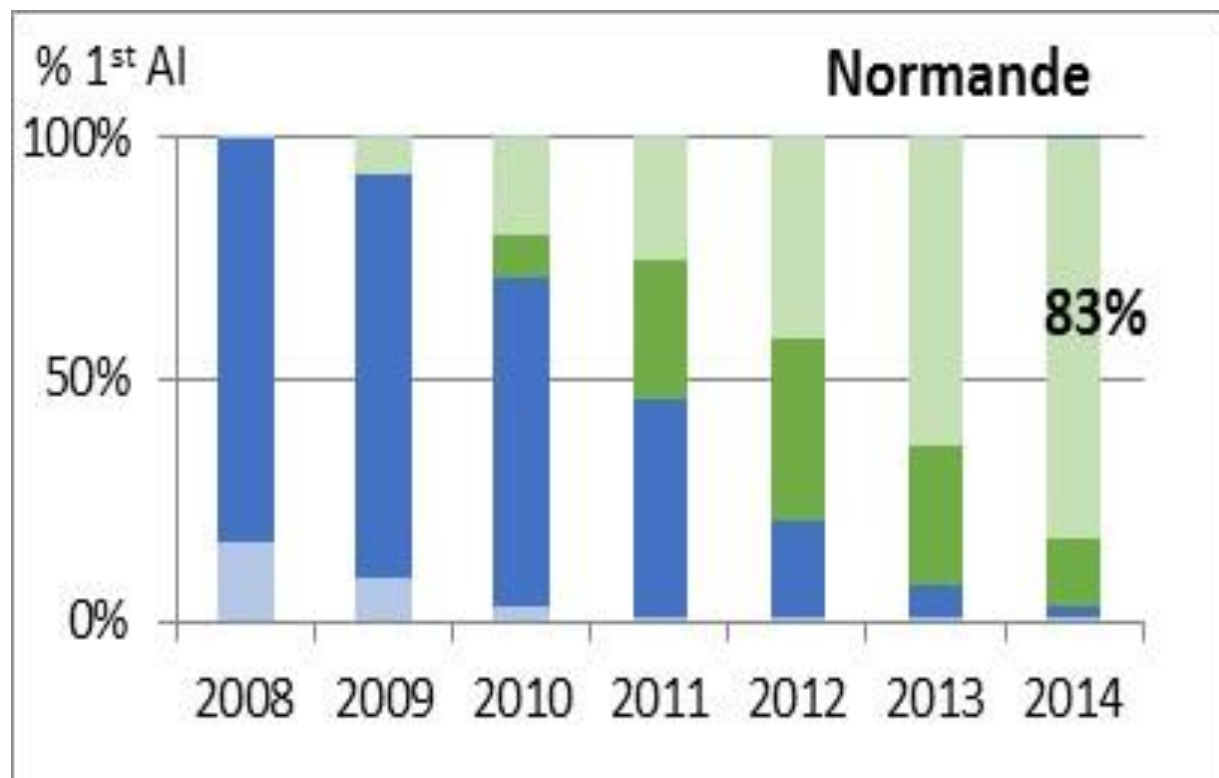Fertility REL   0.60   0.95

=> T shortened by 3-4 years

Quick adoption of GS by breeders: more balanced selection

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

Genomic selection

genetic standard deviation

Milk yield   Udder Health   Fertility   Longevity

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AI % in France

Proven bulls

Bulls under progeny testing

Proven bulls with genomic EBV
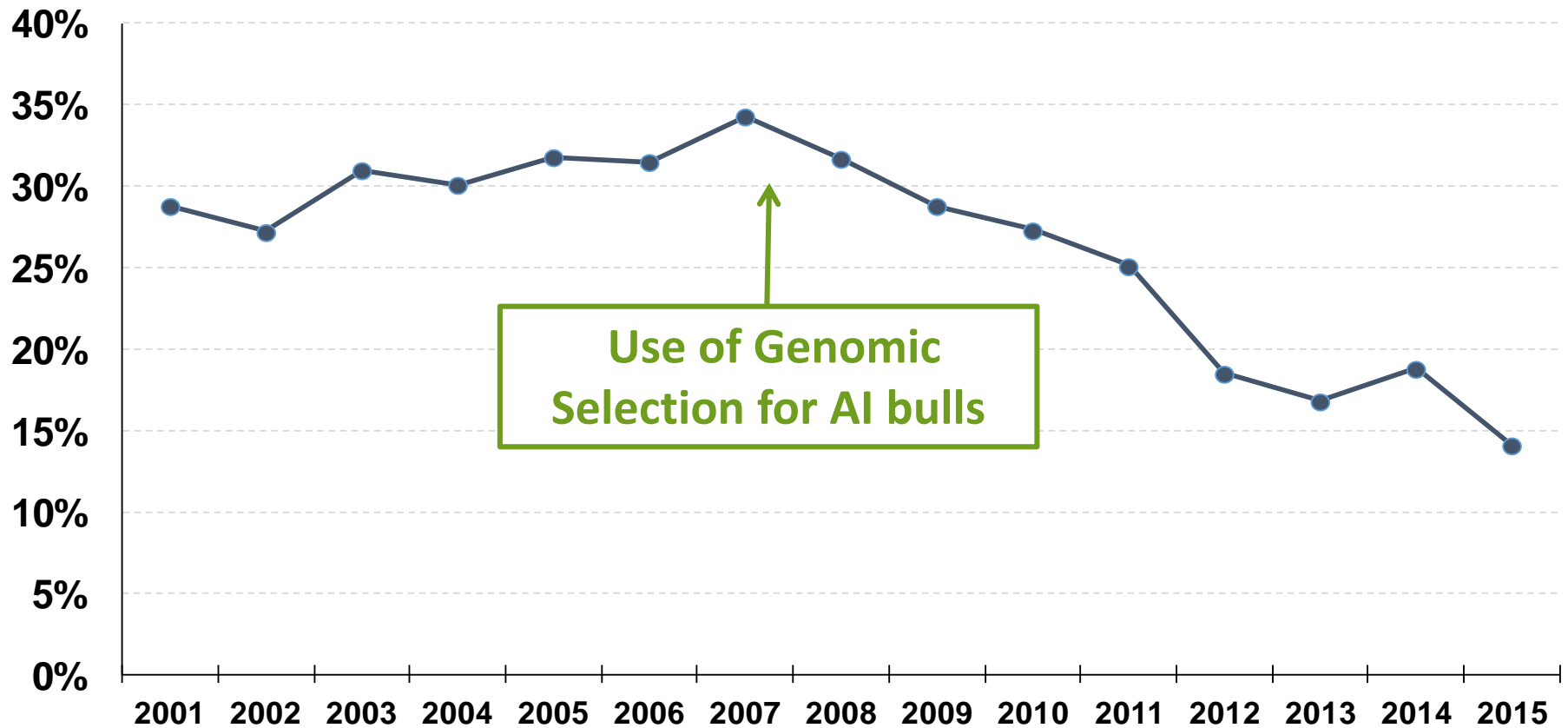
Young bulls with genomic EBV without daughters

Large increase of genotyping
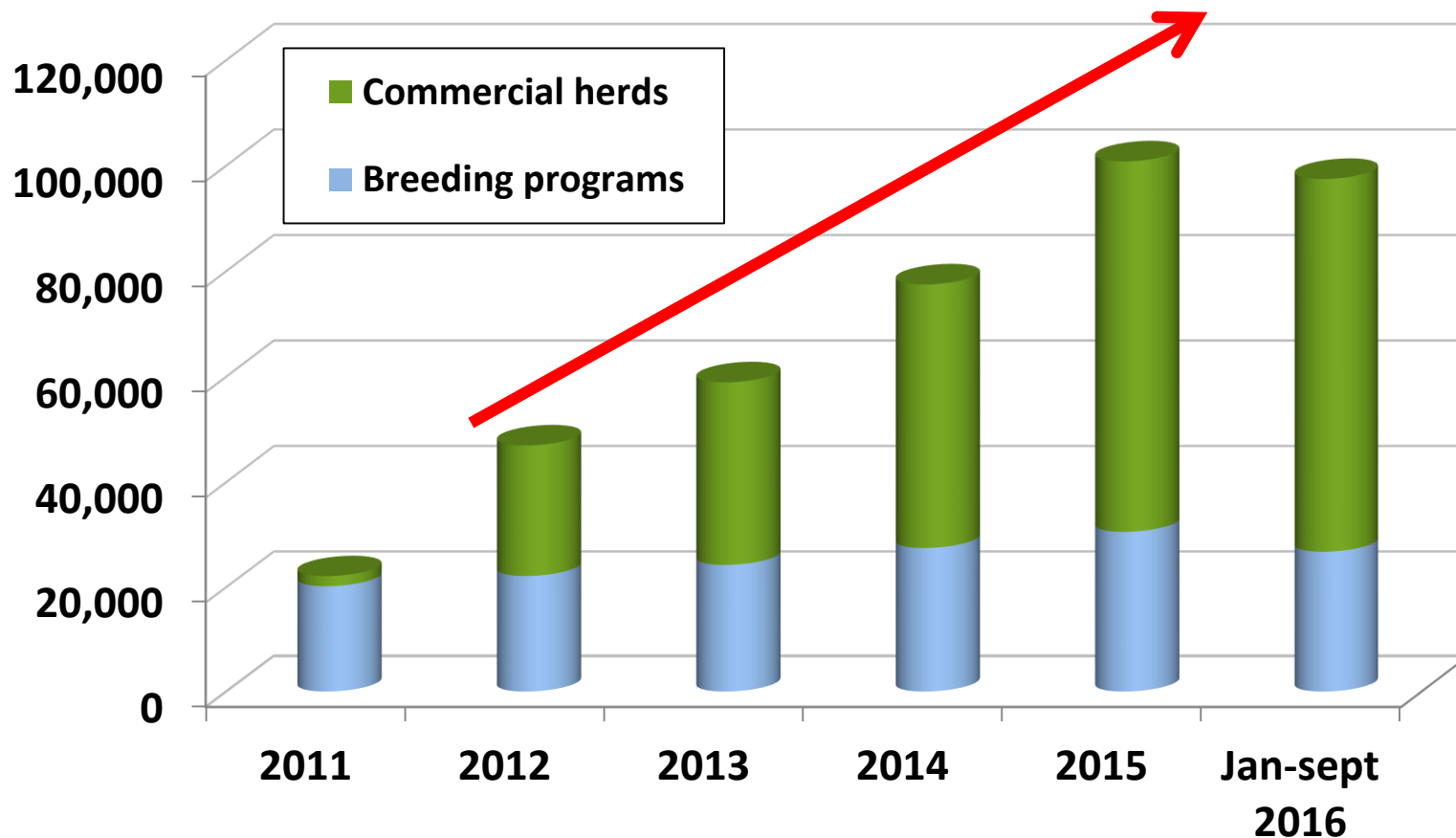
Larger panel of bulls used

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

Use of Genomic
Selection for AI bulls

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Implementation in other breeds and species?

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

- o **same large generation interval**

- o **genetic population size larger**

- o **reference population more difficult to generate**

  - • **less AI use for beef**

  - • **phenotype less precise / DYD**

  - • **smaller population size**

➡ **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

**<u>Good basis</u>
to develop genomic selection for several breeds (imputation)**

⬇

<u>Implementation of Genomic Selection</u>

- o **in Dairy regional breeds**

- o **in large Beef cattle breeds (BLA, CHA & LIM)**

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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
HOLSTEIN	33000	-	[0.55-0.70]
MONTBELIARDE	2800	31000	[0.55-0.70]
NORMANDE	2400	16000	[0.50-0.65]
BROWN	6000	-	[0.45-0.70]
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**

➡ **Different method used for beef cattle with blending of polygenic and genomic results** **(VanRaden et al., 2009)**

Example of reliability gain for young Charolais calf

EBV	Polygenic reliability	Genomic reliability
Birth	0,30	0,40 **(+33%)**
Growth Total Merit Index	0,27	0,33 **(+22%)**
Maternal Total Merit Index	0,25	0,34 **(+36%)**

Reference population for beef cattle breeds

Maternal effects

		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

➡ **Different method used for beef cattle with 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 **sheep**?

► **Less favorable situations for small ruminants**

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

► **already familiar with the use of molecular information (scrapie)**

► **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)

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Different research programs and funding to test GS interest and feasibility in **Dairy sheep**

▶ **Illumina OvineSNP50 chip available since 2009**

▶ **Different goals:**

- ○ **build up reference population**

- ○ **check interest of GS for sheep (with no additional cost)**

- ○ **define the best method to apply on sheep data**

- ○ **test GS in experimental conditions**

- ○ **include new traits**

- ○ **foresee potential impact on selection scheme**

Results for **dairy sheep**

► **QTL detection study: no big QTL found (limited power detection)**

► **ssGBLUP with phantom group**

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

► **Lacaune experimental study:**

Candidate selection (born in 2011)

1/3 Genomic

Classic

Progeny testing

Comparison of Total Merit Index after progeny testing in 2013

$TMI_{genomic} - TMI_{classic} = 0.5\ \sigma_{TMI}$

► **Modeling of different genomic selection pressures on young rams**

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

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

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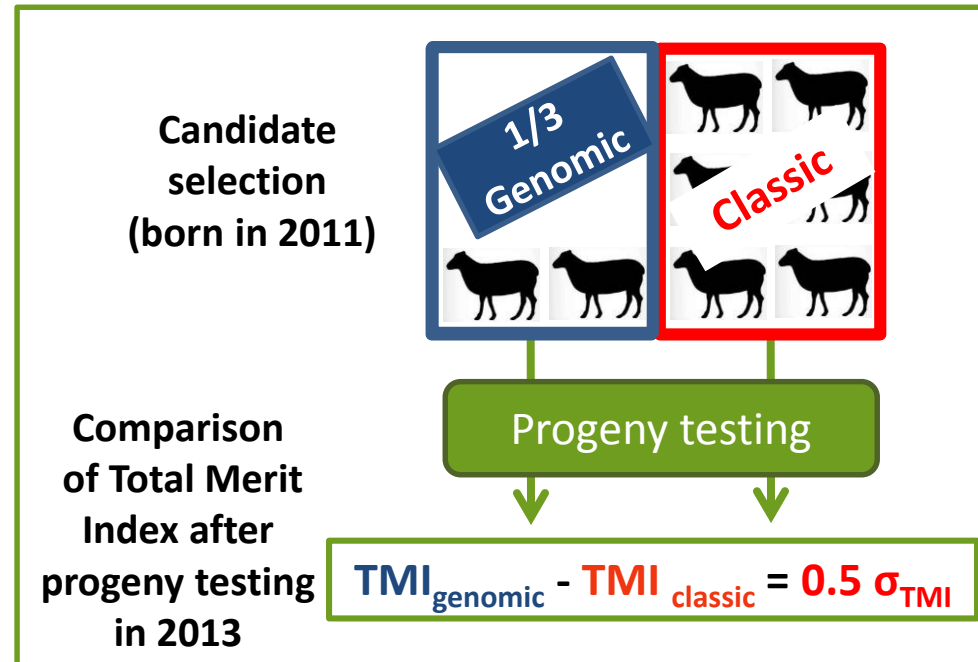
Results for dairy sheep

► <u>Lacaune breed:</u>

=> Studies showed interest of GS for Lacaune breed

=> GS official in 2015 + end of ram progeny testing

=> 7 genomic evaluations /year

► <u>Other dairy sheep breeds:</u>

o reference population smaller

o test of multi-breed evaluations with LATXA Spanish breed

=> GS should take place in 2017.

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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**

► **2 kind of populations for reference population:**
   2 400 females (G + P) and 800 AI bucks

► **Research in progress on:**

   o **combination of the 2 breeds (Alpine and Saanen) + international coll.**

   o **major gene inclusion in genetic evaluation**

   Goal: GS in 2017

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 professional organization structure 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

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► **several challenges:**

o **Private initiatives**

o **Organizational reforms**

o **Reference population maintenance**

o **Competition on new phenotypic recording**

o **Integration of sequence information**

...

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► **http://en.france-genetique-elevage.org**

► **www.idele.fr**

► **www.allice.fr**

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

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English version !

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