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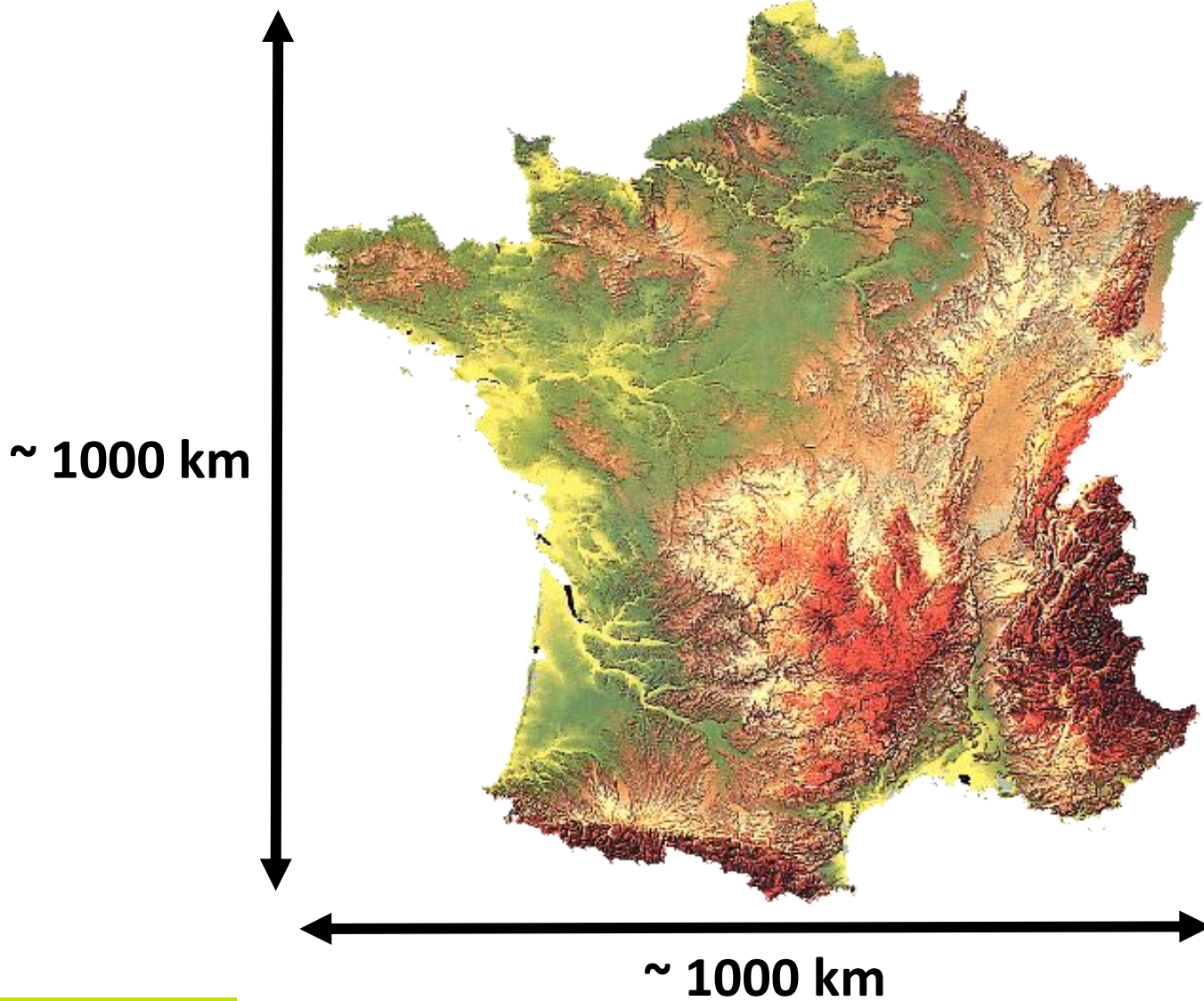
French genomic experience: genomic for all ruminant species

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French specificities

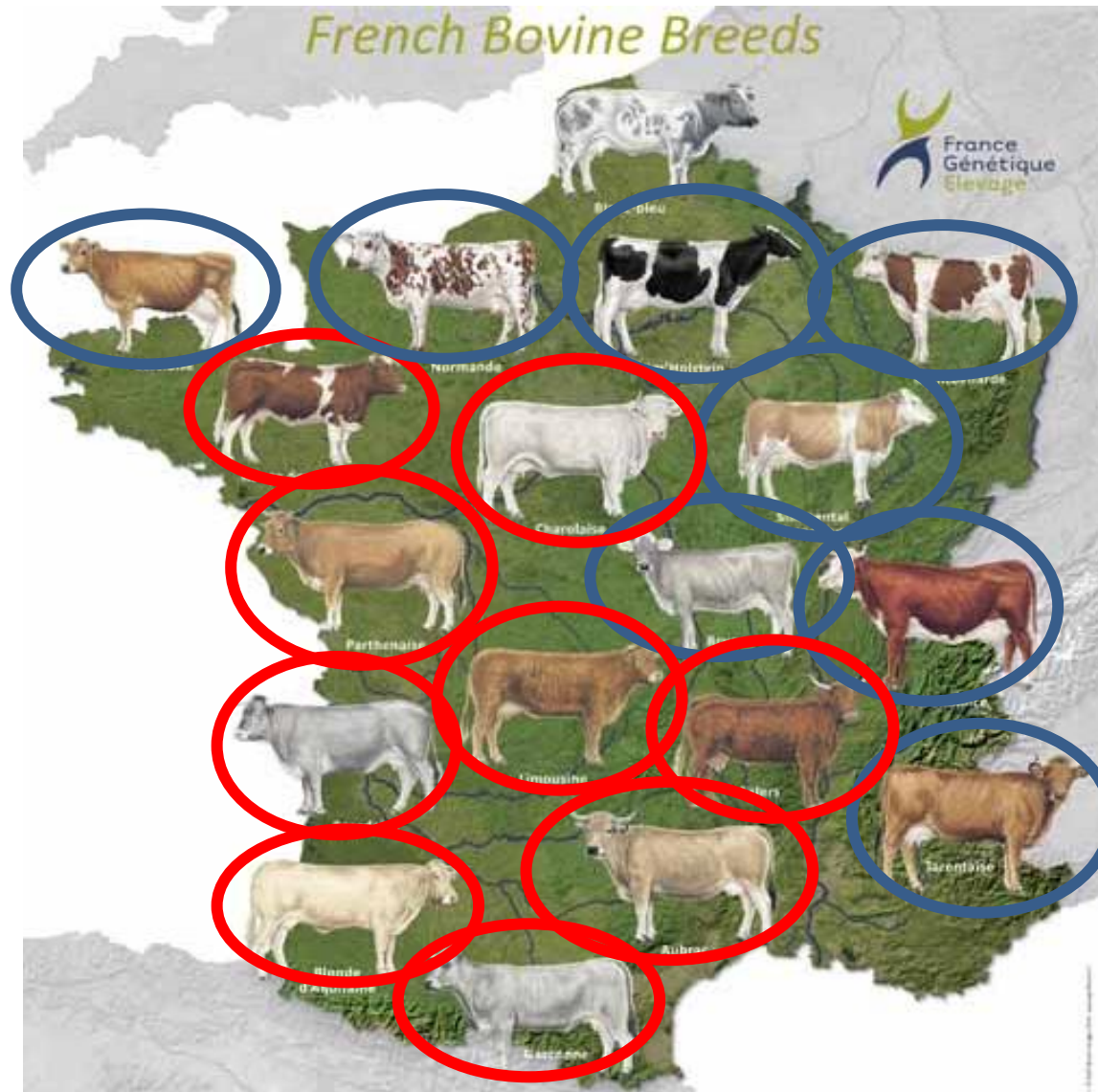


Source: www.CartesFrance.fr

French specificities



Large number of breeds



Small ruminant breeds



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:

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

Reference population size & Accuracy (R)

Reference population per breed and reliability 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



Reference population size & Accuracy (R)

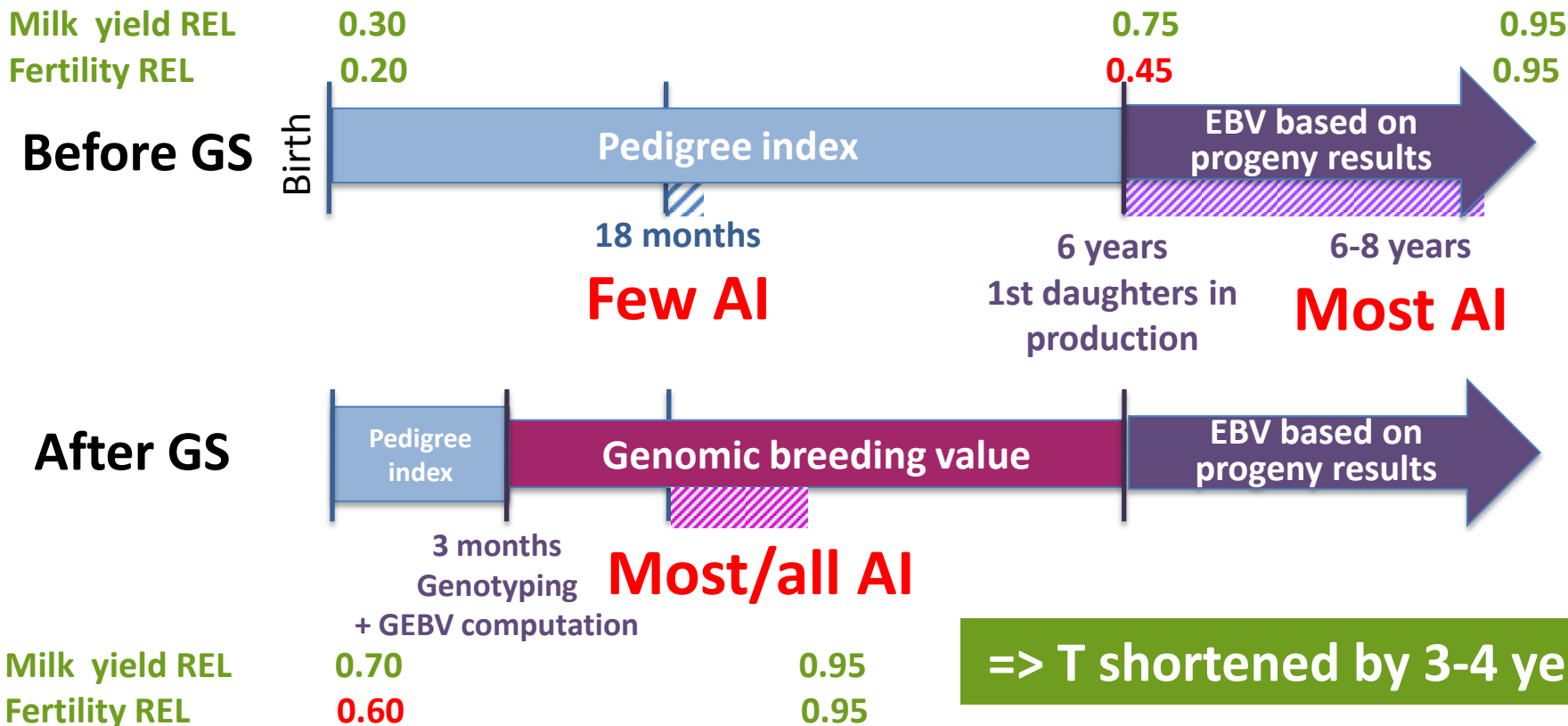
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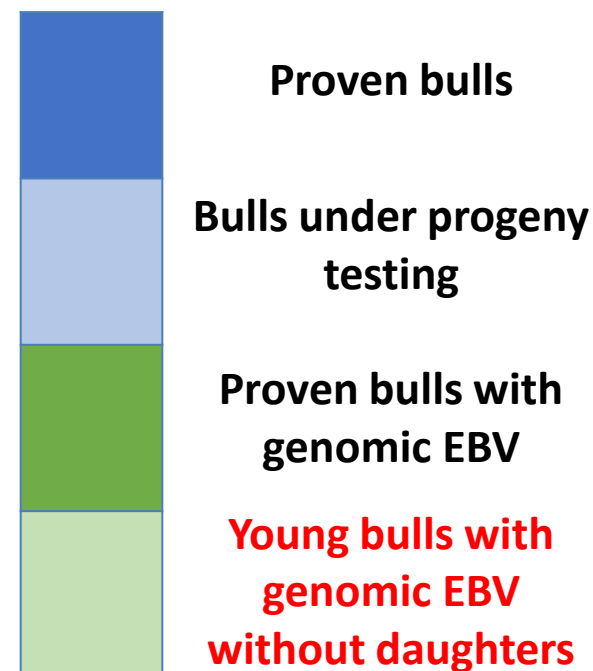
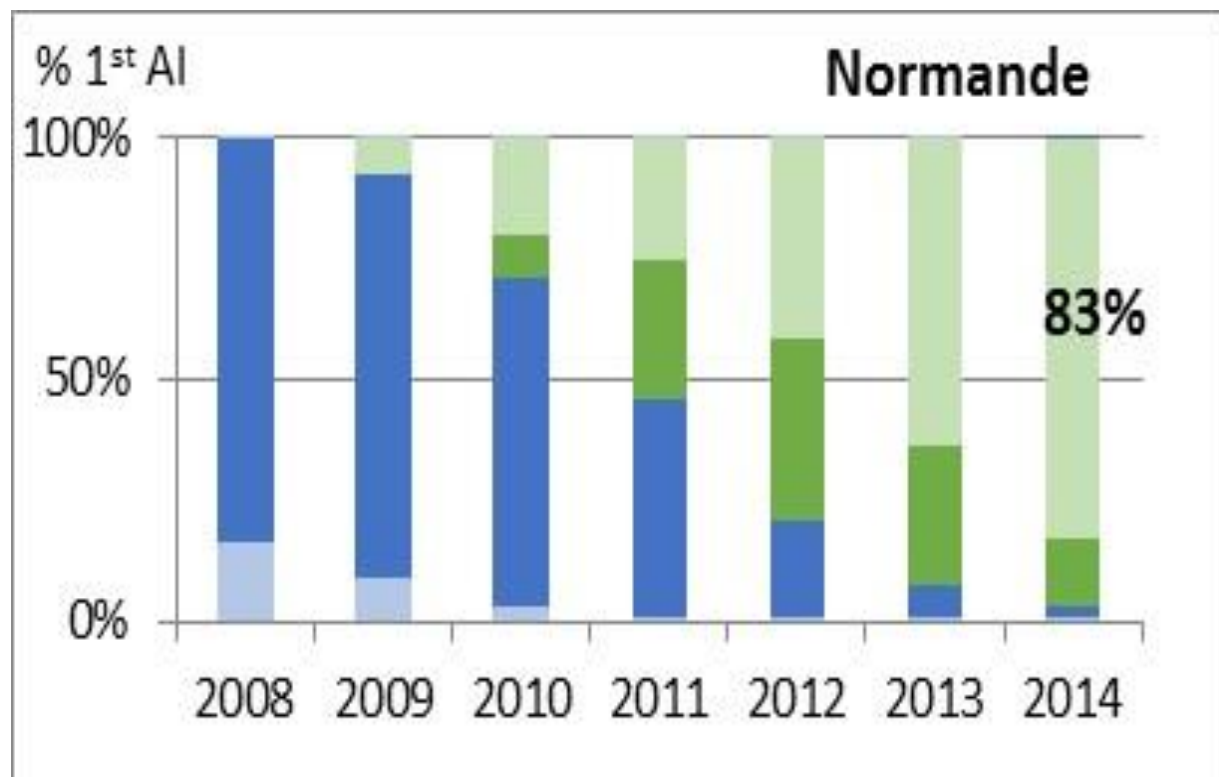
Genomic selection started in 2009 (QTL-GS)
6 times / year with QTL and marker effects estimation
 +
Weekly (without QTL effect estimation)

Reduction of generation interval and more efficient selection on functional traits



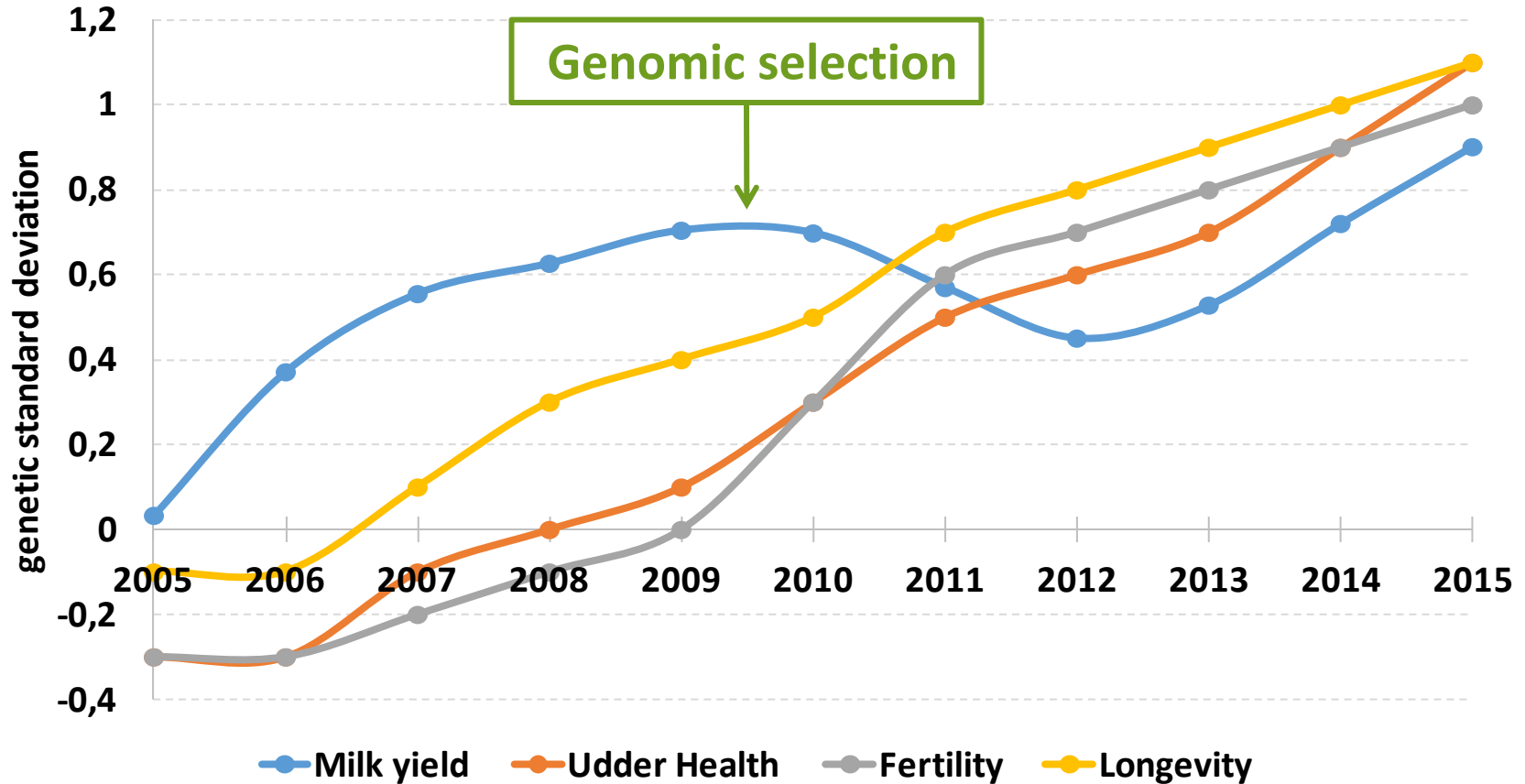
Quick adoption of GS by breeders: use of young genomic bulls

AI % in France

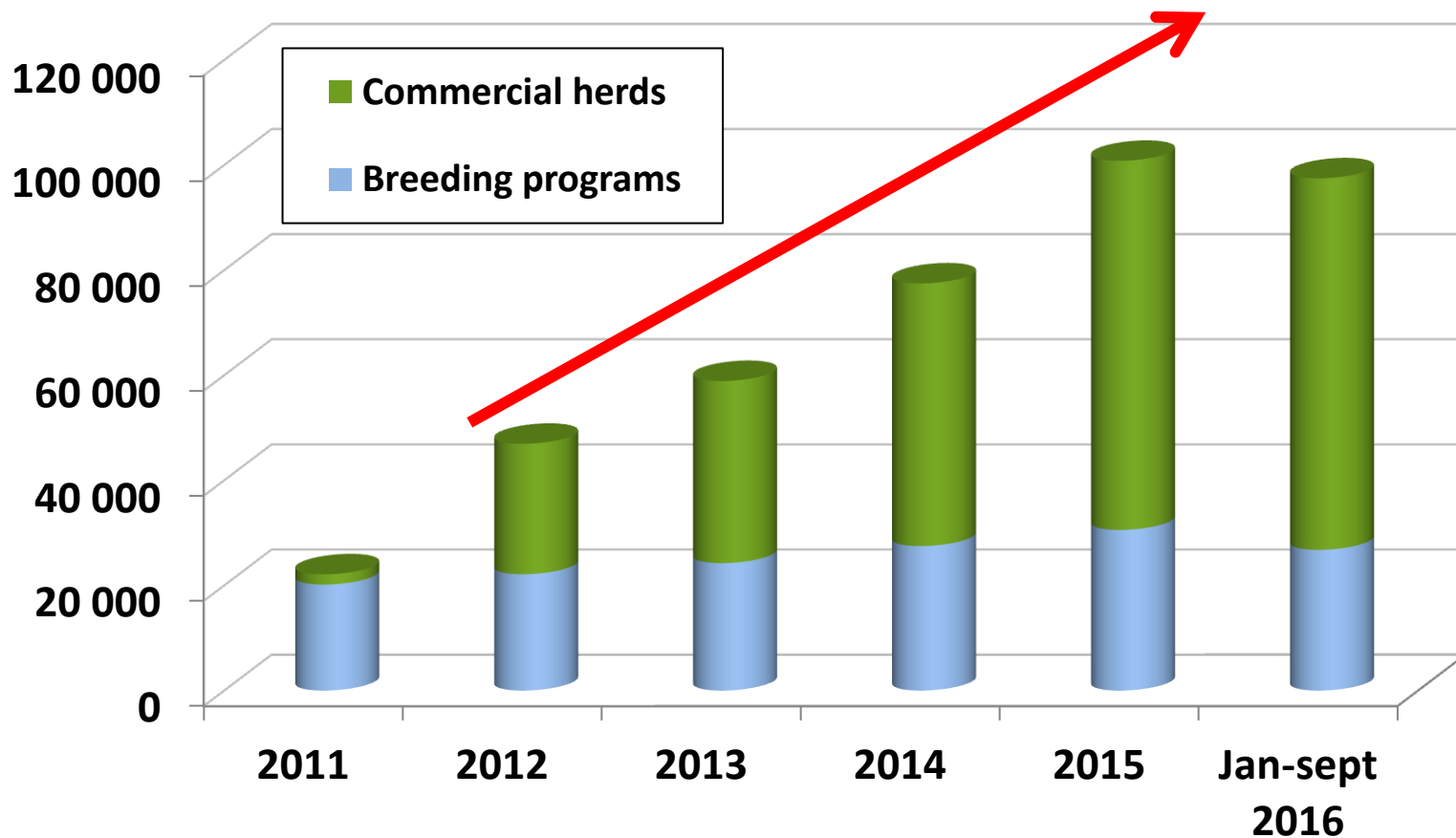


Quick adoption of GS by breeders: **more balanced selection**

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

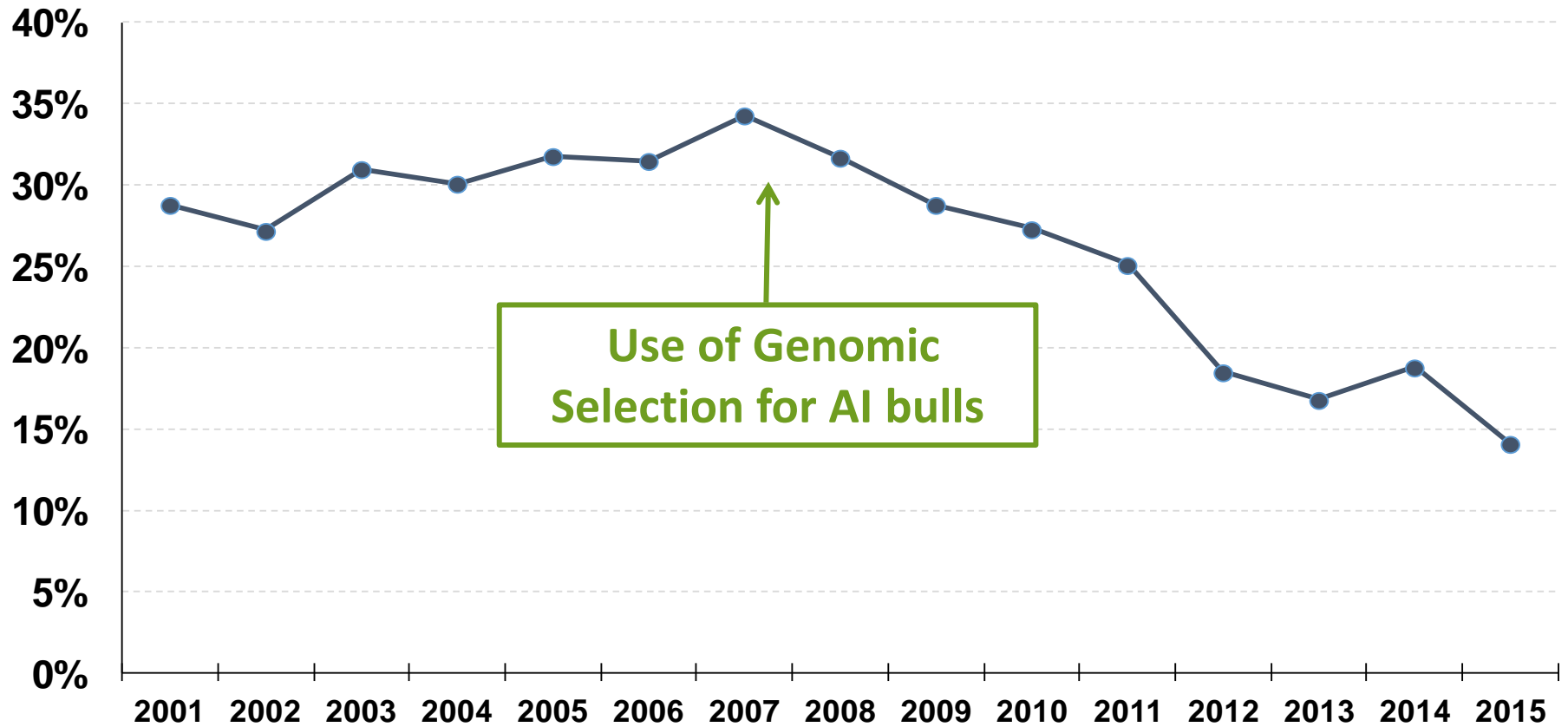


Large increase of genotyping



Larger panel of bulls used

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



Implementation in other breeds and species?

- ▶ Less favorable situation for **Beef cattle breeds**
and **Dairy regional breeds**
 - genetic population size larger
 - reference population more difficult to generate
 - smaller population size
 - less AI for beef breeds
 - phenotype less precise / DYD



Multi-breed option?

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

Genomic selection for regional dairy cattle breeds

Reference population per breed and reliability expected for candidates

Breed	Nb Bulls	Nb Dams	Young candidate REL
ABONDANCE	350	1900	[0.35-0.55]
TARENDAISE	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

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



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

Reference population for **beef cattle breeds**

Maternal effects

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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

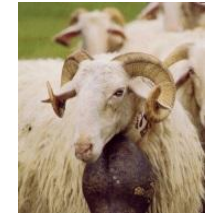
+

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

What about **Small ruminants**?

► Less favorable situation for small ruminants

- cost of genotyping relatively high
- already short generation interval
- use of fresh semen for AI in sheep
- 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

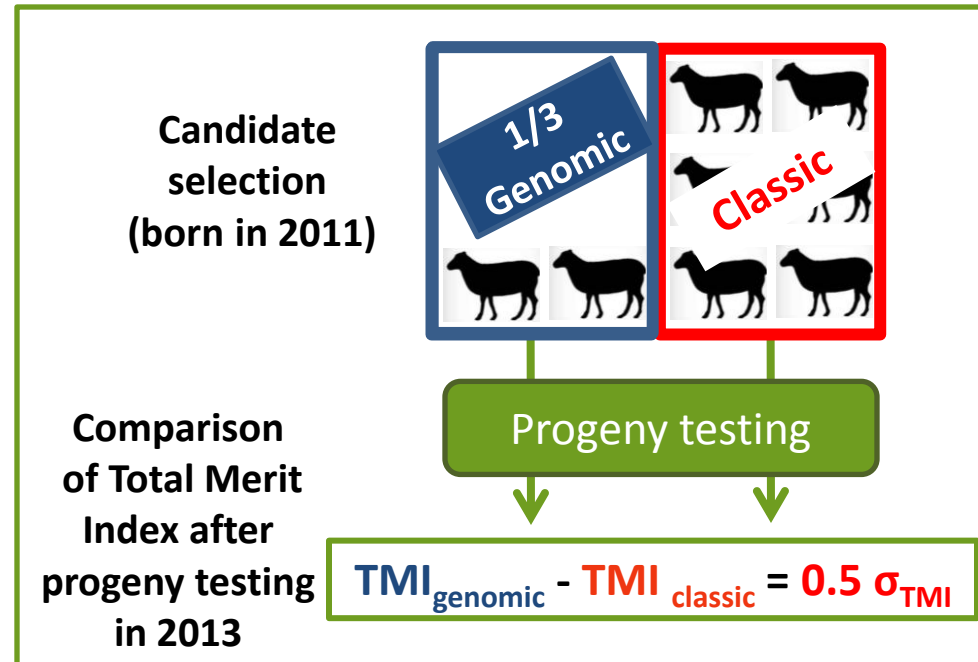
▶ QTL detection studies: no big QTL found (limited power detection)

▶ **ssGBLUP** with phantom group

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

▶ Lacaune experimental study:

▶ different genomic selection pressures on young rams modeled



=> 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:
 - combination of the 2 breeds (Alpine and Saanen)
 - international collaboration
 - major gene inclusion in genetic evaluation



Goal: start of Genomic Selection 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 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

END OF THE STORY? ...

... NO! JUST THE BEGINNING!

► several challenges to come:

- Organizational reforms
- Reference population maintenance
- Competition for new phenotypes
- Integration of sequence information

...



REFERENCES

▶ <http://en.france-genetique-elevage.org>

▶ www.idele.fr

▶ www.allice.fr

▶ http://www.jouy.inra.fr/gabi_eng

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