Swine Genetics: Past and Future

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Genetics has greatly evolved

Ancestors: Europe and Asia – 25 million years ago

Origin of all breeds: European wild boar and Chinese pigs

Domestication of pigs: 6,000 to 8,000 B.C., numerous breeds were created then

http://www.thepigsite.com/info/swinebreeds.php *

*   Various local breeds are excluded from this list
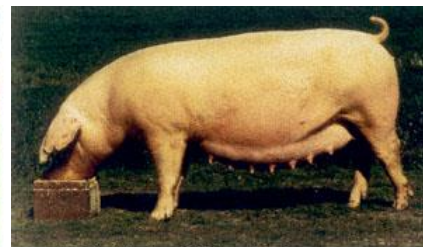

European Wild Boar

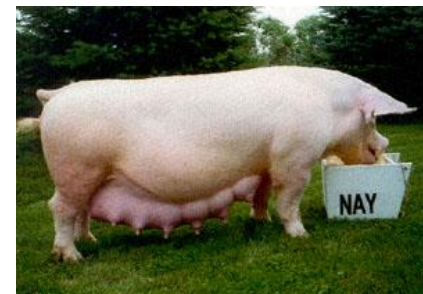Chinese Pig

First a phenotype-based selection

Especially at the turn of the 19th century

On distinct traits:

- **Structure**
- **Head**
- **Ear**
- **Colour**

provided by National Swine Registry

provided by National Swine Registry

And what about the evolution of performances in 30 years!

Trait*	1988 (30-90 kg)**	2017 (30-130 kg)	Difference
Growth (g/d)	880	1,100	+ 220
Back fat (mm)	13.6	9.0	-4.6***
Feed conversion	2.45	2.00	-0.45***

* Average performance in a testing station
**Source: Federal-Provincial Swine Aptitude Control Program. 1988 Annual Report
*** On a pig weighing 40 kg more in the end

Animals with unseen potential

Today's potential reflects tomorrow's performance

2019 nucleus performance

Top 10% for growth: **1.34 kg/day**
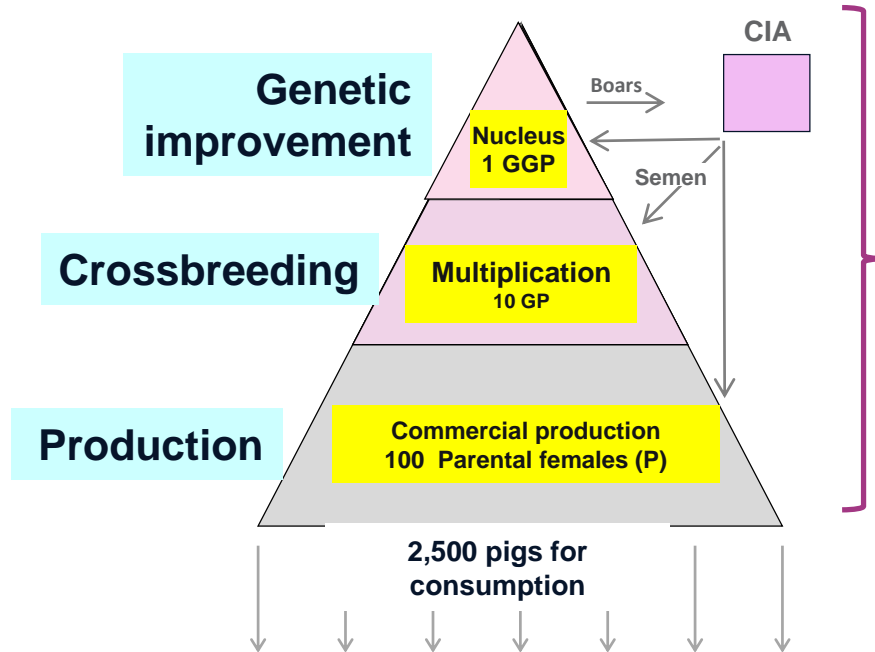
Top 10% for FC: **1.63**

Top 10% of litter sizes: **22.1/litter**

Goals of the presentation

1- Understand the principles governing genetic progress

2- Identify the technologies that have modulated and will modulate genetic progress

3- Evaluate their future impacts on performances

Swine production: A highly hierarchical diagram

Genetic improvement

Crossbreeding

Production

CIA

Boars

Semen

Nucleus
1 GGP

Multiplication
10 GP

Commercial production
100 Parental females (P)

2,500 pigs for consumption
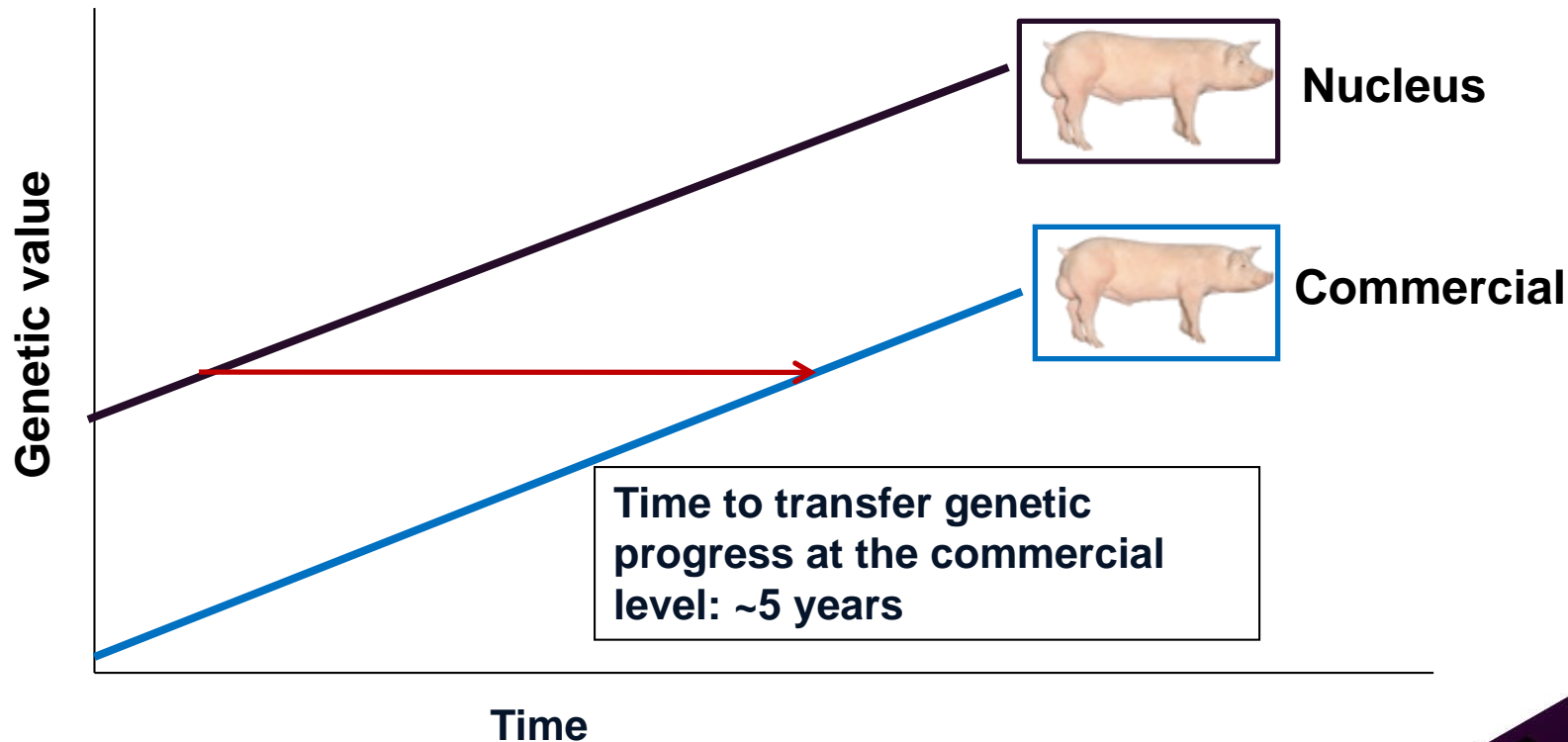
Quebec has 300,000 sows*

Need 150,000 gilts / year and 700 boars / year

18,750 sows being multiplied

1,875 sows female line
450 sows male line

* Active sows excluding pre-herd

Transmission of genetic progress
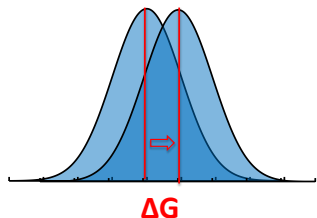

Nucleus

Commercial

Genetic value

Time to transfer genetic progress at the commercial level: ~5 years

Time

Goal of a selection program

1st generation
2nd generation
3rd generation
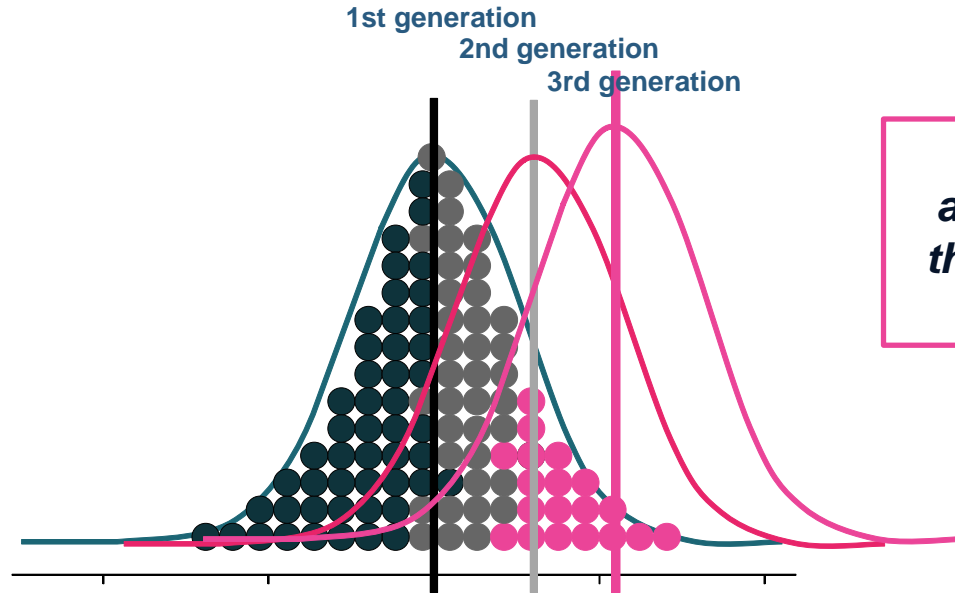
Identify elite animals and use them as breeding pigs

Genetic progress is based on 2 pillars

1. Use levels that maximize the genetic gain

ΔG

$$\Delta G = \frac{\text{Selection intensity (I) x Variance (V) x Accuracy (rIA)}}{\text{Generation interval (t)}}$$
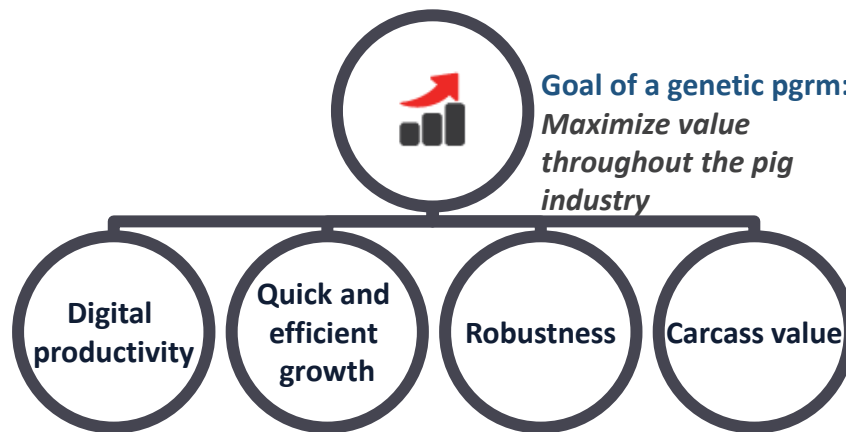
I: proportion of animals kept/ evaluated 1:100 = 2.33 ; 1:10: 1.28

V: new gene vs. consanguinity entry

T: optimize the useful life of elite animals

rIA: influenced by technologies

Justificatif

2. Measure and select what is relevant

Goal of a genetic pgrm:
Maximize value throughout the pig industry

Digital productivity

Quick and efficient growth

Robustness

Carcass value

Produce nutritious, tasty meat at the right price, according to high ethical standards
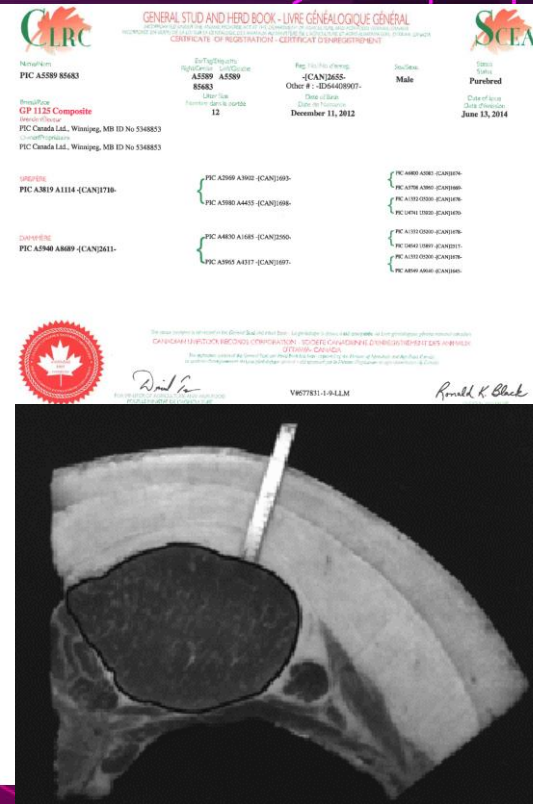
What traits to select?

Often limited by tools and technologies

Herd books
- **Breed recognition, genealogy**
- **Breed standard maintenance**

No genetic selection on traits measured before 1930
- **First testing station - 1935**
- **First farm program - 1956**
  - **Selection based on growth and later on on fat**
  - **Swine then started to change**

The possibilities have now increased tenfold

The list continues to grow

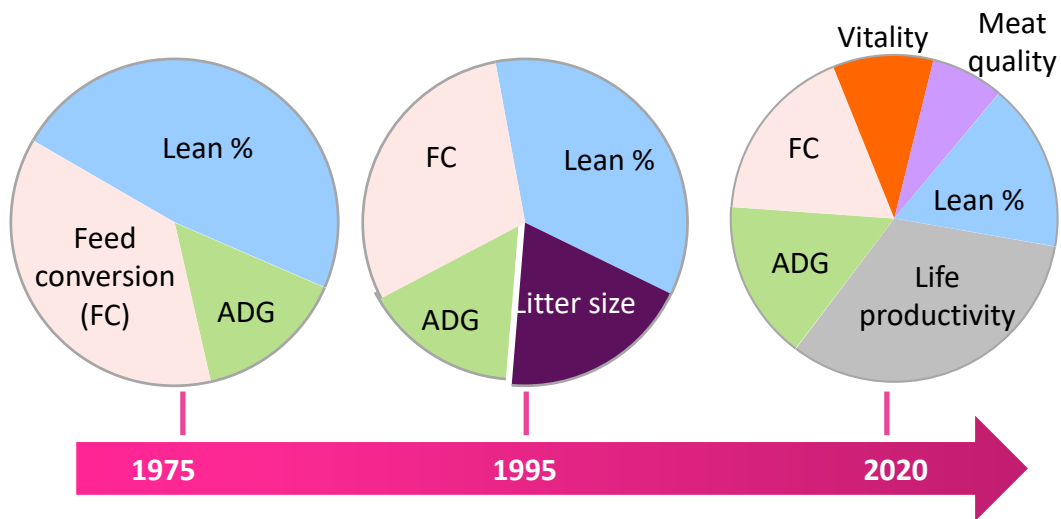Access to technologies helps to measure a growing number of traits

Computers can process information

Costs are the main limitation, more possibilities

We've come a long way in 45 years!

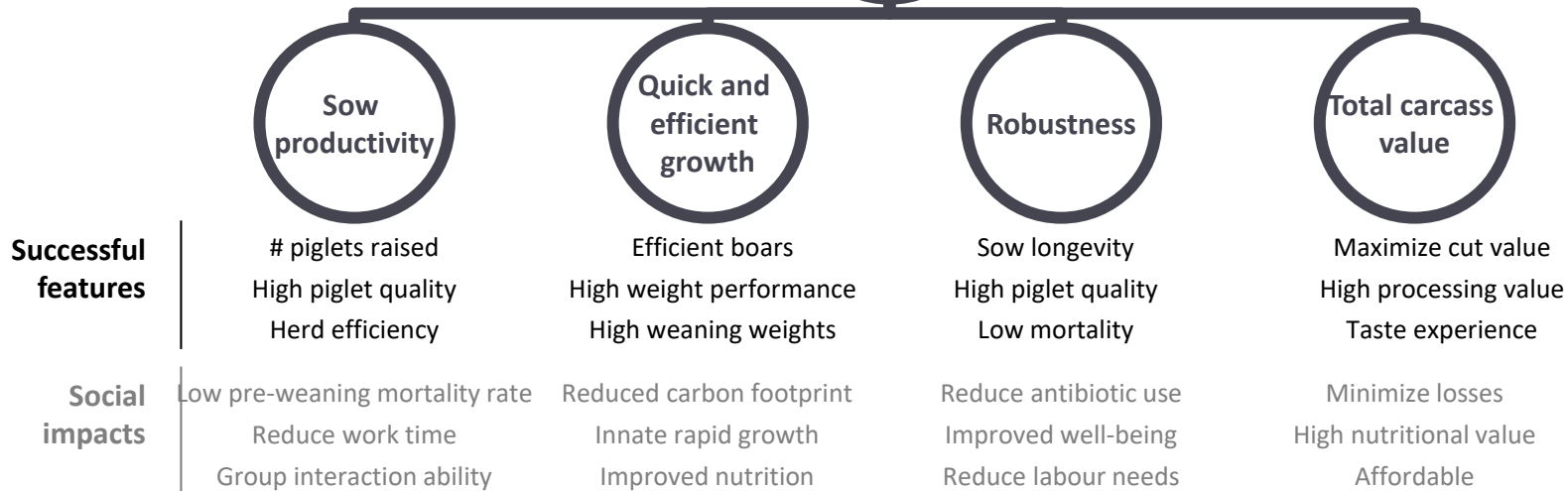## Selection of a growing number of traits

Today's selection criteria must take into account economic and social aspects

Goal of a genetic program:
Maximize value throughout the pig industry

|	**Sow productivity**	**Quick and efficient growth**	**Robustness**	**Total carcass value**
Successful features	# piglets raised High piglet quality Herd efficiency	Efficient boars High weight performance High weaning weights	Sow longevity High piglet quality Low mortality	Maximize cut value High processing value Taste experience
Social impacts	Low pre-weaning mortality rate Reduce work time Group interaction ability	Reduced carbon footprint Innate rapid growth Improved nutrition	Reduce antibiotic use Improved well-being Reduce labour needs	Minimize losses High nutritional value Affordable

← Nutritious, tasty meat at the right price, produced according to high ethical standards →

Levers now maximizing genetic progress

Accurate rIA evaluations are essential

- **The higher the rIA, the more stable the index**
- **In turn, better genetic decisions are made**
- **Genetic progression is also more rapid**

Index =140

High rIA

Low rIA
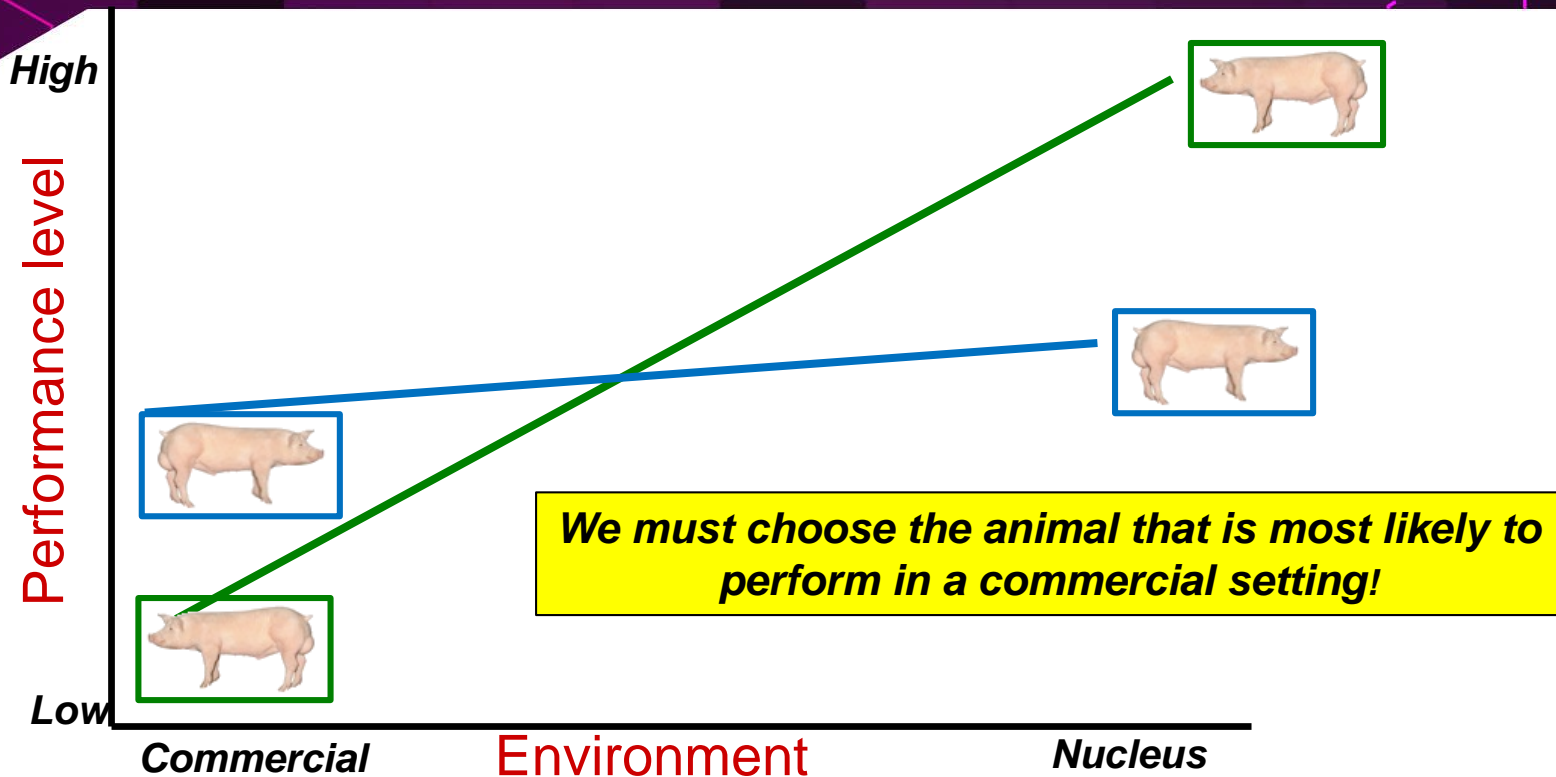
90 110 130 150 170 190
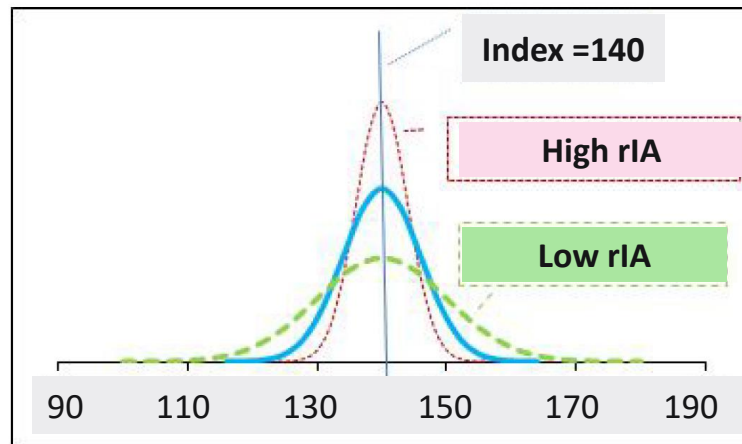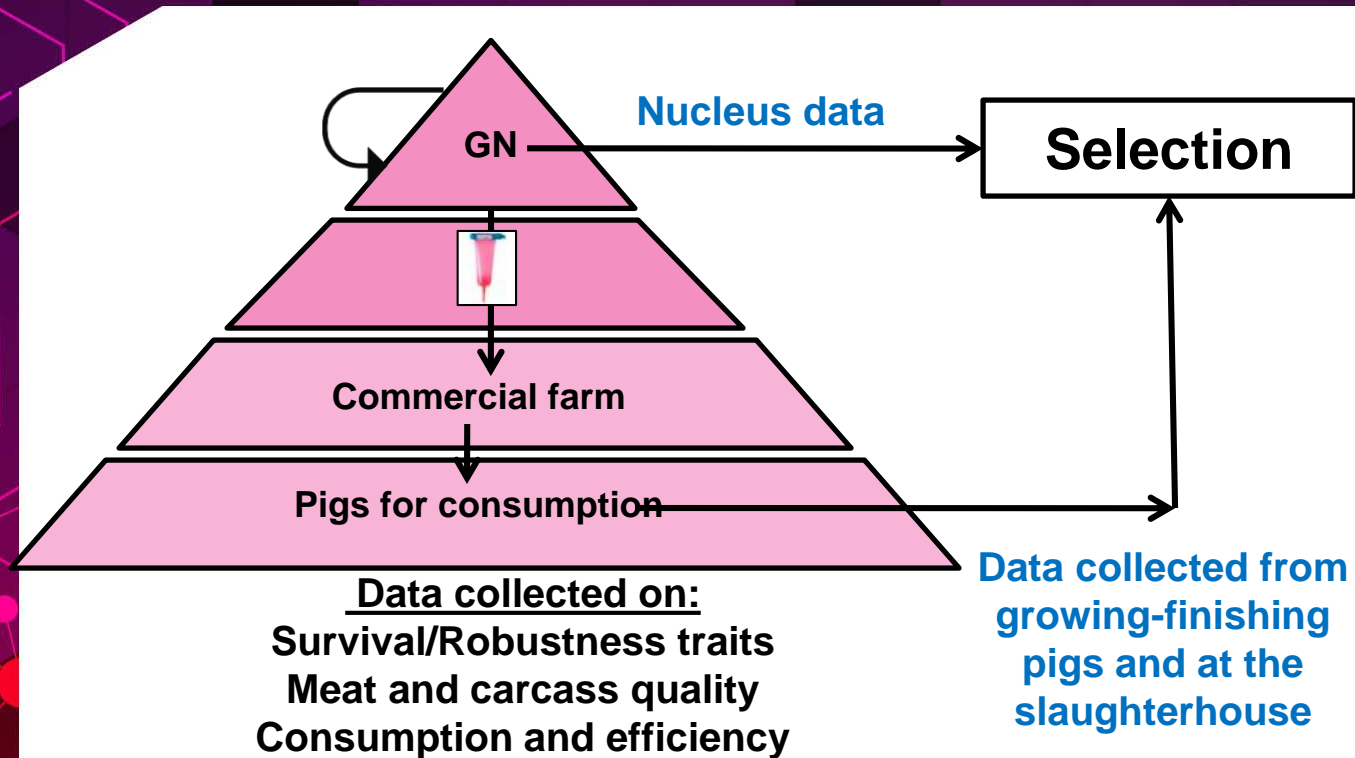
BLUP: The game changer

Statistics tool used to improve index accuracy

1. Uses all available sources of information (individuals, brothers, sisters, half-brothers, half-sisters, etc.)
2. Uses animal genealogy
3. Uses the correlation existing between traits
4. First used for production traits: ADG, fat, FC (1985)
5. Then, breeding traits: end of the 90s
6. It prompted an increase in the number of traits to select

Which 2 boars must we choose?

We must choose the animal that is most likely to perform in a commercial setting!

Measures in a commercial setting

Nucleus data

Selection

GN

Commercial farm

Pigs for consumption

Data collected on:
Survival/Robustness traits
Meat and carcass quality
Consumption and efficiency

Data collected from growing-finishing pigs and at the slaughterhouse

Why measures in a commercial setting?

Information	h² = 0.10	h²= 0.25	h²= 0.40
Own performance	0.32	0.50	0.63
2 parents	0.22	0.35	0.45
5 siblings	0.27	0.38	0.45
100 half-b/s	0.27	0.34	0.40
5 descendants	0.34	0.50	0.60
100 descendants	0.84	0.93	0.96

* c² = 0,05 (B, S, HB, HS)

Data collection on the animal itself is desirable and often more accurate than that collected from parents, siblings or half-b/s.

Regardless of the h², the descendance measurement is always more accurate than those taken on the animal
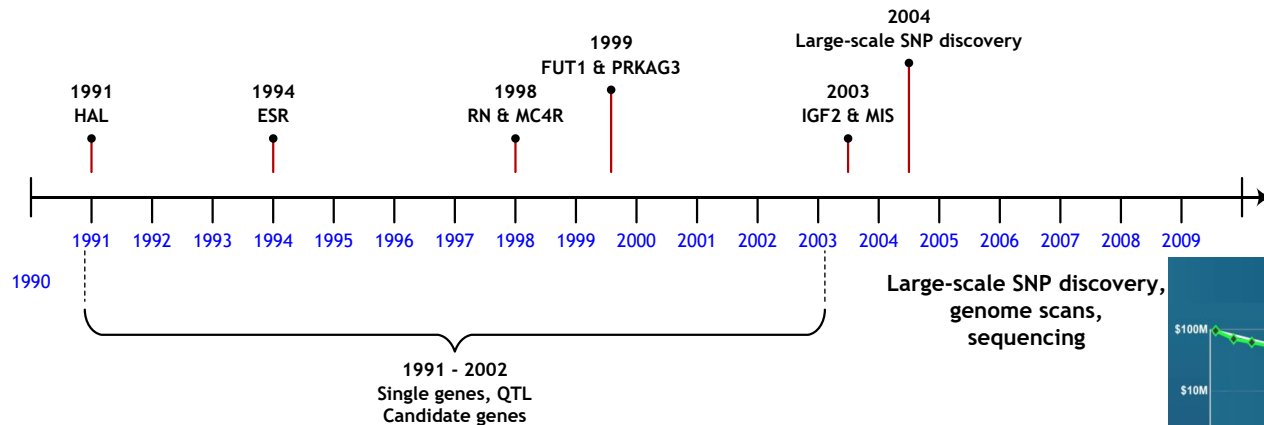
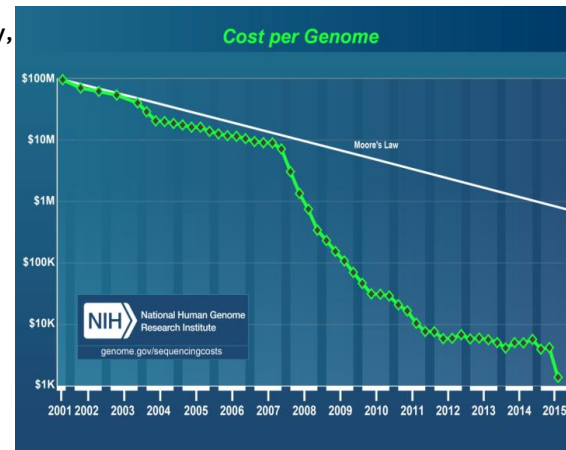# Greater selection accuracy of measures in a commercial setting

**Commercial data→ greater accuracy→
Increased selectivity of elite individuals →
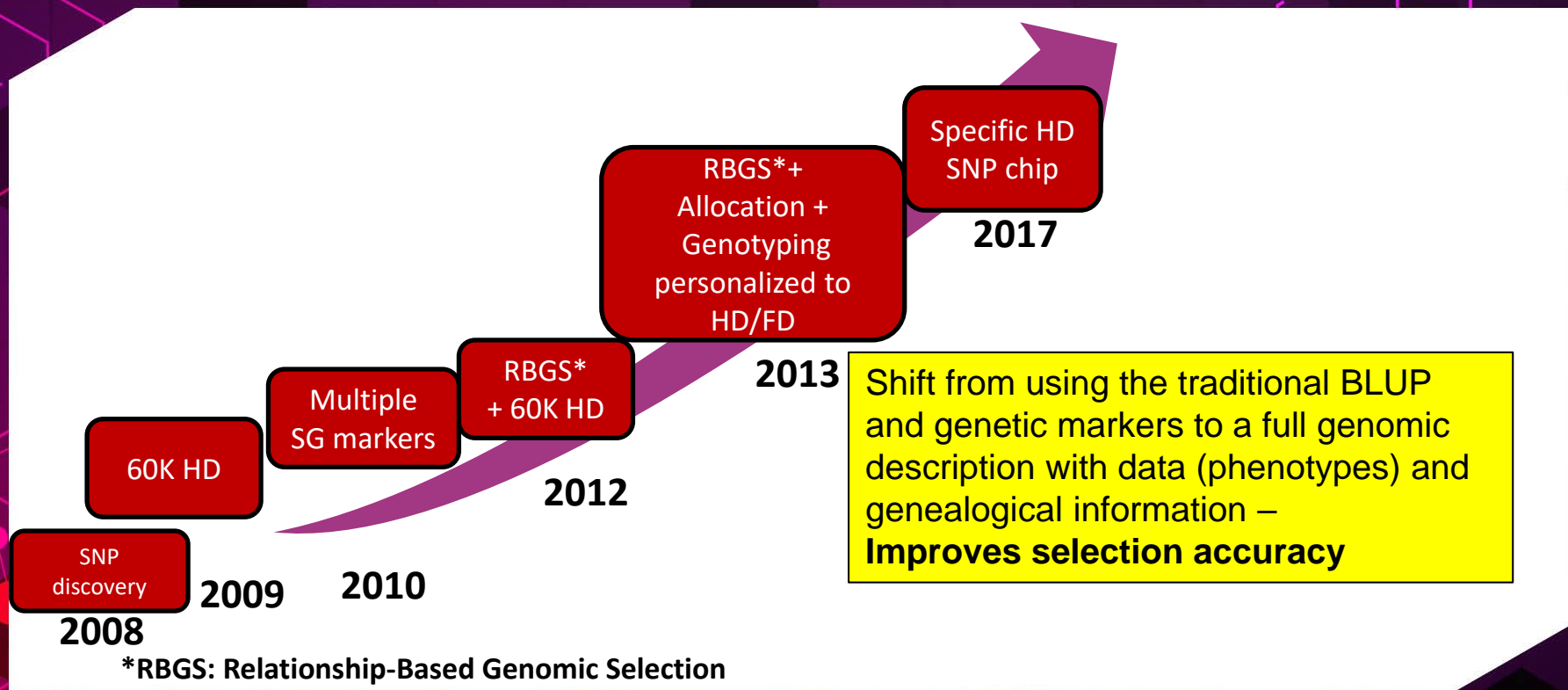Acceleration of annual genetic progress**

+DC

GN
Nucleus

18% improvement
with the addition of
commercial data

Index accuracy
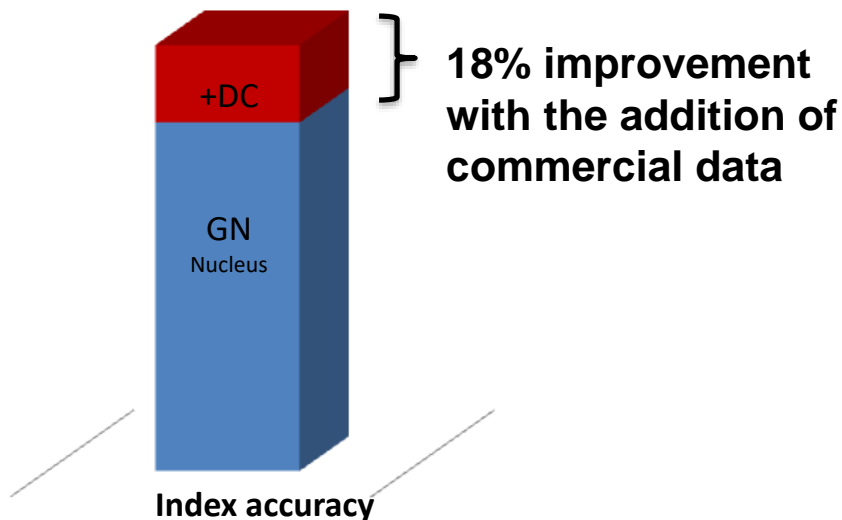
Genomic: On the move for more than 30 years!

1991
HAL

1994
ESR

1998
RN & MC4R

1999
FUT1 & PRKAG3

2003
IGF2 & MIS

2004
Large-scale SNP discovery

1990

1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009

1991 - 2002
Single genes, QTL
Candidate genes

Large-scale SNP discovery,
genome scans,
sequencing

From individual genes, to genetic markers and lastly SNPs…

Cost per Genome

Moore's Law

$100M

$10M

$1M

$100K

$10K

$1K

NIH National Human Genome Research Institute
genome.gov/sequencingcosts

2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015

Evolution in the way genomic is used

SNP discovery

2008

60K HD

2009

Multiple SG markers

2010

RBGS* + 60K HD

2012

RBGS*+ Allocation + Genotyping personalized to HD/FD

2013

Specific HD SNP chip

2017

Shift from using the traditional BLUP and genetic markers to a full genomic description with data (phenotypes) and genealogical information –
Improves selection accuracy

*RBGS: Relationship-Based Genomic Selection

Genomic selection: Yes, but…

Caractère	Lignée A 2005	Lignée A 2009	Lignée B 2005	Lignée B 2009	Lignée C 2005	Lignée C 2009	Lignée D 2005	Lignée D 2009
GMQ	4	13	4	5	3	8	8	4
CMJ	1	10	0	2	2	5	3	8
Gras dorsal	3	11	7	8	5	7	7	6
Épaisseur de longe	1	13	3	6	2	8	6	8
pH24	2	8	2	8	2	4	7	8
Minolta L*	1	1	1	3	1	1	2	3
Mortalité pré-sevrage	0	5	0	4	0	4	0	9
Mortalité en poup.	0	8	0	9	0	5	0	11
Mortalité en crois.-finition	0	7	0	10	0	7	0	14
Hernie scrotale et crypt.	0	0	0	0	0	0	2	4
Cote membres	1	12	6	5	1	9	3	5
Gras intra-musculaire	3	4	2	3	1	1	4	2
Total	**16**	**92**	**25**	**63**	**17**	**59**	**42**	**82**

... It has given way to relationship-based genomic selection

- **Based on science, it's the best genomic application for genetic improvement purposes**

- **It differs from the classic genomic selection that seeks to improve specific traits**

- **It replaces the use of the kinship matrix, which is strictly based on genealogy in the calculation of indices**
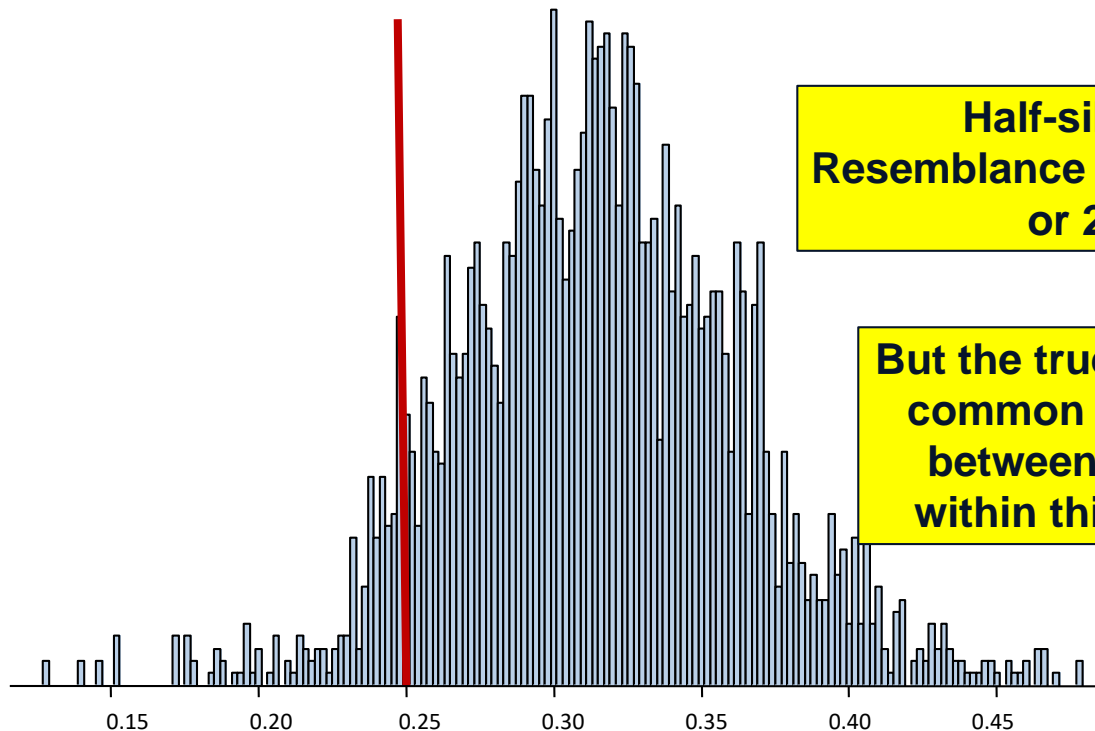

vs

Transforming data into decisions

Les génotypes déterminent le profil génétique

≠ 50%

20%

100%
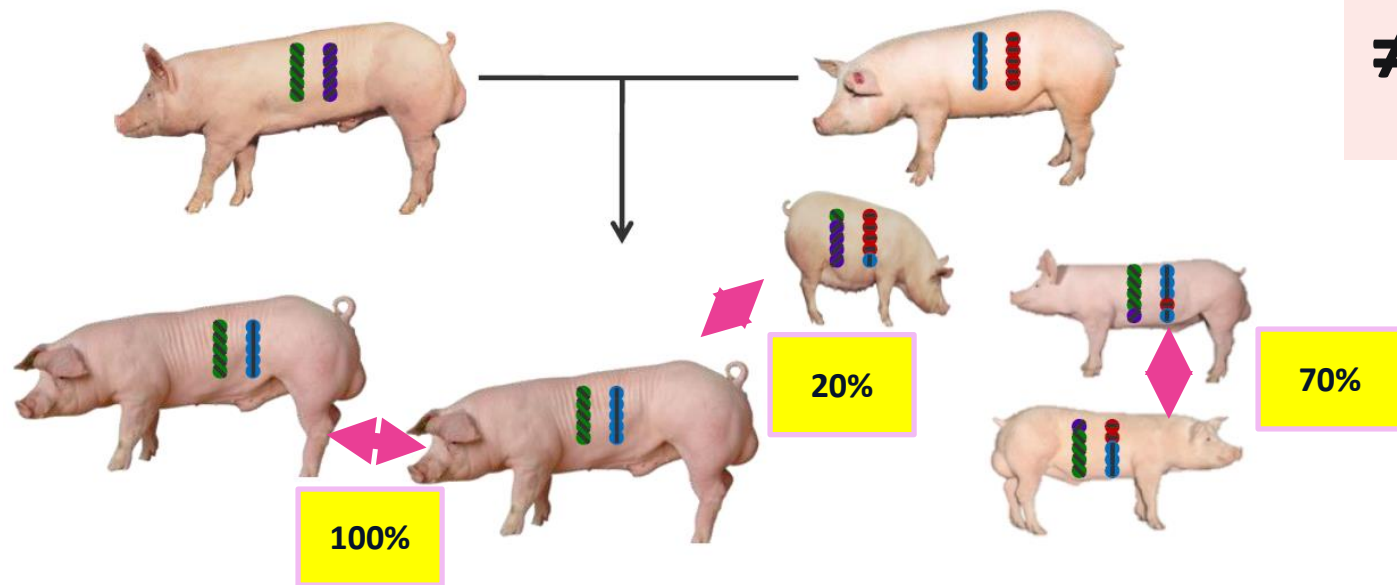
70%

Another example: The relationship between half-siblings

Half-siblings:
Resemblance coefficient= ¼ or 25%

But the true proportion of common alleles varies between 12 and 47% within this population

Goal of the relationship-based genomic selection

More accurate evaluation and identification of elite animals → Acceleration of the genetic progress

- Elite animals
- High-potential animals
- Non-selected animals
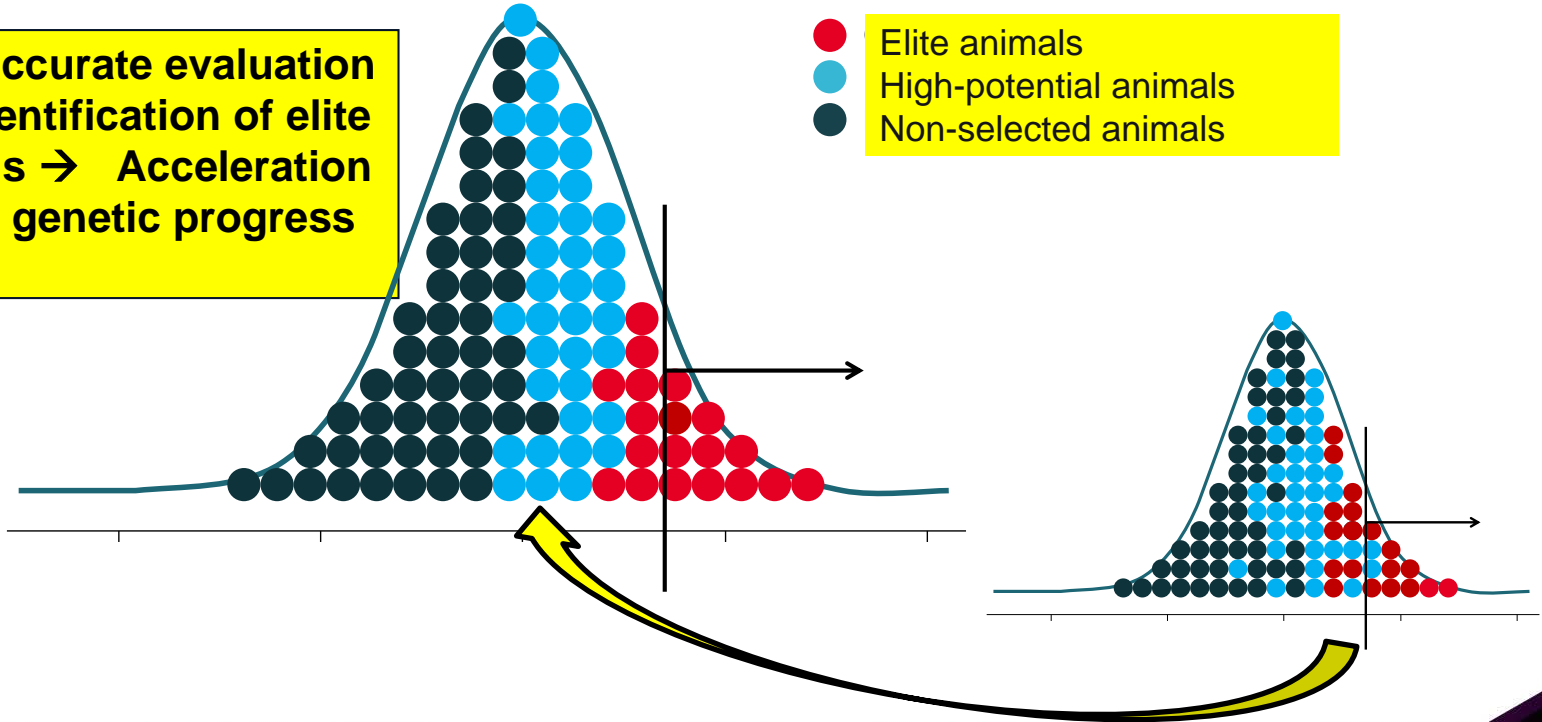
35% genetic progress improvement

Relationship-based genomic selection between individuals vs. BLUP

Commercial genetic trend

Increase in the genetic value created since 2013!

Acceleration
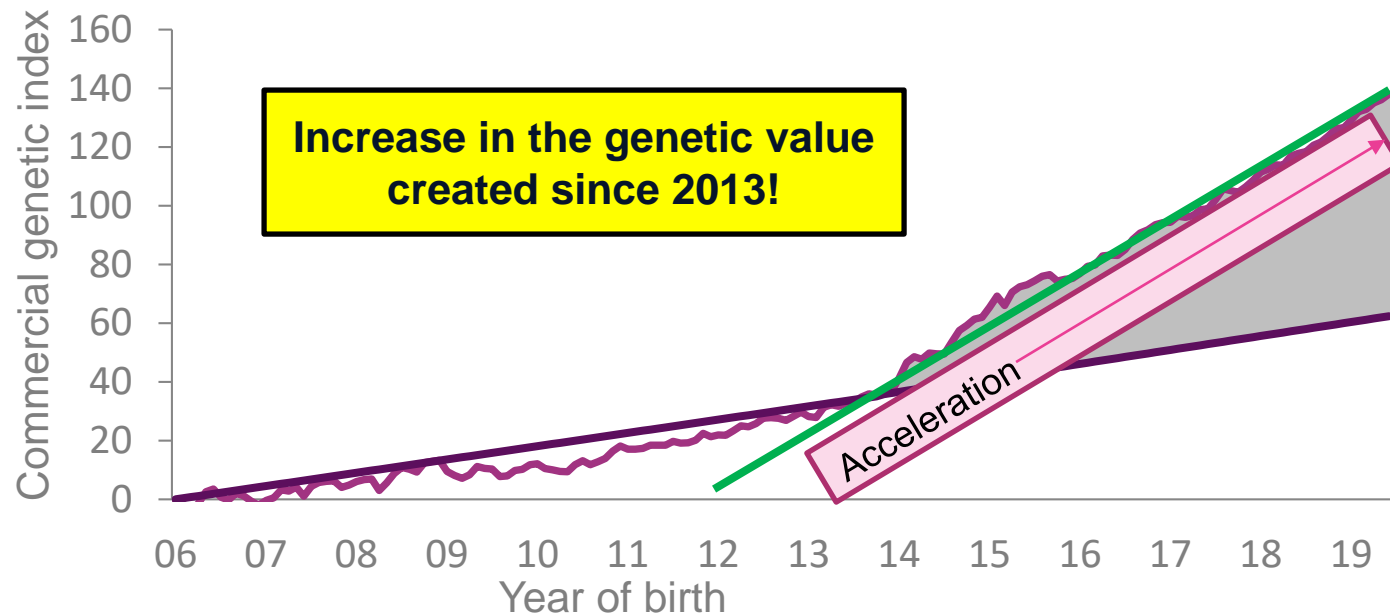
The annual progress made is cumulative

Genomic resemblance — **Basic program** — **Additional cumulative progress**

Additional cumulative value $ / pig

An additional cumulative value of ~5,00 USD in 7 years!

$0.71 $1.42 $2.13 $2.84 $3.55 $4.27 $4.98

2013 2014 2015 2016 2017 2018 2019 2020
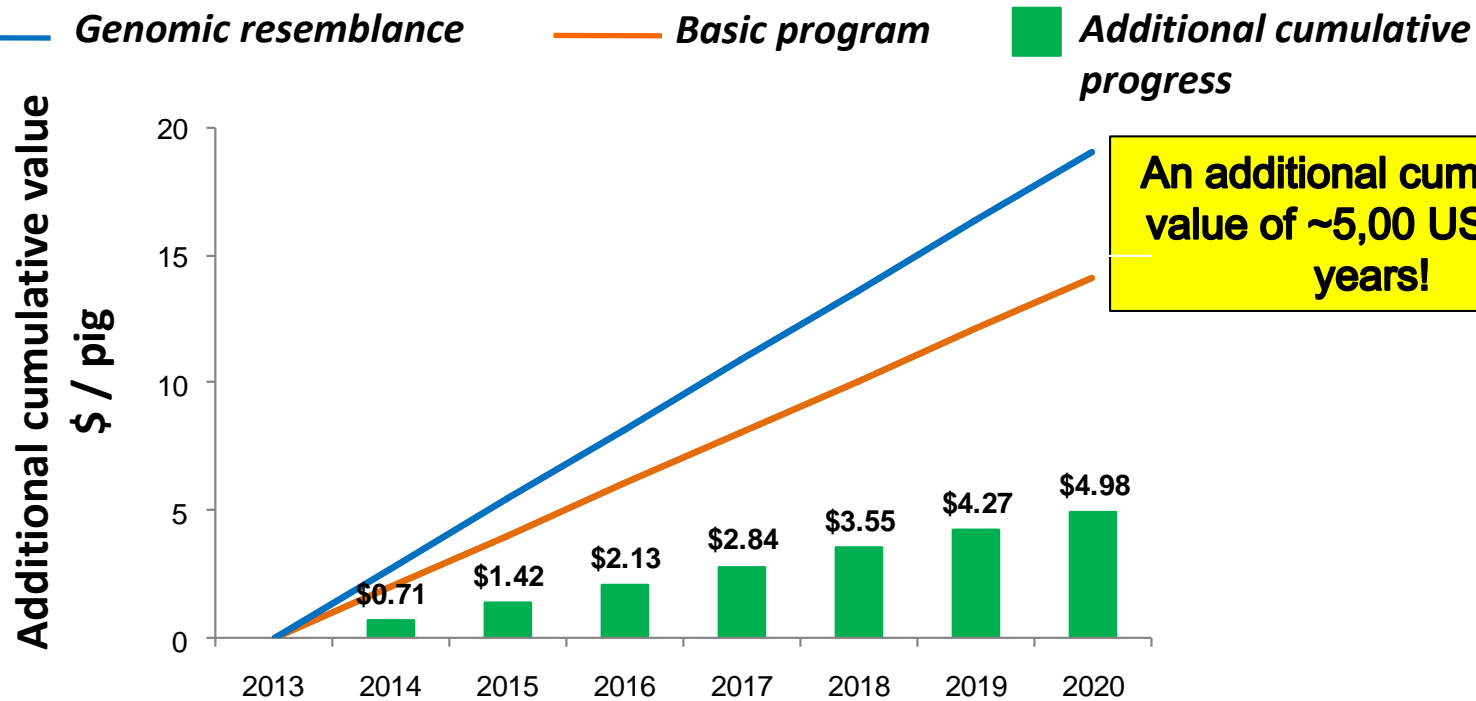
Better mitigating genetic antagonisms
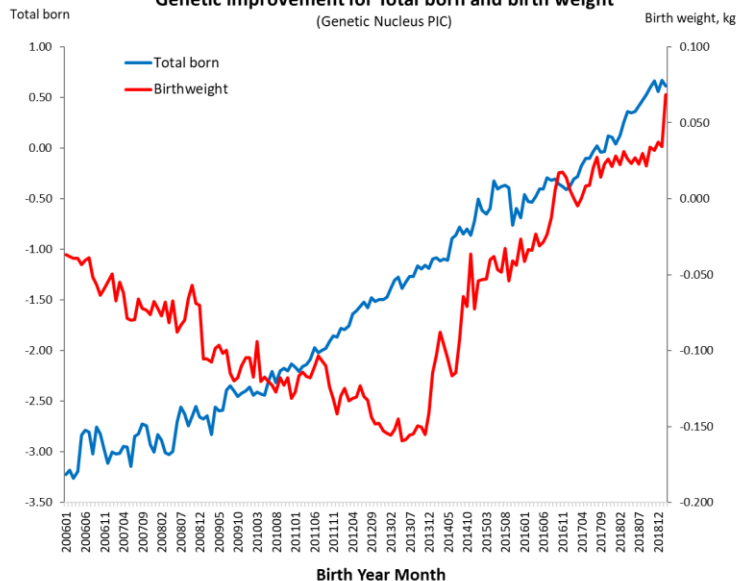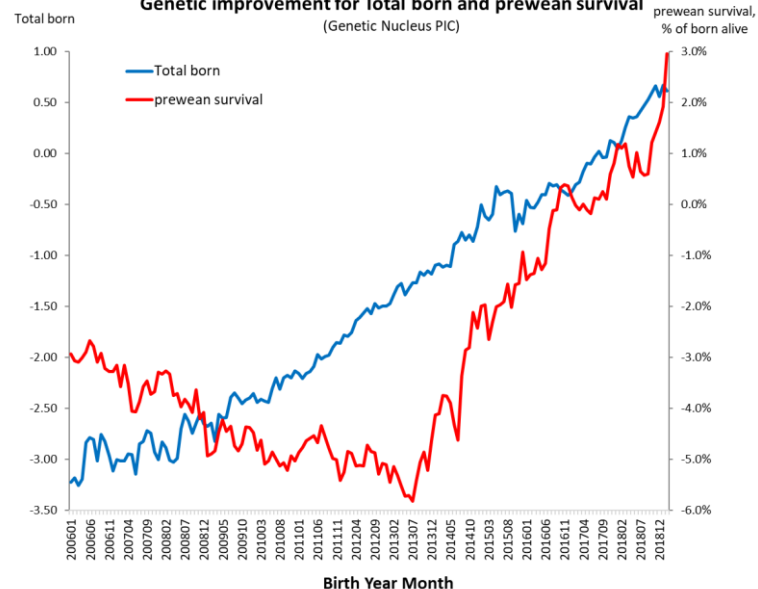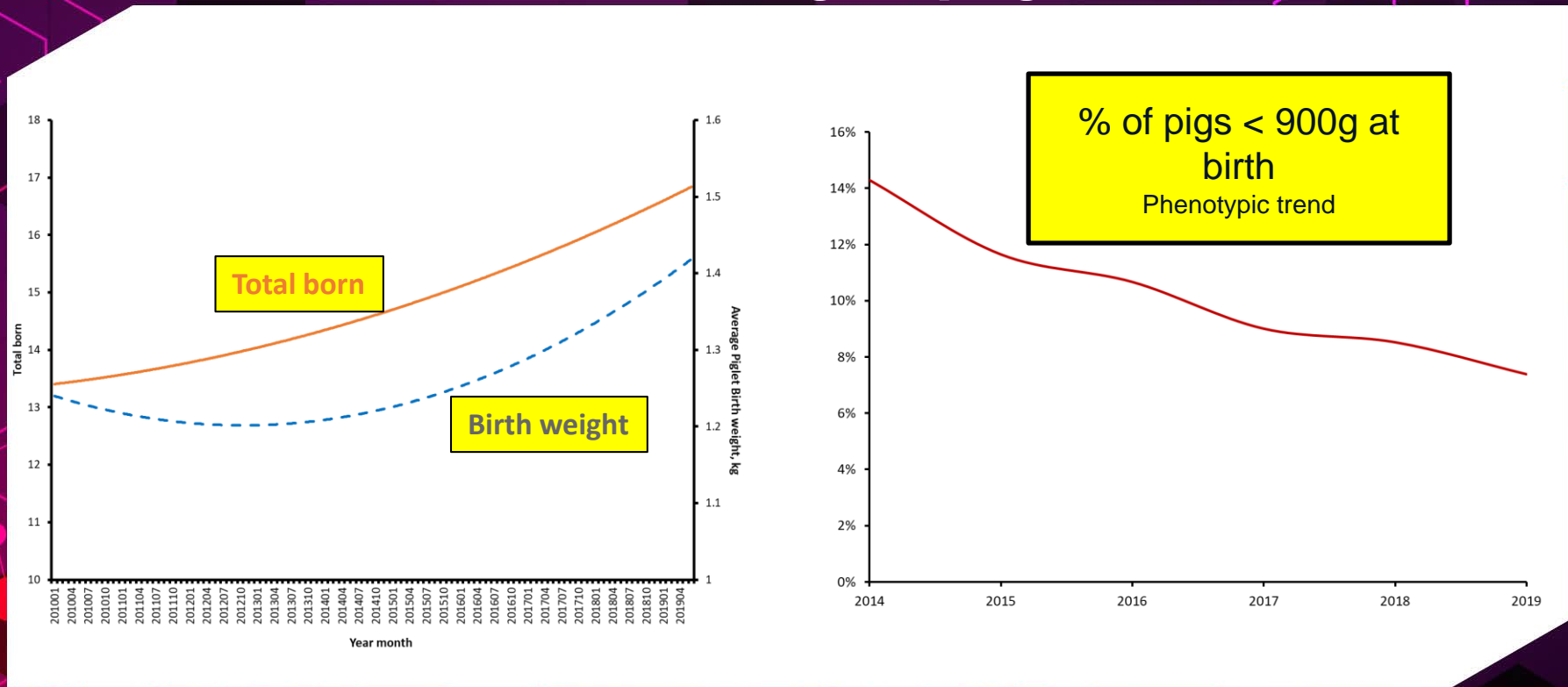
This improvement will be conveyed at the commercial level

| Trait	2018	Annual progress	2028
Piglets/sow/year	33.0	1.1	44.0
Weaned/litter	13.1	0.45	17.6
Weight of weaned piglets/sow/year (kg)	185	6.8	253
Amount weaned/sow/lifetime	60.0	1.3	73.0
Weight sold/sow/year (kg)	3,865	173	5,595
% pigs sold	93	0.35	96.5
Market weight (kg)	130	1.3	143
Post-weaning feed conversion	2.20	0.03	1.90

LE PORCSHOW

What will the next 10-20 years consist of?

1. **Genome sequencing**

2. **Gene editing**

3. **New traits**
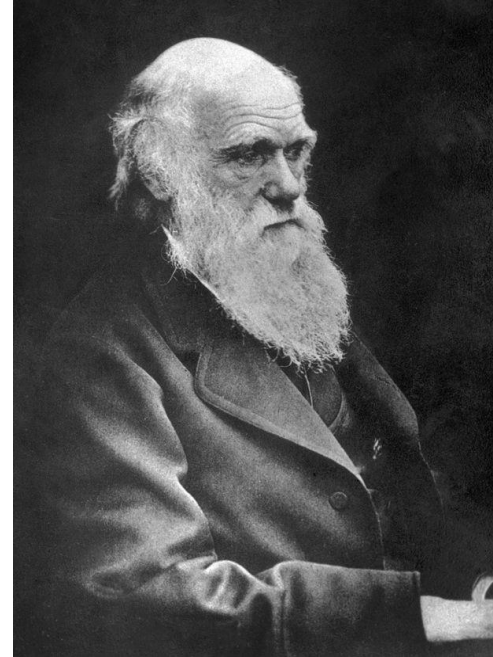
Full genome sequencing

- Identification of the 2 billion+ pairs of nucleotides
- Allocation for genotyped animals with 5K, 15K, 50k, 60k, 80K chips to the full DNA sequence on thousands of animals in the genomic database
- Improvement of the rIA, thus accuracy, thus progress acceleration
- **Discovery of new mutations, new genes of interest**
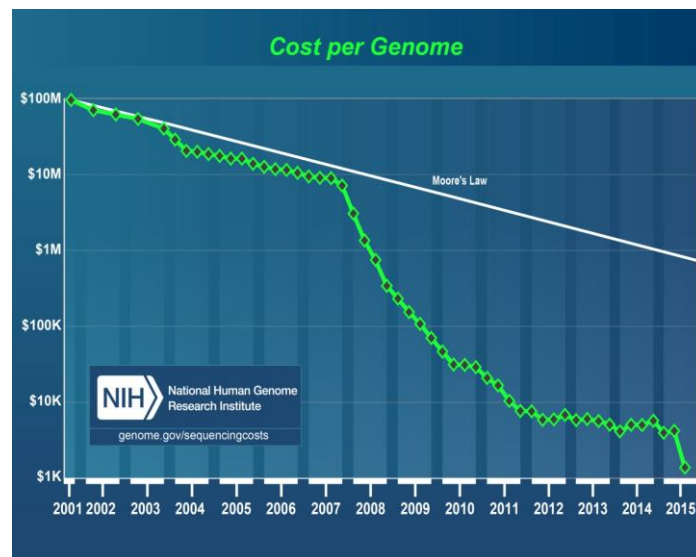
Gene editing

Gene editing is an extremely accurate process

Nucleotides can be:

➢ added

➢ removed

➢ replaced

First results published in December 2015

- **Pigs were created through the genomic editing of a few nucleotides of the CD163 gene. The specific form of this precise gene provides <u>virus resistance</u>**

- **No foreign DNA was inserted in the pig**

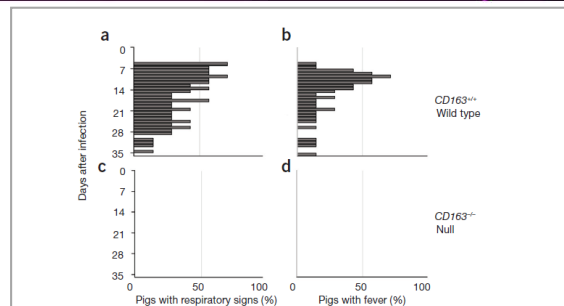- **This discovery has since been confirmed by numerous universities worldwide**

Figure 1 Clinical signs during acute PRRSV infection. (a–d) Results shown are compiled daily assessments for the presence of respiratory signs and fever for $CD163^{+/+}$ ($n = 7$) and $CD163^{-/-}$ ($n = 3$) pigs. The percentage of pigs with respiratory signs (a,c). The percentage of pigs with a fever (b,d). Fever was considered positive if it was ≥104 °F (normal body temperature, 101.6–103.6 °F). Respiratory scores ranged from 0: normal, to 1: mild dyspnea and/or tachypnea when stressed (when handled), 2: mild dyspnea and/or tachypnea when at rest, 3: moderate dyspnea and/or tachypnea when stressed (when handled), 4: moderate dyspnea and/or tachypnea when at rest, 5: severe dyspnea and/or tachypnea when stressed (when handled), 6: severe dyspnea and/or tachypnea when at rest. The percentage of piglets that had a fever or any sign of respiratory stress (a score of ≥1) at the various days of the challenge are shown. Note that the $CD163^{-/-}$ piglets displayed no signs of either respiratory stress or fever.
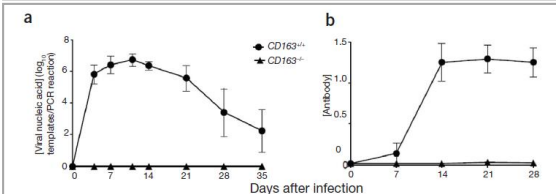
Figure 3 PRRSV-specific nucleic acid and antibody. (a,b) Mean and s.d. of PRRSV nucleic concentrations (a) and antibody (b) in serum from $CD163^{+/+}$ ($n = 7$) and $CD163^{-/-}$ ($n = 3$) pigs (one replication) are shown. Sample to positive ratio = the median fluorescent intensity (MFI) of the sample divided by the MFI of the positive control.

Implementing pigs stemming from gene editing

| Technology	• Confirm the validity of the discovery • Optimize the editing process • Produce pigs stemming from the editing process
Regulation	• *Commitment for approval with the FDA (United States)* • *Initiate contact with international regulatory bodies* • *Cooperate with various bodies of interest*
Product acceptance	• *Make the technology and its benefits known* • *Support public debates* • *Research with the industry & consumers* • *Agreement with meat purchasing countries (ex. China)*

Gene editing potential

➢ **For a set number of selected traits, genetic progression slows down over time**

➢ **Each edited gene brings additional economic value**

➢ **It can be set within a few generations**
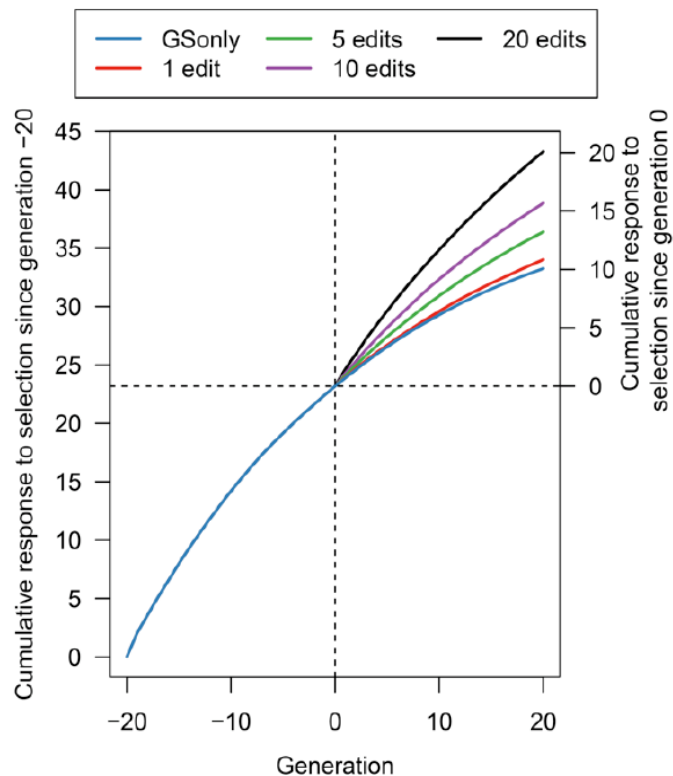
Traits potentially influenced by gene editing

1. **Diseases (African swine fever virus, GET, DEP, influenza)**
   - Existence of vaccines
   - Economic advantages of better control
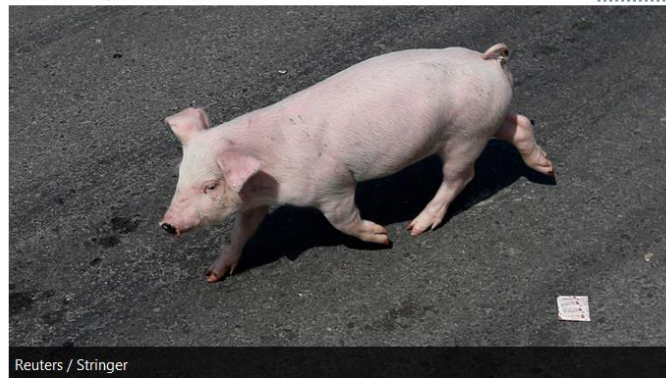   - Resistance ≠ resilience, tolerance

2. **And for the other criteria…**
   - Current selection criteria
   - Sexual smells
   - Others???

New traits

1. **Ability to store and process lots of data**
   - ➤ Computer processing power
   - ➤ Algorithms allowing for information to be pre-processed

2. **Real time measurements will be a game changer**
   - ➤ Increased camera use
   - ➤ Artificial intelligence

New traits

1. **Phenotype measuring from all angles**
   - ➢ Repeated measures
     - ➢ How the animal drinks and eats
     - ➢ When the animal gets sick, isn't feeling well
     - ➢ Etc.
2. **Pig behaviour and animal well-being**
   - ➢ Defining the trait is a challenge in itself
   - ➢ Correlation between piglet<-> fattening pig <-> sow
   - ➢ No evidence today (h2=0)
   - ➢ Data storage and analysis
3. **Other traits**
   - ➢ Function of technologies available and economic interest

Conclusion

1. **A growing range of selection criteria**
2. **Improvement of (rIA) accuracy means**
   - ➤ Genetic progress that keeps getting more rapid
   - ➤ More predictable results (sector)
     1. + piglets born, weaned and at weight + raised
     2. + full value pigs at the slaughterhouse
     3. Very rapid growth and low conversion
     4. Improvement in meat quantity and quality
3. **Challenge for all fields to express the full potential**
   - ➤ Guides and manuals
   - ➤ Farming management, nutrition, health, etc.