REGRESAR MENU

# "Genetic progress in pigs: innovating for the 2025 industry and markets"

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AMVEC 2015

July 31st

# Genetic progress

**Accuracy of selection**
- **Data collection / traits**
- **BVE technology**

**Selection intensity**
- **Population sizes**
- **Selection work**

$$\Delta G_{year} = \sigma_H \times r_{IH} \times \frac{i}{L}$$

**Genetic variation**

**Generation interval**
- **Replacement rate**
- **Age at 1st service**

# Data collection

# Genetic progress

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**Generation interval**
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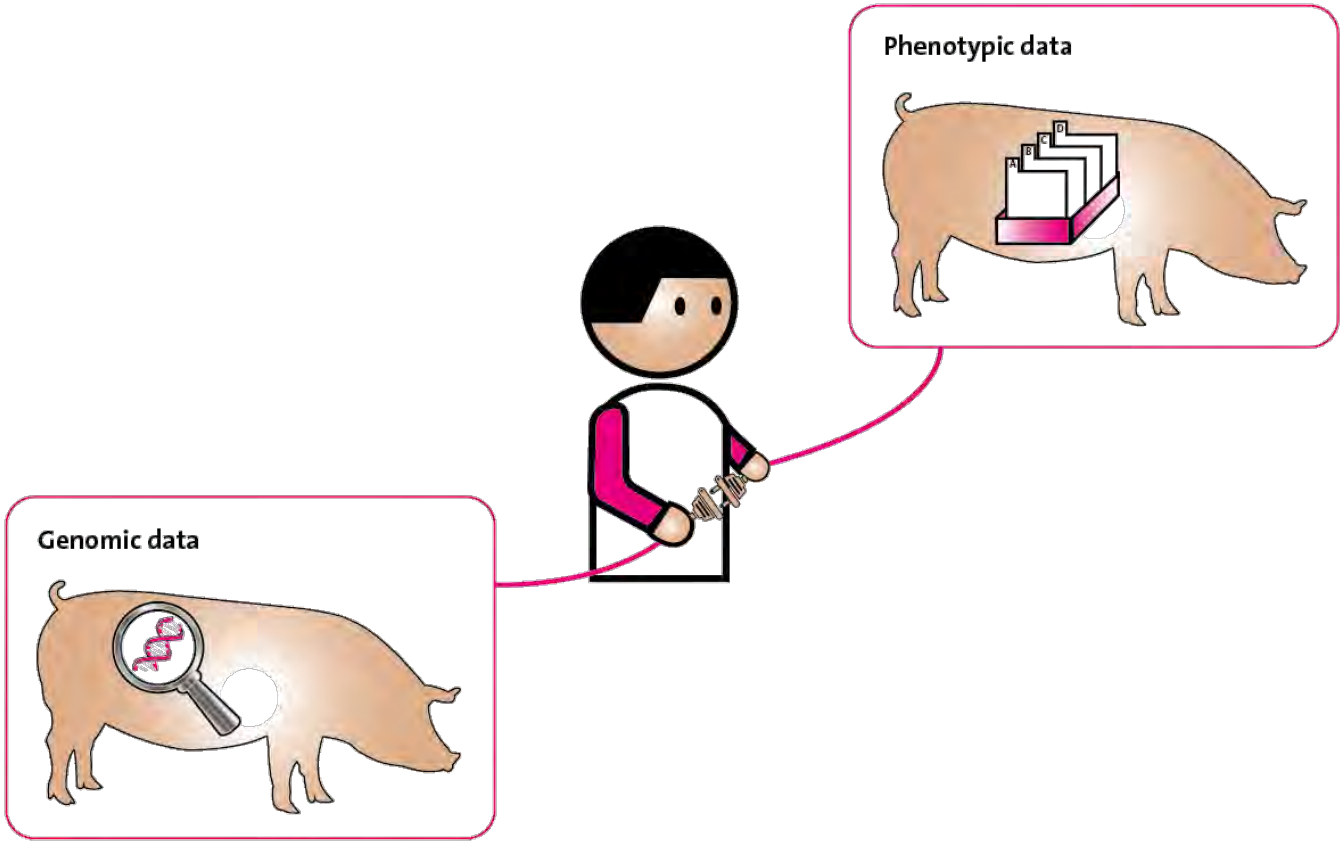
# Genomic selection



# Genotyping tools

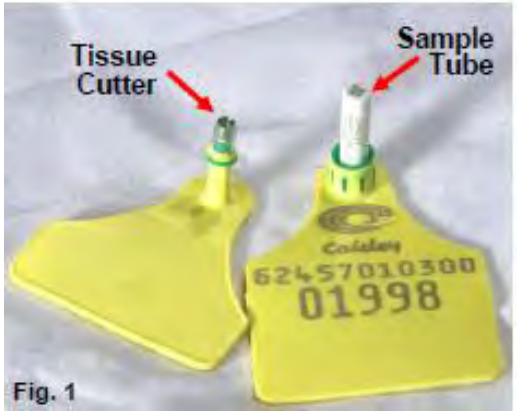
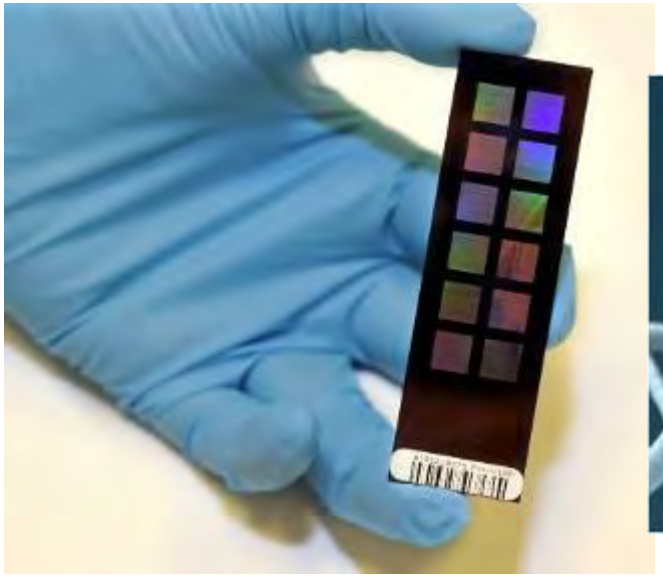


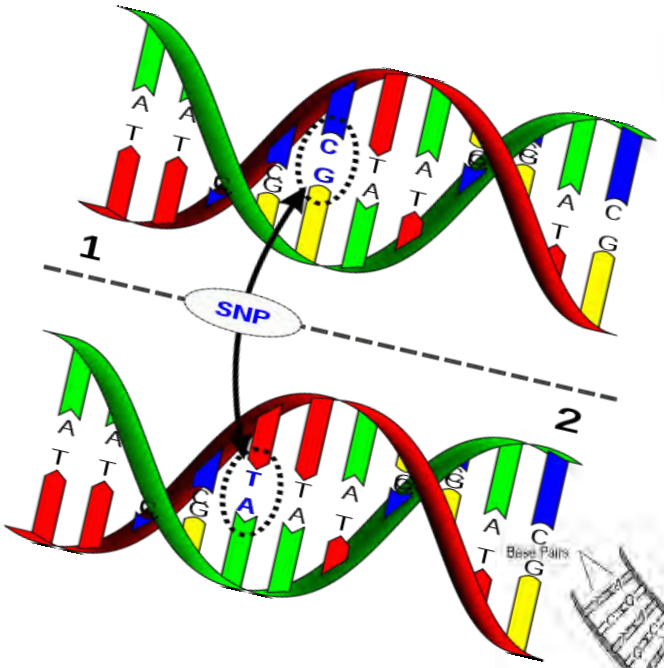
Fig. 1

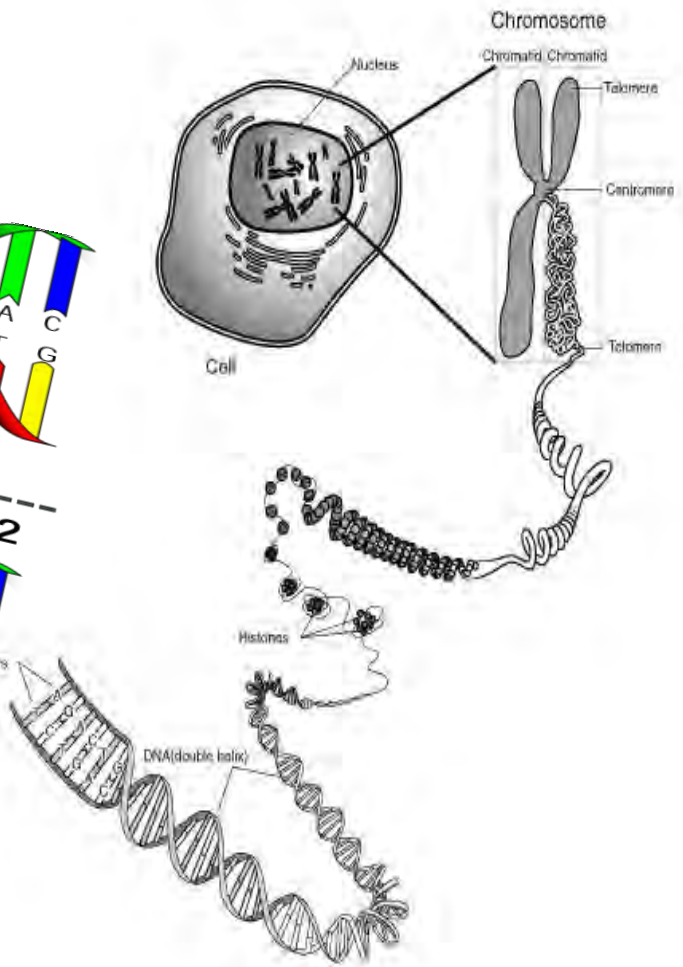

Fig. 6

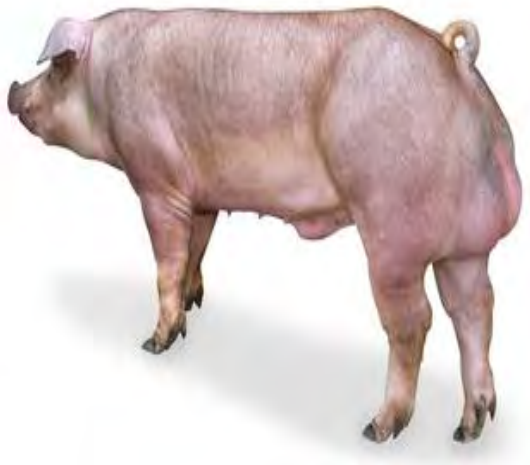


# Some terms and definitions in the era of genomics

# SNP's


1
SNP
2


Chromosome
Nucleus
Chromatid
Chromatid
Telomere
Centromere
Telomere
Cell
Histones
Base Pairs
DNA(double helix)



# DNA and genes

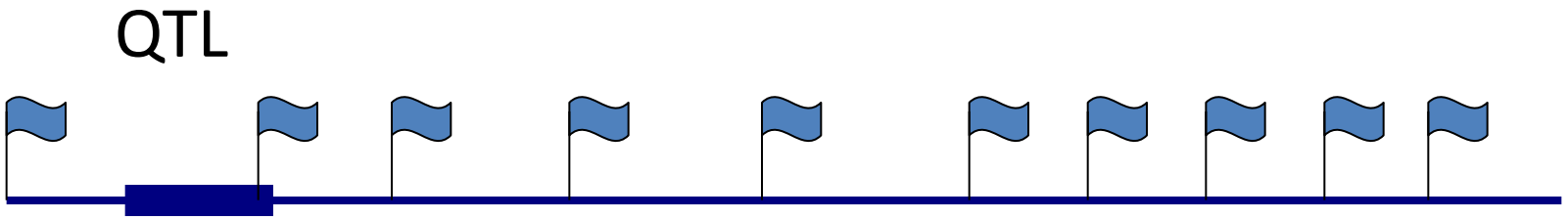

QTL = Quantitative Trait Loci = Gene

*E.g. a piece of DNA with a positive effect on meat quality*

# Marker / SNP


SNP's define a position  on the genome

# SNP panel



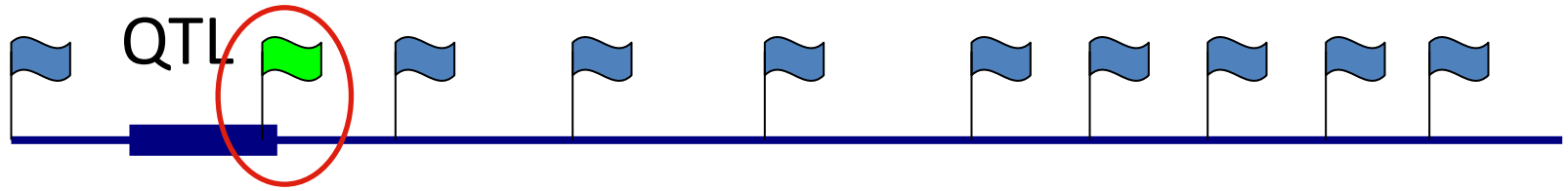

Set of markers

Many SNP’s = many markers = high density

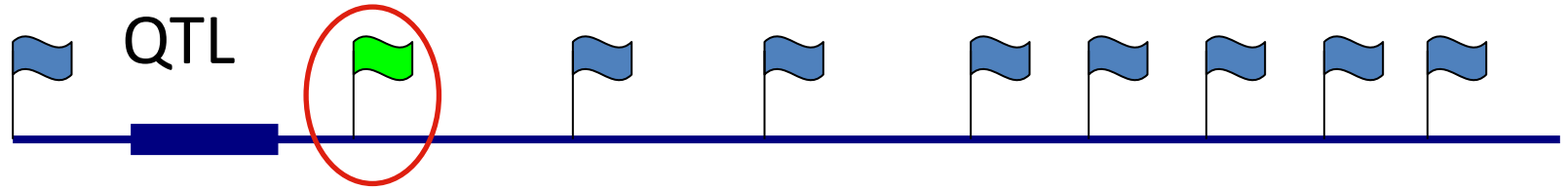
# Training

Markers explaining phenotypic performance:

1. Inside the causative mutation




2. Near the causative mutation

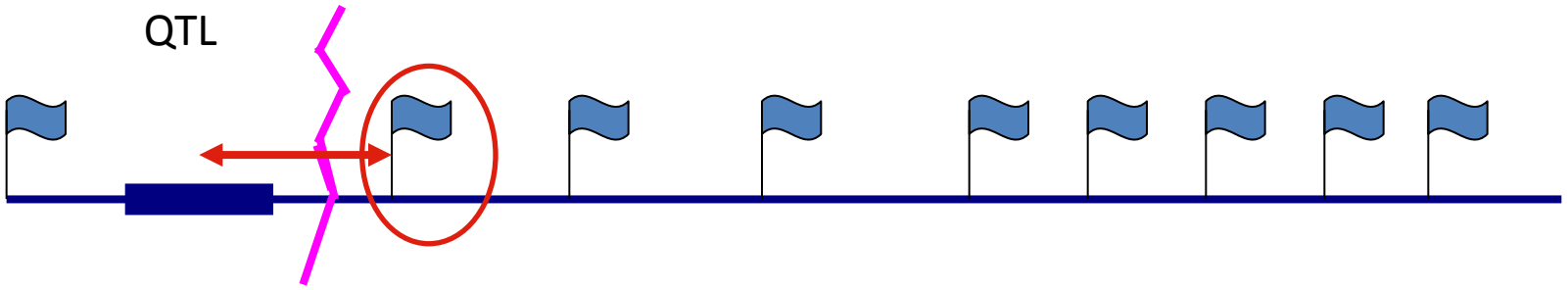


# Recombination

Oocyte/sperm production: mixing DNA of grandparents

*(= Mendelian sampling / crossing-over)*

Marker/SNP – QTL relation can break → **repeat training**

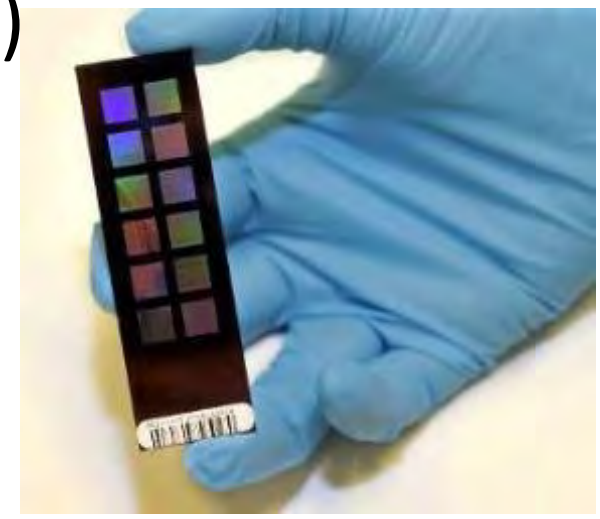


# Genotyping

Different densities:

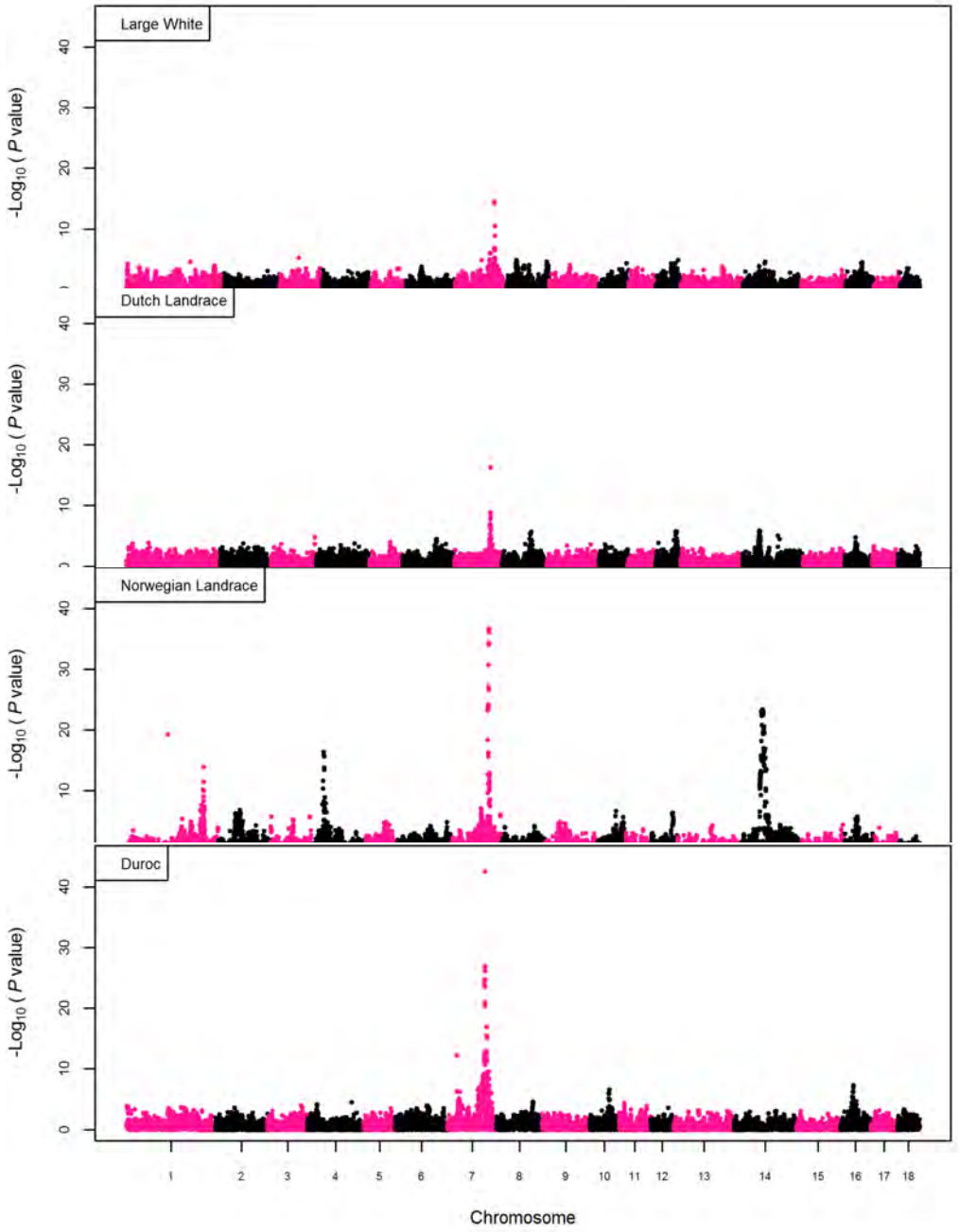
- Full genome sequence (~1M SNPs)
- HD-chip (80k SNPs)
- LD-chip (10k SNPs)

Imputation

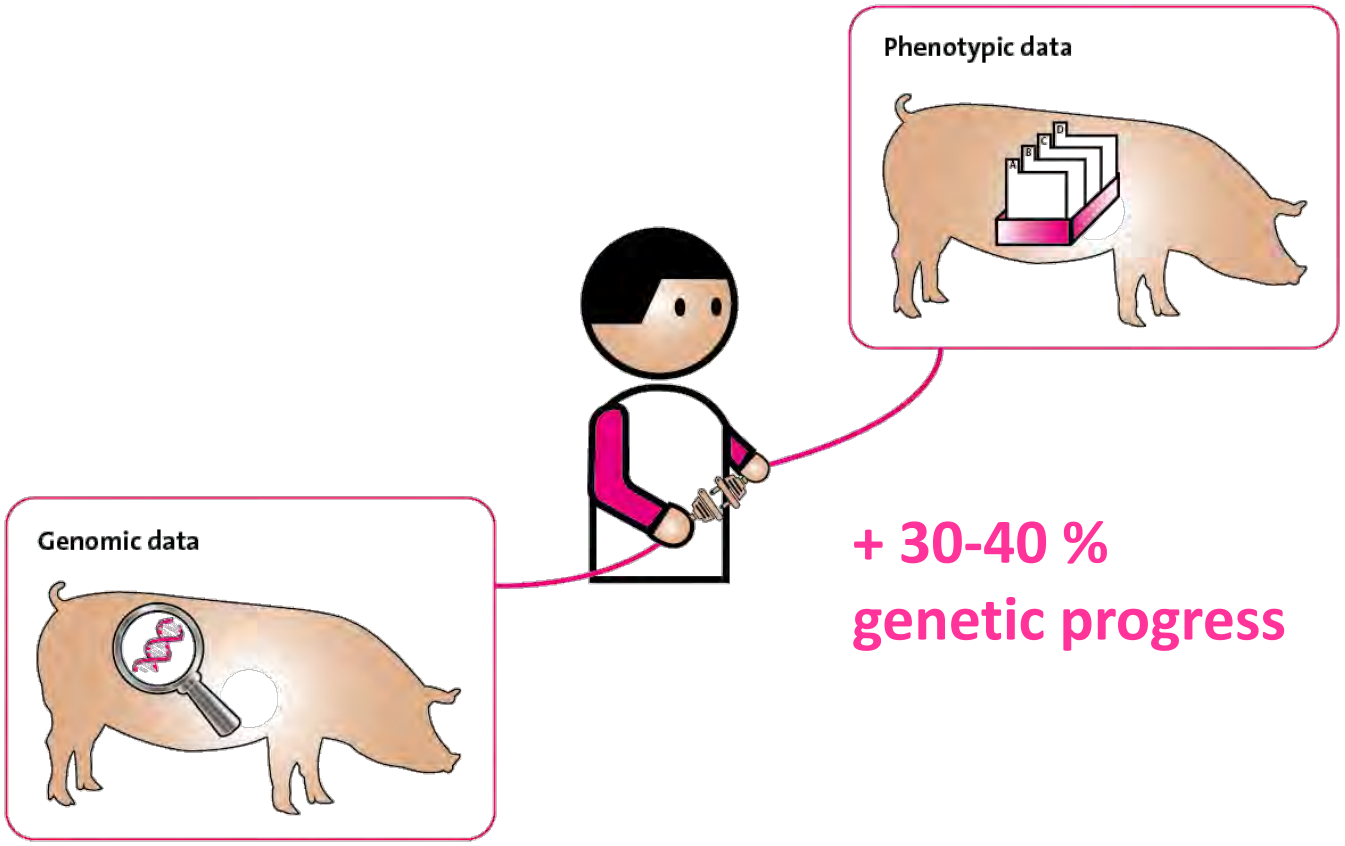


# GWAS
## # of teats

highly significant in all phenotyped lines



# Genomic selection

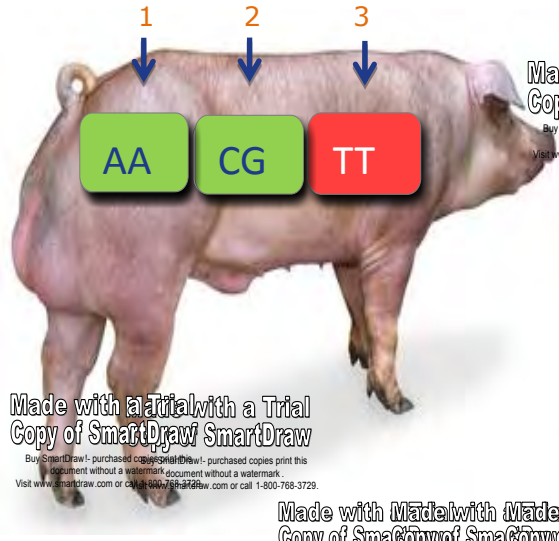


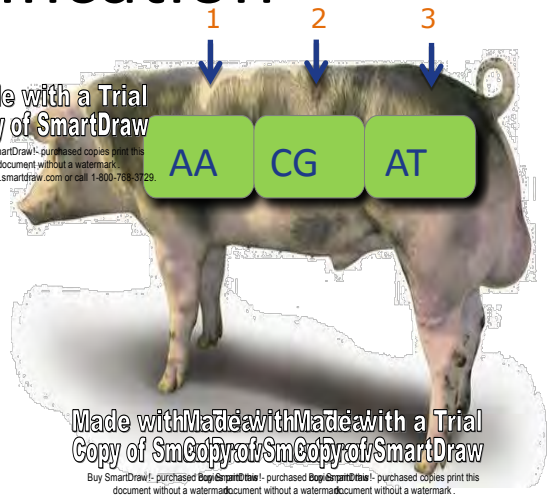
# Added value

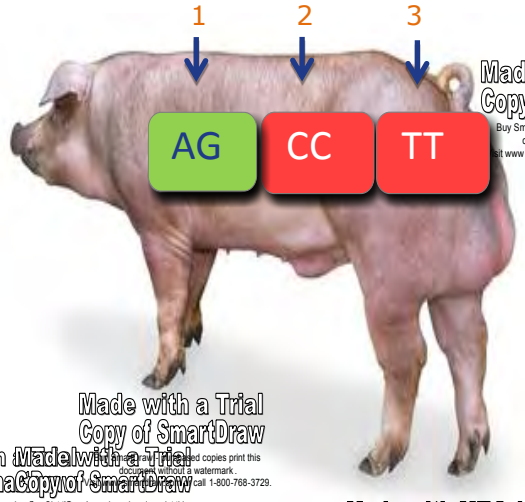
- More reliable breeding values
- Faster genetic improvement (30-40%)
- New selection traits
- More predictable performance in client herds

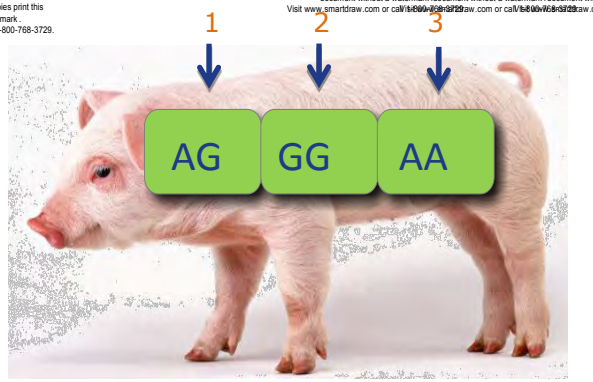
# Reliable pedigree

- Parental Identification



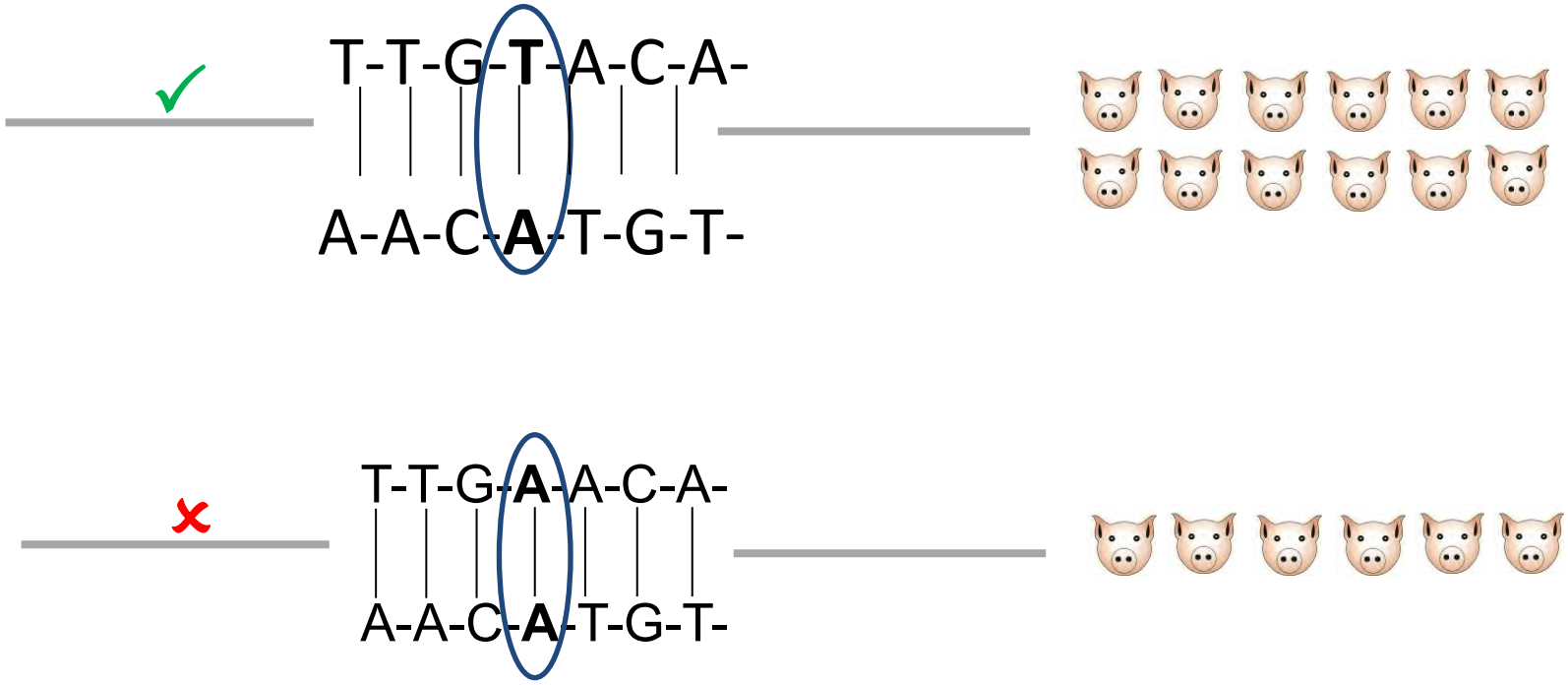



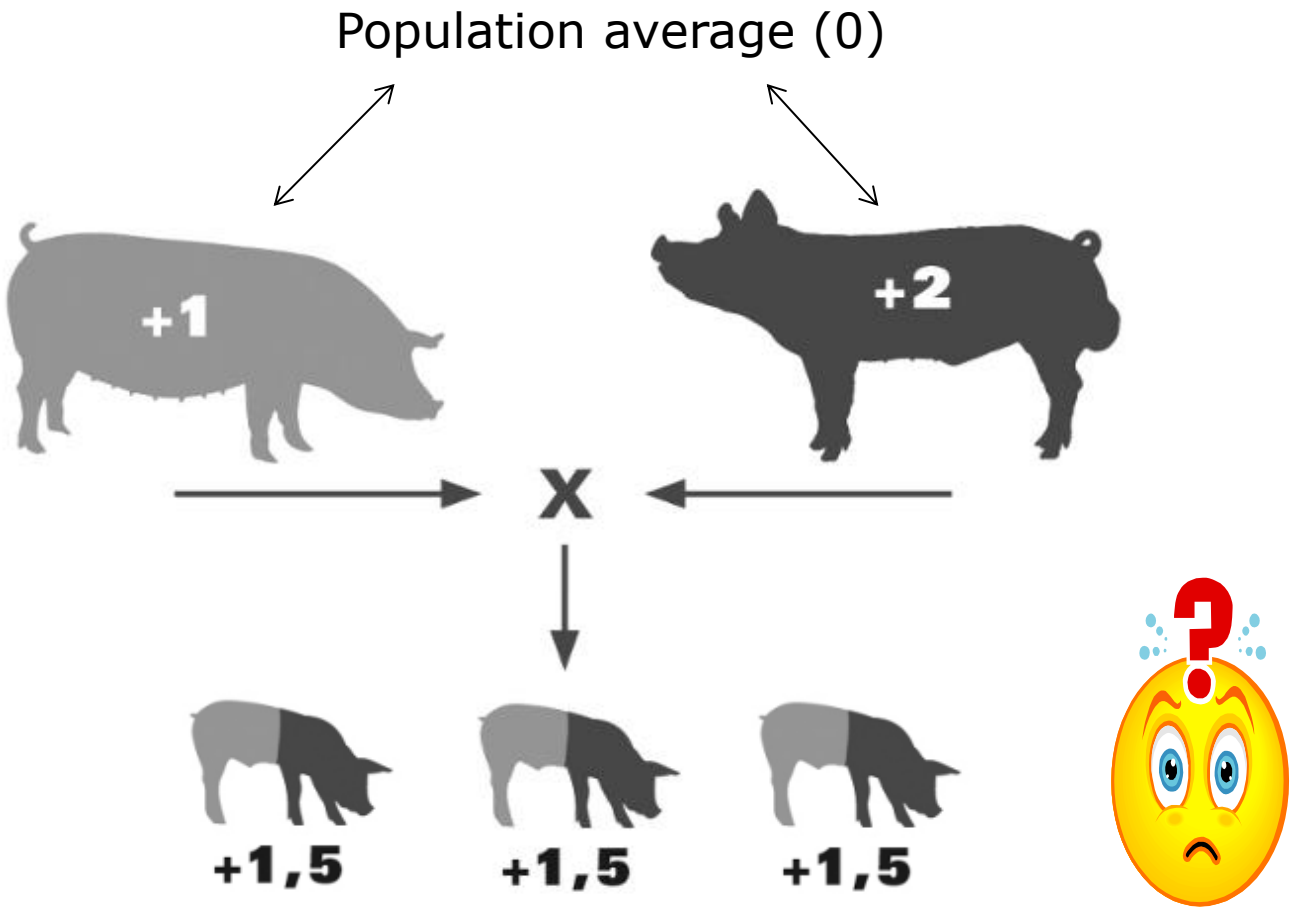
# Specific Markers

*E.g. total number born*

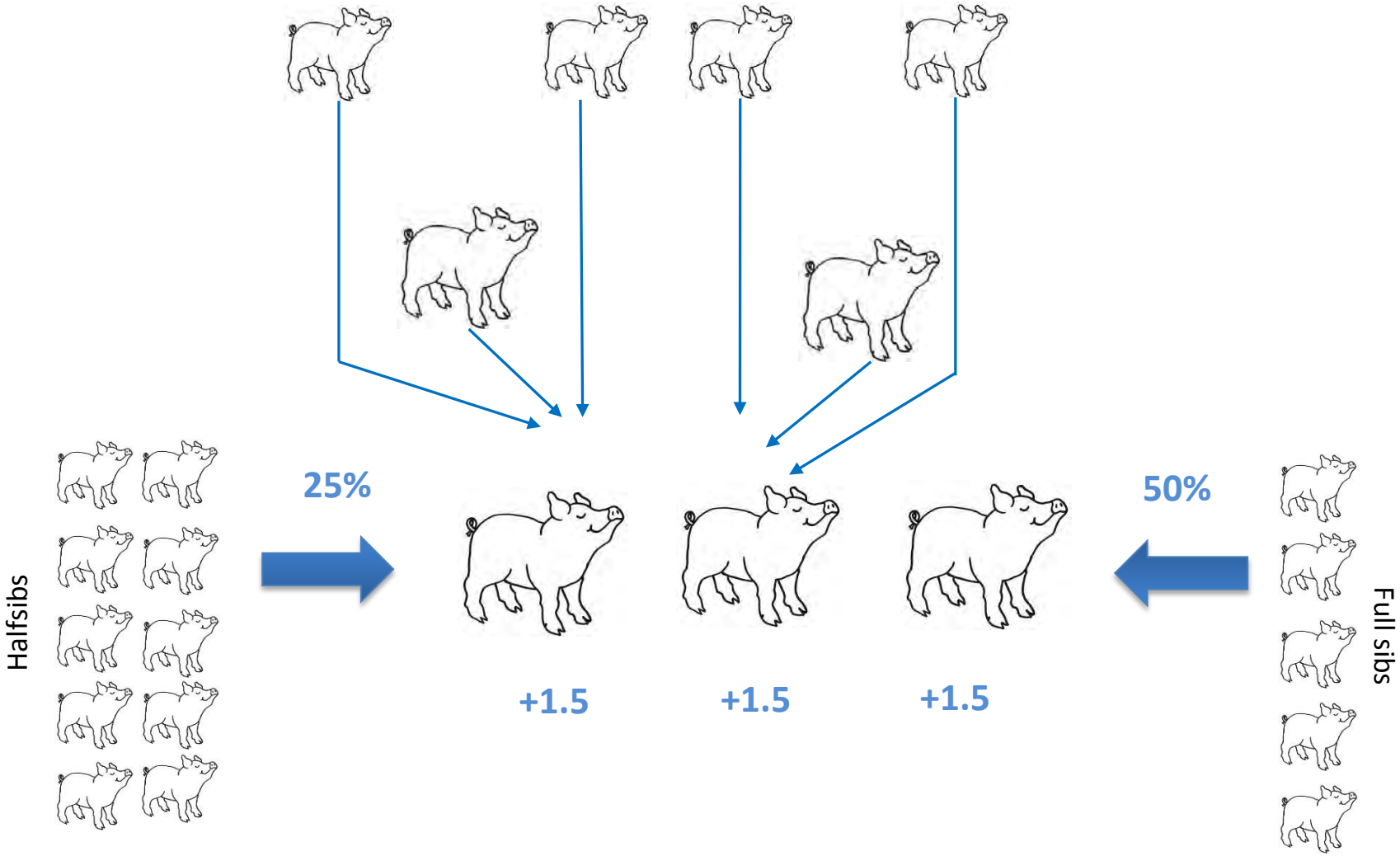


# More accurate relations ($A^{-1}$ ➔ $H^{-1}$)

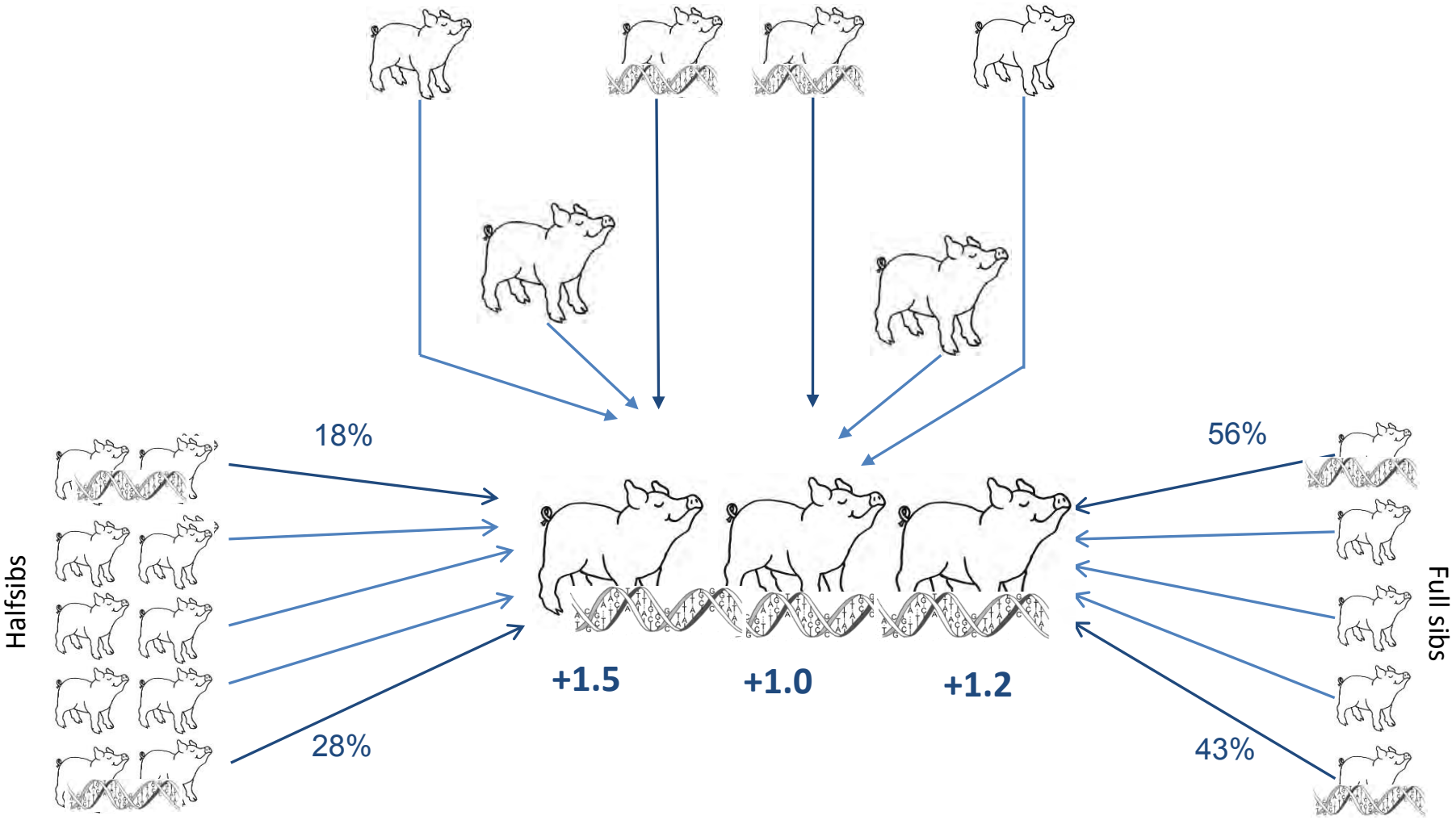
Classical breeding values ($A^{-1}$)



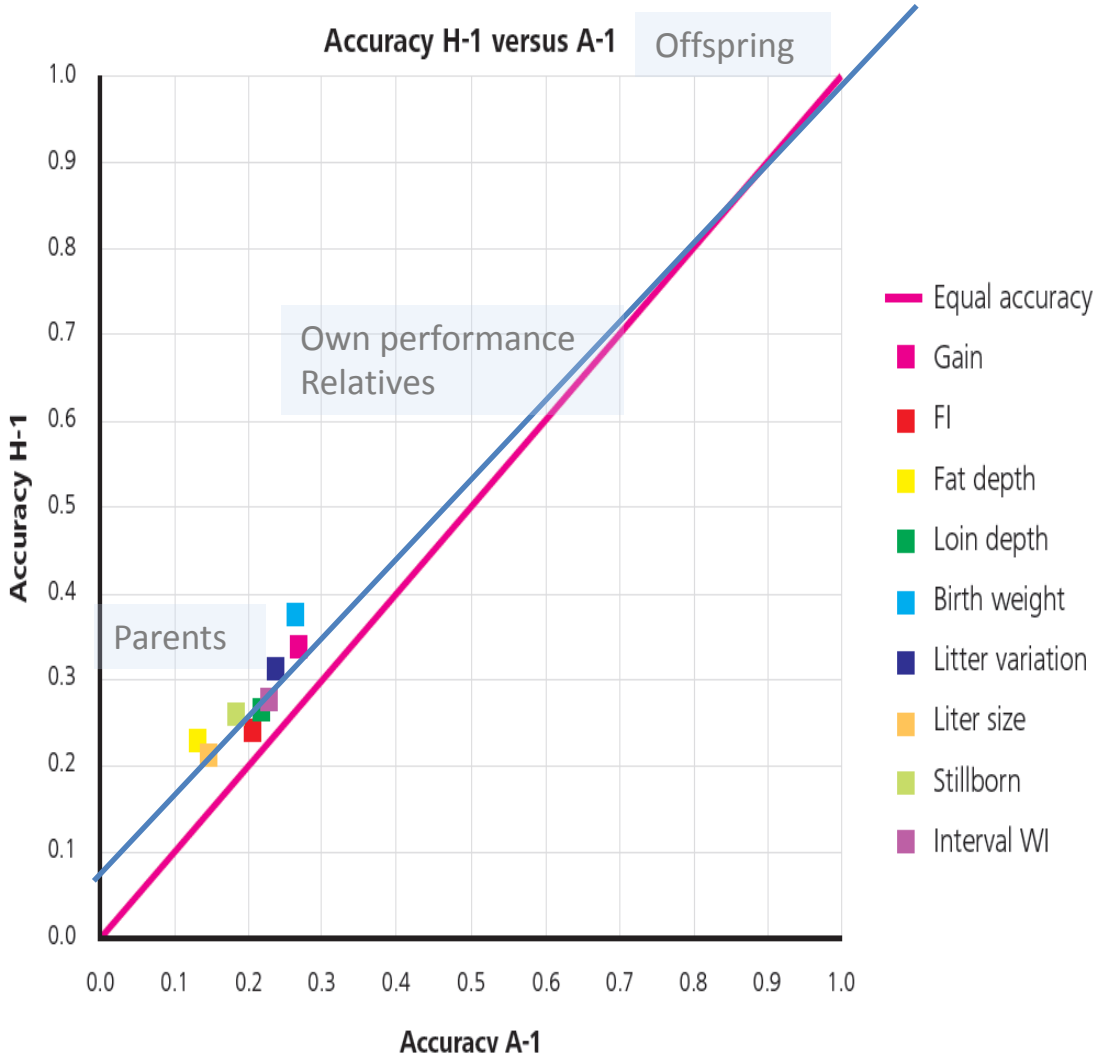
# Traditional family relations ($A^{-1}$)



# Traditional + DNA relations ($H^{-1}$)



# More accurate relations = more accurate EBV

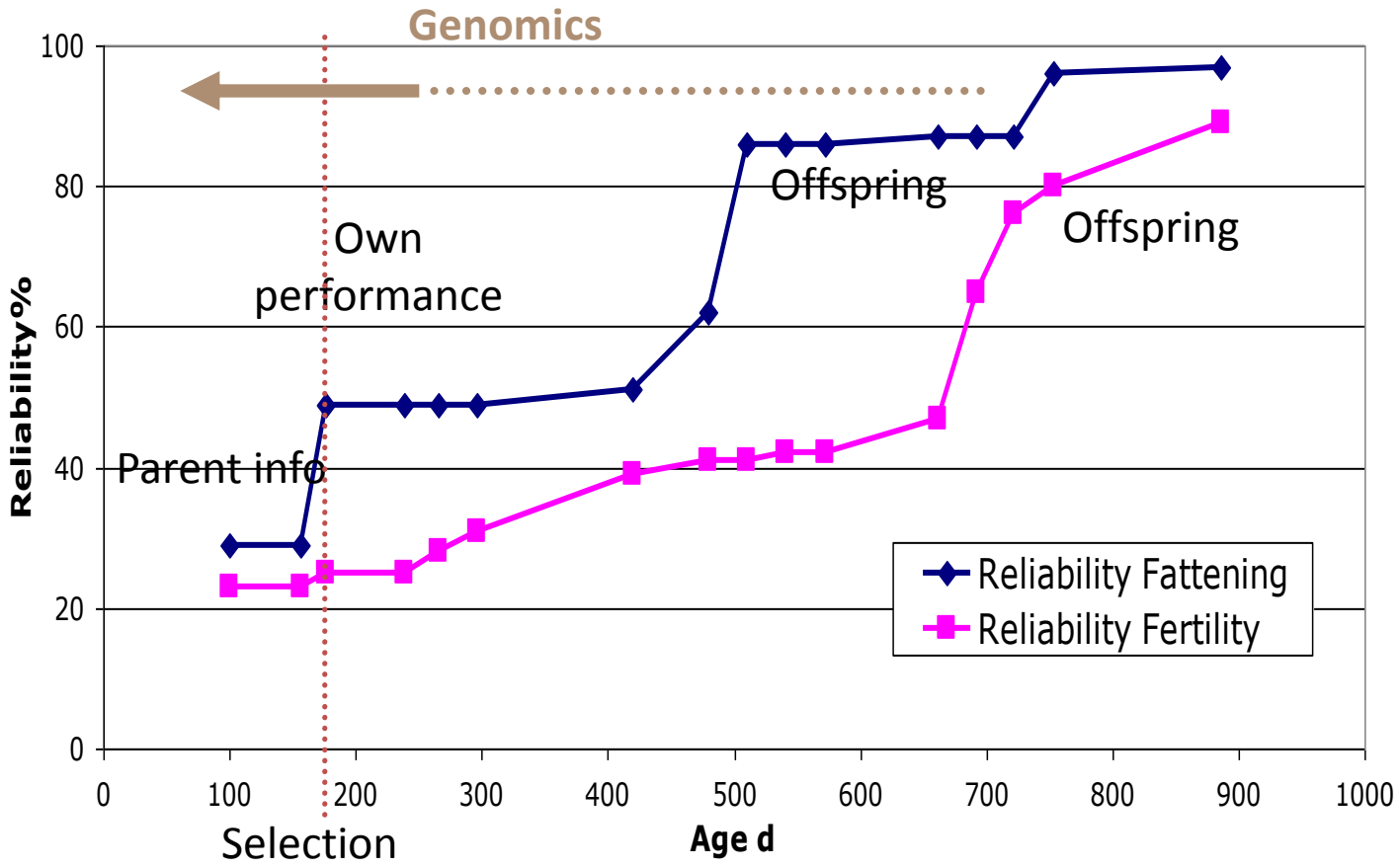


# Added value

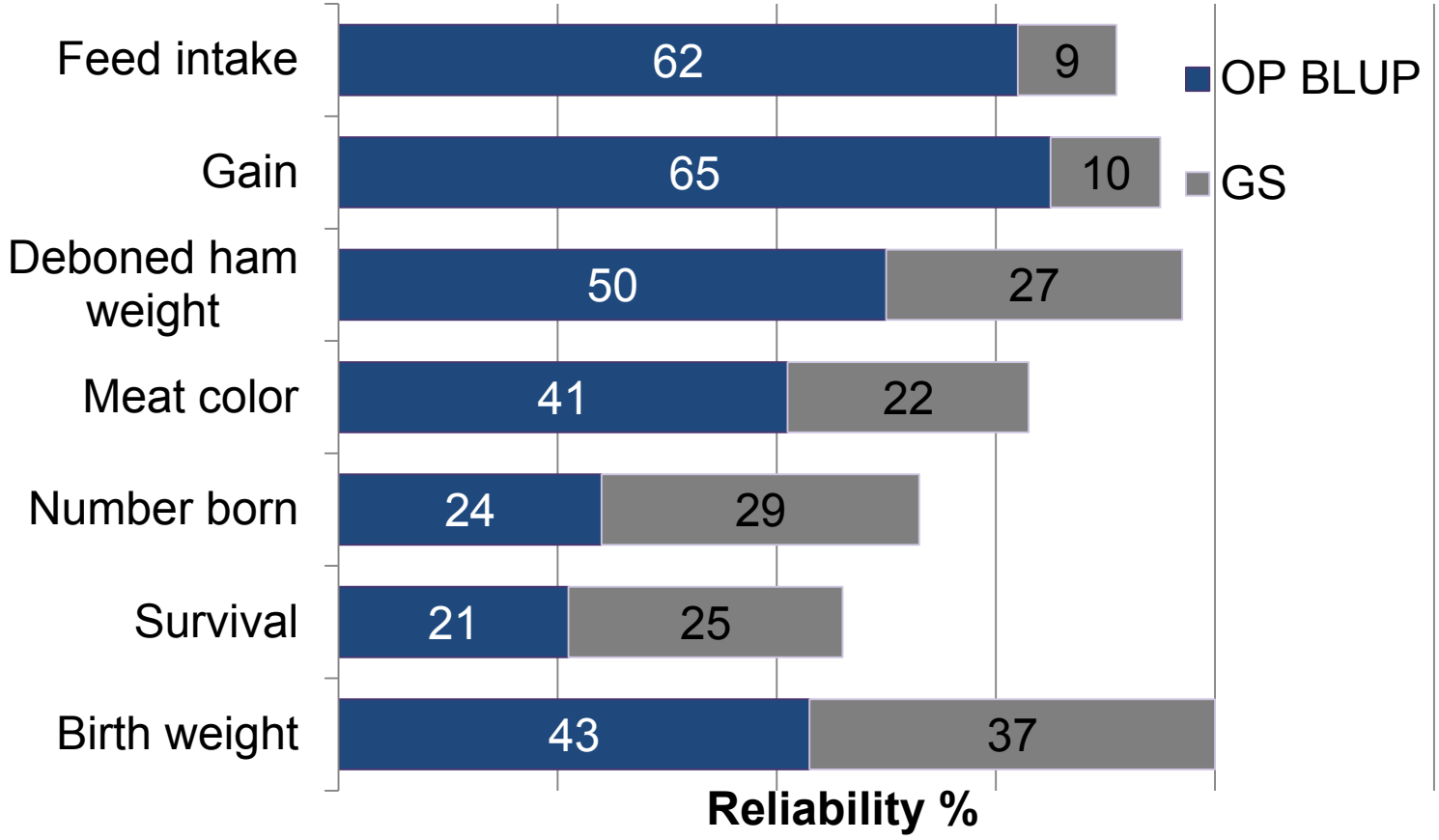
- More △G, via higher accuracy
  - Late in life
  - Low heritability
  - Single sex
  - Expensive/difficult to measure
- Highest added value in dam lines

# Reliability without genomics

Dam line boar



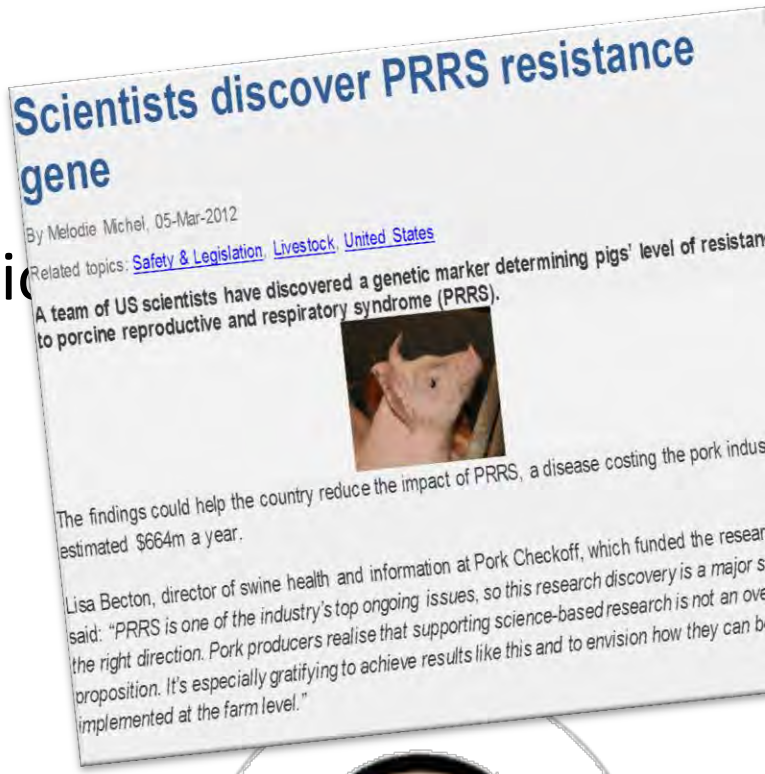
# Reliability breeding values



# New breeding goal traits

Examples:

- Disease resistance requires infecti
  - e.g. PRRS.
- Cured ham quality
  - e.g. Incarlopsa project
- Boar taint
  - e.g. Nador SNP-panel



## Scientists discover PRRS resistance gene

By Melodie Michel, 05-Mar-2012

Related topics: Safety & Legislation, Livestock, United States

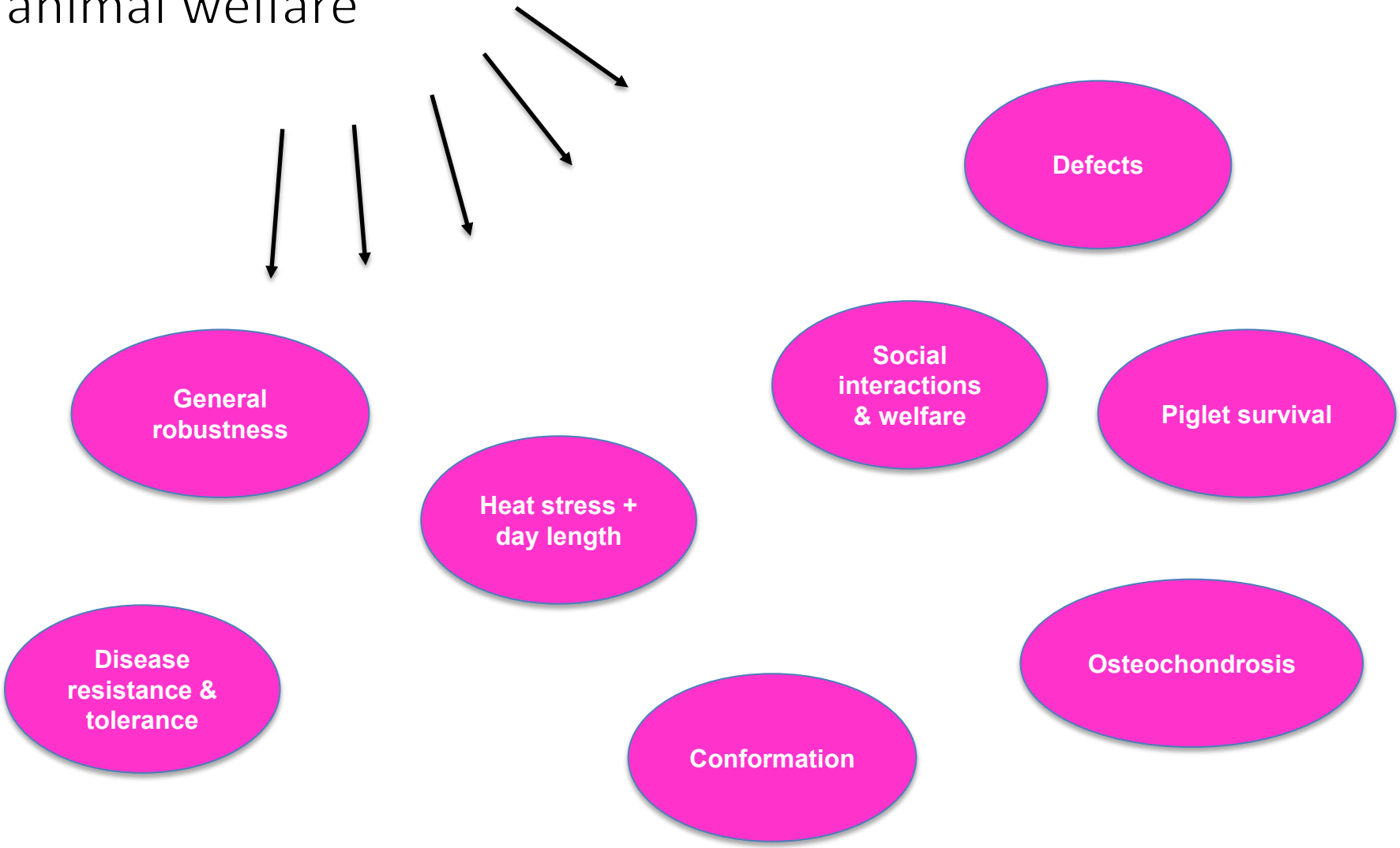
**A team of US scientists have discovered a genetic marker determining pigs' level of resistan to porcine reproductive and respiratory syndrome (PRRS).**

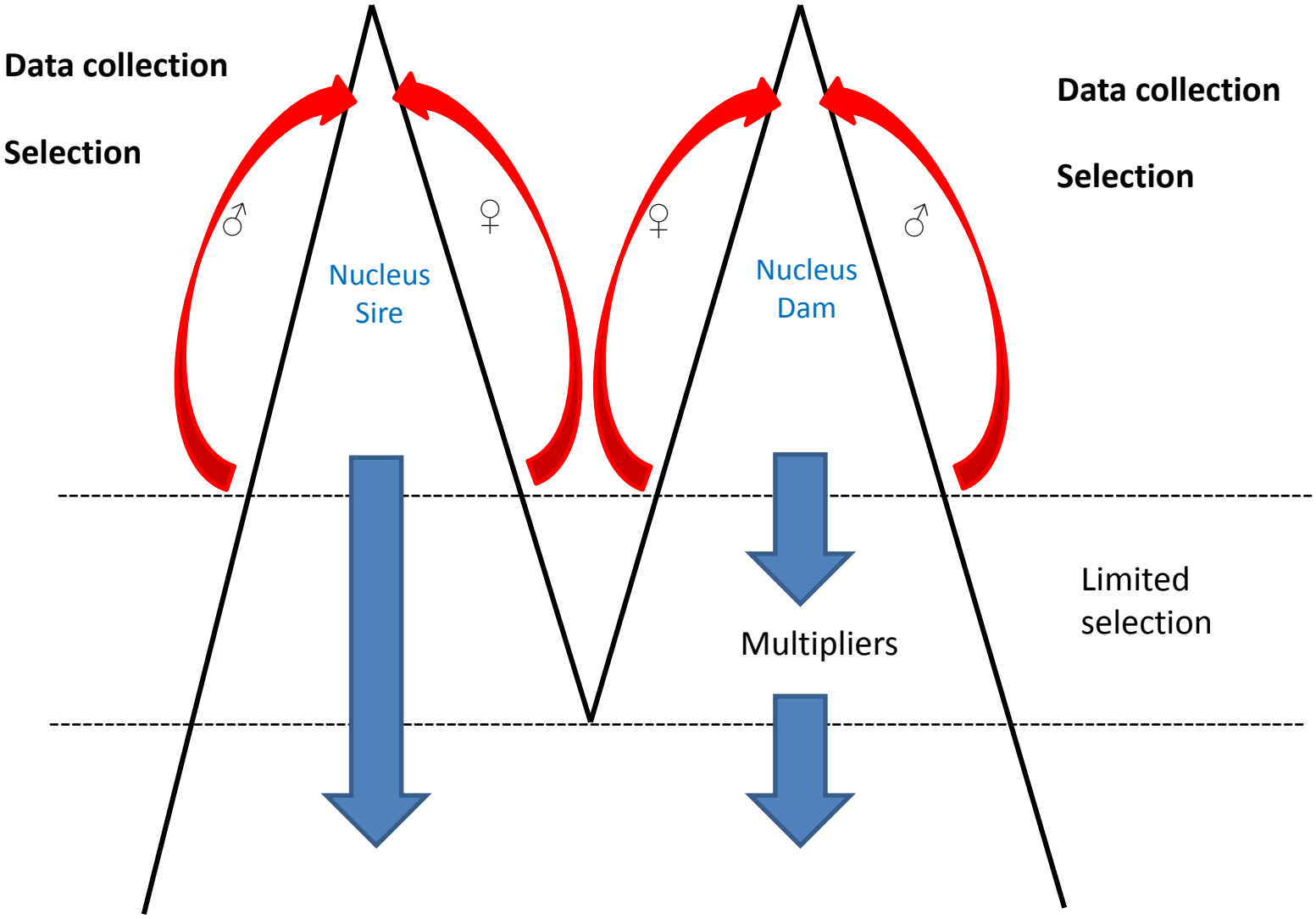
The findings could help the country reduce the impact of PRRS, a disease costing the pork indus estimated $664m a year.

Lisa Becton, director of swine health and information at Pork Checkoff, which funded the resear said: "*PRRS is one of the industry's top ongoing issues, so this research discovery is a major s the right direction. Pork producers realise that supporting science-based research is not an ove proposition. It's especially gratifying to achieve results like this and to envision how they can b implemented at the farm level.*"

What could bring this in relation with welfare and robustness traits?

# Robustness and animal welfare




Data collection
Selection
♂
♀
Nucleus
Sire
♀
♂
Nucleus
Dam
Data collection
Selection
Limited
selection
Multipliers

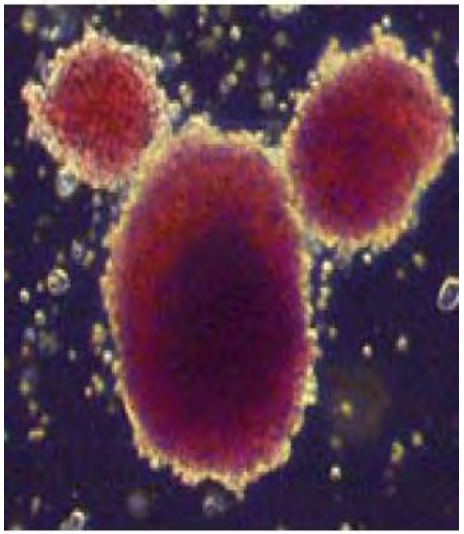
# What will the future bring?

# Stem cell technology

Recipe:

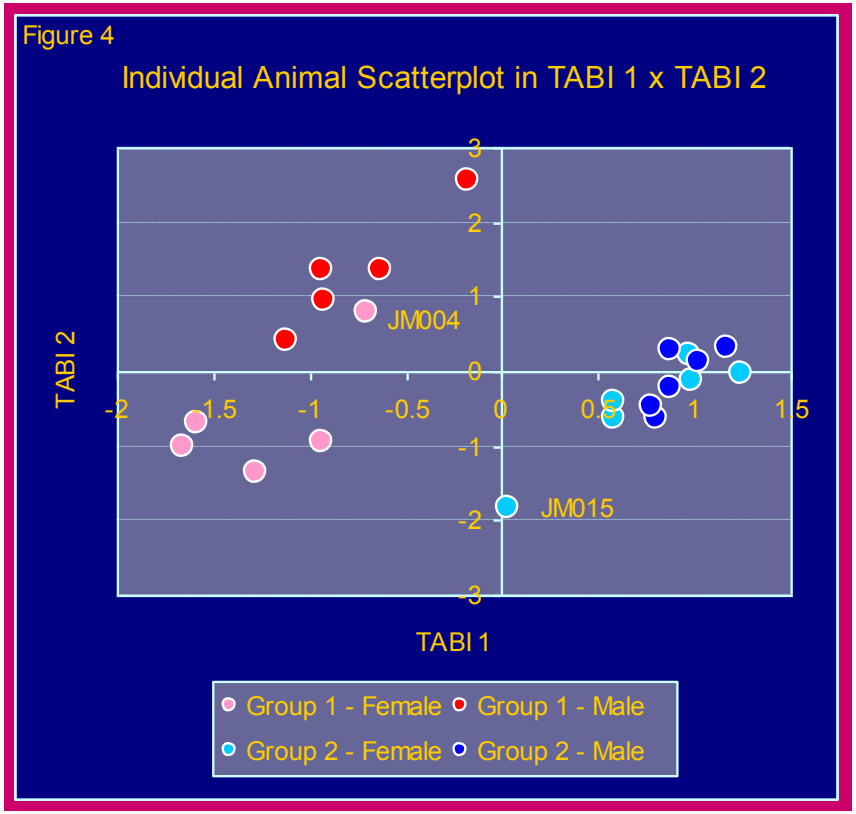
- Kill semen producing cells of AI boar
- Replace with similar cells from high genetic value week old boar piglets
- Save 6 months (or so) of male generation interval

$$\Delta G_{year} = \frac{\sigma_H * r_{IH} * i}{L}$$



# *In vitro* challenge using blood sample

Susceptibility to PMWS (Circo virus)

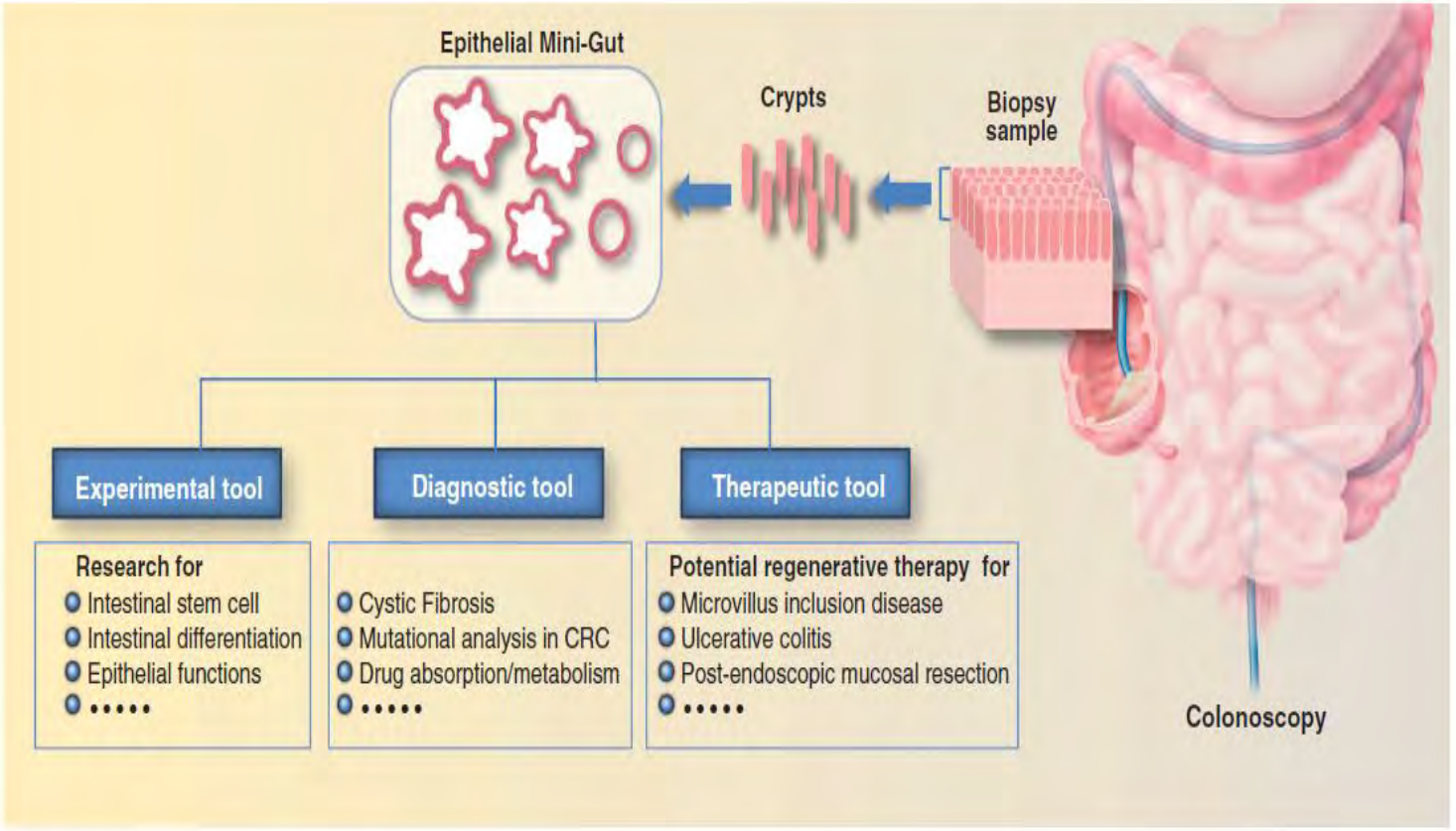



- Group 1: Higher susceptibility
- Group 2: Lower susceptibility

$$\Delta G_{year} = \frac{\sigma_H * r_{IH} * i}{L}$$

Source: Metadis (2011)

# Organoids



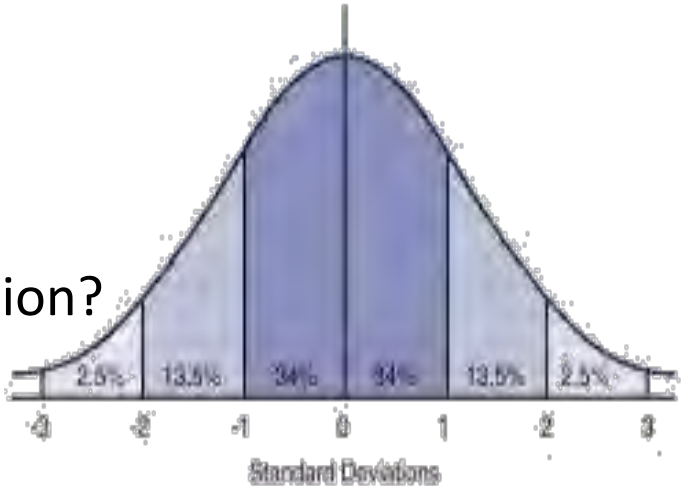

Source: Sato and Clevers. Science 340, 1190 (2013);

$$\Delta G_{year} = \frac{\sigma_H * r_{IH} * i}{L}$$

# Gene editing?

- Ultimate goal: find animal with desired genotype for all SNPs
- Chance of desired genotype:
  - 25% (in case of 50% allele frequency)
  - Reduces rapidly with increasing # SNPs
- Today:
  - Sum of SNP-effects
  - Normal distribution
  - Part of selection index
- Gene editing: future solution?

| | A | a |
|---|---|---|
| A | AA 25% | Aa 25% |
| a | aA 25% | aa 25% |




| SNPs (#) | Chance (1 out of n) |
|---|---|
| 1 | 4 |
| 2 | 16 |
| 3 | 64 |
| 4 | 256 |
| 5 | 1,024 |
| 10 | 1,048,576 |

- Existing variation!
- Healing!
- Still: ethical discussion
  (and high price...)

- Increases genetic standard deviation

Examples of use?
- ❑ F4 (Ecoli receptor)
- ❑ PRRS QTL

$$\Delta G_{year} = \frac{\sigma_H * r_{IH} * i}{L}$$

# Wrapping up:

- Pick up client data (Big Data)
- Precision phenotyping
- Genomics

- Keep it? (optimum cont.)
- Gene editing?

$$\Delta G_{year} = \frac{\sigma_H * r_{IH} * i}{L}$$

More selection candidates to choose from (Blueprint)

Reduce generation interval

# Questions?