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# Genetic improvement of pig : fertility, litter size and piglet viability

Luis Varona

# Magapor<sup>®</sup>



Pig Breeding

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# Piramidal Scheme

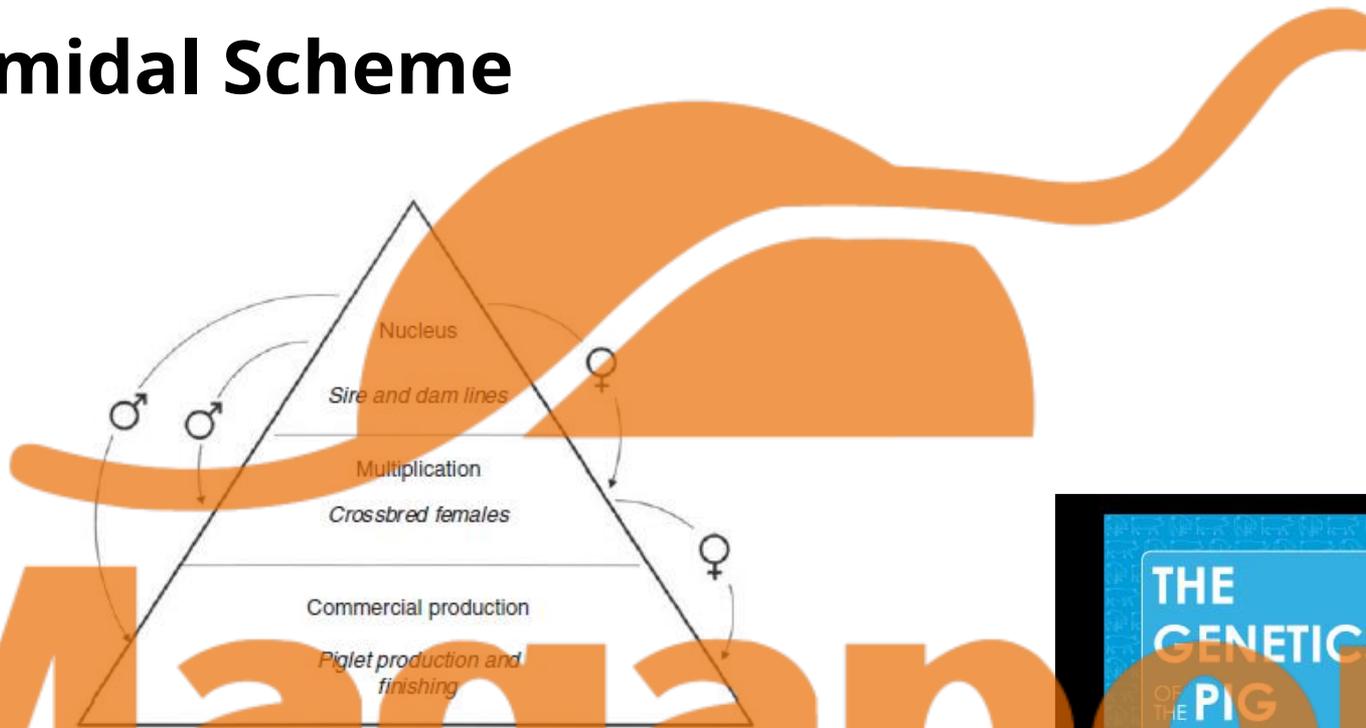
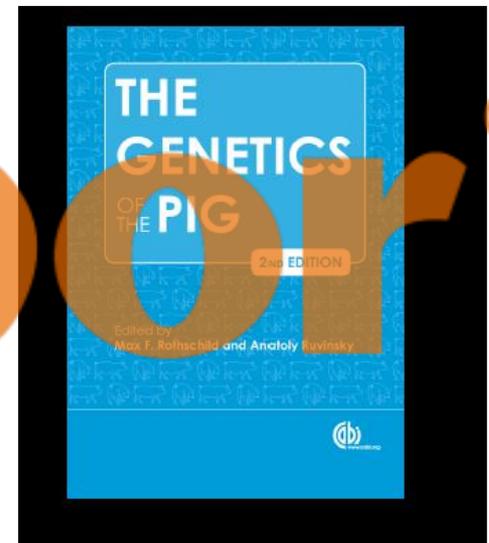
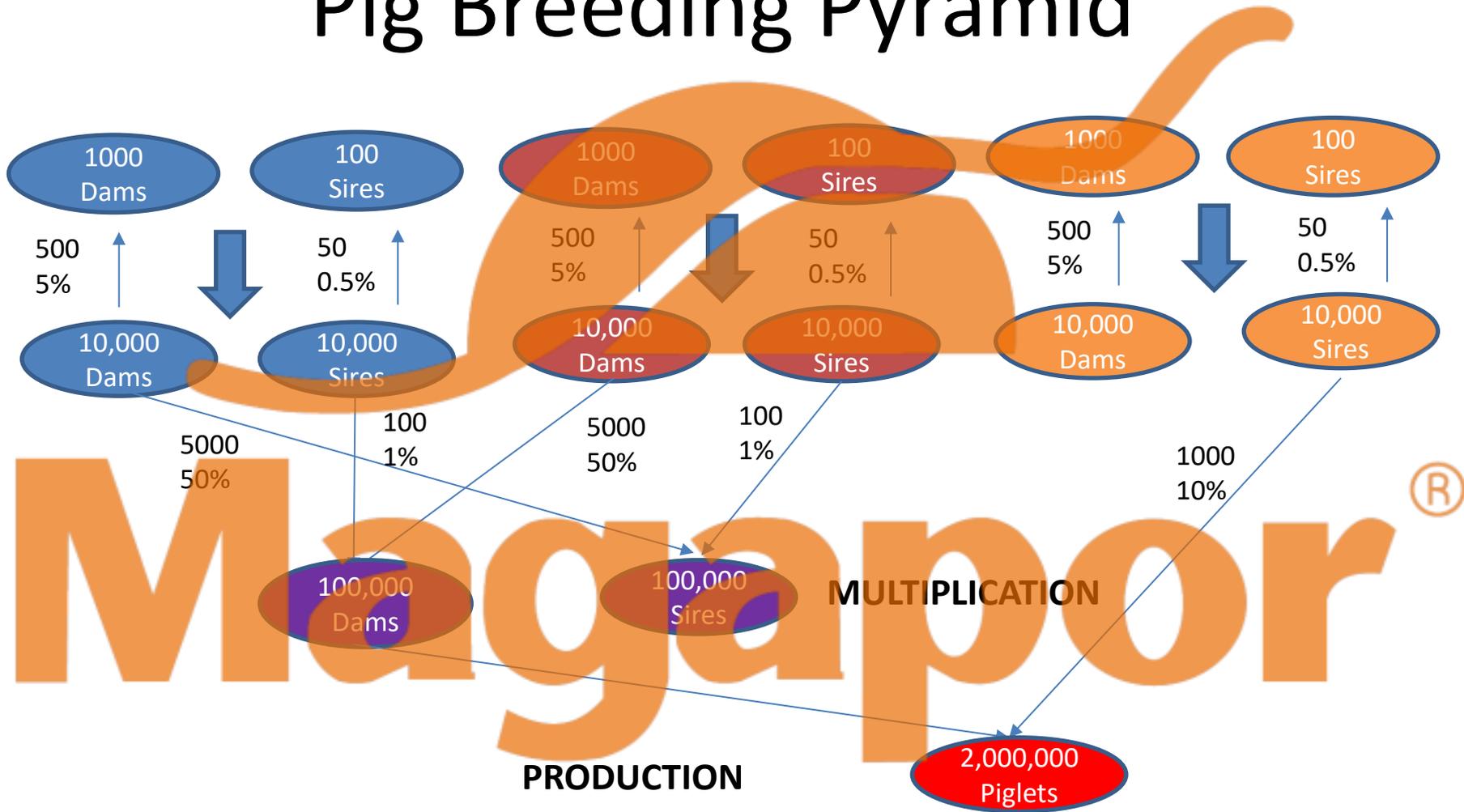


Fig. 16.2. Pig breeding pyramid.

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# Pig Breeding Pyramid



## Selection of pure lines

### Paternal Lines (Terminal Sire)

- Growth
- Feed Conversion Ratio
- % Lean
- Killing out percentage
- Meat Quality

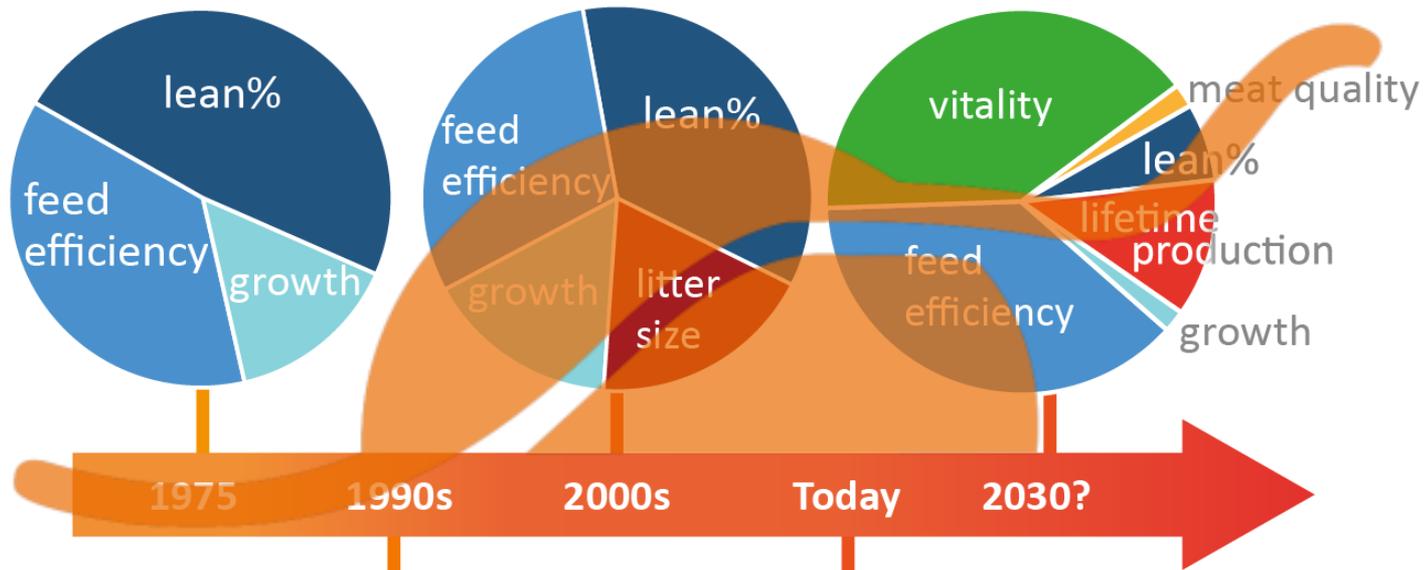
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## Selection of pure lines

### Maternal Lines

- Growth
- Feed Conversion Ratio
- % Lean
- Killing out percentage
- Meat Quality
- Maternal Traits (litter Size, piglet survival, longevity...)

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The word 'Magapor' is written in large orange letters. Two pie charts are overlaid on the letters 'a' and 'p'. The pie chart on 'a' includes segments for reproduction, growth, lean %, feed efficiency, and meat quality. The pie chart on 'p' includes segments for vitality, meat quality, lean %, lifetime production, growth, and feed efficiency.

## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

$i$  : Intensity of Selection

$r(u, \hat{u})$  : Accuracy

$\sigma_u$  : Genetic Standard Deviation

$L$  : Generation Interval

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## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

**$i$** : Intensity of Selection

Very high

$r(u, \hat{u})$ : Accuracy

$\sigma_u$ : Genetic Standard Deviation

$L$ : Generation Interval

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## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

$i$  : Intensity of Selection

$r(u, \hat{u})$ : Accuracy

$\sigma_u$ : **Genetic Standard Deviation**

Population Specific

$L$ : Generation Interval

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## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

$i$  : Intensity of Selection

$r(u, \hat{u})$ : Accuracy

$\sigma_u$ : Genetic Standard Deviation

$L$ : **Generation Interval**

Low

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## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

$i$  : Intensity of Selection

$r(u, \hat{u})$ : Accuracy

$\sigma_u$ : Genetic Standard Deviation

$L$ : Generation Interval

- Heritability

- Phenotypic information (own and from relatives)

- Genomic information

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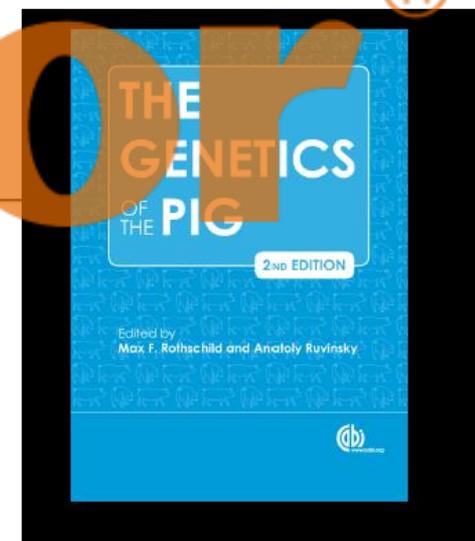
**Heritability**

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**Table 10.3.** Heritability ( $h^2$ ) estimates for female and male reproductive traits in the pig. Adapted from Rothschild and Bidanel (1998).

	Trait	No. of estimates	Mean $h^2$	Range
Female traits	Age at puberty	16	0.37	0–0.73
	Oestrus symptoms	3	0.21	0.09–0.29
	Ovulation rate	18	0.32	0.10–0.59
	Conception rate	3	0.10	0–0.29
	Prenatal survival rate	12	0.15	0–0.23
	Total number born	103	0.11	0–0.76
	Number born alive	118	0.10	0–0.66
	Number weaned	54	0.08	0–1.0
	Farrowing survival rate	12	0.07	0.03–0.14
	Birth to weaning survival rate	12	0.05	0–0.13
	Farrowing length	2	0.07	0.05–0.10
	Litter homogeneity at birth	6	0.08	0.03–0.1
	Litter weight at birth	18	0.24	0–0.54
	Birth assistance	2	0.05	0.05
	Litter weight at 21 days	22	0.14	0.07–0.38
	Weaning to oestrus interval	5	0.22	0.11–0.36
	Rebreeding interval	3	0.23	0.03–0.36
Male traits	Testis width	8	0.37	0.02–0.61
	Testis weight	5	0.44	0.24–0.73
	Semen volume	6	0.19	0.14–0.25
	Sperm concentration	6	0.19	0.13–0.26
	Sperm motility	6	0.11	0.06–0.18
	% Abnormal sperm	4	0.10	0.06–0.17
	Libido	13	0.15	0.03–0.47

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## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

$i$  : Intensity of Selection

$r(u, \hat{u})$  : Accuracy

$\sigma_u$  : Genetic Standard Deviation

$L$  : Generation Interval

- **Heritability (Generally Low)**

- Phenotypic information (own and from relatives)

- Genomic information

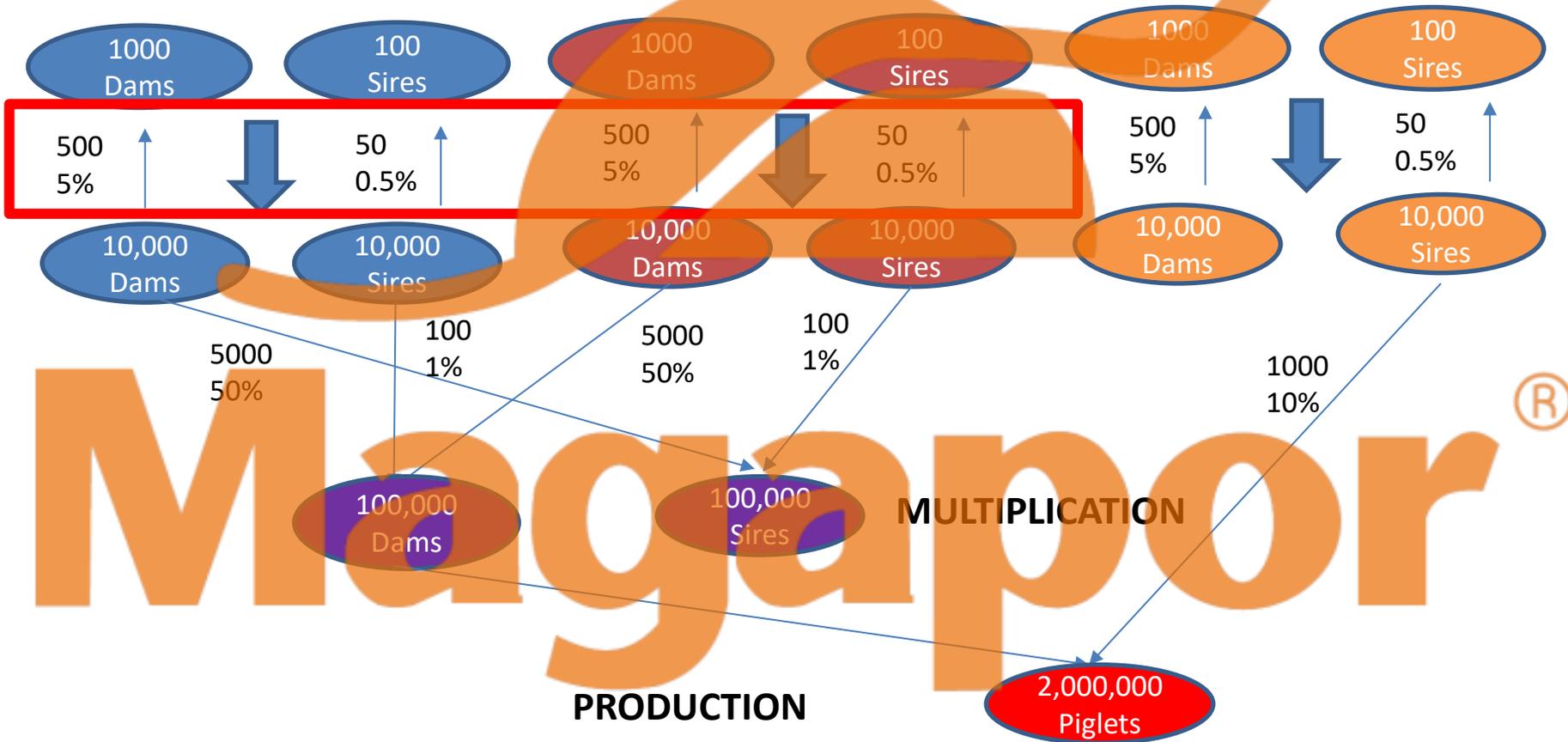
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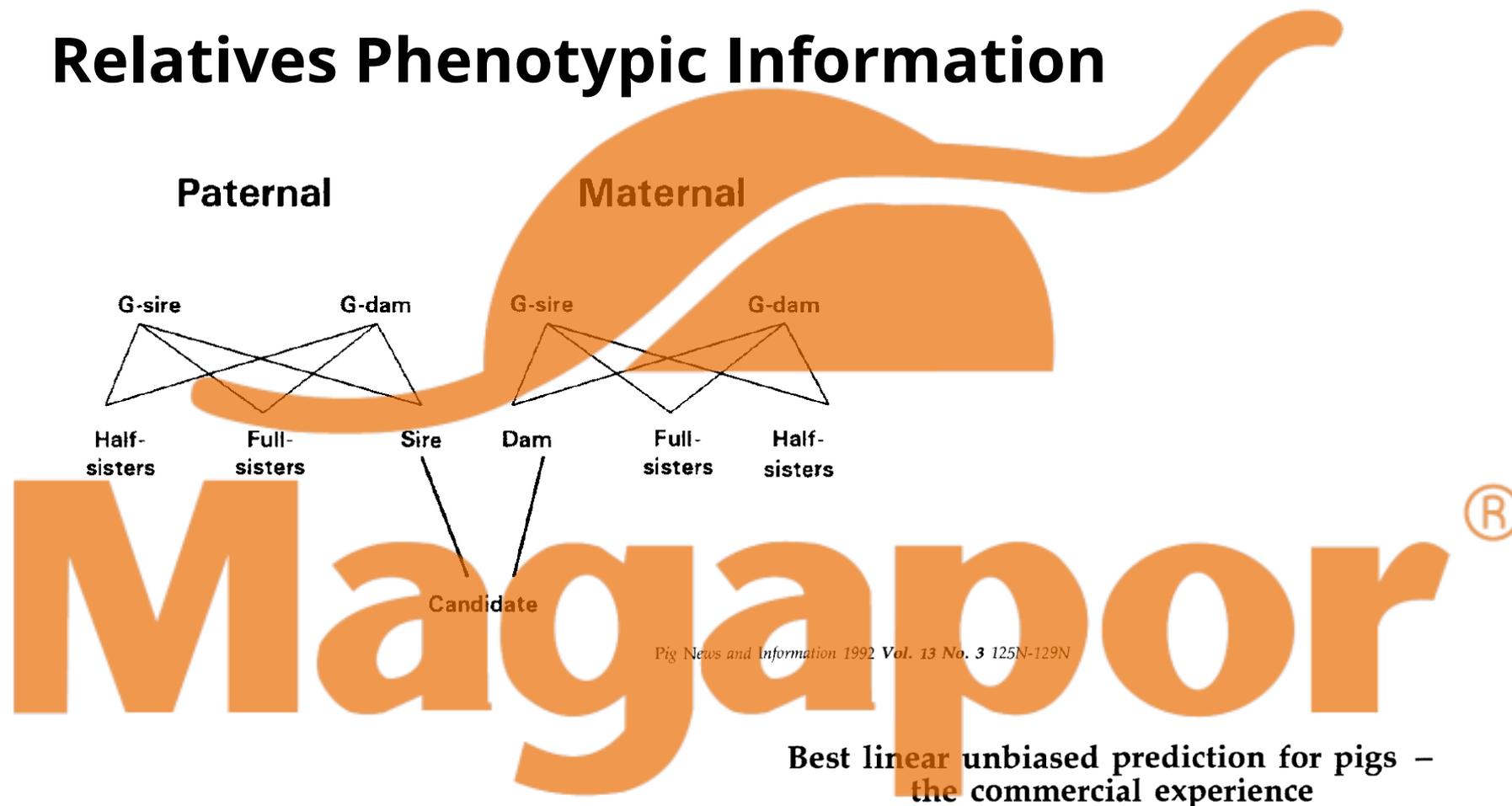
**Phenotypic Information**

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# 3 way- Piramidal Scheme



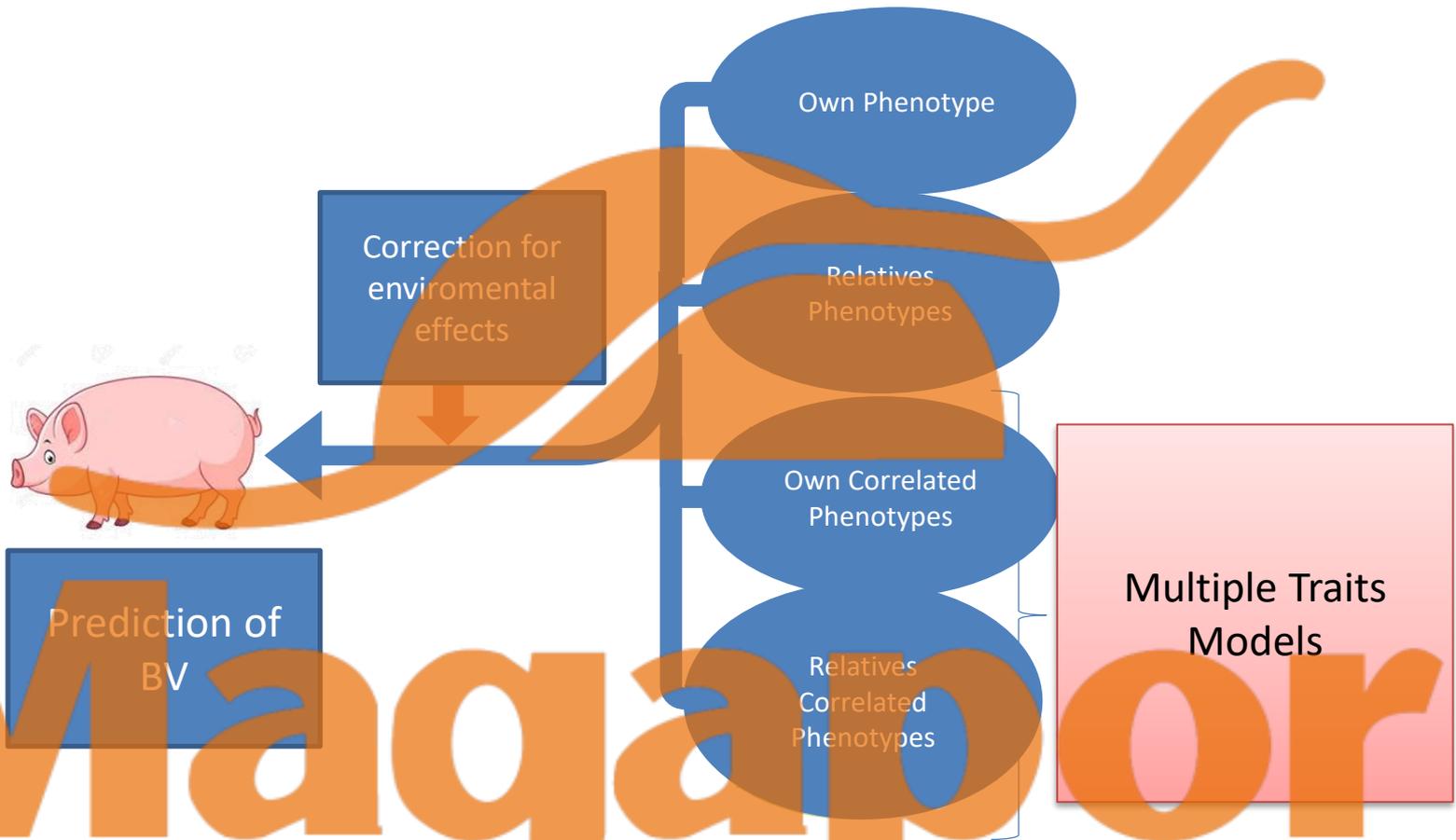
# Relatives Phenotypic Information



*Pig News and Information 1992 Vol. 13 No. 3 125N-129N*

**Best linear unbiased prediction for pigs –  
the commercial experience**

**Paul R. Bampton**  
Cotswold Pig Development Company Limited,  
Rothwell, Lincoln, UK



$$y = Xb + Zu + e$$

$$\begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1} \end{bmatrix} \begin{bmatrix} \sigma_e^2 \\ \sigma_u^2 \end{bmatrix}^{-1} \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

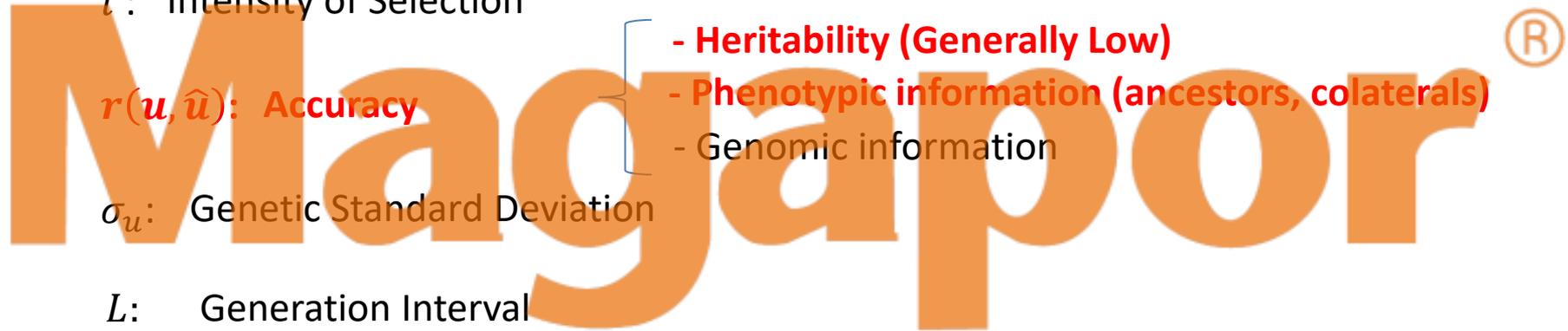
$i$  : Intensity of Selection

$r(u, \hat{u})$  : Accuracy

$\sigma_u$  : Genetic Standard Deviation

$L$  : Generation Interval

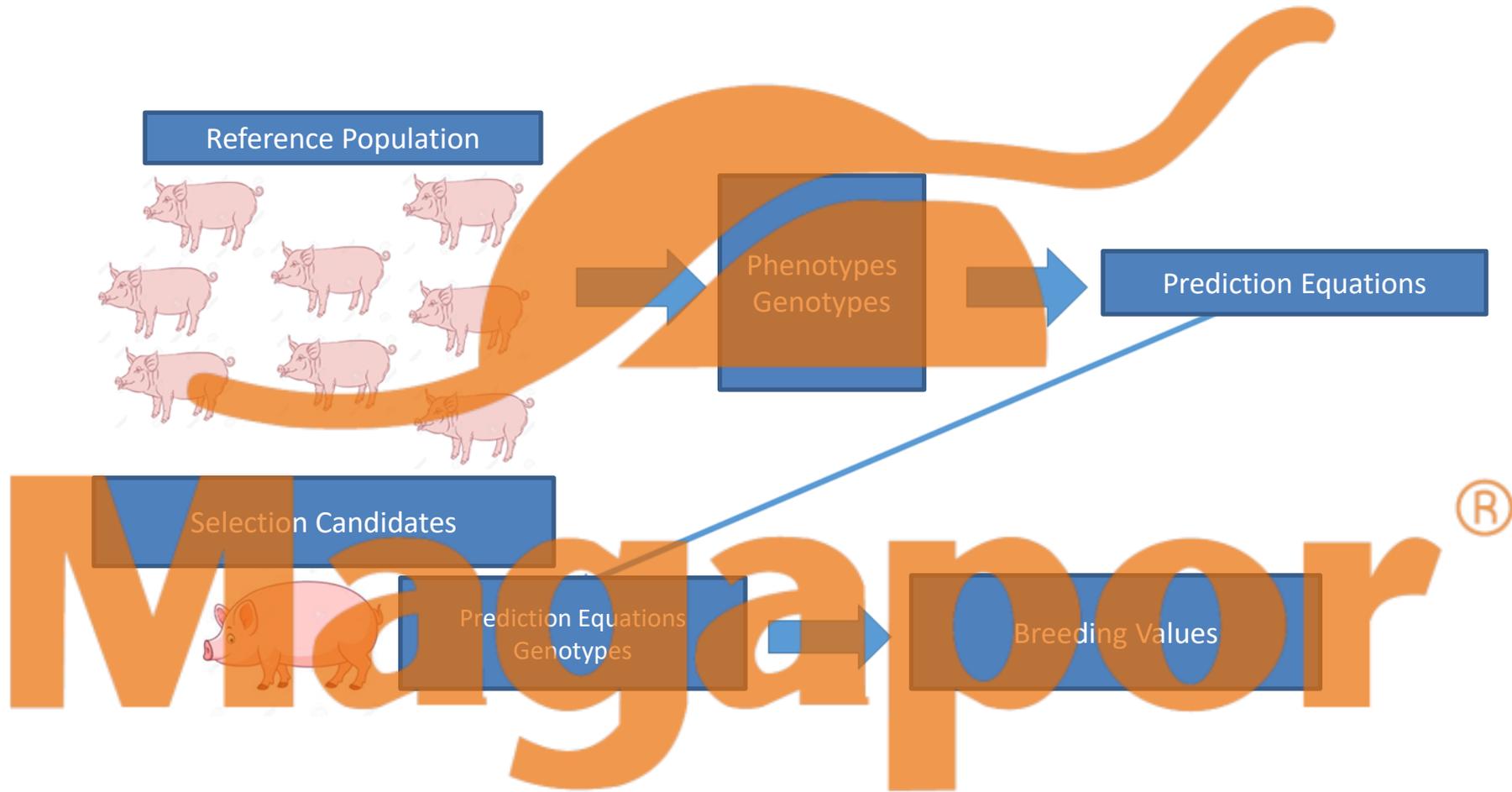
- Heritability (Generally Low)
- Phenotypic information (ancestors, colaterals)
- Genomic information



A large, stylized orange silhouette of an animal, possibly a pig or a dog, is positioned behind the text. The animal is facing right, with its head down and tail up.

**Genomic Selection**

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$$y = Xb + Zu + e$$

$$\begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1} \frac{\sigma_e^2}{\sigma_u^2} \end{bmatrix}^{-1} \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

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- **G: Realized Relationship**
- **A: Expected Relationship**

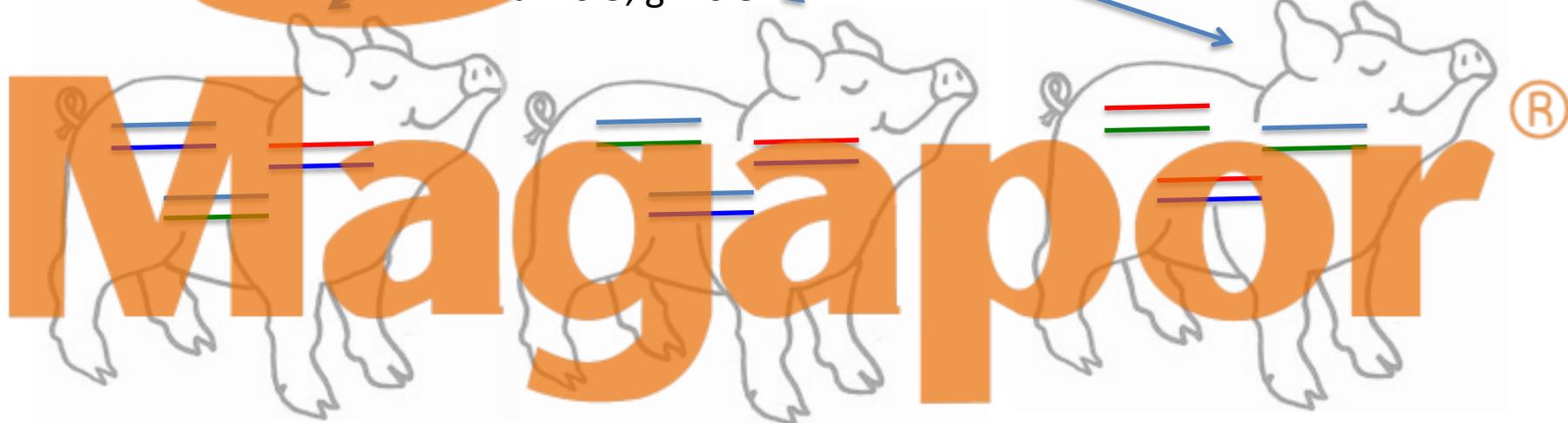
$$\begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + G^{-1} \frac{\sigma_e^2}{\sigma_u^2} \end{bmatrix}^{-1} \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$



$a = 0.5, g = 0.5$

$a = 0.5, g = 0.5$

$a = 0.5, g = 0.5$

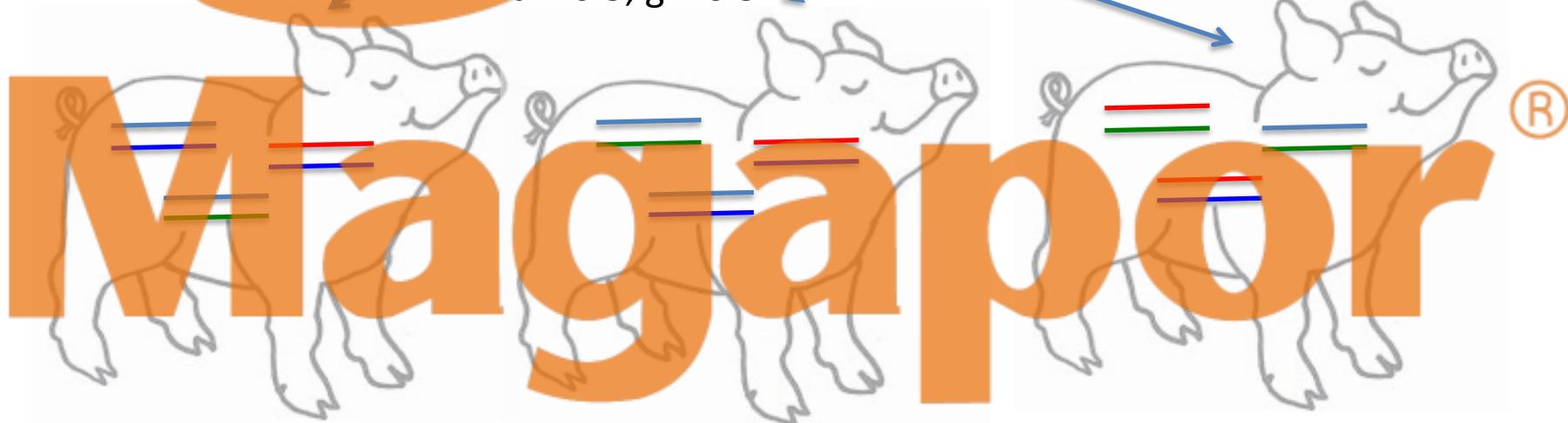




$a = 0.5, g = 0.5$

$a = 0.5, g = 0.5$

$a = 0.5, g = 0.5$







$a = 0.5, g = 0.67$

$a = 0.5, g = 0.33$

$a = 0.5, g = 0.00$



18 Lechones

14 Lechones

10 Lechones

0.5

0.5

0.5

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18 Lechones

14 Lechones

10 Lechones



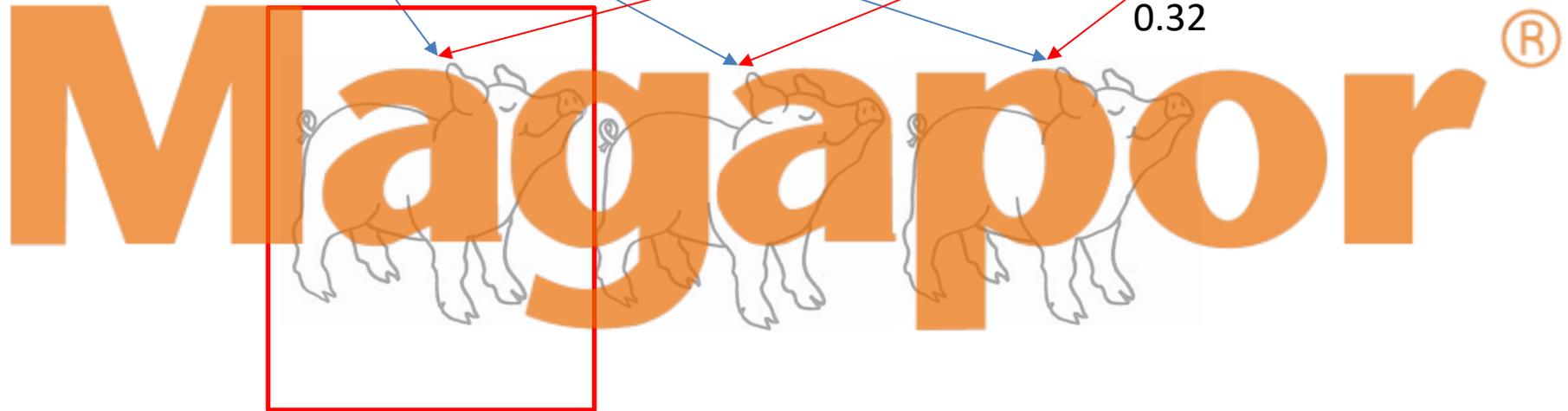
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18 Lechones

14 Lechones

10 Lechones



## Response to Selection (R)

$$R = \frac{i \times r(u, \hat{u}) \times \sigma_u}{L}$$

$i$  : Intensity of Selection

$r(u, \hat{u})$  : Accuracy

$\sigma_u$  : Genetic Standard Deviation

$L$  : Generation Interval

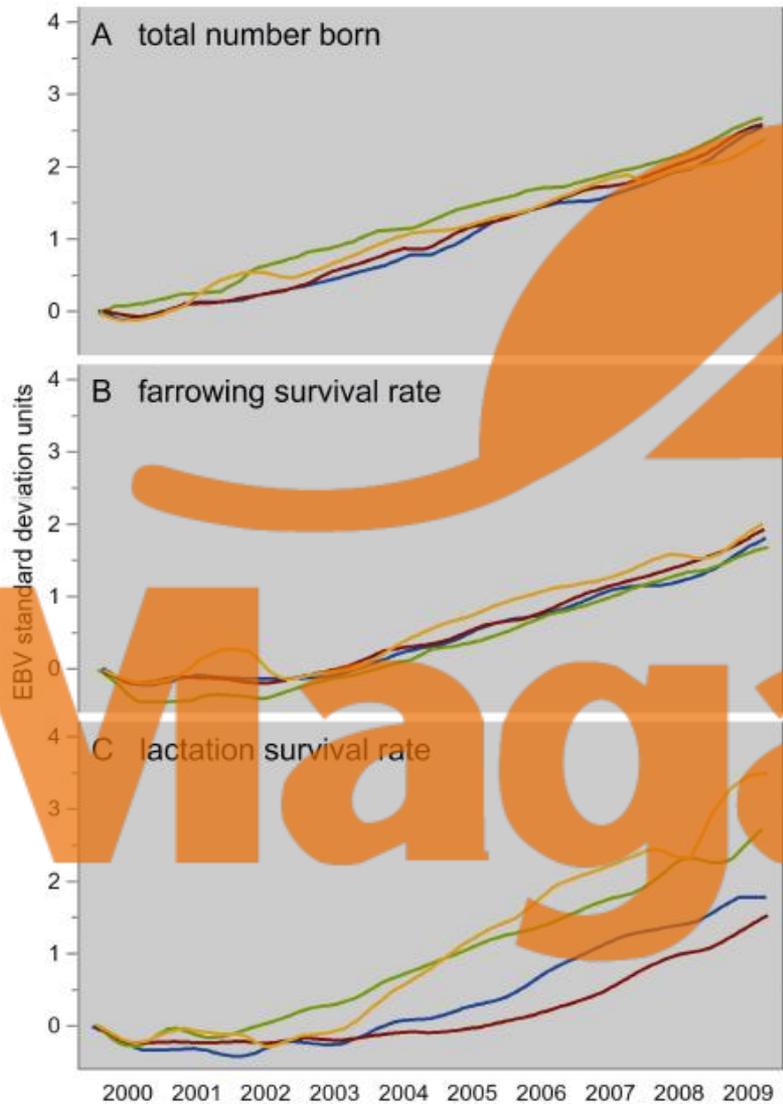
- Heritability (Generally Low)
- Phenotypic information (ancestors, colaterals)
- Genomic information
- Increase accuracy
- Discriminate between full sibs

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Some Results

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Knap et al. 2023. Genetic and phenotypic time trends of litter size, piglet mortality, and birth weight in pigs. *Front. Anim. Sci.*

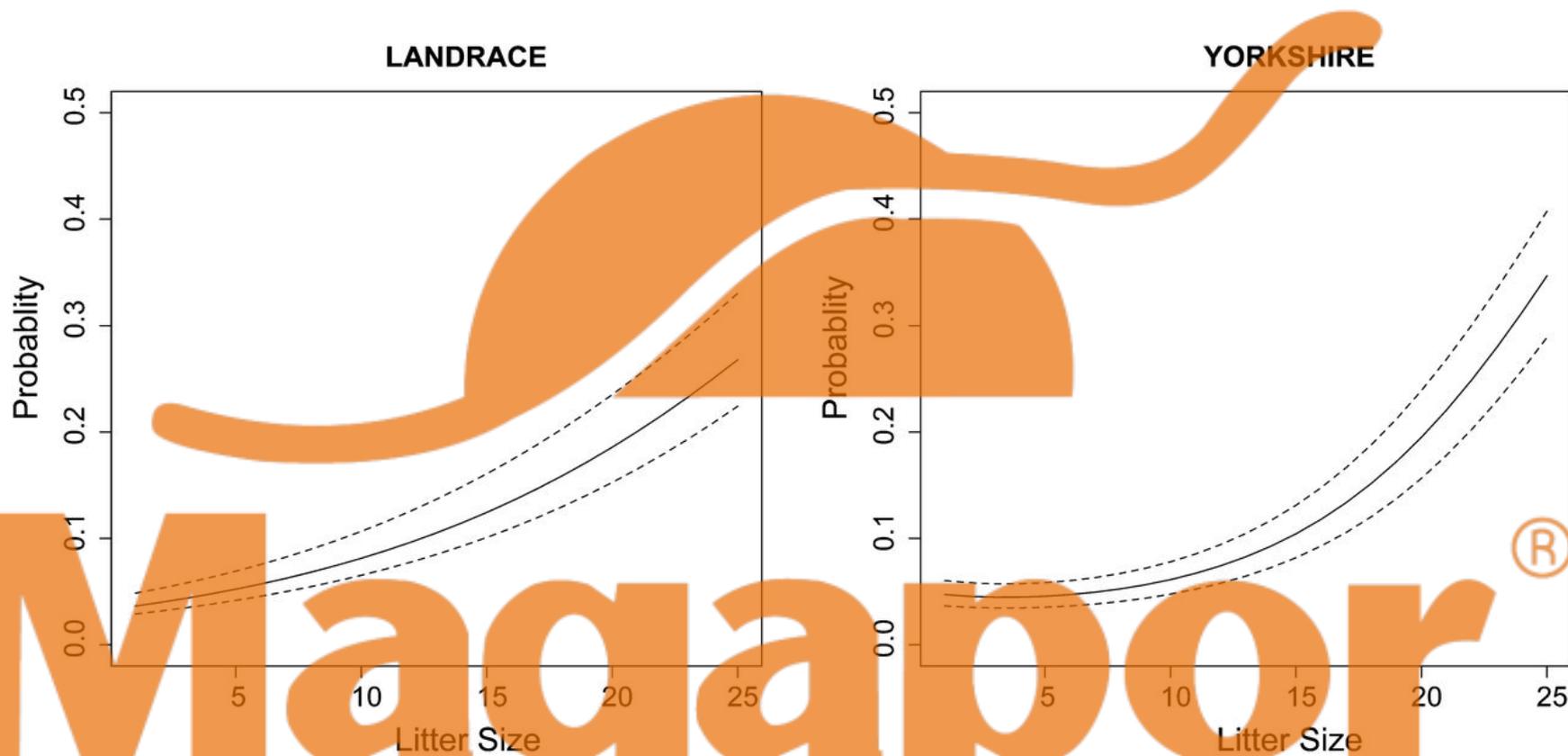
<https://doi.org/10.3389/fanim.2023.1218175>

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**Undesirable Results**

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Varona, L y Sorensen, D. A. 2014. Joint Analysis of Binomial and Continuous Traits with a Recursive Model: A Case Study Using Mortality and Litter Size of Pigs. Genetics 196:643-651.

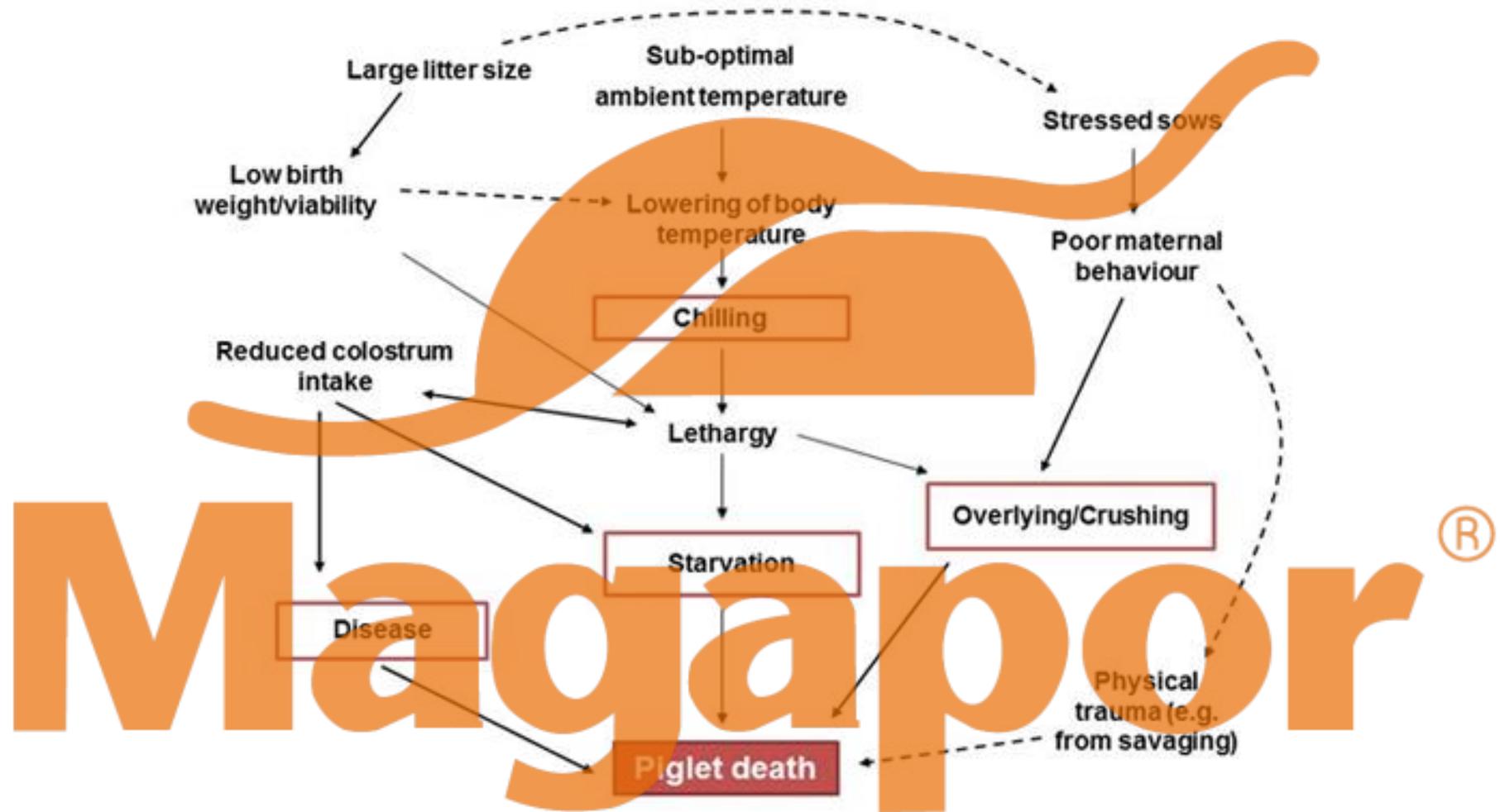


Fig 2. Predisposing risk factors of live-born piglet mortality

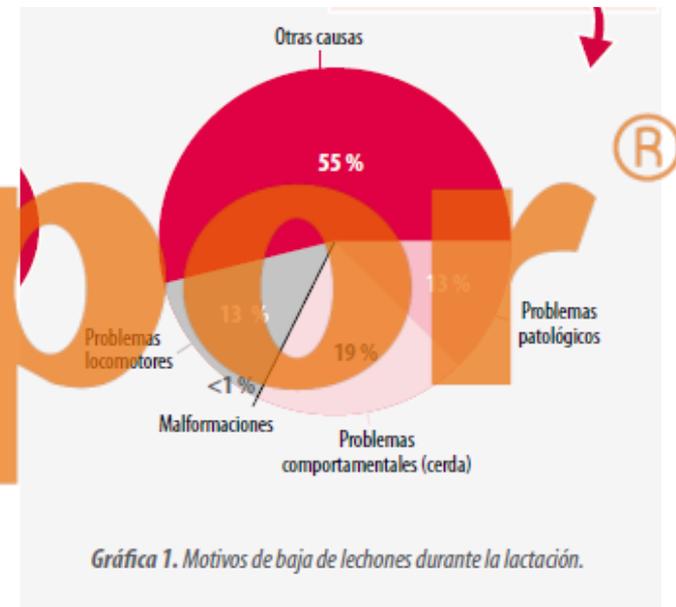
# ¿POR QUÉ Y CUÁNDO SE PRODUCEN LAS BAJAS DE LOS LECHONES EN LACTACIÓN?

Aitor Arrazola, Libertat Tusell, Joaquim Tarrés, Núria Alòs y Raquel Quintanilla  
BDporc. Genética y Mejora Animal. IRTA.

IRTA

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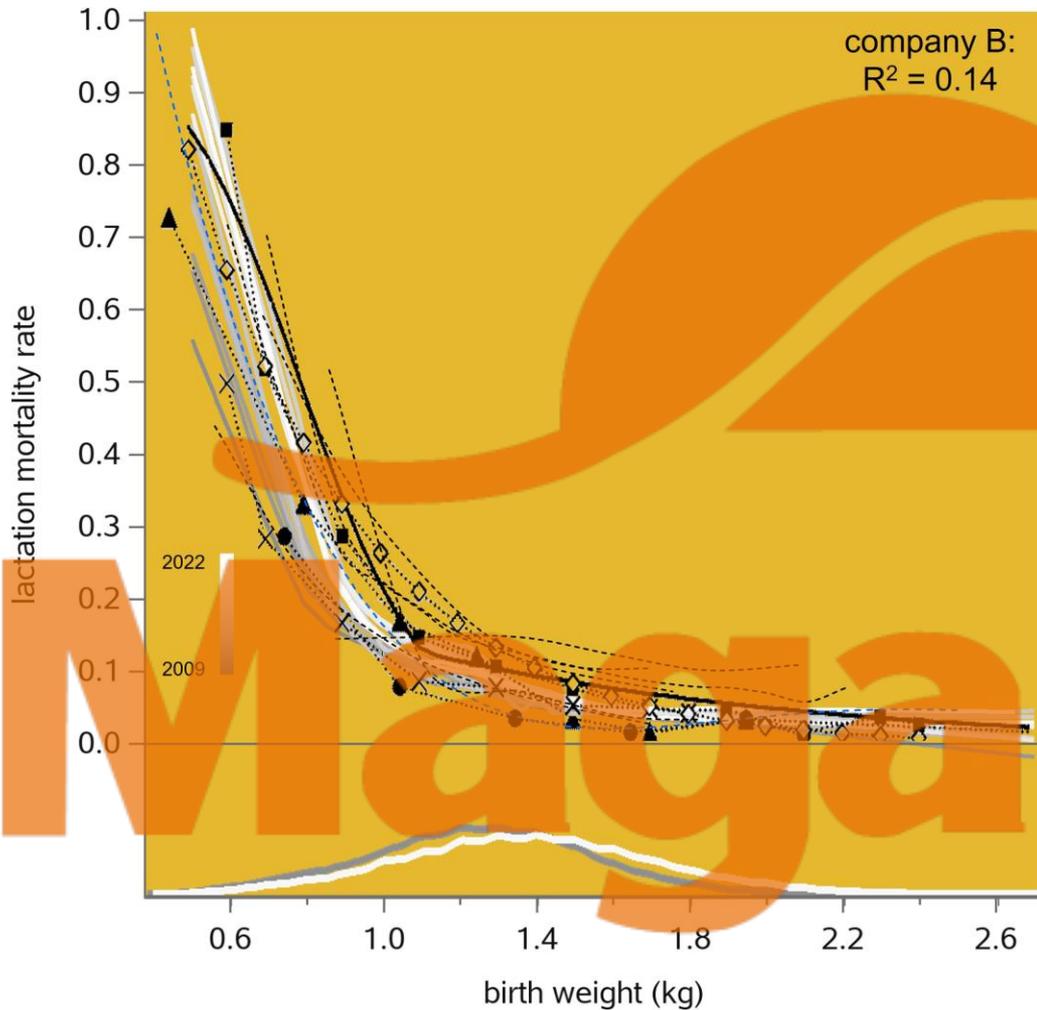


## New Traits

- Piglet Weight
- Uniformity
- Gestation Length
- Farrowing Duration
- Maternal Behaviour
- Congenital Defects

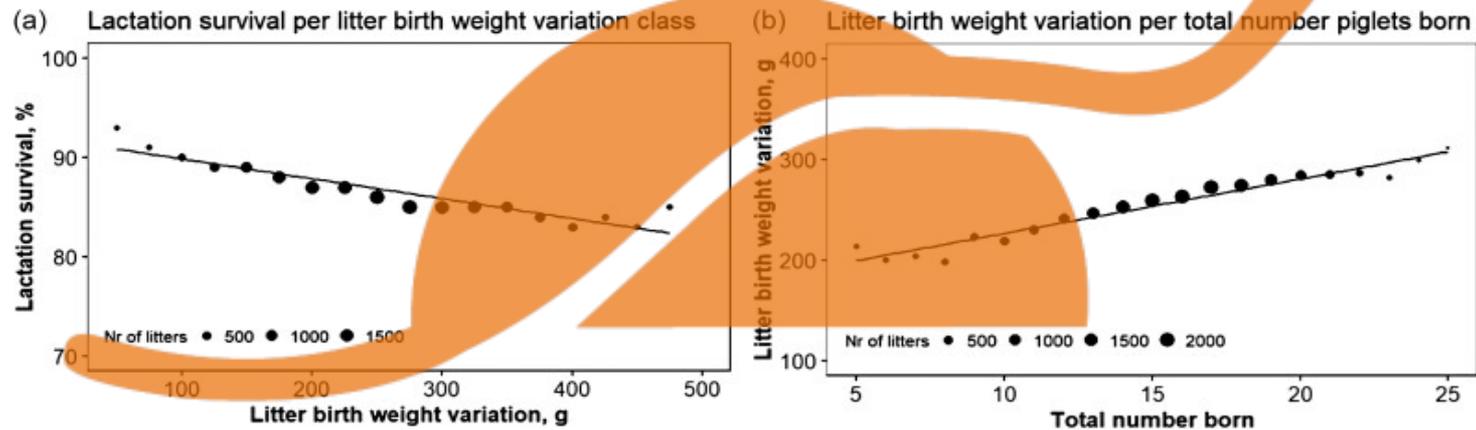


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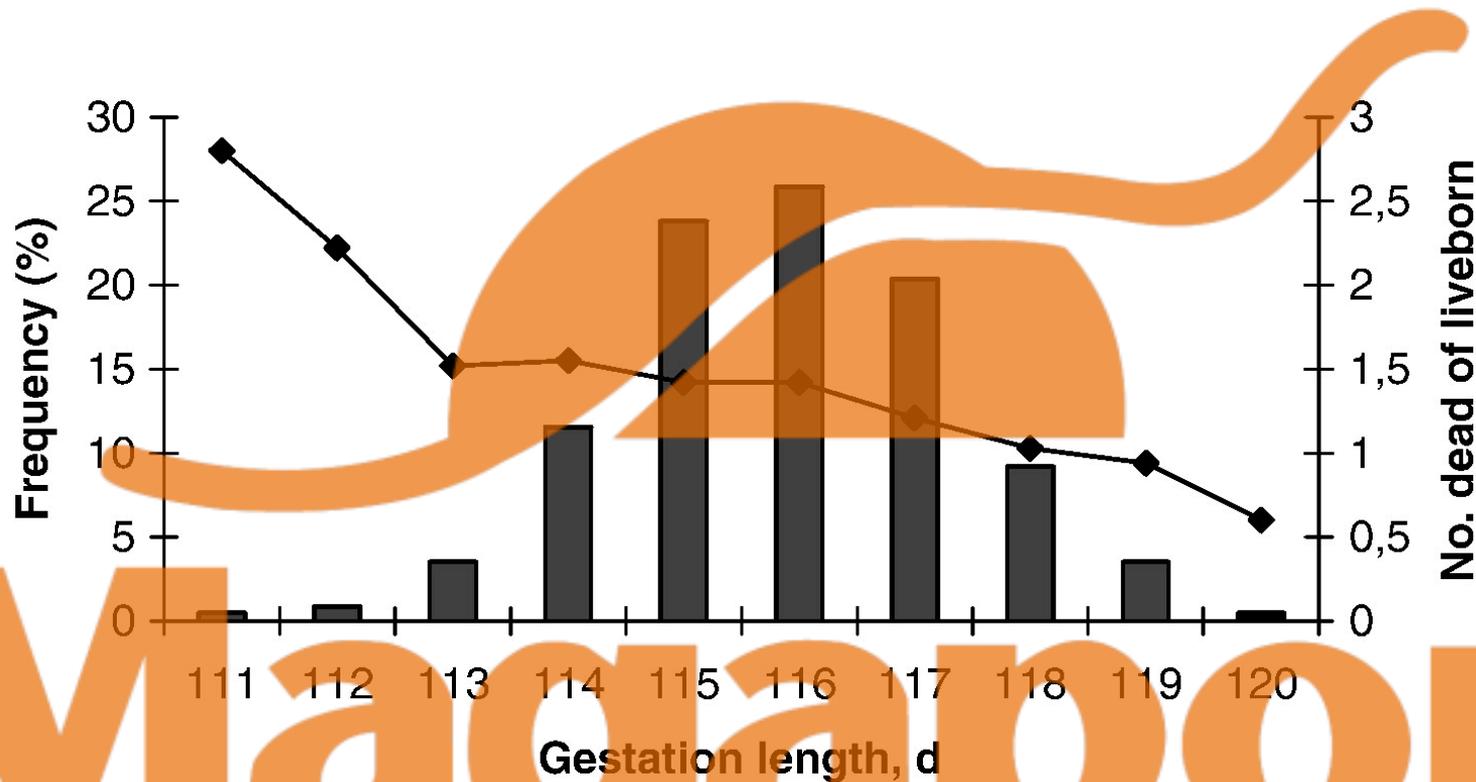
Knap et al. 2023. Genetic and phenotypic time trends of litter size, piglet mortality, and birth weight in pigs. *Front. Anim. Sci.* <https://doi.org/10.3389/fanim.2023.1218175>

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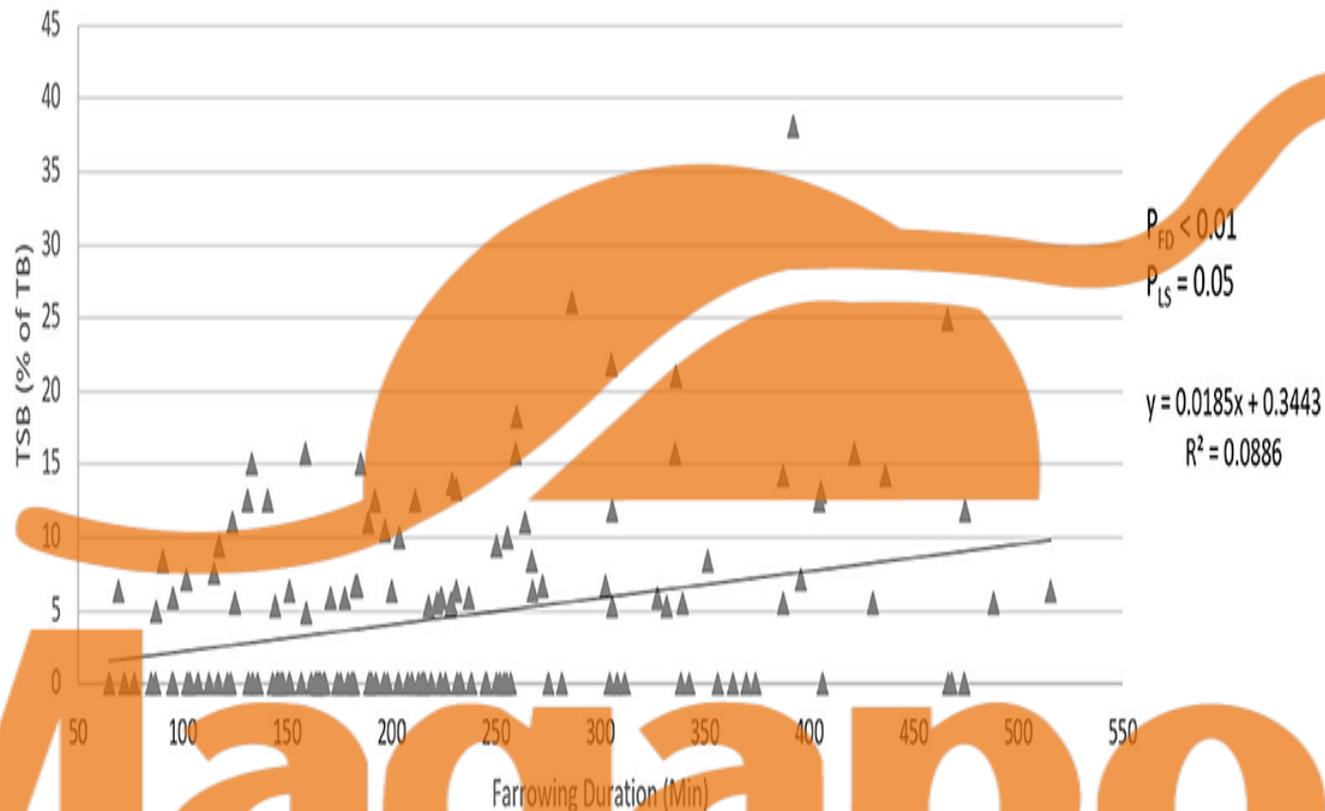
Knol et al., 2022. Genetic aspects of piglet survival and related traits: a review. *J. Anim. Sci.* 100:skac190

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Rydhmer et al., 2008. Genetic correlations between gestation length, piglet survival and early growth. *Lives. Sci.* 115:287-293.

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Van den Bosch et al. 2022. Disentangling Litter Size and Farrowing Duration Effects on Piglet Stillbirth, Acid-Base Blood Parameters and Pre-Weaning Mortality. *Front. Vet. Sci.*  
<https://doi.org/10.3389/fvets.2022.836202>

Low Heritability (0.08-0.10) (Canario et al., 2006; Merour et al. 2010).

*Animal* (2008), 2:9, pp 1273–1280 © The Animal Consortium 2008  
doi:10.1017/S1751731108002504



## Genetic aspects regarding piglet losses and the maternal behaviour of sows. Part 1. Genetic analysis of piglet mortality and fertility traits in pigs

B. Hellbrügge<sup>1</sup>, K.-H. Tölle<sup>2</sup>, J. Bennewitz<sup>1</sup>, C. Henze<sup>1†</sup>, U. Presuhn<sup>3</sup> and J. Krieter<sup>1</sup>

<sup>1</sup>Institute of Animal Breeding and Husbandry, Christian-Albrechts-University, D-24118 Kiel, Germany; <sup>2</sup>Chamber of Agriculture Schleswig-Holstein, LVZ Futterkamp, D-24732 Blekendorf, Germany; <sup>3</sup>Farm concepts GmbH & Co. KG, D-23812 Wahlstedt, Germany

(Received 9 July 2007; Accepted 11 April 2008; First published online 8 July 2008)

**Table 4** Heritabilities ( $\pm$ s.e.), additive genetic variance ( $\sigma^2_a$ ), random permanent sow effect ( $\sigma^2_{sow}$ ), random common litter effect ( $\sigma^2_{ll}$ ) and repeatability ( $t$ ) for the different causes of piglet losses (LOSS)

LOSS	$h^2 \pm$ s.e.	$\sigma^2_a$	$\sigma^2_{sow}$	$\sigma^2_{ll}$	$t$ (%)
Survival rate (SR)	0.03 $\pm$ 0.01	0.03	0.02	0.09	12
Crushing (CRUSH)	0.03 $\pm$ 0.01	0.03	0.01	0.07	10
Crushing – early (CRUSH_E)	0.04 $\pm$ 0.02	0.05	0.02	0.10	15
Crushing – late (CRUSH_L)	0.01 $\pm$ 0.01	0.02	0.02	0.05	7
Crushing heavier piglets (CRUSH_H)	0.03 $\pm$ 0.01	0.03	0.03	0.05	10
Underweight (UW)	0.03 $\pm$ 0.02	0.04	0.07	0.12	18
Runt (RU)	0.05 $\pm$ 0.03	0.06	0.07	0.09	18

$\sigma^2_e$  was set equal to 1.



## Heritability of udder morphology and colostrum quality traits in swine<sup>1</sup>

A. Balzani,<sup>\*2</sup> H. J. Cordell,<sup>†</sup> E. Sutcliffe,<sup>‡</sup> and S. A. Edwards<sup>\*</sup>

<sup>\*</sup>School of Agriculture, Food and Rural Development, Newcastle University, Newcastle upon Tyne, NE1 7RU, UK; <sup>†</sup>Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne NE1 3BZ, UK; and <sup>‡</sup>ACMC Ltd., Upton House, Beeford, Driffield, East Yorkshire, YO258AF, UK

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### Udder morphology

COL	528	25.5	3.50	15.1	35.0	0.35 (0.07)
SAMER	987	104.5	14.45	62.2	154.0	0.37 (0.06)
SAMER SD	987	21.62	7.94	4.8	74.8	0.18 (0.03)
LEN	986	16.1	3.00	7.0	31.3	0.46 (0.04)
LEN SD	986	2.81	2.21	0.0	11.34	0.42 (0.1)
DIA	987	10.5	1.70	4.6	16.2	0.53 (0.02)
DIA SD	987	1.77	1.38	0.1	9.4	0.11 (0.03)
AML	987	61.2	10.88	30.0	105.0	0.22 (0.04)
AML SD	987	17	4.95	5.0	47.8	0.19 (0.03)
OR	987	0.9	0.21	0.0	1.0	0.14 (0.03)
NoFun	987	0.04	0.05	0.0	0.4	0.22 (0.05)
TT	987	15.6	1.12	12.0	19.0	0.42 (0.02)
DEV	987	2.24	0.51	1.0	3.0	0.25 (0.04)

<sup>1</sup>SAF = sow age at current farrowing; GLEN = sow gestation length; NBA = number of piglets born alive; TB0 = total number of piglets born; LW0 = litter weight at birth excluding stillborns; LS10 = litter size at 10 d after farrowing; LW10 = litter weight at 10 d after farrowing; LiveD = total number of piglets born alive that died during the first 10 d of age; STB = number of stillborn piglets; COL = colostrum IgG concentration; SAMER = interteat distance within the same row; LEN = teat length; DIA = teat diameter; AML = teat distance from the abdominal midline; OR = proportion of teats oriented perpendicular to the udder; NoFun = proportion of nonfunctional teats; TT = total number of teats present in both rows; DEV = udder development score; ADG = ADG during gilt test 30 to 100 kg (g); BFAT = backfat thickness at end of test.

<sup>2</sup>Number of observations.

Smart Agricultural Technology 5 (2023) 100246



Contents lists available at ScienceDirect

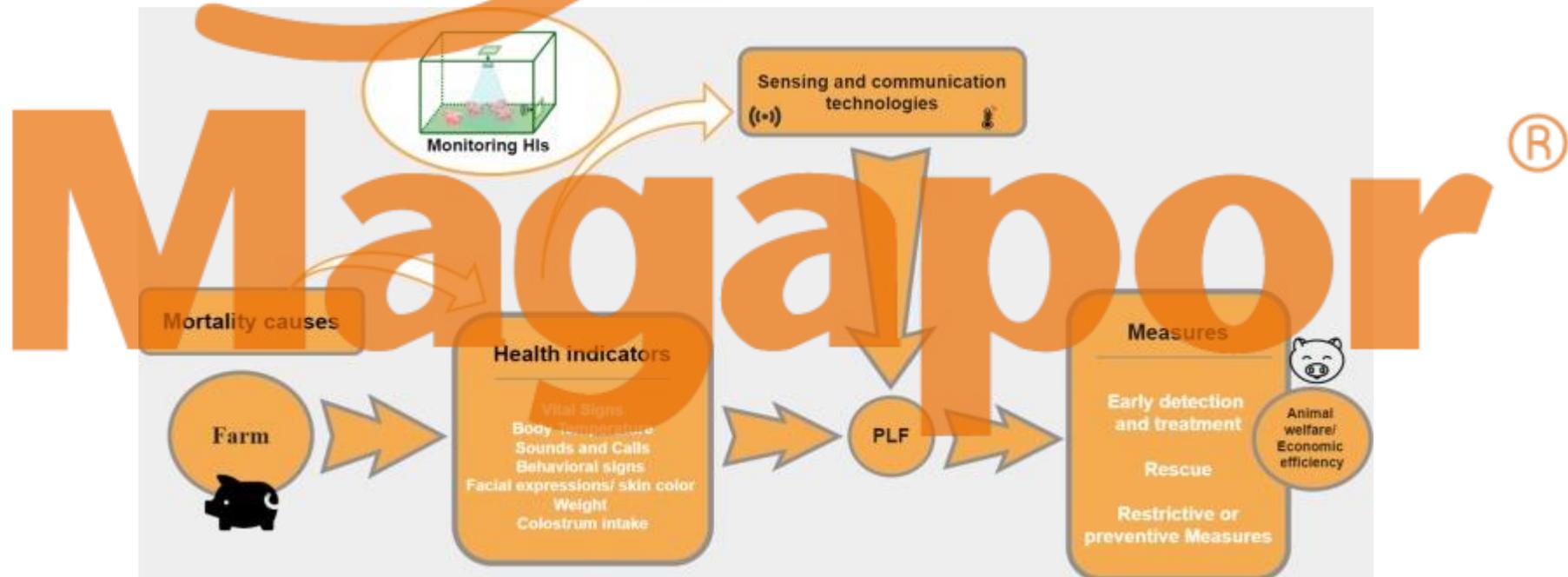
## Smart Agricultural Technology

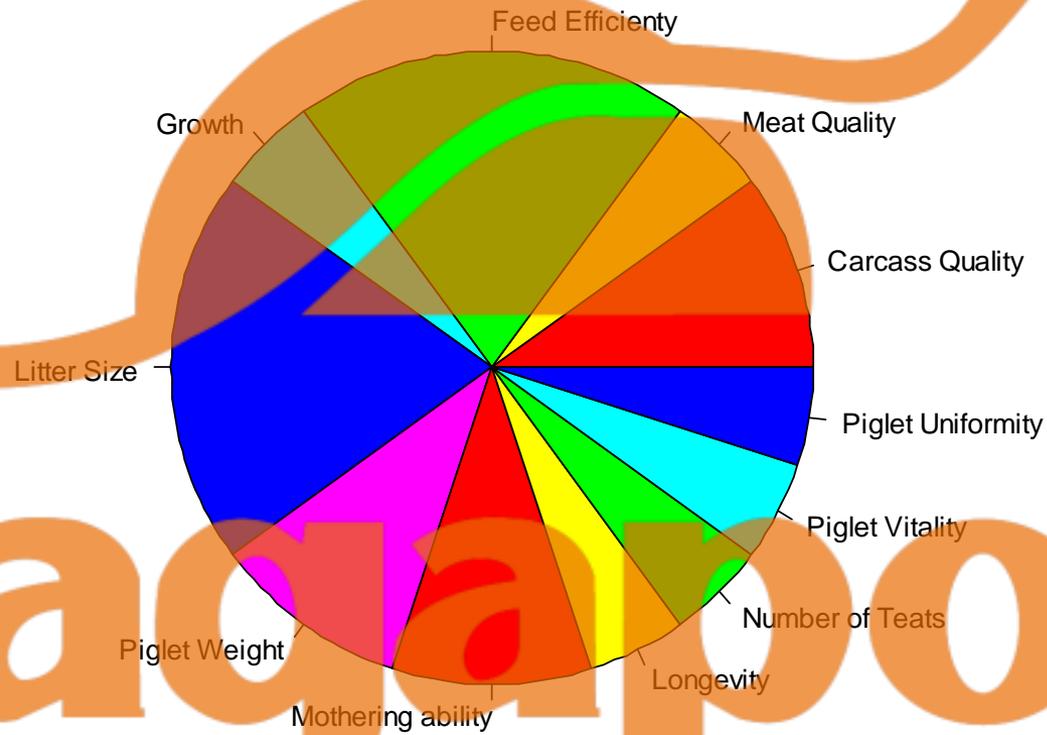
journal homepage: [www.journals.elsevier.com/smart-agricultural-technology](http://www.journals.elsevier.com/smart-agricultural-technology)



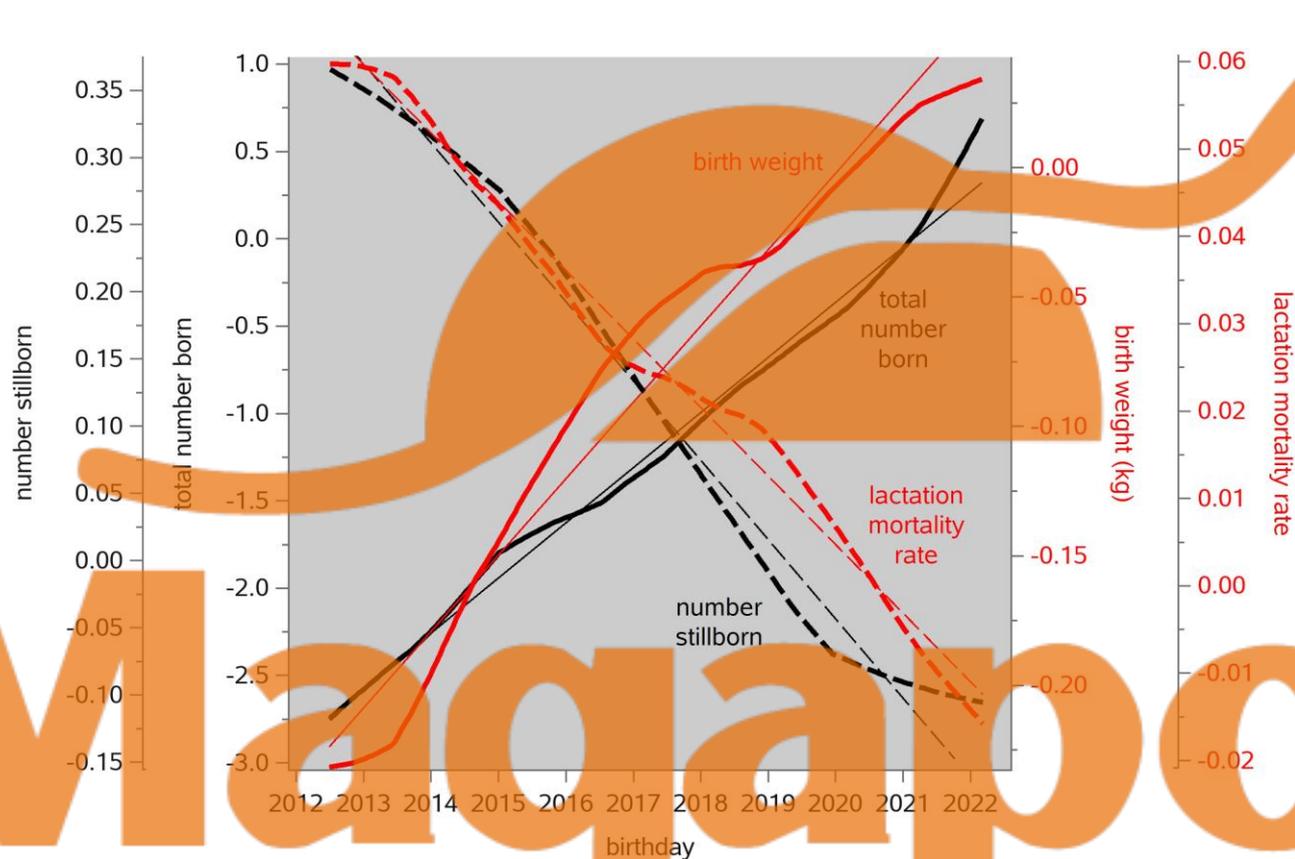
### Improving piglets health and well-being: A review of piglets health indicators and related sensing technologies

Ehsan Sadeghi \*, Claudie Kappers, Alessandro Chiumento, Marjolein Derks, Paul Havinga





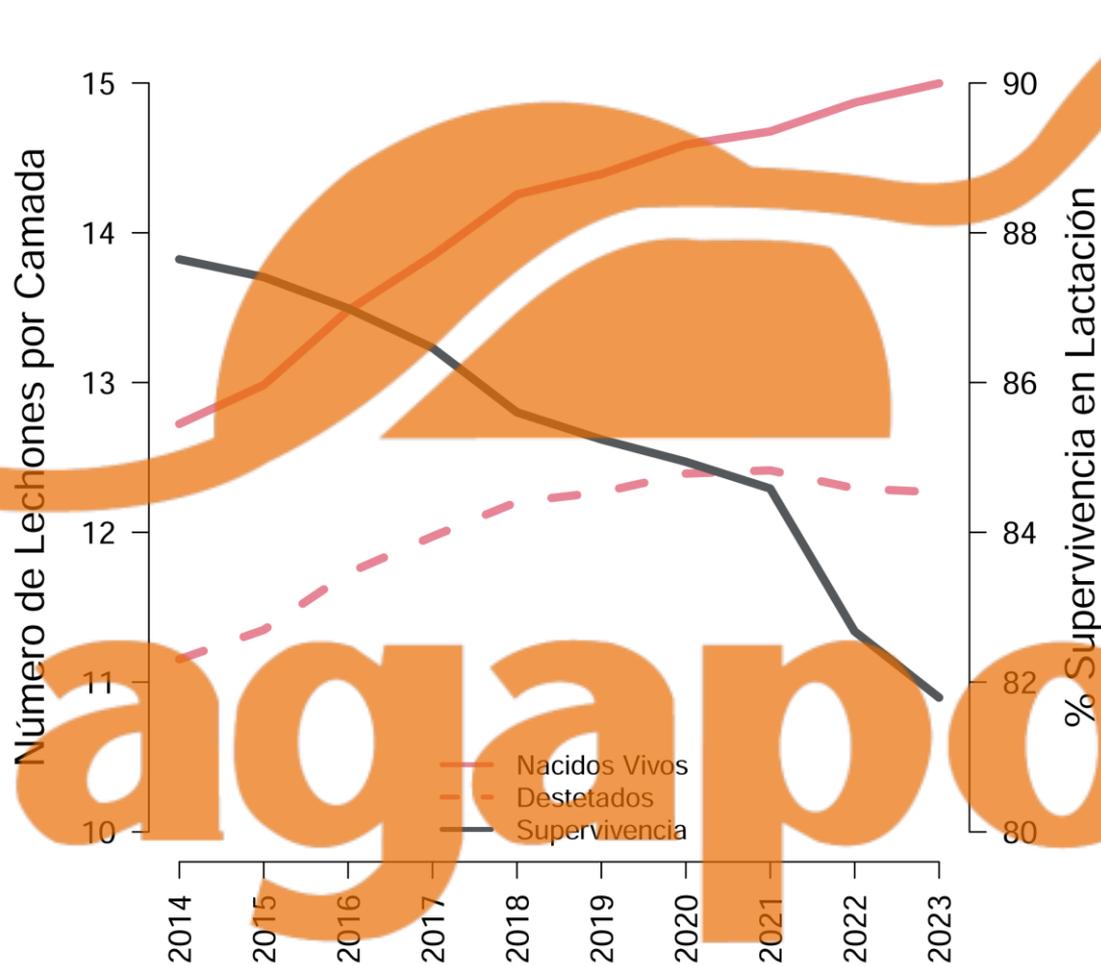
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Knap et al. 2023. Genetic and phenotypic time trends of litter size, piglet mortality, and birth weight in pigs. *Front. Anim. Sci.*

Sci. <https://doi.org/10.3389/fanim.2023.1218175>

However?



<https://bdporc.irta.es/>

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**Crossbreeding Genomic  
Selection**

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## BOARD INVITED REVIEW: The purebred-crossbred correlation in pigs: A review of theory, estimates, and implications<sup>1</sup>

Y. C. J. Wientjes<sup>2</sup> and M. P. L. Calus

Wageningen University and Research, Animal Breeding and Genomics, 6700 AH Wageningen, The Netherlands

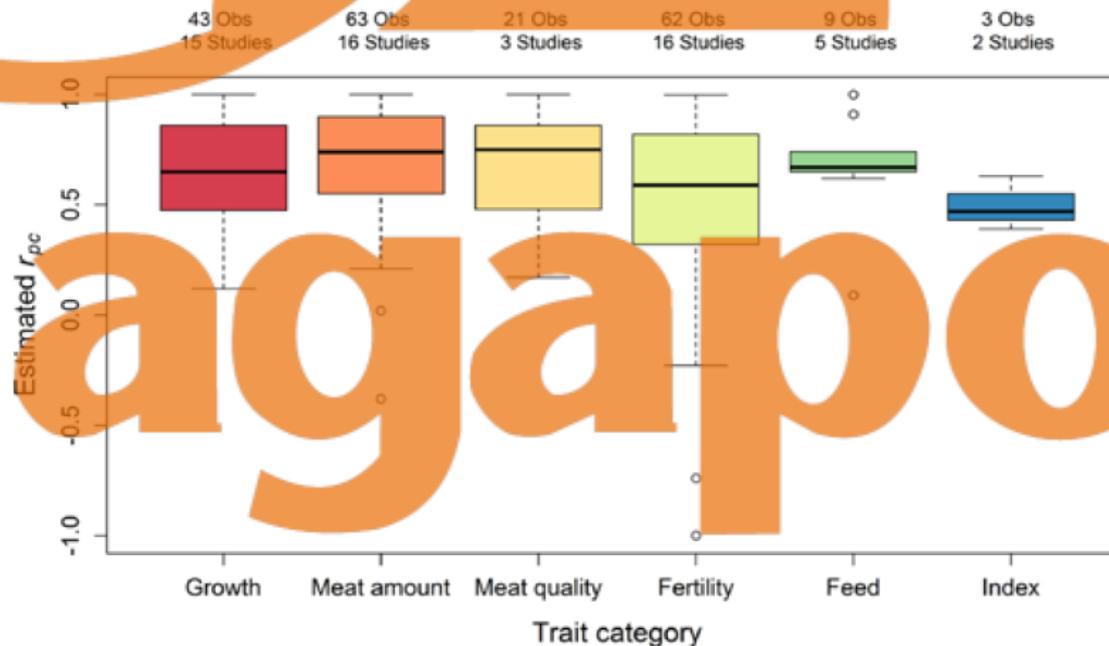


Figure 3. Estimated  $r_{pc}$  values for the 6 different trait categories.

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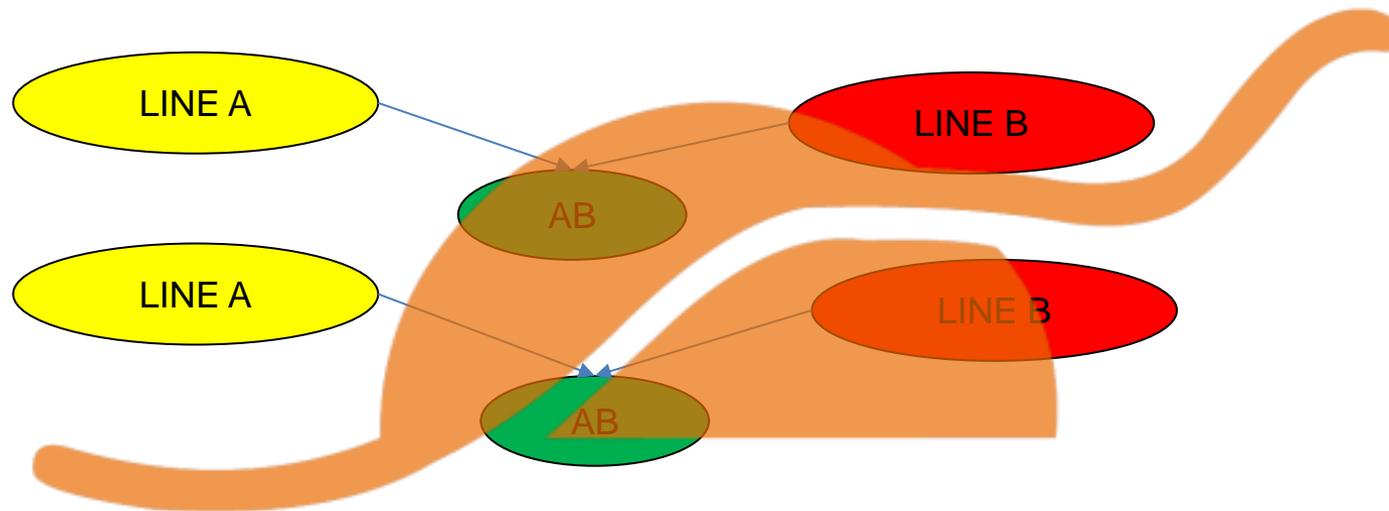


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- Genes involved in piglet survival may differ between environments.

- Individuals with the best genotype in one environment can not be the best in other environment.



- Selection is based on crossbred individuals performance
- It maximized long term response in the crossbred population
- It is slow, because it requires the phenotypes of crossbred individuals
- It is specific for a particular cross and environment

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Journal of Animal Science, 2021, Vol. 99, No. 8, 1–24

<https://doi.org/10.1093/jas/skab205>

Advance Access publication July 05, 2021

Received: 12 March 2021 and Accepted: 2 July 2021

Animal Genetics and Genomics

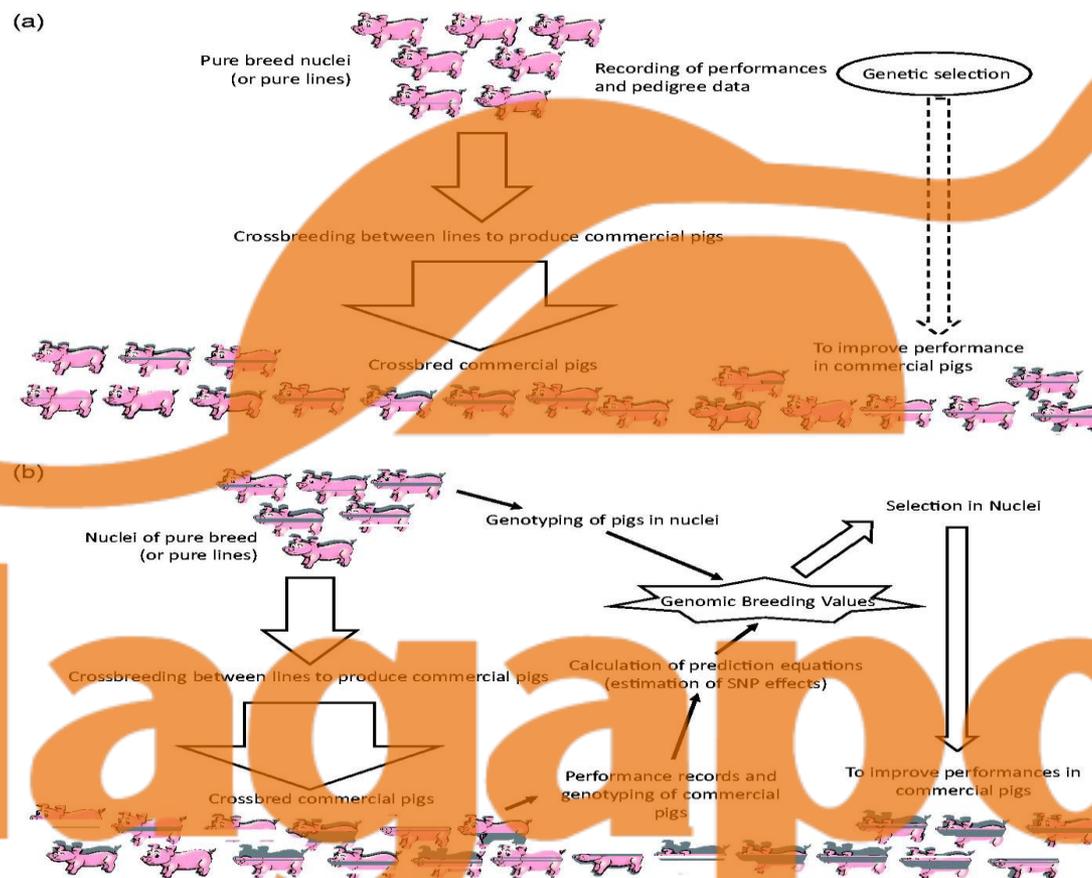
ANIMAL GENETICS AND GENOMICS

## Review: optimizing genomic selection for crossbred performance by model improvement and data collection

Pascal Duenk, Piter Bijma, Yvonne C. J. Wientjes, and Mario P. L. Calus

Animal Breeding and Genomics, Wageningen University and Research, P.O. Box 338, 6700 AH Wageningen, The Netherlands

- If the correlation between purebreds and crossbreds is less than 0.8, the cause is genotype-by-environment interaction.
  - The benefit of phenotyping crossbred individuals increases as the correlation decreases and with larger populations.
  - The benefit of phenotyping crossbred individuals requires knowledge of their pedigree and/or genomic information.
- 



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THANKS

GRACIAS

Luis Varona

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