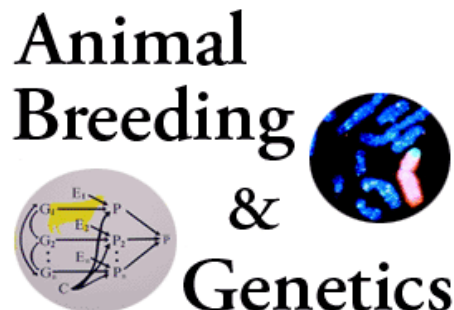


Genomic Selection in pigs

Jack Dekkers

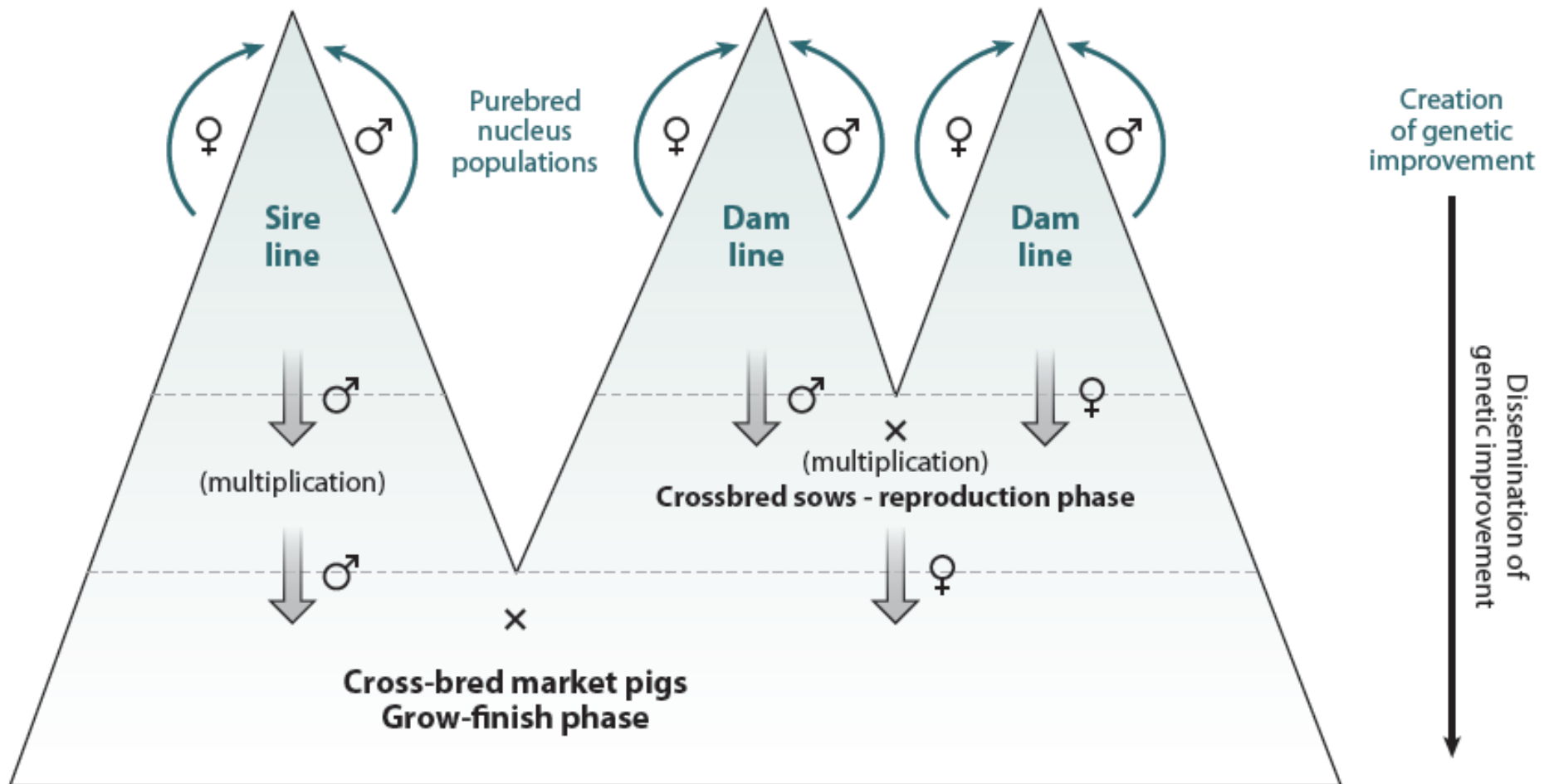
Animal Breeding & Genetics
Department of Animal Science
Iowa State University

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ANIMAL
SCIENCE

Typical Breeding Pyramid for Pigs

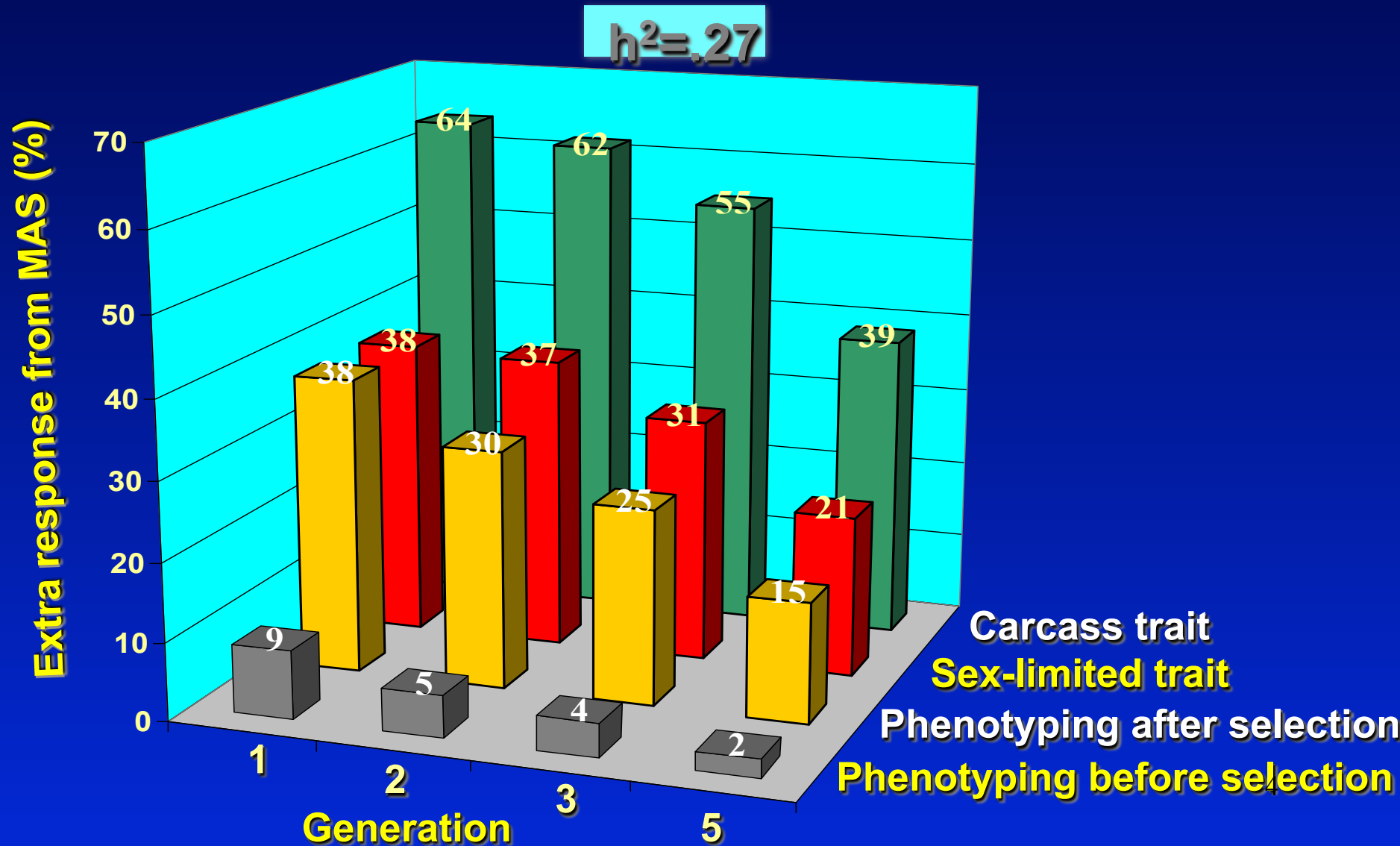


- Limited opportunities to reduce generation intervals
- Challenges:
 - Preselection for entry of candidates into further testing
 - Selection for female reproduction and longevity
 - Selection for feed efficiency
 - Selection for carcass/meat quality traits
 - Selection for commercial crossbred performance
 - Selection for Disease resistance/resilience/robustness
 - Limited size of individual nucleus populations

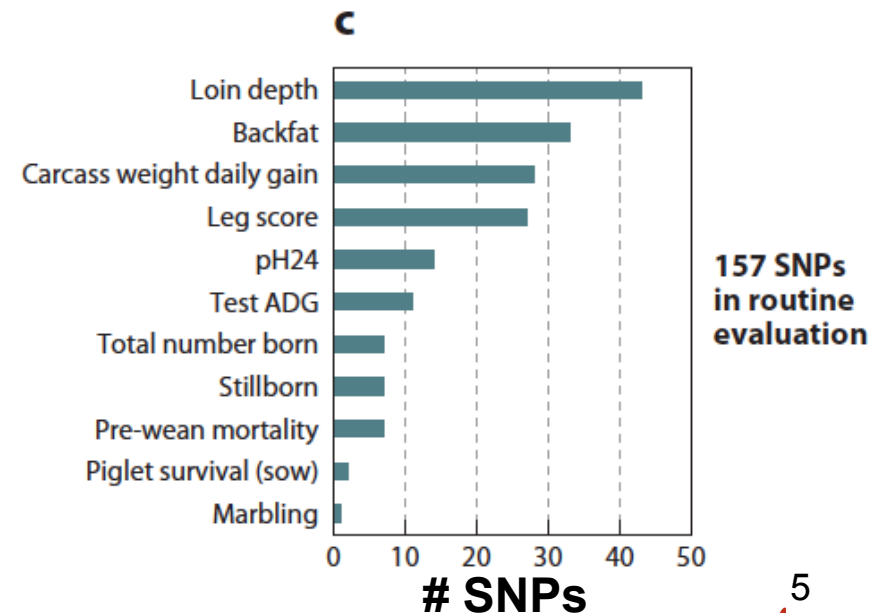
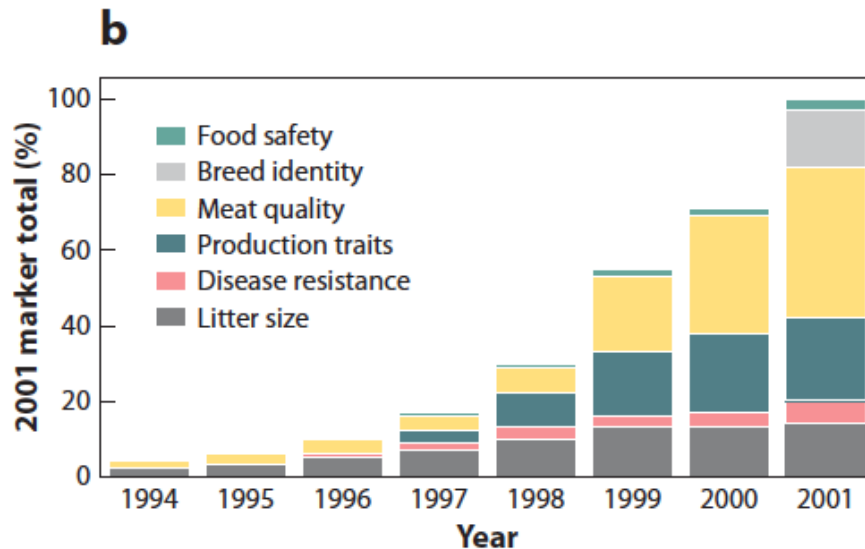
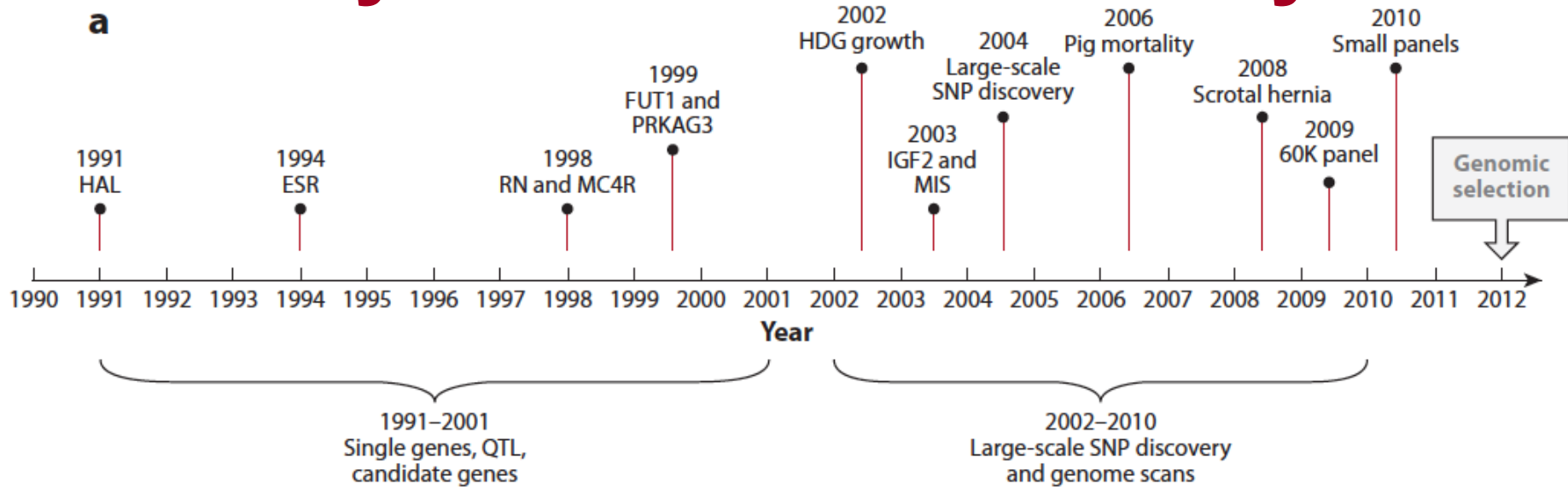
Gains from LE-MAS

Meuwissen & Goddard, 1996

QTL with 1/3 of genetic variance haplotype-marked



History of use of markers by PIC



Single step genomic evaluation

- Accuracy improvement for **non-genotyped** progeny of genotyped sires and dams*

Trait	ACC EBV	ACC GEBV	Increase
Total number born	0.35	0.39	11%
Stillborn	0.33	0.37	12%
Survival birth-weaning	0.23	0.29	26%
Litter wean weight	0.32	0.40	25%
Interval wean-mate	0.32	0.35	9%

*Sires and dams have few or no daughters

- Full siblings have the same breeding value
- Accuracy improvement for **60k genotyped** progeny of genotyped sires and dams

Trait	ACC EBV	ACC GEBV	Increase
Total number born	0.36	0.62	71%
Total number born xbred	0.22	0.39	75%

Genomic selection for two traits in a maternal pig breeding scheme¹

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^{*}Nofima AS, N-1430 Ås, Norway and [†]Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, N-1430 Ås, Norway

ABSTRACT: The objective of this study was to compare different implementations of genomic selection to a conventional maternal pig breeding scheme, when selection was based partly on production traits and partly on maternal traits. A nucleus pig breeding population with size and structure similar to Norwegian Landrace was simulated where equal weight was used for maternal and production traits. To genotype the boars at the boar station and base the final selection of boars on genomic breeding values increased total genetic gain by 13% and reduced the rate of inbreeding by 40%, without significantly affecting the relative contribution of each trait to total genetic gain. To increase the size of the reference population and thereby accuracy of selection, female sibs in the selected litters can also be genotyped to increase genetic gain for maternal traits more than for production traits, thereby resulting in an increased relative contribution of maternal traits to total genetic gain. Genotyping 2,400 females each year increased the rela-

tive contribution of maternal traits to total genetic gain from 16 to 32%. Performing preselection of males by allowing genotyping of 2 males per litter and allowing for selection across and within litters before the boar test increased genetic gain by 5 to 11%, compared with genotyping the boars at the boar station, without significant effects on the relative contribution of each trait to total genetic gain. Genotyping more animals consequently increased genetic gain. Genotyping females to build a larger reference base for maternal traits gave similar genetic gain as genotyping the same amount of additional males but with a lower rate of inbreeding and a greater contribution of maternal traits to total genetic gain. In conclusion, genotyping females should be prioritized before genotyping more males than the tested boars if the breeding goal is to increase maternal traits specifically over production traits or genomic selection is used as a tool to reduce the rate of inbreeding.

Key words: breeding design, genomic selection, multitrait selection, pig

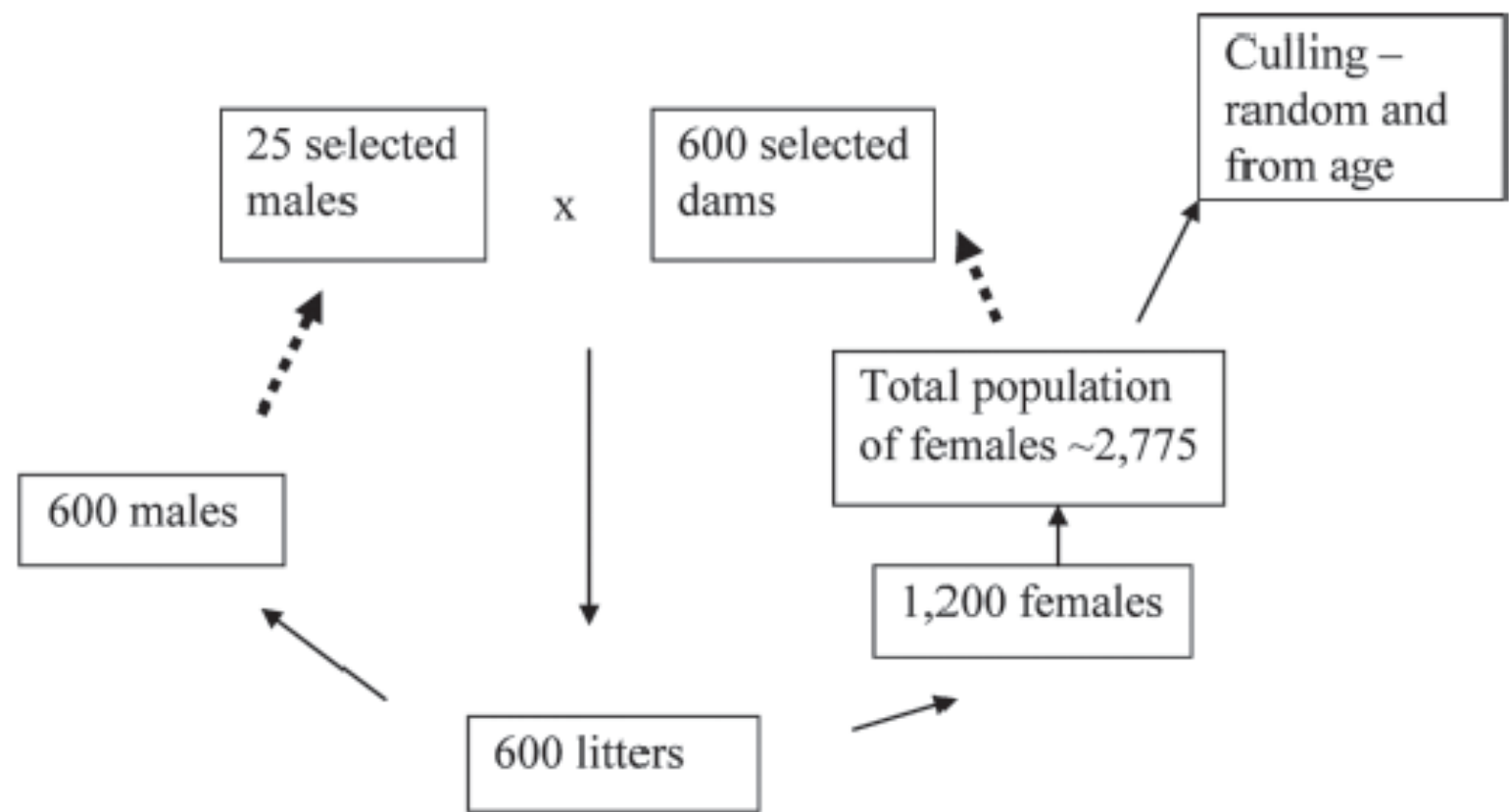


Figure 1. Overview of the breeding population structure of the conventional scheme (CONV-BLUP). Dotted arrows represent selection.

Selection for a trait measured on females after 1st litter – $h^2=0.1$.

2 rounds of selection/year.

Each round, 600 dams selected to produce selected litters.

Within each selected litter, 1 male and 2 female piglets randomly picked as selection candidates

CONV-BLUP: Selection of males on parental average EBV for maternal traits. Generation interval = 2 rounds

PROG-BLUP: Selection of males based on progeny-test EBV from 40 progeny. Generation interval = 5 rounds

Table 1. An overview of the different breeding schemes¹

Scheme ²		Genotyped males ³	Genotyped females ³	Increase in reference population ³	Male candidates per litter
CONV-BLUP		0	0	—	1
PROG-BLUP		0	0	—	1
CONV-GEbv_0	Random fraction of dams genotyped	600	0	25	1
CONV-GEbv_0.2		600	240	265	1
CONV-GEbv_0.3		600	360	385	1
CONV-GEbv_0.4		600	480	505	1
CONV-GEbv_0.5		600	600	625	1
CONV-GEbv_1		600	1,200	1,225	1
WL2-GEbv_0.5	# males genotyped per litter	1,200	600	625	2
WL3-GEbv_0		1,800	0	25	3
WL3-GEbv_1		1,800	1,200	1,225	3

¹The number of genotyped animals is per selection round (6 mo).

²Breeding scheme: CONV-BLUP = conventional scheme; PROG-BLUP = progeny testing scheme, in which selection is based on BLUP breeding values. CONV-GEbv_x = genomic selection applied for final selection of sires, with x referring to the fraction of dams genotyped; WLy-GEbv_x = multiple males genotyped from each litter, where x refers to the fraction of dams genotyped and y refers to the number of males genotyped per litter.

³Per round of selection.

Genomic Selection (GEbv):

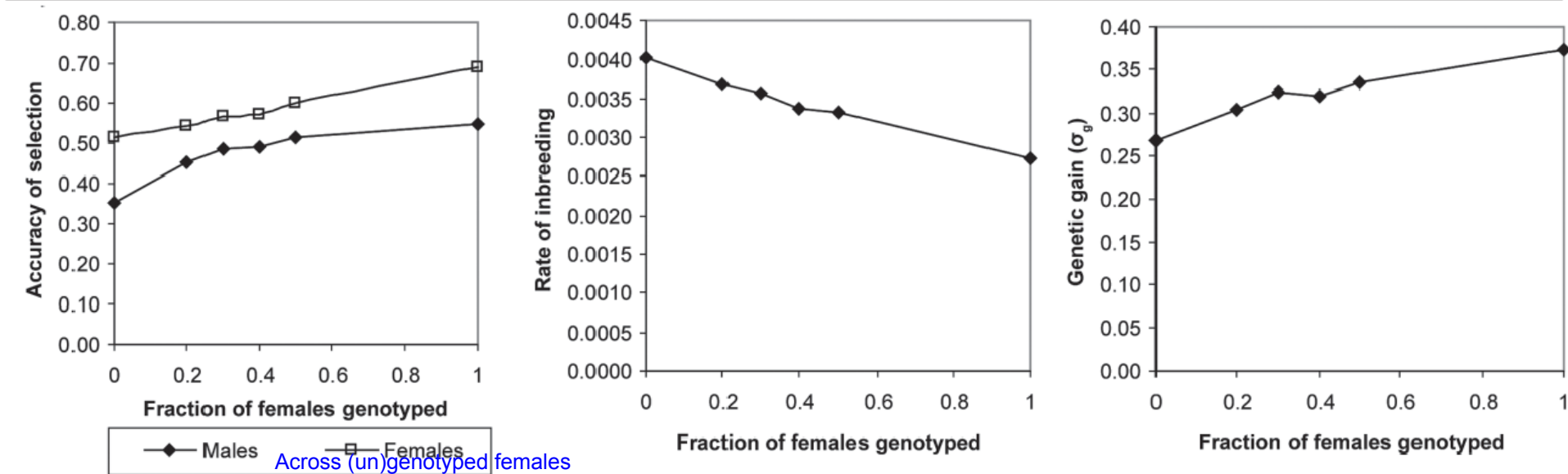
Training population = 450 animals from the base generation with 40 progeny with 1 record each
+ new genotyped animals generated from the breeding scheme
when they got a record (dams) or a DYD (sires).

25 males selected on GEbv from among those genotyped (1/litter for CONV-GEbv; >1/litter for WLy-GEbv)

Selection of females on (G)EBV across genotyped and ungenotyped candidates.

Table 2. Results from the main breeding schemes - Last 10 of 20 rounds of selection

Scheme ¹	Genetic gain (σ_g) ²	Rate of inbreeding ²	Acc. (males) ³	Acc. (females) ³
CONV-BLUP	0.22	0.0077	0.21	0.50
PROG-BLUP	0.24	0.0011	0.70	0.46
CONV-GEV_0	0.27	0.0040	0.35	0.51
CONV-GEV_0.5	0.33	0.0033	0.51	0.60
CONV-GEV_1	0.37	0.0027	0.55	0.69
WL2-GEV_0.5	0.36	0.0033	0.51	0.61
WL3-GEV_0	0.30	0.0050	0.34	0.56
WL3-GEV_1	0.42	0.0029	0.56	0.72



- 1) GS can increase gain for maternal traits and reduce inbreeding through greater accuracy of EBV of young males
- 2) It is essential to genotype females to ensure high accuracy of EBV
- 3) With >1 male genotyped/litter → within-litter selection and >1 sires from best litters → higher gain, less inbreeding
- 4) At same cost, genotyping females → greater increase in genetic gain than genotyping more males

Efficiency of genomic selection in a purebred pig line¹

T. Tribout,*^{†2} C. Larzul,*[†] and F. Phocas*[†]

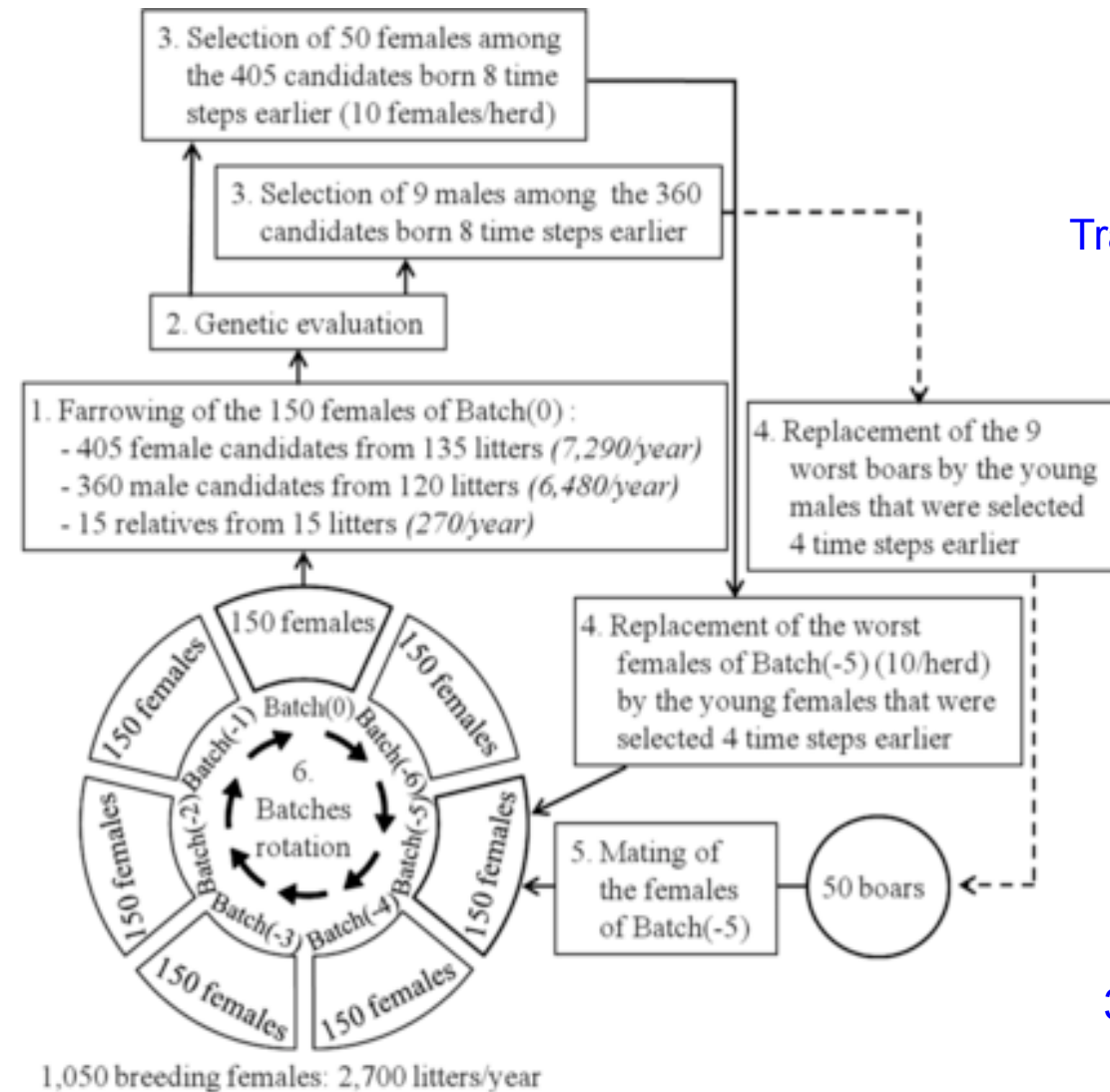
*INRA, UMR1313 Génétique Animale et Biologie Intégrative, F-78350 Jouy-en-Josas, France;
and [†]AgroParisTech, UMR1313 Génétique Animale et Biologie Intégrative, F-75231 Paris, France

ABSTRACT: Stochastic simulation was used to compare the efficiency of 3 pig breeding schemes based on either traditional genetic evaluation or genomic evaluation. The simulated population contained 1,050 female and 50 male breeding animals. It was selected for 10 yr for a synthetic breeding goal that included 2 traits with equal economic weights and heritabilities of 0.2 or 0.4. The reference breeding scheme, named BLUP-AM, was based on the phenotyping of all candidates (13,770 animals/yr) for Trait 1 and of relatives from 10% of the litters (270 animals/yr) for Trait 2 and on BLUP-Animal Model genetic evaluations. Under the first alternative scenario, named GE-1TP, selection was based on genomic breeding values (GBV) estimated with one training population (TP) made up of candidate relatives phenotyped for both traits, with a size increasing from 1,000 to 3,430 over time. Under the second alternative scenario, named GE-2TP, the GBV for Trait 2 were estimated using a TP identical to that of GE-1TP, but the GBV for Trait 1 were estimated using a large TP made up of candidates that increased in number from 13,770 to 55,080 over time. Over the simulated period, both genomic breeding schemes generated 39 to 58% more accurate EBV for Trait 2 than the reference scheme,

resulting in 78 to 128% (GE-1TP) and 63 to 84% (GE-2TP) greater average annual genetic trends for this trait. For Trait 1, GE-1TP was 18 to 24% less accurate than BLUP-AM, reducing average annual genetic trends by 27 to 44%. By contrast, GE-2TP generated 35 to 43% more accurate EBV and 8 to 22% greater average annual genetic trends for Trait 1 than the reference scheme. Consequently, GE-2TP was 27 to 33% more efficient in improving the global breeding goal than BLUP-AM whereas GE-1TP was globally as efficient as the reference scheme. Both genomic schemes reduced the inbreeding rate, the greatest decrease being observed for GE-2TP (−49 to −60% compared with BLUP-AM). In conclusion, genomic selection could substantially and durably improve the efficiency of pig breeding schemes in terms of reliability, genetic trends, and inbreeding rate without any need to modify their current structure. Even though it only generates a small TP, limited annual phenotyping capacity for traits currently only recorded on relatives would not be prohibitive. A large TP is, however, required to outperform the current schemes for traits recorded on the candidates in the latter.

Key words: breeding scheme, genomic selection, pig, production traits, simulation

Simulation of purebred terminal sire population with 1,050 breeding females and 50 breeding males, resembling French Piétrain breed.



Population structure of the simulated breeding scheme and chronological order of events occurring at each simulated time step of 3 wks.

Selection for breeding goal with 2 traits with equal economic weights/genetic SD

Trait 1 = fattening trait that is cheap and easy to record on a large number of candidates (e.g., growth rate, ultrasonic backfat thickness, or loin depth)

Trait 2 = a trait that is too difficult or too expensive to measure on a large scale (e.g., meat quality, feed efficiency, and intramuscular fat).

BLUP-AM = selection BLUP-EBV using phenotypes of all candidates for Trait 1 and limited # relatives for Trait 2 – selected on parental EBV

GE-1TP - No pheno on candidates – Pheno + Genotype on relatives only
Initial training = 1,000 both traits

GE-2TP – pheno + genotype on all candidates for Trait 1; relatives Trait 2.
Initial training 13,770 trait 1; 1,000 trait 2

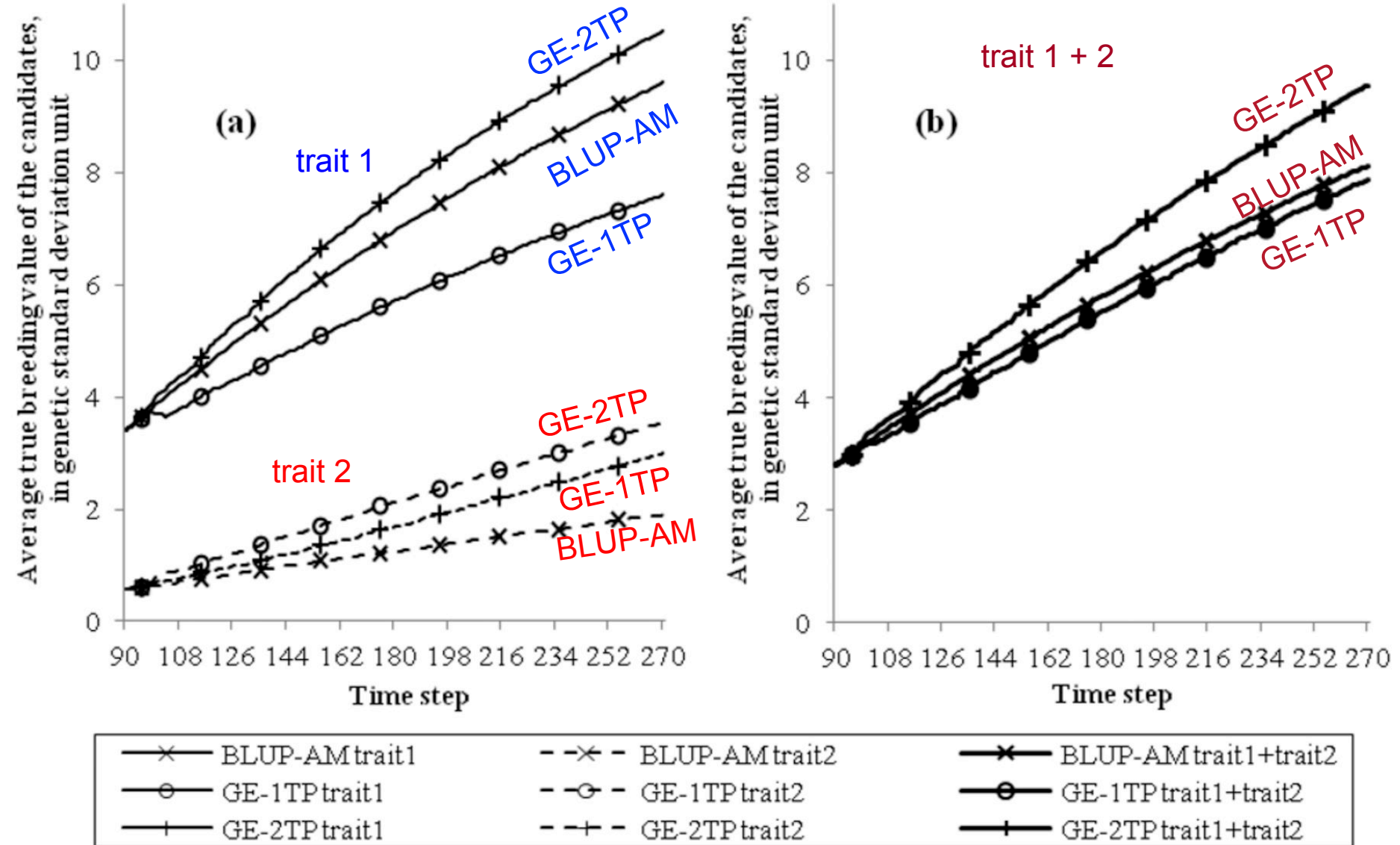
3 sets of heritabilities for Trait 1 and Trait 2

$MMh^2 = 0.4$ and 0.4

$MLh^2 = 0.4$ and 0.2

$LLh^2 = 0.2$ and 0.2

3 QTL densities: 10/30/60 QTL/Morgan



Realized genetic trends for Traits 1 and 2 (a)
 and for the global breeding goal (Trait 1 + Trait 2) (b)
 under 3 scenarios during the last 10 yr simulated,
 with an initial QTL density of 60 QTL/M for each trait,
 initial heritability of Trait 1 = 0.4, and initial heritability of Trait 2 = 0.2.

Efficiency of genomic selection in a purebred pig male line

T. Tribout, C. Larzul and F. Phocas

J ANIM SCI 2012, 90:4164-4176.

CONCLUSIONS

- GS can substantially and durably improve the efficiency of pig breeding schemes in terms of accuracy, genetic gain and inbreeding, without a need to modify their current structure
- Even though it only generates a small training population, limited annual phenotyping capacity for traits currently only recorded on relatives would not be prohibitive
- A large training population is, however, required to outperform the current schemes for traits recorded on the candidates.

RESEARCH

Open Access

Economic aspects of implementing genomic evaluations in a pig sire line breeding scheme

Thierry Tribout^{1,2*}, Catherine Larzul^{1,2} and Florence Phocas^{1,2}

Abstract

Background: Replacing pedigree-based BLUP evaluations by genomic evaluations in pig breeding schemes can result in greater selection accuracy and genetic gains, especially for traits with limited phenotypes. However, this methodological change would generate additional costs. The objective of this study was to determine whether additional expenditures would be more profitably devoted to implementing genomic evaluations or to increasing phenotyping capacity while retaining traditional evaluations.

Methods: Stochastic simulation was used to simulate a population with 1050 breeding females and 50 boars that was selected for 10 years for a breeding goal with two uncorrelated traits with heritabilities of 0.4. The reference breeding scheme was based on phenotyping 13 770 candidates per year for trait 1 and 270 sibs of candidates per year for trait 2, with selection based on pedigree-based BLUP estimated breeding values. Increased expenditures were allocated to either increasing the phenotyping capacity for trait 2 while maintaining traditional evaluations, or to implementing genomic selection. The genomic scheme was based on two training populations: one for trait 2, consisting of phenotyped sibs of the candidates whose number increased from 1000 to 3430 over time, and one for trait 1, consisting of the selection candidates. Several genomic scenarios were tested, where the size of the training population for trait 1, and the number of genotyped candidates pre-selected based on their parental estimated breeding value, varied.

Results: Both approaches resulted in higher genetic trends for the population breeding goal and lower rates of inbreeding compared to the reference scheme. However, even a very marked increase in phenotyping capacity for trait 2 could not match improvements achieved with genomic selection when the number of genotyped candidates was large. Genotyping just a limited number of pre-selected candidates significantly reduced the extra costs, while preserving most of the benefits in terms of genetic trends and inbreeding. Implementing genomic evaluations was the most efficient approach when major expenditure was possible, whereas increasing phenotypes was preferable when limited resources were available.

Conclusions: Economic decisions on implementing genomic evaluations in a pig nucleus population must take account of population characteristics, phenotyping and genotyping costs, and available funds.

Are additional
expenditures
more
profitably
devoted to
implementing
genomic
evaluations
or to
increasing
phenotyping
capacity?

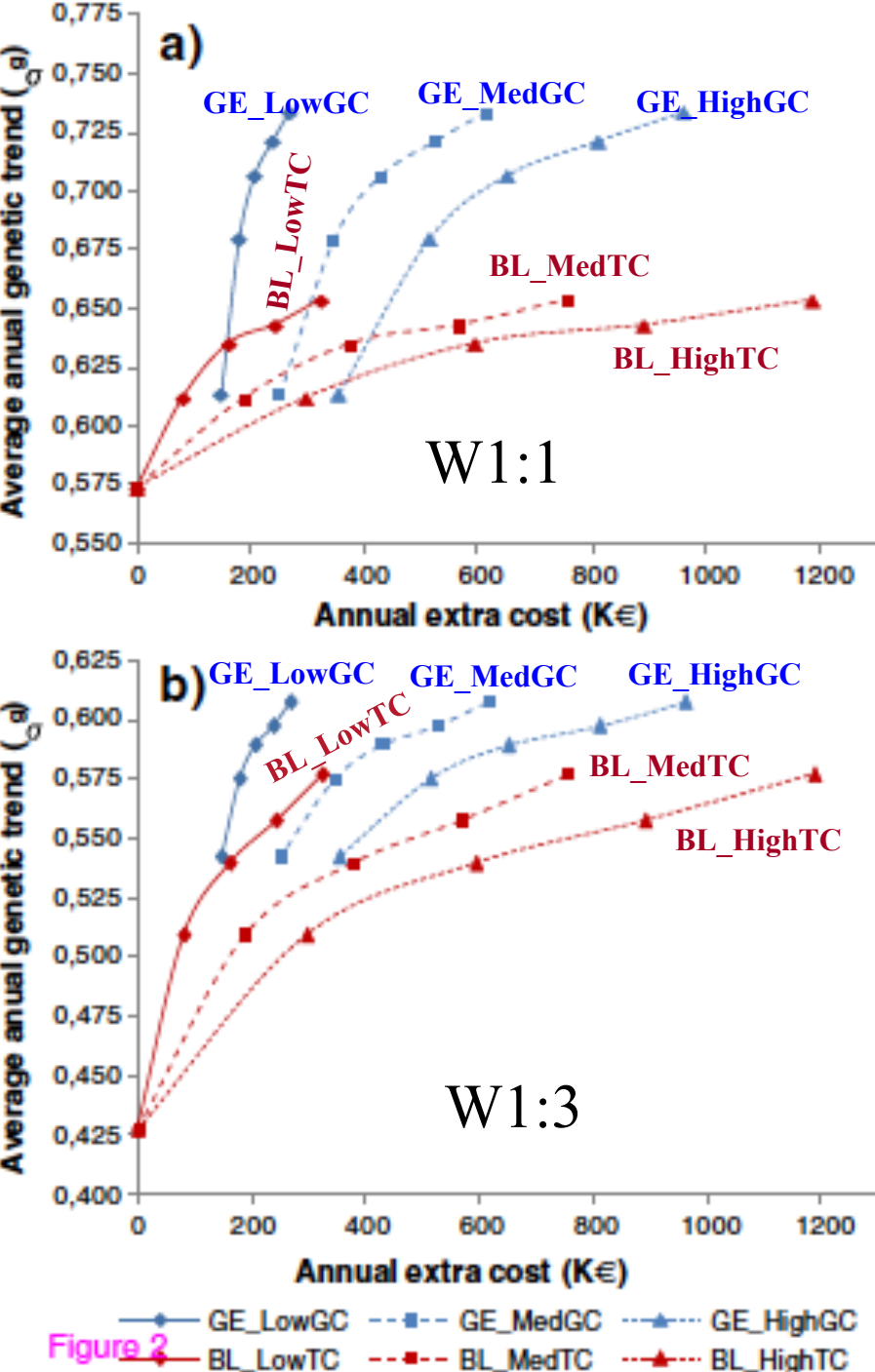


Figure 2 Average annual genetic trend for the breeding goal under genomic and pBLUP scenarios, based on the additional annual cost compared to the reference scheme.

Three levels of genotyping and phenotyping costs:

BL_LowTC, **BL_MedTC** and **BL_HighTC** = pBLUP breeding scheme with low, medium and high testing station costs:

550, **350** or **150** Euro per extra sib phenotyped for trait 2

GE_LowGC, **GE_MedGC** and **GE_HighGC** = GE with low, medium and high genotyping costs

Boars and sows used for breeding were genotyped with the porcine60SNP beadchip

Selection candidates and phenotyped sibs were genotyped with a lower density beadchip.

High density: **150** or **120** or **90** Euro/animal

Low density: **50** or **30** or **10** Euro/animal

for **High / Med / Low** genotyping costs

RESEARCH

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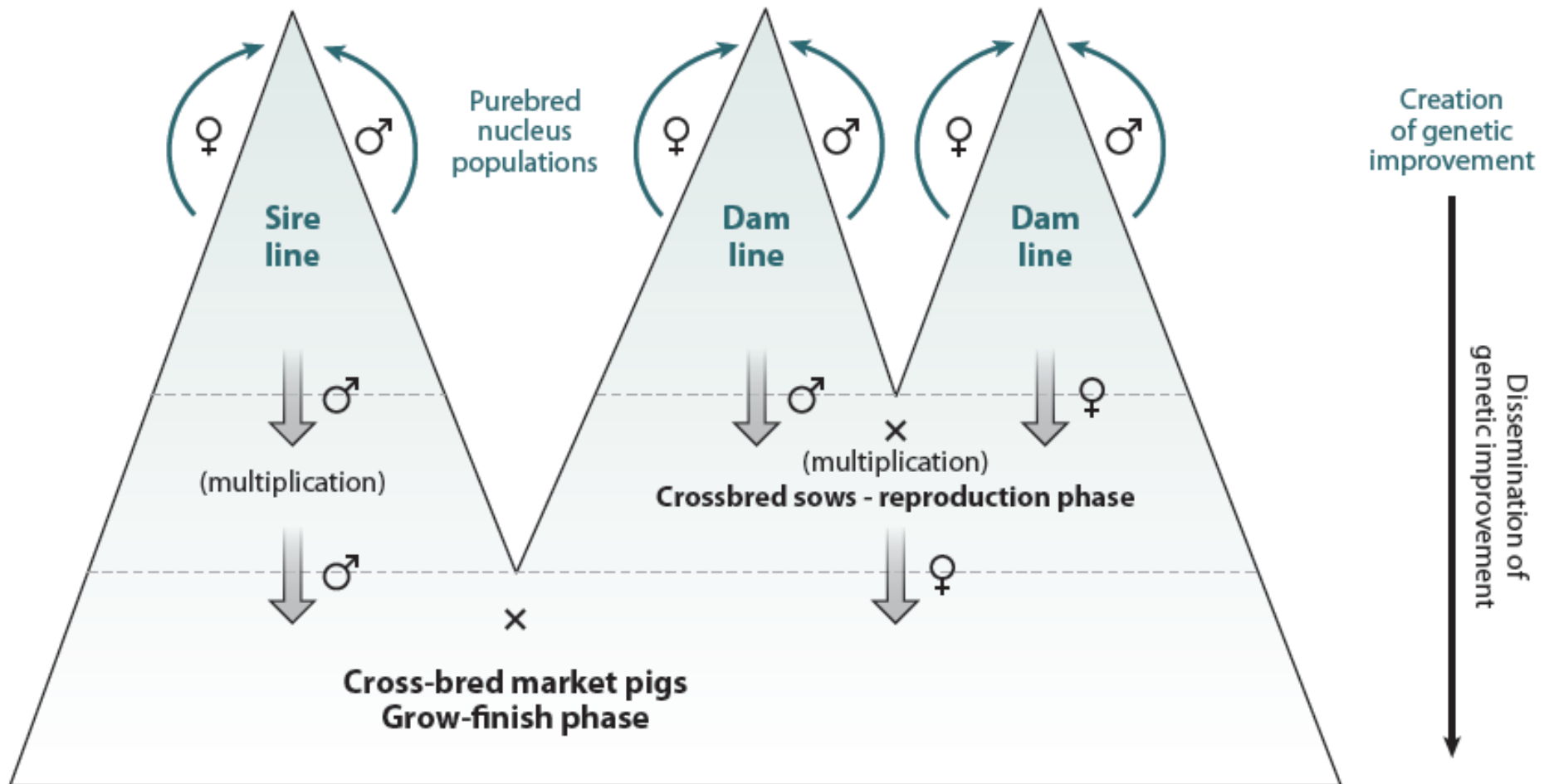
Economic aspects of implementing genomic evaluations in a pig sire line breeding scheme

Thierry Tribout^{1,2*}, Catherine Larzul^{1,2} and Florence Phocas^{1,2}

CONCLUSIONS

- The potential improvements provided by implementing genomic evaluations significantly exceed the possible benefits of increasing phenotyping capacities for the most limited traits while retaining traditional pBLUP EBV.
- Implementing a genomic breeding scheme would generate large additional costs.
 - However, substantial savings could be achieved by pre-selecting the candidates to be genotyped based on their parental EBV, and still maintain an advantage over the traditional pBLUP scheme.
- From an economic point of view, implementing genomic evaluations is not always the most efficient investment to improve the efficiency of a breeding scheme
 - but a threshold for additional annual expenses can be determined, below which increasing the number of phenotyped sibs while maintaining pBLUP evaluations is preferred, and above which genotyping animals to implement genomic evaluations is more efficient. This threshold depends on the cost of phenotyping additional sibs, on genotyping costs in combination with the imputation strategy, on the breeding goal and on the size of the nucleus population.
- Therefore, a breeding company must consider the relevance of implementing genomic evaluations based on the characteristics of the population and its possible annual financial commitment..

Typical Breeding Pyramid for Pigs



**Is Genomic Selection the solution
for all traits?**

**Genomic vs. Marker-assisted
Selection**