

Genetic improvement of pigs

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▶ To cite this version:

Jean Pierre Bidanel. Genetic improvement of pigs. Master. Animal breeding and reproduction biotechnology, Valencia, Spain, Spain. 2017, pp.58. hal-03364808

HAL Id: hal-03364808 https://hal.inrae.fr/hal-03364808

Submitted on 4 Oct 2021

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Genetic improvement of pigs

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Outline

- Some elements on pig production
- Genetic improvement of pigs
 - General principles
 - Definition of the breeding goal
 - Genetic variability of economically important traits
 - Breeding schemes : development and optimisation
 - Use of crossbreeding
 - Controlling the efficiency of pig breeding schemes
 - What does genomics bring to pig breeding schemes

O1 Some elements on pig production





GLOBAL MEAT DEMAND GROWTH ESTIMATES 2010 - 2030



=> Further improvements in efficiency are required







Meat Consumption and CO₂ Emissions

According to a report by the United Nations Food and Agriculture Organization, livestock generates 18 percent of greenhouse gas emissions. The problem is expected to grow, as developing countries increase their consumption of meat and byproducts.



Source: "Livestock's Long Shadow," by the United Nations Food and Agriculture Organization, 2006; Lantmannen THE NEW YORK TIMES

Increasing welfare concerns









02 Genetic improvement of pigs – General principles – Elements on pig production

Main characteristics of pig production

Homogeneity of production conditions

A dominant production system

The Objective : production of (reasonable) quality meat at the

lowest price

✓ Standardised housing, feed & management conditions

Some exceptions

✓ Example : Local breeds (e.g. Iberian pigs), organic production

Homogeneity of the pig produced

Slaughtered at a given target weight

✓ (90 – 115 kg on average - differences between regions/countries

✓ Some "heavy pig" chains (ex : Italy for Parme ham production)

Main characteristics of pig production

Conversely, pig meat is consumed in many different ways

- Fresh meat
- Many processed products
 - ✓ « cooked » or « dry » ham & sausages, "ready to use" dishes,...



Economic efficiency of pig production

Production costs

- 1. Production cost of piglets (up to 25 kg)
 - Is mainly a function of herd numerical productivity
- 2. Cost of the growth period :
 - Growth rate (cost of housing)
 - Feed conversion ratio (amount of feed consumed)
 - Mortality

Usage value of the slaughter pig

- 1. Quantitative aspect = dressing percentage
- 2. Qualitative aspects
 - Carcass composition (lean meat content)
 - Meat and fat quality (not paid to farmers except boar taint)



= Number of piglets produced per sow per unit of time









Related to the duration of the period from 25 kg to slaughter (D) Low D 🛙 reduced housing cost

Some characteristics of pig growth :

- Birth weight x 2 within 8 days
- x 5 within 3 weeks
- x 20 within 8 weeks
 - -x 80 within 6 months !!

Growth curve = sigmoid, with an inflexion point around puberty



Food conversion ratio = amount of feed (kg) necessary for 1 kg live weight gain

Considerable economic impact

Production costs In weaning – fattening herds



Individual measurement : Automatic feeders







Definition of a carcass EU regulation n°3220/84, modified by regulation n°3513/93)

Dressing percentage

100 * Ratio of carcass to liveweight



Traits of economic interest CARCASS TRAITS

Estimation of carcass composition Through ultrasonic backfat depth







LOIN HAM SHOULDER BELL **LEAF FAT REAR LEG** FRONT LEG



X-ray tomography



The different aspects of meat quality Dietetic qualities

Consumers nutritional requirements

Hygienic qualities Consumer health

Organoleptic qualities Consumers satisfaction

Technological qualities Meat processing





Economic consequences of product quality

no payment for meat quality Some meat defaults can be forbidden

> For slaughterhouses : Weight losses through exudation (1 - 3%)

For distributors : Weight losses through exudation (1 - 3%) Selling difficulties

> For processing units Weight losses at cooking (1 - 10%) Losses when making slides (0 - 50%) Losses when conservation is poor

For consumers:

Weight losses at cooking (1 - 10%)







... measured on different muscles

Technological yields (Napole, cooking or drying %) Fibre characteristics (?)



Fat quality criteria



Firmness Rancid character % water, % lipids Fatty acid composition (polyinsaturated/saturated)

... + organoleptic and dietetic quality

Boar taint (androstenone, skatole)





Intramuscular fat content (% IMF) Shear force



... usually measured on the loin

Tenderness Juiciness Flavour

Consumer panel tests

03 From pig production to pig breeding

Characterisation – use of genetic variability within ... and between breeds



Large White



provided by National Swine Registry

Hampshire



Landrace



Provided by Gregorio Hernandez Silva

Iberian pig



Duroc



Bayeux



Piétrain



provided by Tran Thi Dan Mongcai



Wutsusan



Meishan



Fengjing



JinHua

.026

Using pedigree, phenotypic ... and, more recently, molecular information





















A breeding goal (BG) is characterised by :

The set of traits we want improve or to control
The relative weights of these traits
global genetic value H = a₁ T₁ + a₂ T₂ + ... + a_i T_i

A correct definition of the BG is of major importance

- determines the future of the population
- the breeding structures and tools
 - \checkmark example: including meat quality in the BG
 - move from individual selection to selection on sibs

Definition of a breeding goal Determining trait weights – economic approach

✓ Use of an economic function

$$FE = f(x_1, x_2, ..., x_n, z_1, ..., z_p)$$

x₁,...,x_p = traits related to animal characteristics
z₁,...,z_p = other traits

✓ Weight computation

$$\mathbf{a} = \left(\frac{\partial \mathbf{F}\mathbf{E}}{\partial \mathbf{x}_{\mathbf{i}}}\right) \Delta \mathbf{x}_{\mathbf{i}}$$

using analytic, graphical or finite difference methods



Simple économic fonction : profit/slaughtered pig

Hypotheses: 1) Pig production efficiency ~ Pig producer annual profit PA 2) $PA = \sum_{i=1}^{n} P_i$ The herd profit is the sum of profit/pig P_i





Use of « finite difference » metod

$$a_{LS} = PC_{\mu+\Delta} - PC_{\mu}$$

Strong variations with average LS

→ Needs to be periodically recomputed



Definition of breeding goals

Trait choice

Specialised lines / populations

- ✓ (Grand)sire line BG = Production
- ✓ (Grand)dam lines BG = Production + reproduction

Economic approach

✓ Trait choice based on a . h^2 a = economic weight h^2 : trait heritability Biological approach

 \checkmark Improve the efficiency of biological functions

Ex: lean growth efficiency

Desired gains

Maintaining meat quality or food consumption at a desired level
Selection for an optimum

Selection against environmental variability (canalisation)

Definition of breeding goals Main traits of economic interest

9 8 6 5 3 C ADG (25-100kg) FCR (25-1054) Martality (25-100kg) tetmetig ADG worky Nortality Age of puberty Drudin 1 Pathwaring FCR ₩. ركالما بيبيد وتقاله ADdi Present

heigthe economic volue (C/sd witt)
04 Genetic variability of economically important traits

Variation between breeds Major pig breeds

Landrace



Large White

Piétrain





Duroc



provided by National Swine Registry



Table 10.1. Examples of comparative reproductive performance of some pig breeds.ª

	Large	White				
Trait	Dam line	Sire line	Landrace	Duroc	Piétrain	Reference
Total number born	14.2	_	14.6	9.9	-	DSP, 2008
Total number born	14.8	12.0	13.7	-	10.0	
Number born alive	13.6	11.0	12.5	-	9.3	IFIP, 2009
Number weaned	11.4	9.4	10.8	-	7.8	

*Standard errors of breed means range from 0.03 to 0.1.

Such comparisons are necessary, but should be interpreted with caution (vary according to the environment, time, sampling,...)





CR : conception rate; PS : prenatal survival; LWB, LW21d = litter weight at birth and 21 d of age, respectively; BWSURV : birth to weaning survival; TNB : total number born; NBA : number born alive; NW : number weaned; WOI ; weaning to oestrus interval; OR: ovulation rate

Within breed variation Genetic parameters of production traits

Heritability values for meat quality traits





Within breed variation Genetic parameters

Genetic correlations between production traits

	FCR	Dressing %	Lean%	
ADG	-0,4 à -0,5	-0,3 à -0,2	-0,3 à +0,1	
FCR		-0,2 à +0,1	-0,2 à -0,8	
Dressing %			0,0 à +0,3	

Genetic correlations between sow reproductive traits

Table 10.4. Means of literature estimates of genetic and phenotypic correlations^a among reproductive traits.

	AP	OR	PSR	TNB	FSR	NBA	BWSR	NW	LBW	L21W	ABW
AP		-0.06	-0.08	-0.04	_	0.07	-	0.09	-0.10	-0.15	-
OR	0.05		-0.36	0.32	-0.27	0.24	-0.38	0.01	0.24	0.03	-0.23
PSR	-0.01	0.14		0.50	0.3	0.55	-0.25	0.42	0.30	0.10	-0.41
TNB	-0.03	0.13	0.60		-0.25	0.92	-0.15	0.73	0.62	0.40	-0.41
FSR	-	0.06	-0.15	-0.08		0.01	0.17	-0.01	-0.10	0.05	0.22
NBA	-0.03	0.12	0.40	0.91	0.15		-0.14	0.81	0.64	0.55	-0.34
BWSR	_	-0.11	-0.14	-0.12	0.08	-0.22		0.15	-0.07	0.65	0.15
NW	-0.01	0.03	0.36	0.71	0.47	0.79	0.55		0.67	0.81	-0.23
LBW	-0.03	0.07	0.55	0.79	0.43	0.82	0.09	0.71		0.65	0.43
L21W	-0.04	0.02	0.08	0.42	0.36	0.46	0.65	0.80	0.61		0.60
ABW	-	-0.17	-0.32	-0.40		-0.44		-0.17	0.10	0.07	

^aGenetic correlations above the diagonal, phenotypic correlations below.

AP, age at puberty; OR, ovulation rate; PSR, prenatal survival rate; TNB, total number born; FSR, farrowing survival rate; NBA, number born alive; BWSR, birth to weaning survival rate; NW, number weaned; LBW, litter weight at birth; L21W, 21-day litter weight; ABW, average birth weight.

Bidanel, 2011



Main results of table 10.4

- Age at puberty has low genetic correlations with sow productivity traits
- Ovulation rate, litter size and litter weight have positive genetic correlations
- Litter size and weight have negative, i.e. unfavourable correlations with the numbers and proportions of dead embryos / piglets as well as with average birth weight



Genetic correlations between production and female reproduction traits

	Growth rate	Lean %	Meat quality
Age at puberty	favourable (-0,2)	-0.2 to 0.2	<0 with GP
Litter size	-0,4 à +0,2	0 à -0,3	= 0 with GP
fertility	Low & u	incertain ?	?
Teat number	Indep	?	
longevity	Indep	?	



Genetic correlations between meat quality traits

	Drip loss	Cooking loss	Tenderness
pH 1h post mortem	-0.27	-0.14	0.27
pH 24h post mortem	-0.71	-0.68	0.49
Reflectance	0.49	0.26	-0.16
Water holding capacity	-0.94	-0.25	-0.46
% intramuscular fat	-0.08	0.07	0.15



Genetic correlations between meat quality and production traits

	Average daily gain	Lean%	Fat%
pH 1h post mortem	0	0.10	0.26
pH 24h post mortem	0	-0.13	0.15
Reflectance	0	0.16	-0.21
Water holding capacity	0	-0.19	0.02
% intramuscular fat	0.40	-0.34	0.30

Genetic correlations of production traits with nitrogen (N) and phosphorus (P) excretions

	Daily feed intake	Daily gain	Lean meat content
N excretion	0.55	-0.46	-0.72
P excretion	0.54	-0.50	-0.66

Saintilan et al (2013), J Anim Sci 91, 2542-2554



Normal allele *N* Mutant allele *n*

3 genotypes :



HAL is the Ryanodine Receptor 1 (RYR1) locus (chromosome 6)



Economic interest of heterozygous pigs



The RN gene

RN = acid meat gene

Normal allele *rn*⁺ Mutant allele *RN*⁻

3 genotypes :



RN is the PRKAG3 (Protein kinase AMP-activated gamma 3-subunit) locus (chromosome 15)



*except flavour



Major gene effects

Other major genes identified or suspected

-IGF2

-ESR

-A-FABP, H-FABP

-MC4R



Quantitative trait loci

> 16000 QTL detected <u>PigQTLdb</u> <u>http://w</u>

http://www.animalgenome.org/

2015

Traits	Number of QTL
Drip loss	945
Average backfat thickness	158
Loin muscle area	132
Backfat at last rib	125
Carcass length	122
Average daily gain	82
Cervical vertebra length	80
Backfat at tenth rib	79
Teat number	74
Lean meat percentage	65
Ham weight	64
Intramuscular fat content	63
PH 24 hr post-mortem (loin)	59
PH for Longissmus Dorsi	54
Adipocyte diameter	52

Top 15 QTL/associations

Traits	Number of QTL
Drip loss	1,071
Average daily gain	568
Mean corpuscular volume	344
Average backfat thickness	332
Loin muscle area	322
Intramuscular fat content	244
Red blood cell count	244
Hematocrit	244
Teat number	241
Backfat at last rib	240
Age at puberty	237
Mean corpuscular hemoglobin content	236
Enterotoxigenic E. coli susceptibility	218
Shear force	192
Backfat at tenth rib	190

2017

Quantitative trait loci

1071 QTL detected for drip loss

PigQTLdb

Drip loss QTL



Quantitative trait loci

139 QTL detected for litter size

Total Number born





Figure 1.1 A. Distribution of additive (QTL) effects from pig experiments, scaled by the standard deviation of the relevant trait, and distribution of gene substitution (QTL) effects from dairy experiments scaled by the standard deviation of the relevant trait. B. Gamma Distribution of QTL effect from pig and dairy experiments, fitted with maximum likelihood.

Master ANIMAL BREEDING AND REPRODUCTION BIOTECHNOLOGY

Genetic improvement of pigs – Part 2

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 - Example of the French breeding scheme
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- High reproductive efficiency
 - Large number of offspring / female

CattlePigs4.8 offspring /cow4.6 litters/sow4.8 * 0.5 * 0.84.6 * 0.5 * 10≈ 1.9 daughters /dam≈ 23 daughters /dam

- Generalised use of crossbreeding
- Development of Al
 - Essentially fresh semen
 - Frozen semen : recent improvements



- Favourable aspects
- Short generation interval
- Traits (growth carcass) that are :
 - heritable
 - Measured early in life
 - Measure on all candidates from both sexes
- Homogeneity of breeding /management conditions
 - (conventional breeding)
- Homogeneity of slaughter pigs
 - (90- 115 kg live weight)



- Constraints
- Sanitary constraints
 - « Vertical » diffusion of breeding pigs : one single provider
 - No breeding pig in testing station
- Diversity of final products
 - Fresh meat
 - Processed products
 - Dry / cooked ham
 - Sausages
 - Processed dishes



Impact of pig biological characteristics on pig improvement schemes

- Constraints (2/2)
- Fast and decentralised breeding decisions
 - Fast information flow required
- Some traits are more difficult to select
 - Reproduction traits : late and sex-limited expression
 - Meat quality : measured after slaughter
- Development of AI, BLUP (and GS ?)
 - Adverse effects on genetic variability

05 Optimisation of breeding schemes



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1) Genetic factors



- 2) <u>Economic factors</u>
 - Selection costs
 - Max(DG) for a given testing capacity
- 3) Technical factors
 - Phenotype measurement
 - Information processing

Interest of Nucleus herds in pigs

(Smith, 1959, Anim Prod, 1, 113-121)

Hypothesis: N=5000 tested candidates, T = 1000 breeding pigs necessary

	Open system	Nucleus	
Selected pigs	1000	20 (50 offspring each)	_
N/T DG	5 1,36 h² s _P	250 2,70 h ² s _P	
Generation 0	0	0	-
1	<mark>0,68 h²</mark> Ծթ	0	Nucleus creation
2	1,36 հ² Ծ _P	0	Selection
3	2,04 հ ² Ծթ	1,35 h² σ _P	Multiplication
4	2,72 հ² Ծթ	2,70 հ² σ _P	
5	3,40 h ² σ _P	4,05 h ² σ _P	



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Optimisation of a breeding scheme - Genetic factors -Effect of population size on the efficiency of selection : the case of a maternal line (de Vries et al, 1989)





Selection with BLUP - AM

Allows non contemporary animals to be compared

Theoretically, rules for age at culling are not necessary, as candidates can be directly compared to older animals

 \Rightarrow Sows can be selected sequentially, which to an extra genetic gain of 3 - 4 %)

 \Rightarrow Sequential selection of boars also possible, but may lead to an over-use the best boars

=> Optimum values established with standard selection theory remain close to optimum

Optimisation of a breeding scheme - Technical factors -

Integration of meat quality in the breeding goal

Goal : avoid any deterioration of MQ

• Pb : MQ cannot be measured on the live animal

• Can this goal be reached by acting on the weights of production traits (PT) included in the selection objective

• No, as MQ is unfavourably related to PT, a deterioration of MQ is obtained whatever the weights of PT

=> MQ has to be included as a selection criterion

•MQ cannot be measured on living pigs

=> Moving from individual testing to combined testing
06 Use of crossbreeding



- 1 Exploiting heterosis effects
- 2 Taking profit of complementarity effect
- 3 Using breed additive differences
- 4 Increasing genetic variability
- 5 Using major genes



Heterosis

 For a given trait, mean deviation between F1 performance and the average of parental breeds





Deviation between F1 mean performance (AB+BA)/2 and Purebred mean performance (A+B)/2 Deviation between the mean performance of pigs from F1 sows [C(AB)+C(BA)]/2 and that of pigs from purebred sows (CA+CB)/2

Mean heterosis values for some traits of economic interest in pigs

Trait	Heterosis				
	Direct	Maternal			
Age at 1 st oestrus (d)	-12 (6%)	0			
Total piglets born/litter	+0,25 (2%)	+0,66 (6%)			
Weaned/litter	+0,49 (4%)	+0,84 (8%)			
Piglet weaning weight (kg)	+0,5 (5%)	0,23 (2%)			
Average daily gain (g/d)	+37 (6%)	0			
Feed conversion ratio	-0,11 (4%)	0			
Body composition	0	0			
Meat quality	0	0			



ne complementarity effect

• Definition

 Complementary aptitudes that are present either in one breed or in the other, but can hardly be present in a single breed

Χ

• Example

Sire breed with a high muscular Growth potential Dam breed with good Reproduction and maternal abilities Use of the complementarity effect in pigs

• Related to the expression of profit : $P = FM - SC/P_N$

	Breed A	Breed B
Sow annual cost (€)	700	700
« Production » margin	77	70
Numerical productivity	20	25
Profit/pig	77-(700/20)	70-(700/25)
	= 42	= 42

- A x B cross : P = 73,5 (700/25) = 45,5
- Gain due to the use of specialised lines = 3,5 €

• = COMPLEMENTARITY

Using additive differences between breeds

- Absorption cross
 - Replacement of one population by another one with higher performances
 - Example: quasi-absorption of French Piétrain population by the German one
- Improvement cross
 - Limited introgression of genes from a higher performing breed
 - Example : introduction of English Large White (LW) in French LW during the 70's



Genotype	NN	Ns	SS
Viability	++	++	
Muscle content	0	+	++
Meat quality	++	+(+)	
Prolificacy	0	0	0
Feed conversion ratio	0	0	0

• Heterozygote pigs are the most interesting ones



Paternal genotype with a high frequency of s allele

Х

Maternel genotype free of the s allele



Classical selection for production traits



Selection for production and reproduction Elimination of the s allele

.024



.025



Allows to take profit of direct heterosis on :

Growth rate	+37g	+0,80 €
Feed conversion ratio	-0,11	+1,40 €
Litter size at weaning	+0,5	+1,25 €
Total		+3,45 €

- + Use of Hal gene
- + Use of complementarity effect
- Maternal heterosis effects cannot be exploited

Comparative	e interest of cross 3-way cross	breeding p	lans
× W			
* *	• Use of direct hete	erosis effects :	
	Growth rate	+0,80 €	
	FCR	-0,11	+1,40 €
	LS at weaning	+0,5	+1,25 €
	 Use of maternal h 	eterosis effects	5
	LS at weaning	+0,84	+2,10€
	Sexual maturity	-12	+0,10 €
	TOTAL		+5,65 €
 + Use of Hal gene 			
• + Use of compleme	entarity +	3,50€	



- No use of Hal gene
- No use of complementarity

Comparative interest of crossbreeding plans

4-way cross



• Use of direct heterosis effects :

Growth rate	+37g	+0,80€
FCR	-0,11	+1,40 €
LS at weaning	+0,5	+1,25€
Use of materna	l heterosis e	effects
LS at weaning	+0,84	+2,10€
Sexual maturity	-12	+0,10 €
TOTAL		+5,65€
	+3 50 £	

- + (Partial) use of Hal gene
- + Use of complementarity
- + Heterosis on (young) boar characteristics



Same advantages as a 4-way cross (but a longer time is necessary for improved genes to reach the commercial level

Main advantage : it is easier to keep the property of purebred animals

Selection and crossbreeding

- 1 effects of selection on between-breed variability
 - Is crossbred performance the same as purebred performance ?
 - Effects of selection on heterosis
- 2 Specialisation of selection goals
- 3 Selection for crossbred performance
 - Recurrent selection
 - Combined purebred crossbred performance (CCPS)
 - Interest of genetic markers



h2 estimates at different stages of a crossbreeding scheme

h2	LR	LW	DU	F1	PT
ADG	0,21	0,23	0,20	0,31	0,33
BFT	0,52	0,46	0,36	0,26	0,39

Genetic correlations between ADG and BFT at different stages







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EBV computed from both Purebred and crossbred information



Requires good pedigree information at the commercial level

Figure 2 Relative merits of three different methods of selection assuming fixed total progeny for all methods. Crossbred responses from (a) PLS and (b) CS are given as a percentage of response from CCPS. Results are plotted as a function of h_c^2 for r_{ac} values of 1.0, 0.7, 0.5 and 0.3.

08 Controlling the efficiency of pig breeding schemes



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.036

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Checking the efficiency of breeding schemes Control of « terminal products »

- Sample of slaughter pigs from different breeding organisations compared in an official test station
- Results officially published by the ministry of Agriculture



Carcass index; 10 points = 3.08 euros

Growth index; 10 points = 2.30 euros



Meat quality index; 10 points = 1.16 euros



Ex: 24rd TP test



Checking the efficiency of breeding schemes Use of frozen semen

SMITH, 1976 : use of frozen semen



1978 : stock of frozen semen of 1977 LW boars

1999 : INRA, ITP & French Ministry of Agriculture reproduction, production, quality



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Checking the efficiency of breeding schemes Use of frozen semen



Experimental design

Reproduction traits

production traits

meat and fat quality

Estimation of genetic trends using frozen semen results

Carcass leanness

	Mean perf.	σ_{ph}	∆G	P-value for H0 ∆G=0
ham weight (kg)	9.7	0.50	+0.56	0.0053
loin weight (kg)	10.5	0.68	+0.85	0.0043
loin eye thickness (mm)	52.1	5.4	+5.97	0.0054
carcass lean content (kg/100kg)	55.7	3.5	+8.60	<0.0001

09 Use of genomic information



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Use of genomic information in pig breeding schemes

First utilisations

Parentage control

> Control / production of given genotypes for major genes

Genotype / marker assisted introgression

- Genotype / marker assisted selection (MAS)
- Characterisation / management of genetic variability

>individual / breed Traceability



Marker Assisted Selection (MAS) in pigs

Apart from major genes (Hal, RN, IGF2,...), limited use... and limited efficiency of first generation MAS (with microsatellites) in pigs. Why ?

- Most QTL mapped in experimental populations between divergent populations (LW x MS, LW x wild boar, ...) : => QTL explain breed differences; they are not necessarily segregating within commercial populations
- 2. Most QTL were mapped with a low accuracy
- First generation MAS used within-family LD => uneasy to use,
 limited gains in pigs
- 4. Few QTL were common between studies => validation required

Genomic selection : General Principle

With low density marker panels (100-200/genome)

Linkage equilibrium



The QTL genotype can be inferred from Marker information only within-family

With high density marker panels (at least 10³ or 10⁴ markers)

Full disequilibrium



The QTL genotye can be inferred from marker information at the population level

Genomic selection : General Principle

<u>Step 1</u> :

Phenotype and genotype individuals for several thousand SNP = reference population => estimate the effect of each chromosomal fragment

Step 2 : **genotype** candidates and compute a genomic EBV from genomic information and segment effects

Or

Single step : genomic information is used to modify the relationhip matrix

Benefits from genomic selection ?

• A higher genetic trend ?



- increase selection intensity ?
- increase accuracy of EBV ?
- reduce generation interval ?
- Decreasing selection costs? NO

increase accuracy of EBV ?

Average CD (correlation(EBV,BV)²) with BLUP-AM evaluation

	Age100	BF100	ADG	FCR	DFI	KO%	LEAN%	MQI	Teats	NBA
Active AI boar	0.68	0.73	0.34	0.37	0.28	0.24	0.51	0.23	0.65	0.26
Active on-farm boar	0.63	0.69	0.29	0.32	0.22	0.18	0.46	0.17	0.59	0.25
Active sow	0.58	0.66	0.28	0.32	0.22	0.18	0.44	0.18	0.54	0.36
Piglet at birth	0.31	0.34	0.15	0.17	0.12	0.10	0.23	0.10	0.29	0.16
Young candidates (end of test)	0.52	0.60	0.23	0.27	0.17	0.13	0.39	0.13	0.48	0.16

Gain in accuracy of young animals' EBV



From Hendrix Genetics

.049

Genomic selection in pigs

Genomic selection in a sire line : a simulation study

Sire pig population :

- ~1000 sows (5 herds). 50 boars
- 7 reproduction batches; overlapping generations
- Sire line selected for a combination of 2 production traits :

VGEglob = 1*VGEcar1 + 1*VGEcar2

Reference scenario : AM - BLUP

- car 1 : measured on of & Q candidates (many records)
- car 2 : measured on a limited number of sibs (few records)

Alternative scenarios: Genomic evaluations

- Genotyped ♂ & ♀ candidates
 - ightarrow estimated genomic value

2 scenarios for reference populations

Tribout et al (2012; 2013)
Genomic selection in a sire line : a simulation study



<u>Genome</u> :

• 10 pairs of chromosomes of 1M length (genome = 10 M)

each chromosome carries 1500 SNP (MAF > 0.05)

mean distance between 2 SNP = 67 Kb

minimum distance between 2 SNP = 28 Kb

each chromosome carries

- 10, 30 or 60 QTL for trait 1

- 10, 30 or 60 QTL for trait 2

the 2 traits are genetically independent at the beginning

Tribout et al (2012; 2013)

Genomic selection in a sire line : a simulation study



Response to selection



Tribout et al (2012; 2013)

Genomic selection in a sire line : a simulation study



Inbreeding



Tribout et al (2012; 2013)

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Genomic selection in a sire line : a simulation study



Tribout et al (2012; 2013)

New goals / criteria that are difficult to measure

- Feed intake, manure production
- Behaviour
- Health
- 🗧
- → Major interest for the selection of such traits
- But their economic interest and their genetic architecture has to be known before integrating them in selection schemes



Other potential interest of genomic selection :

Select populations for crossbreeding

<u>Current principle</u>: « Improving purebred performances also increases performances in crossbreeding »

BUT : Performance at the selection level ≠ performance at the commercial level (rg [0,4 à 0,9])

► Genetic trend commercial level ≤ Genetic trend selection level

<u>Hypothesis</u> :

- 1. Reference population of crossbred pigs »
 - phenotyping and genotyping with SNP microarray
 - estimation of chromosomal fragment effects on phenotypes
- 2. Genotyping purebred candidates
 - Computing EBV from the crossbred reference population
 - NO NEED TO COLLECT PEDIGREE INFORMATION

Higher genetic trend at the commercial level

 h^2 purebred performance (PP) = h^2 crossbred performance (CP) = 0,4 Genetic correlation (PP, CP) = 0,7



From Dekkers, 2007

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Genomic selection : impact on inbreeding



Single step genomic BLUP



y = Xb + Wu + e

$$Var(u) = H \otimes G_0$$
 $Var(e) = I \otimes R_0$

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}W \\ W'R^{-1}X & W'R^{-1}W + H^{-1} \otimes G_0 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ W'R^{-1}y \end{bmatrix}$$

H genomic relationship matrix

See e.g. Legarra et al., 2014, Livest. Sci. 166:54-65

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14-15/03/2017

Use of Single step genomic BLUP In French Landrace breed



Bouquet et al., 2017, J. Rech. Porc 49: 31-36

07 Example of the French breeding scheme



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Selection : pure breeds and lines



(Source : IFIP - Le porc par les chiffres



Commercial level : crossbred slaughter pigs

Most frequent crossbreeding system in France



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The French national pig breeding scheme Breeding goal (2010 – 2014)

Large White – dam line









D% 19%

11%

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French national pig breeding scheme

on-farm performance test

production traits Young male and female candidates

- age at 100 Kg



- backfat thickness at 100 Kg
- Loin depth (male lines)
- (Meat quality)

« reproduction » traits

- numbers of live born piglets
- number of functional teats

station performance test

slaughtered sibs from young candidate males



- average daily gain
- daily feed intake
- feed conversion ratio



- dressing percentage
- carcass lean content
- meat quality index





e French national pig breeding scheme

Genetic evaluation

- Based on animal model BLUP (until 2016) Single step genomic selection since 2016
- Evaluation performed independently in each population
- Joint evaluation for production and reproduction traits
- Evaluation performed every week
- Performed by IFIP (French Pig Institute)

National genetic evaluation of pigs Combined EBVs

EBVs for each trait are combined as follows :



National genetic evaluation of pigs Results sent to breeders

after each evaluation :

Growth, carcass and reproduction EBVs + accuracies

- of all boars and sows of the herd
- of all AI boars
- of young males and females tested on farm
- every six months :

Estimated genetic trends (per breed, herd, sex) Estimated breeding values of pigs sent to multiplication herds

Elements on Connectedness, management of genetic variability