The Potential of Genomic Selection to Improve Litter Size in Pig Breeding Programs

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- Conventional marker assisted selection was (with some exceptions) moderately unsuccessful in pig breeding
- The concept of genomic selection appears promising and is successfully implemented in dairy cattle (and chicken) breeding
- In dairy cattle genomic selection works through reduced breeding costs and shortened generation intervals on the paternal paths (Schaeffer, 2006)
- In pig breeding the major potential for genomic selection presumably is through higher accuracy of genomic breeding values and increased selection intensities

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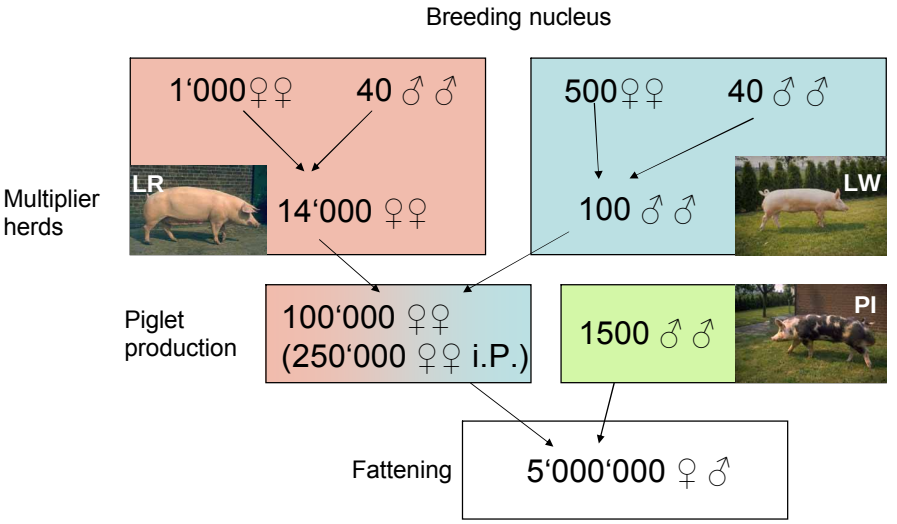
A model breeding program



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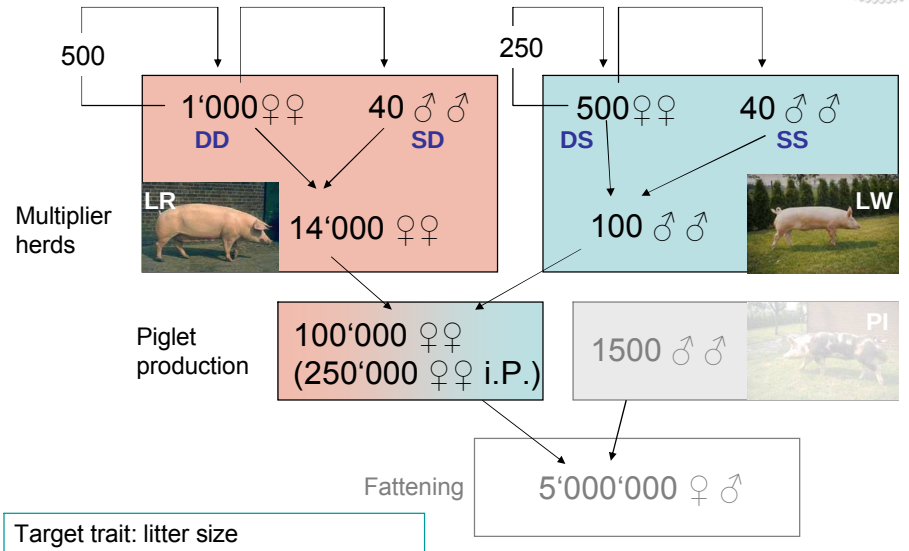
A model breeding program



Target trait: litter size
(number of piglets born alive, h^2 =0.1)

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Conventional breeding scheme

Group	tested	selected	i	r_{AI}	i × r_{AI}	ΔT
DD (LR)	1000	500	.798	0.4	.319	1.42
SD (LR)	1000	40	2.154	0.35	.754	1.17
DS (LW)	500	250	.798	0.4	.319	1.42
SS (LW)	500	40	1.858	0.35	.650	1.17
				Sum	2.042	5.18

$$\Delta G/a = \frac{(i \times r_{AI})_{DD} + (i \times r_{AI})_{SD} + (i \times r_{AI})_{DS} + (i \times r_{AI})_{SS}}{\Delta T_{DD} + \Delta T_{SD} + \Delta T_{DS} + \Delta T_{SS}} \times \sigma_A$$

$$\Delta G/a = \frac{2.042}{5.18} \times 0.71 = 0.280$$

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Accuracy of genomic breeding values

(Daetwyler et al., 2008)

h^2 of the trait
(r^2 when using EBVs/DYDs)

Size of the callibration set N

Effective number of segregating QTL k

$$r_{AI} = \sqrt{\frac{Nh^2}{Nh^2 + k}}$$

N = 1000 boars with
n = 40 daughters
r^2 = 0.506
k = 1000

$$r_{AI} = \sqrt{\frac{1000 \times 0.506}{1000 \times 0.506 + 1000}} = .58$$

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Conventional

Group	tested	selected	i	r_{AI}	i × r_{AI}	ΔT
DD (LR)	1000	500	.798	0.4	.319	1.42
SD (LR)	1000	40	2.154	0.35	.754	1.17
DS (LW)	500	250	.798	0.4	.319	1.42
SS (LW)	500	40	1.858	0.35	.650	1.17
				Sum	2.042	5.18

$$\Delta G / a = \frac{2.042}{5.18} \times 0.71 = 0.280$$

Genomic

Group	tested	selected	i	r_{AI}	i × r_{AI}	ΔT
DD (LR)	1000	500	.798	0.4	.319	1.42
SD (LR)	500 (g)	40	1.858	0.58	1.078	1.17
DS (LW)	500	250	.798	0.4	.319	1.42
SS (LW)	500 (g)	40	1.858	0.58	1.078	1.17
				Sum	2.794	5.18

$$\Delta G / a = \frac{2.794}{5.18} \times 0.71 = 0.383$$

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Economic assessment

Returns

conventional	genomic	
+ 0.280	+ 0.383	piglets born alive per litter
x 2.1	x 2.1	litters per year in piglet production
x 250‘000	x 250‘000	sows in piglet production
x 25 €	x 25 €	marginal benefit per additional piglet in a litter
= 3‘675‘000 €	= 5‘027‘000 €	economic benefit per year

+36.7%

Genotyping costs

1000 x 150 € = 150‘000 € calibration
1000 x 150 € = 150‘000 € selection candidates

Calibration costs are depreciated over 3 years

Return on Investment

Extra return:	5‘027‘000 € - 3‘675‘000 €	= 1‘352‘000 €
Extra cost:	150‘000 € + 0.33 x (150‘000 €)	= 200‘000 €

1‘352‘000 €/200‘000 € = 6.76 Extra return for each Euro invested in genomic selection

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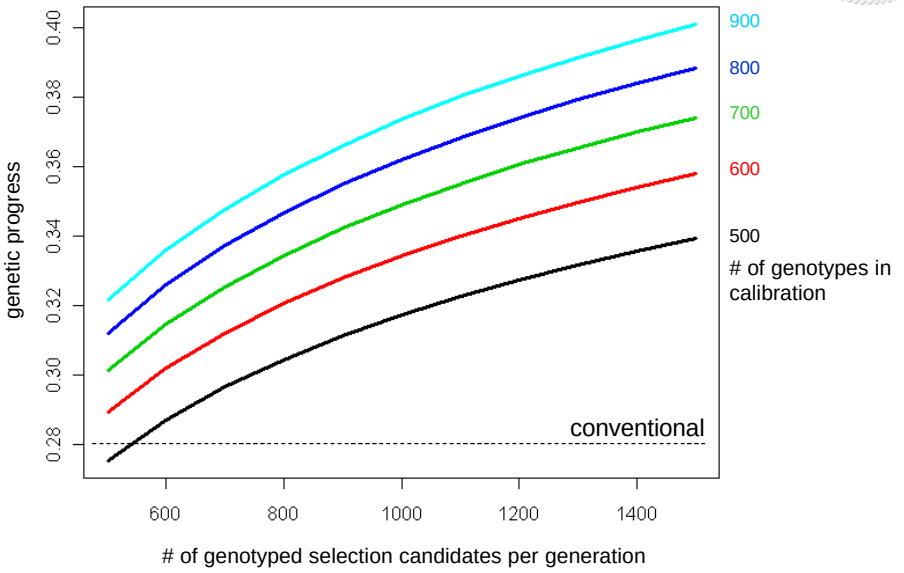
Genetic progress as function of the number of genotypings in calibration and selection



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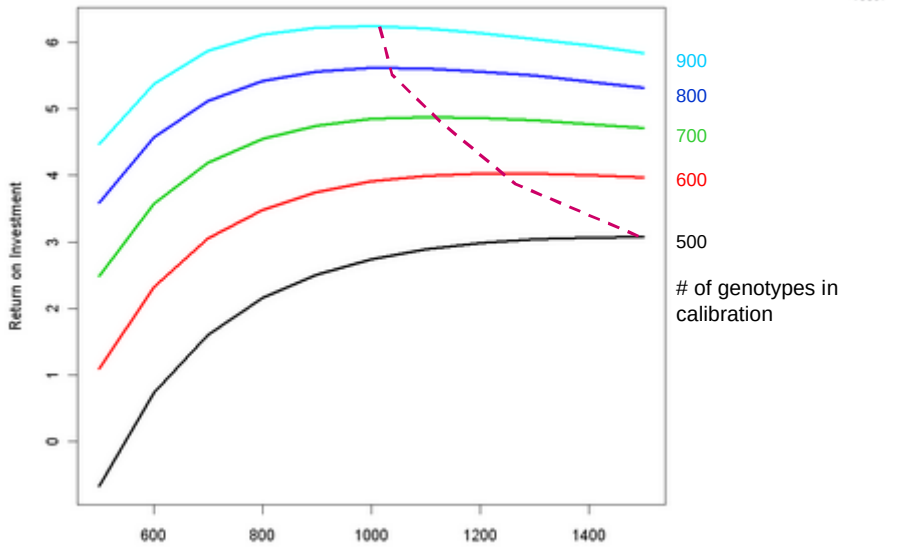
Return on investment as function of the number of genotypings in calibration and selection



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Factors determining the efficiency of genomic selection in pig breeding programs

1. Costs of genotyping vs. value of trait/value of a breeding animal
   - High initial investment (calibration study) and running costs
   - Genotyping costs ↘ or marker density ↗
   - SNP selection, low-density-chip

2. Size of breeding nucleus vs. production population
   - Size and number of purebred populations and number of mutiplier levels
   - Biological limits, inbreeding, time lag

3. Accuracy of genomic breeding values
   - theoretical expectation needs to be assessed with real data
   - relative increase of accuracy higher for low heritability traits
   - availability of DNA samples of enough progeny tested boars with EBVs/DYDs for all relevant traits
   - Combination of genomic and pedigree information

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