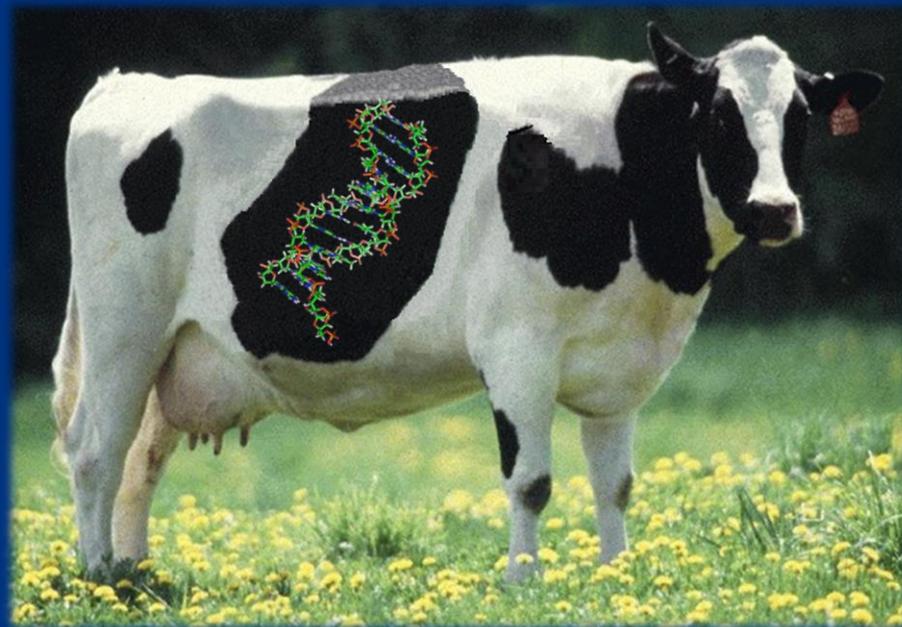


Current status of genomic evaluation for U.S. dairy cattle



See: <http://aipl.arsusda.gov/publish/present.htm>

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ORIGINAL ARTICLE

Strategy for applying genome-wide selection in dairy cattle

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Summary

Animals can be genotyped for thousands of single nucleotide polymorphisms (SNPs) at one time, where the SNPs are located at roughly 1-cM intervals throughout the genome. For each contiguous pair of SNPs there are four possible haplotypes that could be inherited from the sire. The effects of each interval on a trait can be estimated for all intervals simultaneously in a model where interval effects are random factors. Given the estimated effects of each haplotype for every interval in the genome, and given an animal's genotype, a 'genomic' estimated breeding value is obtained by summing the estimated effects for that genotype. The accuracy of that estimator of breeding values is around 80%. Because the genomic estimated breeding values can be calculated at birth, and because it has a high accuracy, a strategy that utilizes these advantages was compared with a traditional progeny testing strategy under a typical Canadian-like dairy cattle situation. Costs of proving bulls were reduced by 92% and genetic change was increased by a factor of 2. Genome-wide selection may become a popular tool for genetic improvement in livestock.

Table 1 Schedule of progeny testing activities

Time (months)	Activity
0	Elite dams chosen and bred.
9	Bull calves born from elite dams
21	Test matings of young bulls made
30	Daughters of young bulls born
45	Daughters of young bulls bred
54	Daughters calve and begin first lactation
57	First estimated breeding values for young bulls from test day model
64	Daughters complete first lactations, keep or cull young bulls

Table 2 Four pathways of selection, progeny testing

Pathway	Selection %	Accuracy		Generation	
		i	r_{TI}	Interval, L	$i \times r_{TI}$
Sire of bulls	5	2.06	0.99	6.5	2.04
Sire of cows	20	1.40	0.75	6	1.05
Dams of bulls	2	2.42	0.60	5	1.45
Dams of cows	85	0.27	0.50	4.25	0.14
Total				21.75	4.68

Table 3 Four pathways of selection, genome-wide strategy

Pathway	Selection %	Accuracy		Generation	
		i	r_{TI}	Interval, L	$i \times r_{TI}$
Sire of bulls	5	2.06	0.75	1.75	1.54
Sire of cows	20	1.40	0.75	1.75	1.05
Dams of bulls	2	2.42	0.75	2	1.82
Dams of cows	85	0.27	0.50	4.25	0.14
Total				9.75	4.55

Economic evaluation of genomic breeding programs

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ABSTRACT

The objective of this study was to compare a conventional dairy cattle breeding program characterized by a progeny testing scheme with different scenarios of genomic breeding programs. The ultimate economic evaluation criterion was discounted profit reflecting discounted returns minus discounted costs per cow in a balanced breeding goal of production and functionality. A deterministic approach mainly based on the gene flow method and selection index calculations was used to model a conventional progeny testing program and different scenarios of genomic breeding programs. As a novel idea, the modeling of the genomic breeding program accounted for the proportion of farmers waiting for daughter records of genotyped young bulls before using them for artificial insemination. Technical and biological coefficients for modeling were chosen to correspond to a German breeding organization. The conventional breeding program for 50 test bulls per year within a population of 100,000 cows served as a base scenario. Scenarios of genomic breeding programs considered the variation of costs for genotyping, selection intensity of cow sires, proportion of farmers waiting for daughter records of genotyped young bulls, and different accuracies of genomic indices for bulls and

cows. Given that the accuracies of genomic indices are greater than 0.70, a distinct economic advantage was found for all scenarios of genomic breeding programs up to factor 2.59, mainly due to the reduction in generation intervals. Costs for genotyping were negligible when focusing on a population-wide perspective and considering additional costs for herdbook registration, milk recording, or keeping of bulls, especially if there is no need for yearly recalculation of effects of single nucleotide polymorphisms. Genomic breeding programs generated a higher discounted profit than a conventional progeny testing program for all scenarios where at least 20% of the inseminations were done by genotyped young bulls without daughter records. Evaluation of levels of annual genetic gain for individual traits revealed the same potential for low heritable traits ($h^2 = 0.05$) compared with moderate heritable traits ($h^2 = 0.30$), preconditioning highly accurate genomic indices of 0.90. The final economic success of genomic breeding programs strongly depends on the complete abdication of any forms of progeny testing to reduce costs and generation intervals, but such a strategy implies the willingness of the participating milk producers.

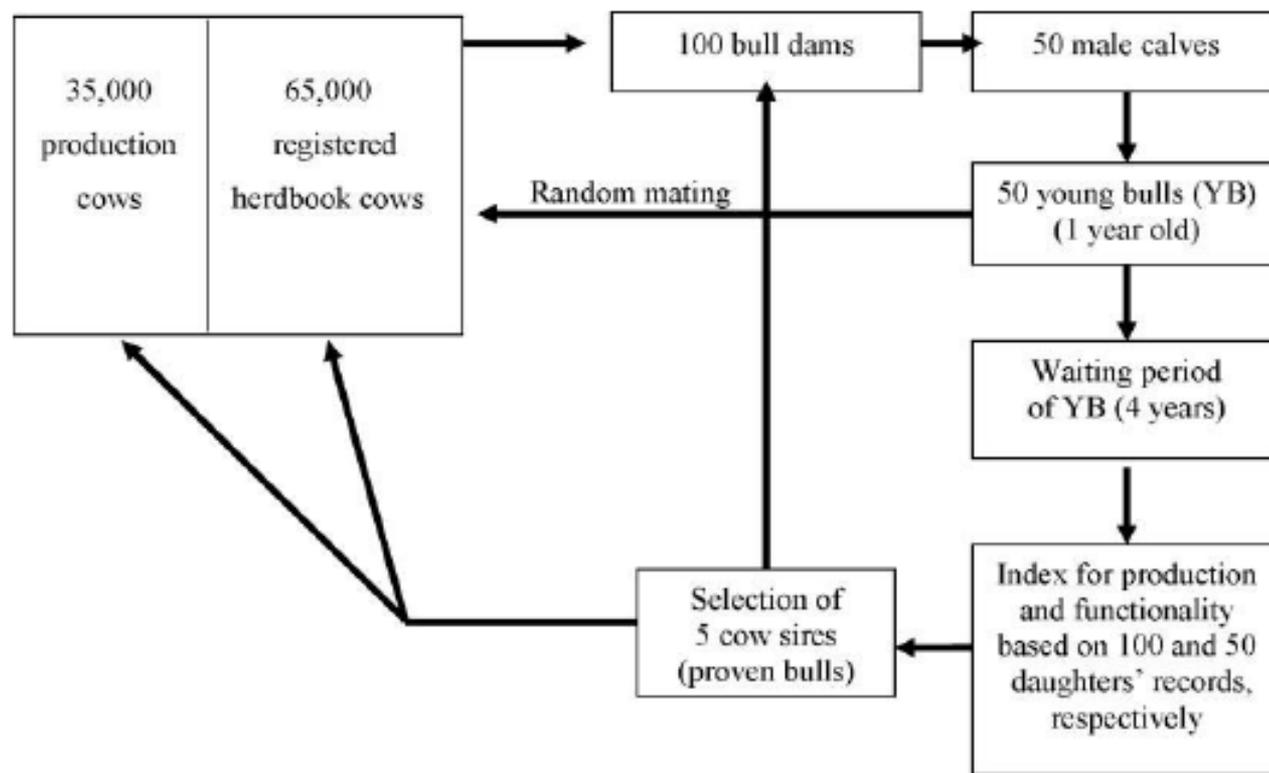


Figure 1. Conventional progeny testing program (CPTP) for the final selection of 5 cow sires per year.

Table 1. Gene flow matrix for conventional progeny testing program (CPTP); arrows indicate the gene flow

Item	Selection group		
	Proven bulls (PB)	Herdbook cows (HC)	Production cows (PC)
PB	1. PB ¹ → PB	2. HC ² → PB	—
HC	3. YB ³ → HC	5. HC ⁴ → HC	—
PC	4. PB ¹ → HC	—	7. PC → PC
	6. PB → PC		

¹PB = proven bulls used as bull and dam sires.

²HC = herdbook cows used as bull dams.

³YB = young bulls used as cow sires.

⁴HC = herdbook cows used as cow dams.

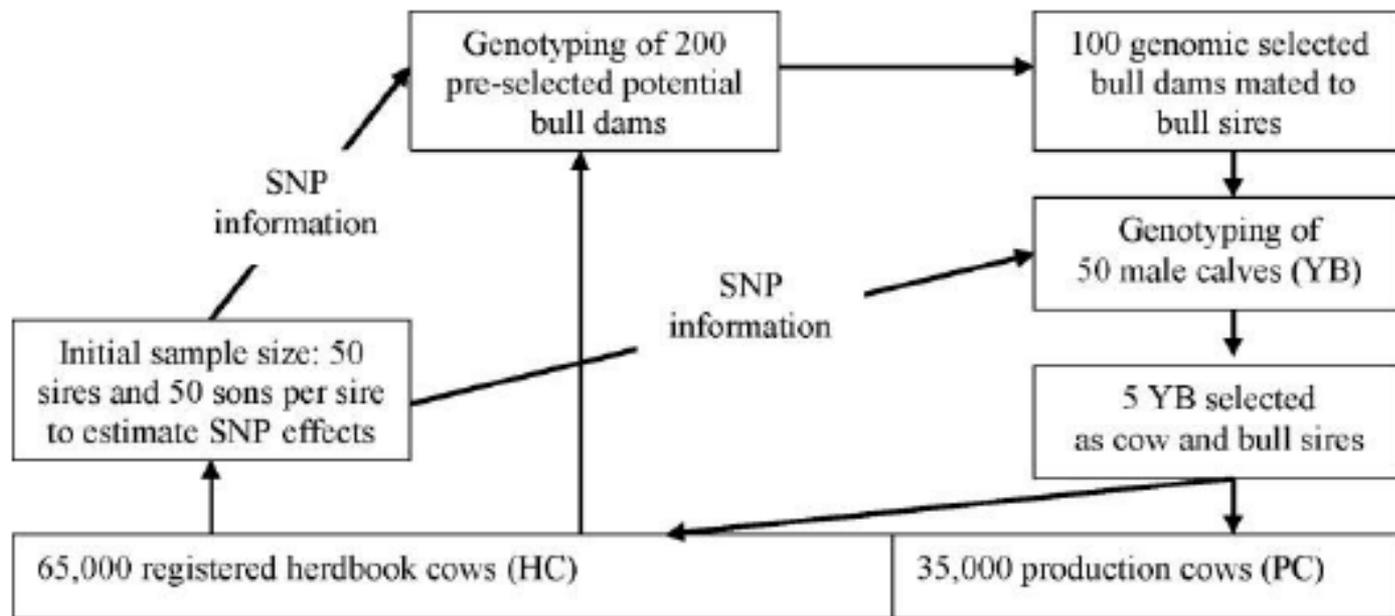


Figure 2. Possible genomic breeding program (GBP) for the final selection of 5 cow sires per year.

Table 2. Gene flow matrix for genomic breeding program (GBP); arrows indicate the gene flow

Item	Selection groups		
	Young bulls (YB)	Herdbook cows (HC)	Production cows (PC)
YB	1. YB ¹ → YB	2. HC ² → YB	—
HC	3. YB ¹ → HC 4. YB-D ⁴ → HC	5. HC ³ → HC	—
PC	6. YB → PC 7. YB-D → PC	—	8. PC → PC

¹YB = genotyped young bulls without daughter records used as cow or bull sires, or both.

²HC = herdbook cows used as bull dams.

³HC = herdbook cows used as cow dams.

⁴YB-D = genotyped young bulls with daughter records used as cow sires.

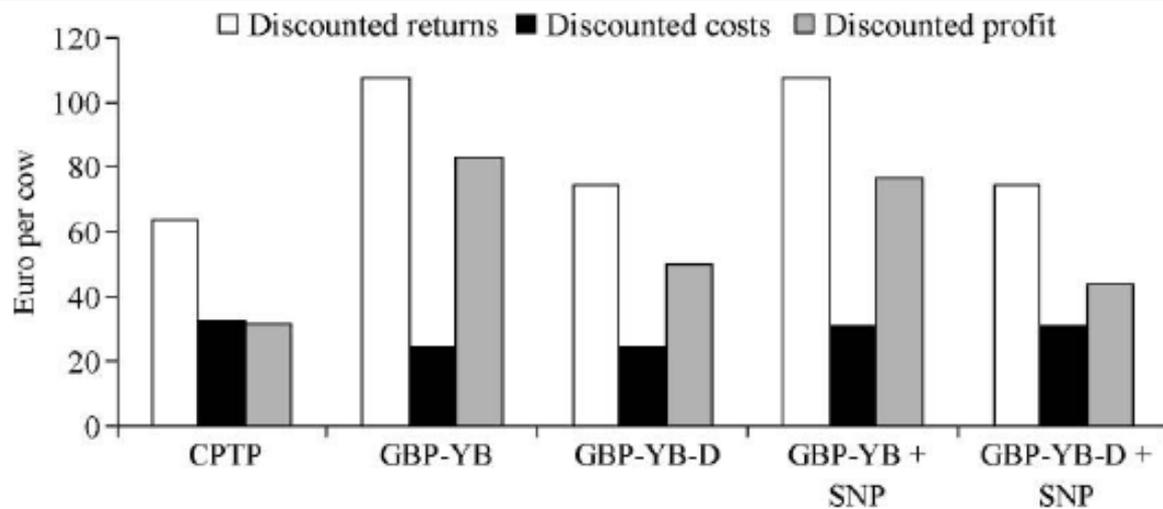


Figure 3. Discounted returns, costs, and profit for a conventional progeny testing program (CPTP) and 4 different scenarios of a genomic breeding program (GBP-YB = 100% of inseminations are done by genotyped young bulls without records; GBP-YB-D = 50% of inseminations are done by young bulls with daughter records; SNP = estimation of SNP effects in the initial sample size of 2,500 bulls).

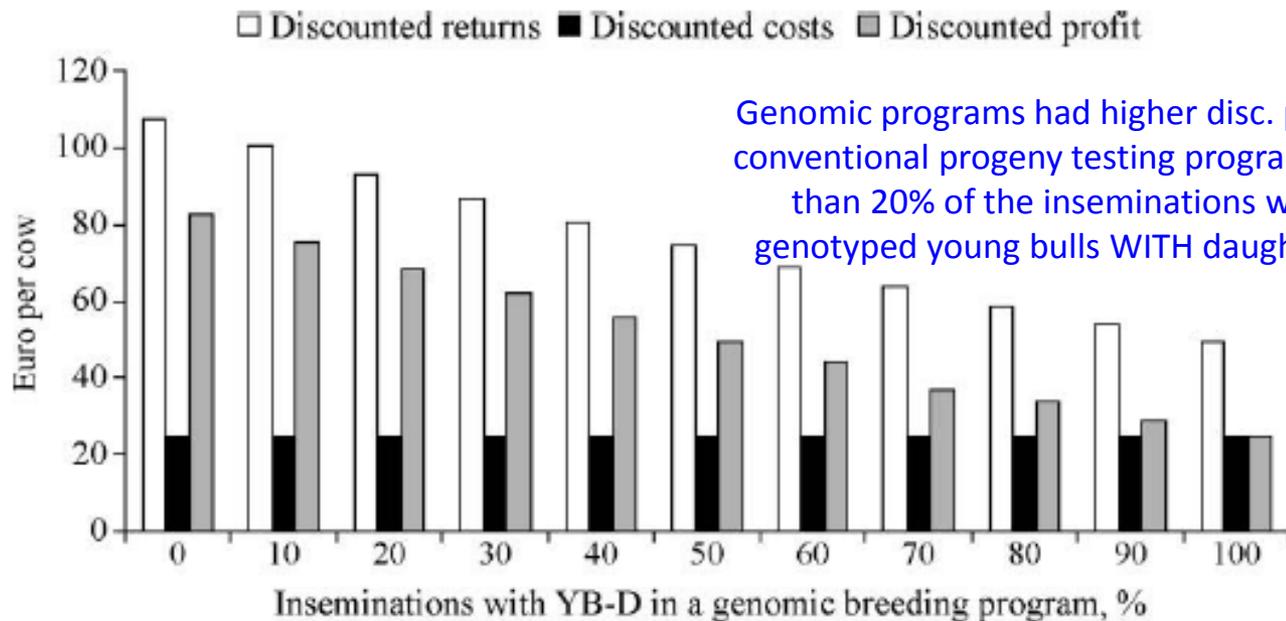


Figure 4. Discounted returns, costs, and profit for a genomic breeding program (GBP-YB) when different percentages of cows in the population are inseminated with genotyped young bulls having daughter records (YB-D).



Optimal strategies for the use of genomic selection in dairy cattle breeding programs

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ABSTRACT

The objective of the present study was to conduct a stochastic simulation study on the possible benefits of an application of genomic selection in dairy cattle breeding programs according to a variety of selection schemes. In addition, the heritability of the trait in question, the accuracy of genomic breeding values, and the number of animals to be genotyped were varied. Specifically, the question of genotyping males, females, or both, was addressed. Selection schemes were compared with a young bull breeding program. The main criterion for comparison was the average of true breeding values of selected young males to be used as replacements for artificial insemination bulls. Stochastic simulations were run with 50 repetitions each to generate individuals with phenotypes, breeding values estimated by BLUP, and true breeding values. Genomic breeding values were generated from true breeding values with defined accuracy. Examined scenarios included a group of selection schemes that featured genotyping of parents of future bulls only.

Such schemes can be viewed as improvements of young bull programs, and they were found to be competitive with or superior to a classical young bull program. However, a genomic breeding program usually involves at least genotyping young male candidates. A second group of selection schemes reflected this requirement. Scenarios in this group were found to be superior over the young bull program by 1.0 to 1.2 standard deviations of the average true breeding value of young male candidates. Within this group of scenarios, one scheme referred to an ideal situation under which genotypes for male calves were available without limitation. Using the average of true breeding values as the criterion for comparison, this idealistic scenario was competitive with other scenarios only if the reliability of genomic breeding values was larger than 0.50. Conventionally not all males available will have genotypes, and the 2 most promising scenarios included a preselection step for dams of future bulls. This preselection step can be based on conventional BLUP estimated breeding values for bull dams, because differences with a scheme under which both parents and the resulting male offspring are genotyped were marginal. Genotyping of young male candidates should be the focus of activities of today's breeding organizations.

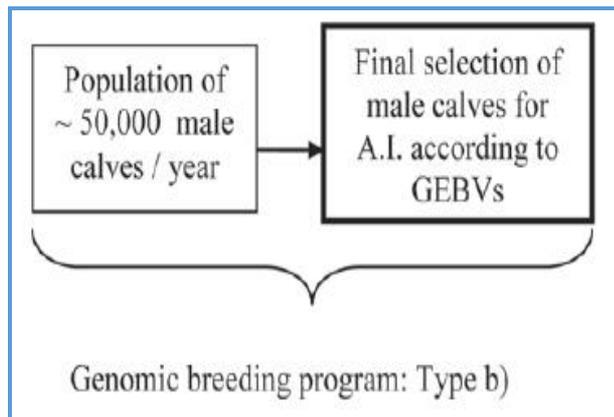
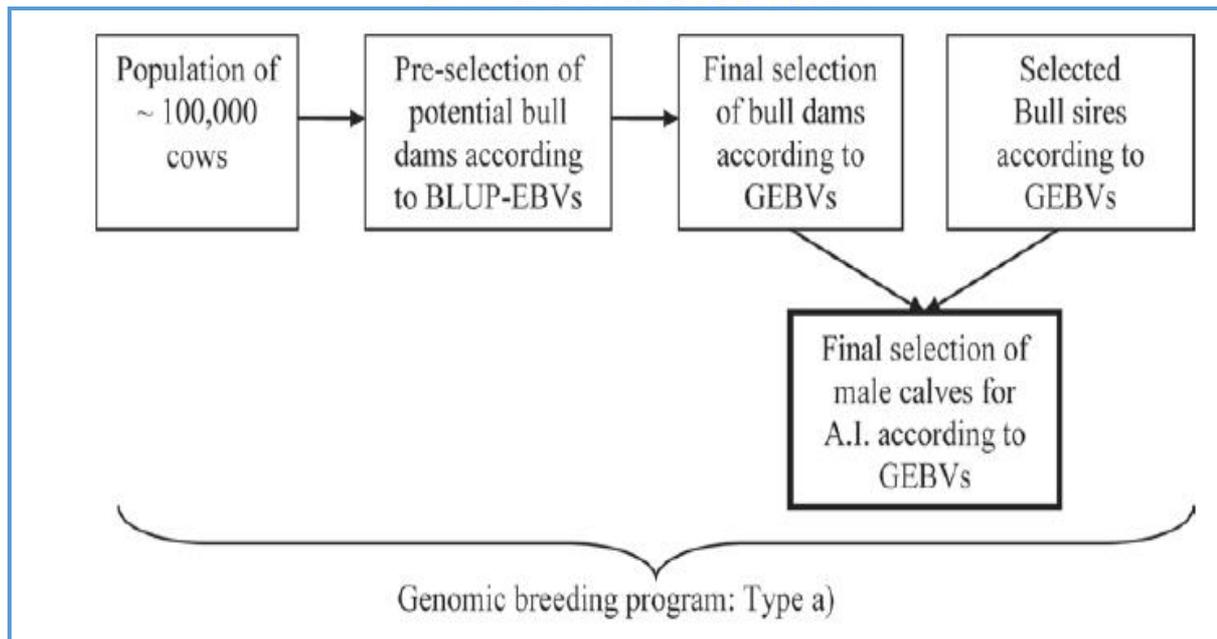


Figure 1. Comparison of 2 different genomic breeding programs: Type a) 2-step selection approach when considering bull dams; Type b) 1-step selection approach for the direct selection of male calves. GEBV = genomic EBV.

GPROG – Bull calves are genotyped

ALL All bull calves are genotyped	RANDOM n bull calves are genotyped at random	BD_BLUP n bull dams are pre-selected based on BLUP-EBV, their bull calves are genotyped	BD_PHEN n bull dams are pre-selected based on phenotype, their bull calves are genotyped	BD_HERD n bull dams are pre-selected from specific herds, their bull calves are genotyped	BD_GENO n bull calves are pre-selected on PI-GBV and genotyped
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GPAR – Parents are genotyped, bull calves are not

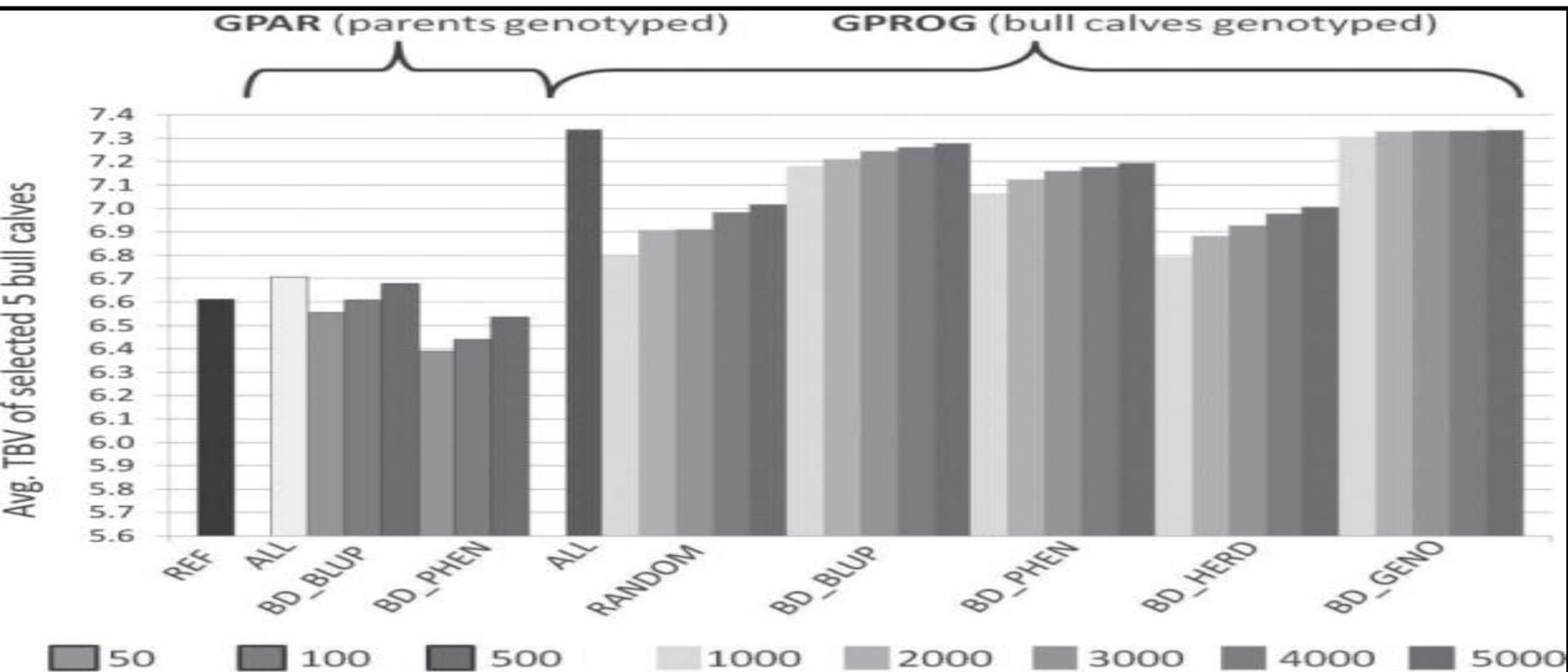
ALL All parents are genotyped; No shortage of bull dams with genotypes	BD_BLUP Pre-selection of n bull dams based on BLUP-EBV	BD_PHEN Pre-selection of n bull dams based on phenotype
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REF – Bull calves are selected on pedigree index

Figure 1. Characteristics of the simulated scenarios. PI-GBV = genomic pedigree index, calculated as average genomic breeding value (GBV) of parents.

$h^2=0.3$

$r_{MBV} = 0.9$



The Future of Dairy Cattle Breeding

**How can AI companies maintain
market share?**

When Everyone

- **has access to superior genetics**
- **can identify such genetics using genomics**
- **and market that genetics using genomics**

How can differentiate your product?

Reference Population for 'New Traits'

If # phenotypes is limited and genotyping is not:
Genotype individuals with phenotype, rather than parents

Grevenhof, Bijma, van Arendonk GSE 2012

