NON-ADDITIVE GENETIC EFFECTS
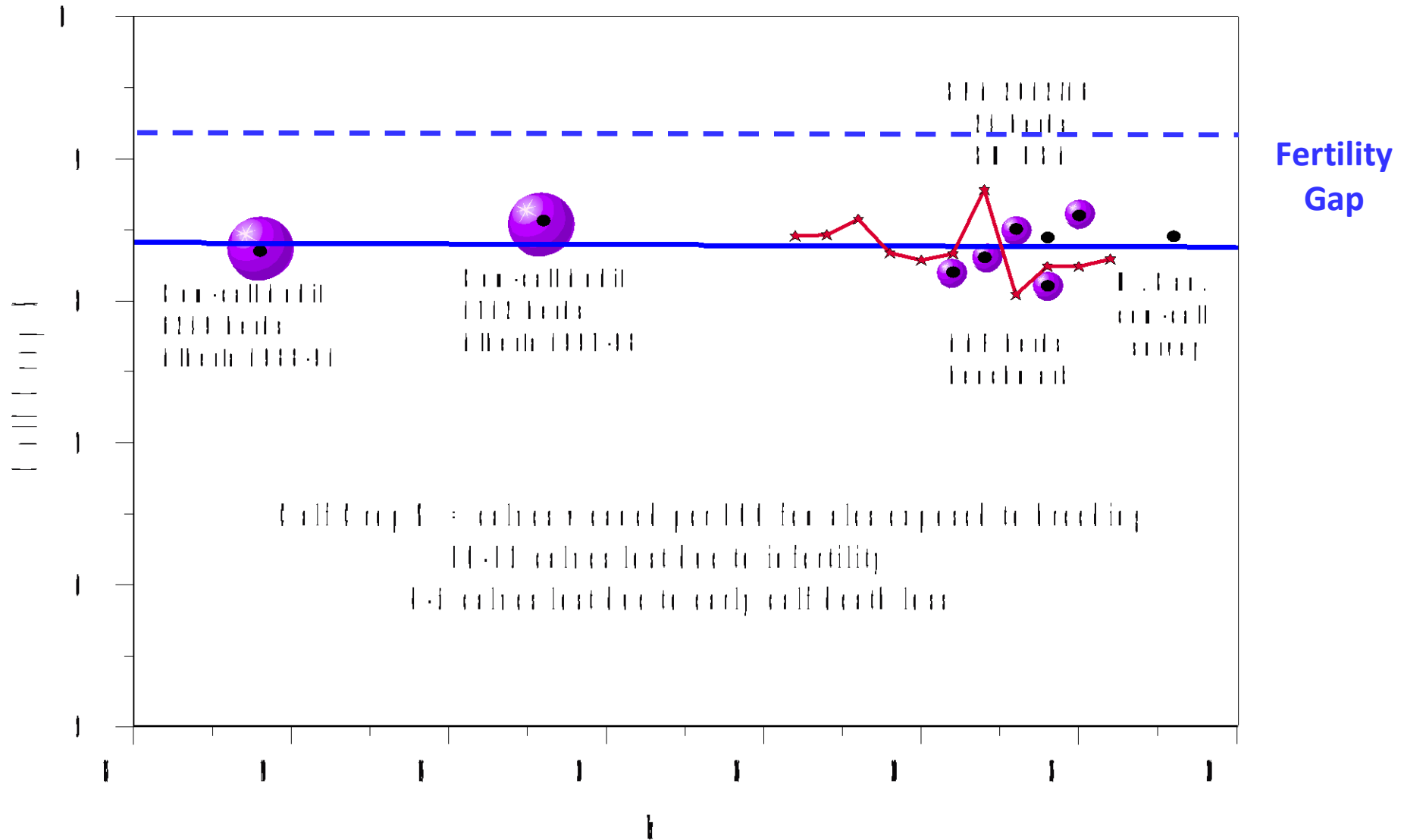**Use in replacement heifer selection**

JA Basarab, T. Valente, C. Li, G. Plastow

Beef Improvement Federation, 5 July 2023
Calgary, Alberta

Improving feed efficiency, product quality, profitability, environmental impact and food security

50

TREND: Calf crop % has remained constant at 83-85% over the last 25-30 years

Fertility Gap

Crossbred Cow-Calf herds in western Canada

TREND: Steady decline in heterosis due to single breed use since early 2000s

- ❖ Measured using genomic breed composition and retained heterozygosity

- ❖ Heterosis is proportional to heterozygosity

- ❖ Heterosis increases fertility, longevity and lifetime productivity by 20-30%

- ❖ > 40% of cows & calves would benefit from a 30% increase in heterosis (n>14,000)

Relative Value of traits to the cow-calf sector

Fertility traits	Growth traits	Carcass traits
10	**2**	**1**

Fertility traits

Heifer pregnancy
Cow pregnancy
Days in the herd
Lifetime productivity
Survival 1st to 5th parity
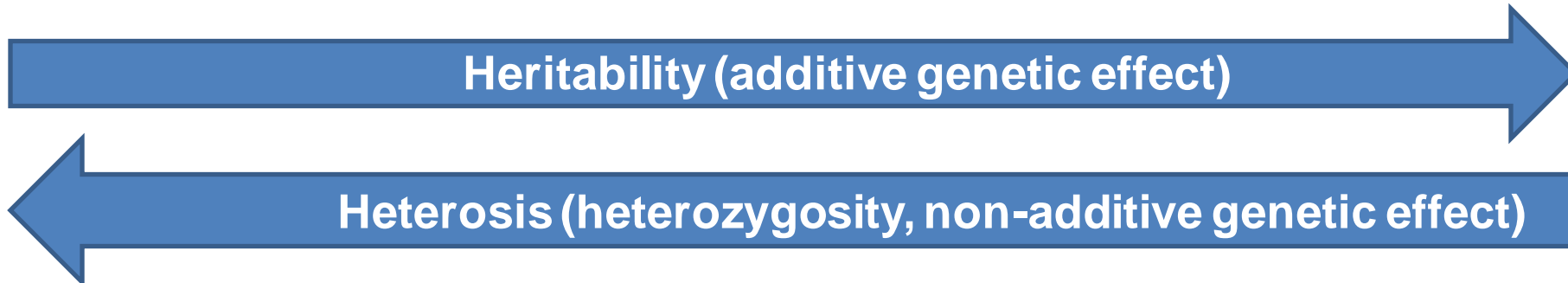Stayability
Longevity

Growth traits

Birth weight
Calving ease
Weaning weight
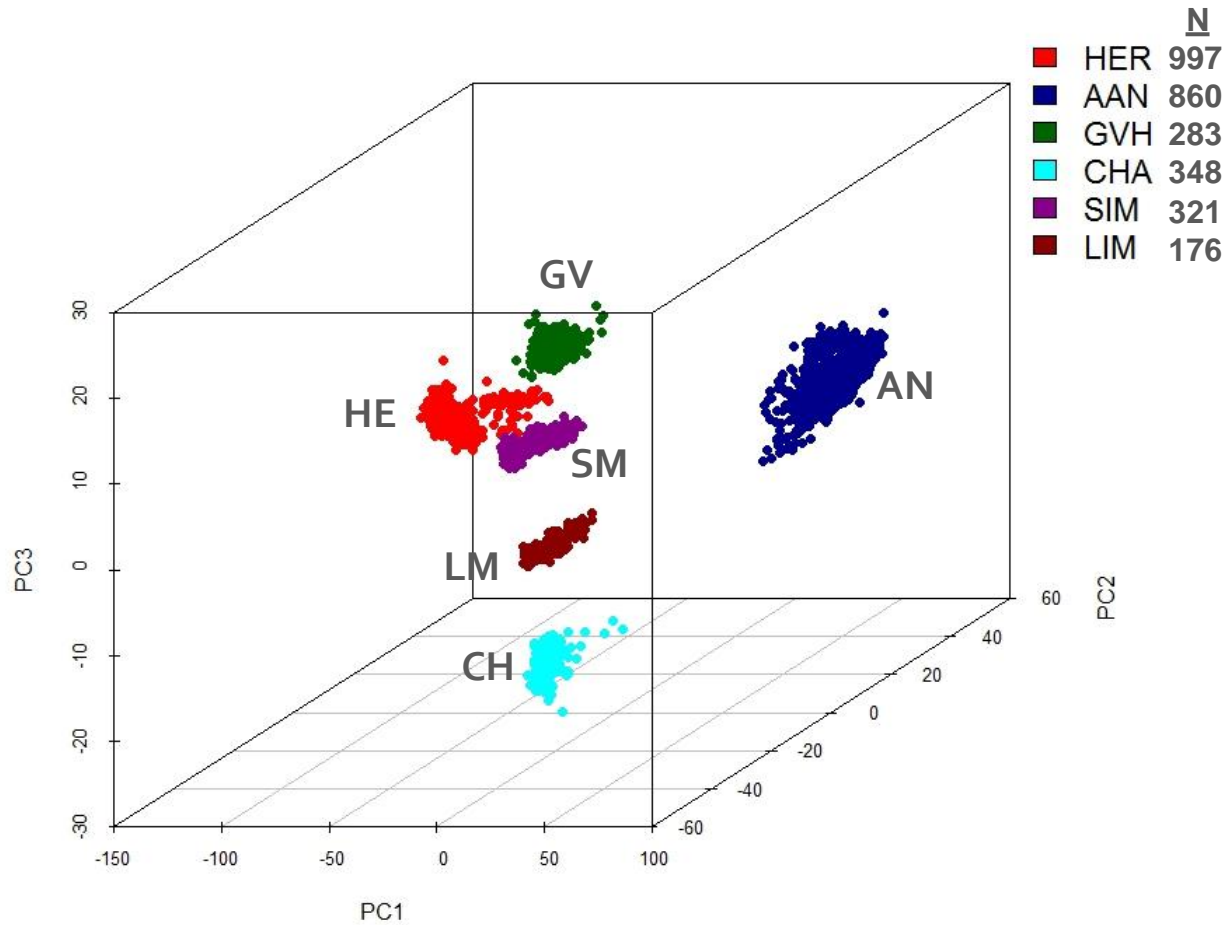Pre-wean gain
Yearling weight
Feedlot gain
Feed efficiency

Carcass traits

Back fat thickness
Ribeye area
Marbling
Lean meat yield
Tenderness
Hot carcass weight

Heritability (additive genetic effect) →

← **Heterosis (heterozygosity, non-additive genetic effect)**

Trenkle & Willham 1977; Melton 1994; Barwick & Nicol 1993

Genomic breed composition

Population structures identified by principal components using 50K for purebred Canadian beef cattle (Abo-Ismail et al. 2016)
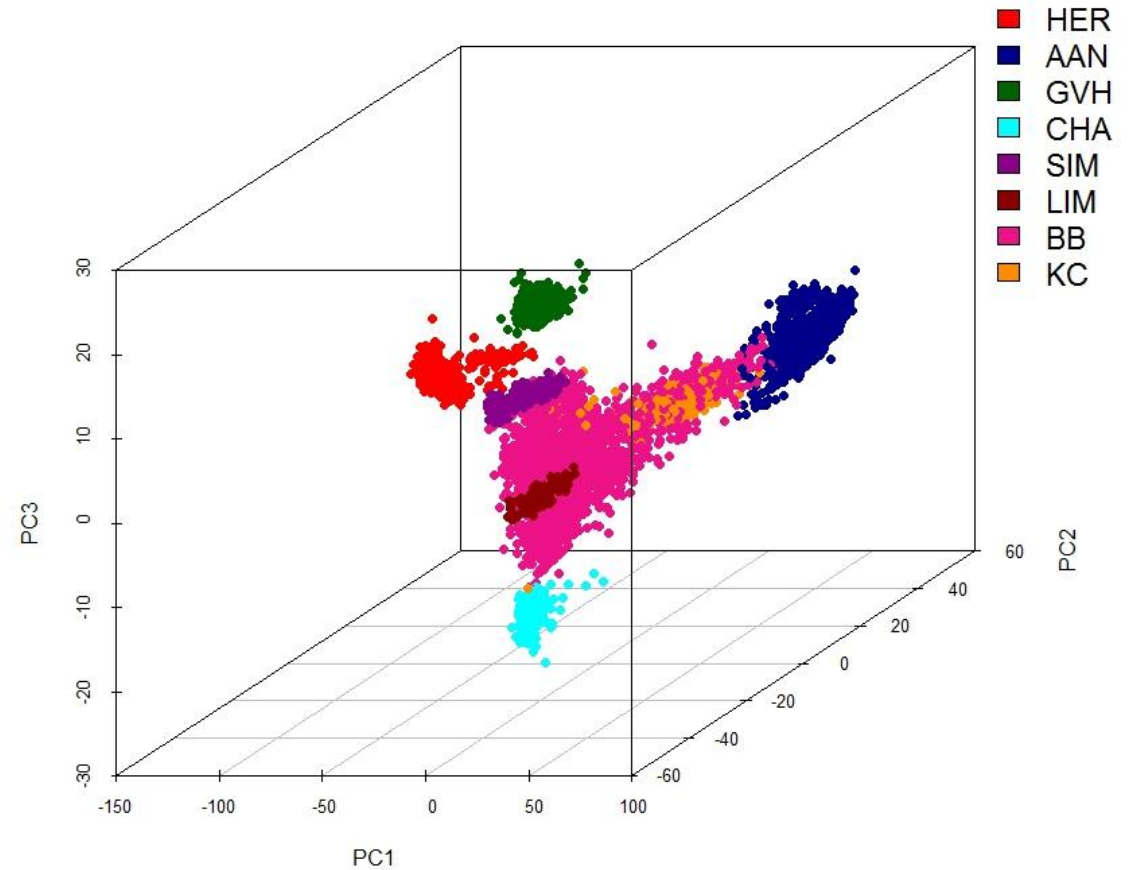
Population structures identified by principal components using 50K including composite animals (BB = 2029 cattle, Abo-Ismail et al. 2016)

Genomic breed composition

Reference Data Set- 14 breeds (n=5,520; Li et al. 2020)

Numbers of purebred animals in the refined breed composition prediction panel	
Breed	
Charolais	465
Simmental	267
Hereford	657
Red Angus	626
Black Angus	1465
Limousin	161
Gelbvieh	179
Salers	133
Maine Anjou	134
Shorthorn	684
Holstein	322
Brown Swiss	163
Jersey	163
Galloway	101
Total	5520

Genomic breed composition

D6574

Angus	**= 52.9%**
Simmental	**= 39.6%**
Charolais	**= 5.9%**
Others	**= 1.6%**
RFI-fat	**= -0.02**

Genomic indicator of heterosis

$$RHET = 1 - \sum_{i=1}^{n\ breeds} p_i^2$$

Hybrid Vigor Score = 55.9%

ARTICLE

Genomic retained heterosis effects on fertility and lifetime productivity in beef heifers

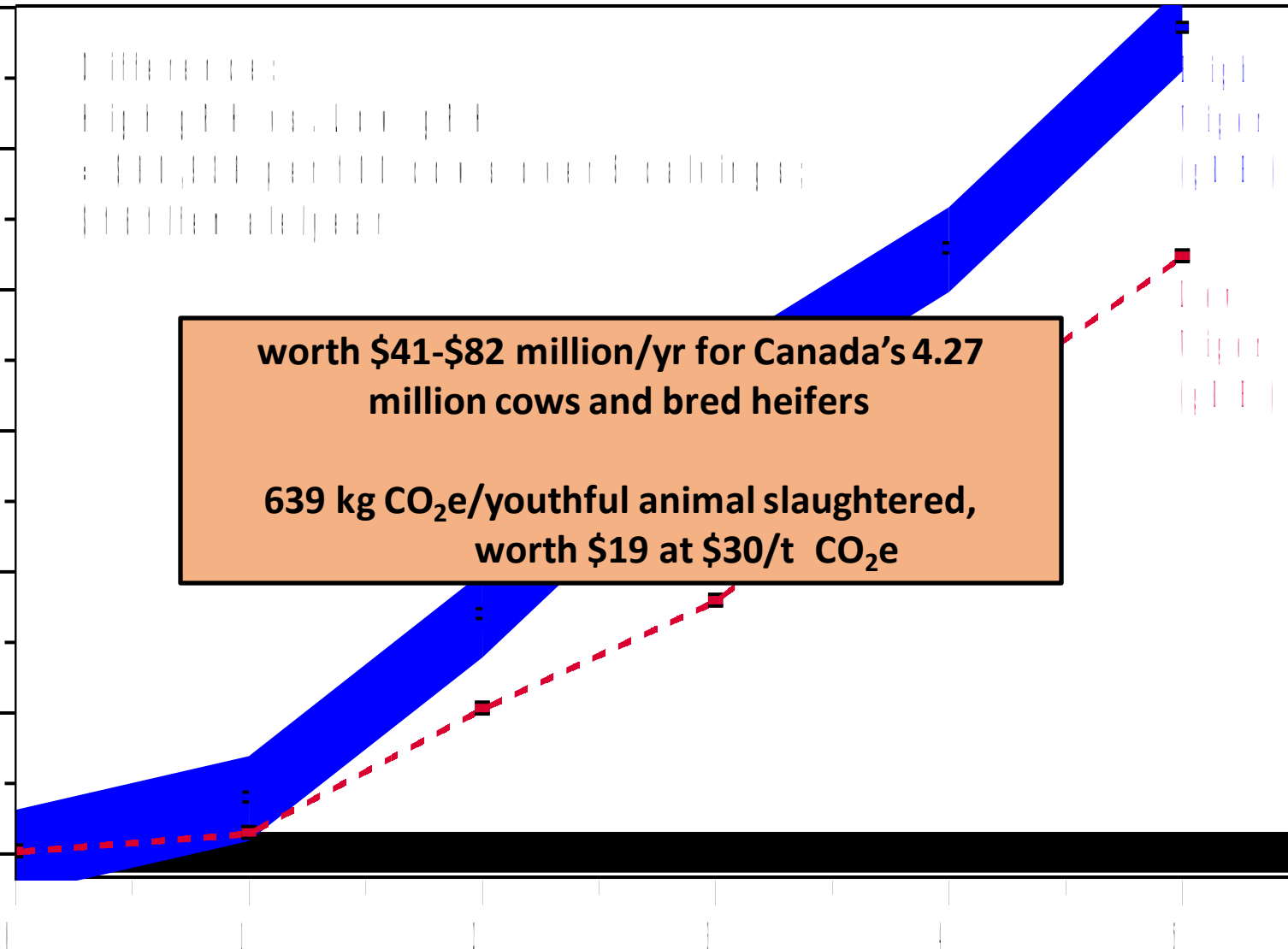J.A. Basarab, J.J. Crowley, M.K. Abo-Ismail, G.M. Manafiazar, E.C. Akanno, V.S. Baron, and G. Plastow

Abstract: This study evaluated the effects of three genomic indicators of heterosis on female fertility and lifetime productivity, and quantified changes over 11 production cycles in a crossbred cow herd. Pedigree-based breed composition (pBC) was determined and used to calculate retained heterozygosity for 412 replacement heifers born from 2004 to 2014 at the Lacombe Research and Development Centre (AB, Canada). Heifers were followed as cows over 1050 mating opportunities, 11 production cycles, and five parities. Heifers and their sires (51) were genotyped and these genotypes were used to predict each animal's genomic breed composition (gBC) and three genomic indicators of heterosis: (1) retained heterozygosity (RHETg), (2) heterozygous proportion (H), and (3) retained heterosis (RHg). Correlations between pedigree and genomic breed fractions for Angus, Hereford, and Charolais were high (r_p = 0.74–0.94; $P < 0.001$). Genomic indicators of heterosis were highly related (r_p = 0.61 for RHETg vs. H; 0.71 for RHg vs. H; 0.96 for RHETg vs. RHg; $P < 0.001$). Each 10% change in RHETg resulted in 51 ± 20 d longer survival ($P = 0.011$) in the herd and 35.7 ± 15.2 kg more ($P = 0.019$) calf wean weight per cow exposed to breeding when summed over five parities. These differences resulted in an extra $161 per heifer in a year. Optimizing heterosis using genomic tools can be very beneficial for the cow herd if applied correctly.

Canadian Journal of Animal Science,

https://doi.org/10.1139/CJAS-2017-0192

Hybrid Vigour Score

Linear effects of genomic retained heterozygosity

200-d weaning weight	**+3 lb/10% change**
Age at first calving	**-2 days/10% change**
Pregnancy rate	**+2 points/10% change**
Weaning rate	**+3 points/10% change**
Lifetime productivity	**+79 lb over 5 parities per 10% change**
Days in the herd	**+51 days/10% change**

Genomic retained heterozygosity is our genomic measure of hybrid vigor or heterosis

worth $41-$82 million/yr for Canada's 4.27 million cows and bred heifers

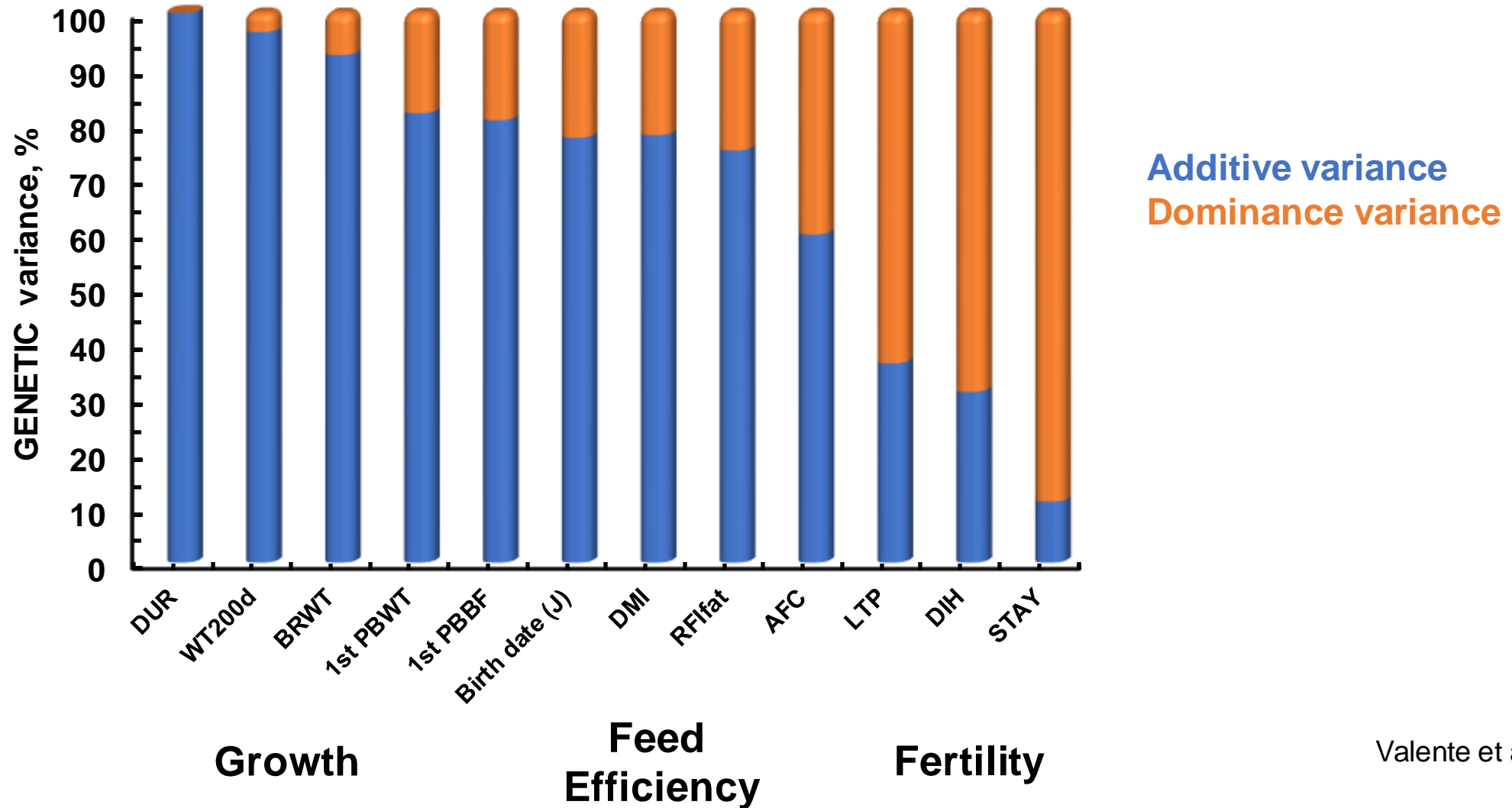639 kg CO_2e/youthful animal slaughtered, worth $19 at $30/t CO_2e

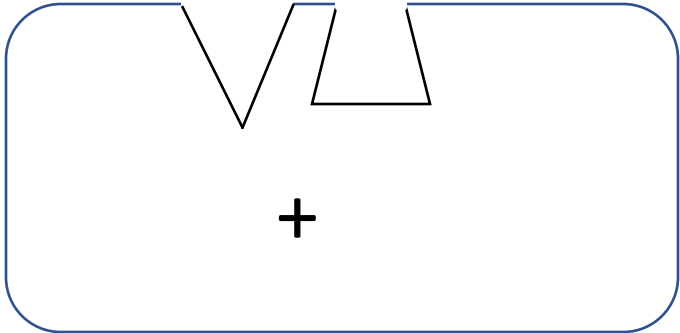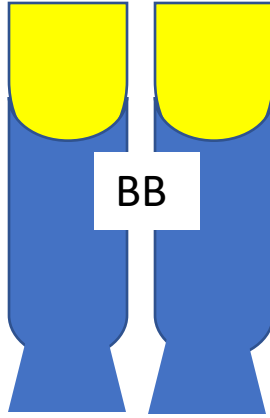# Genetic variance as a percentage of total phenotypic variance
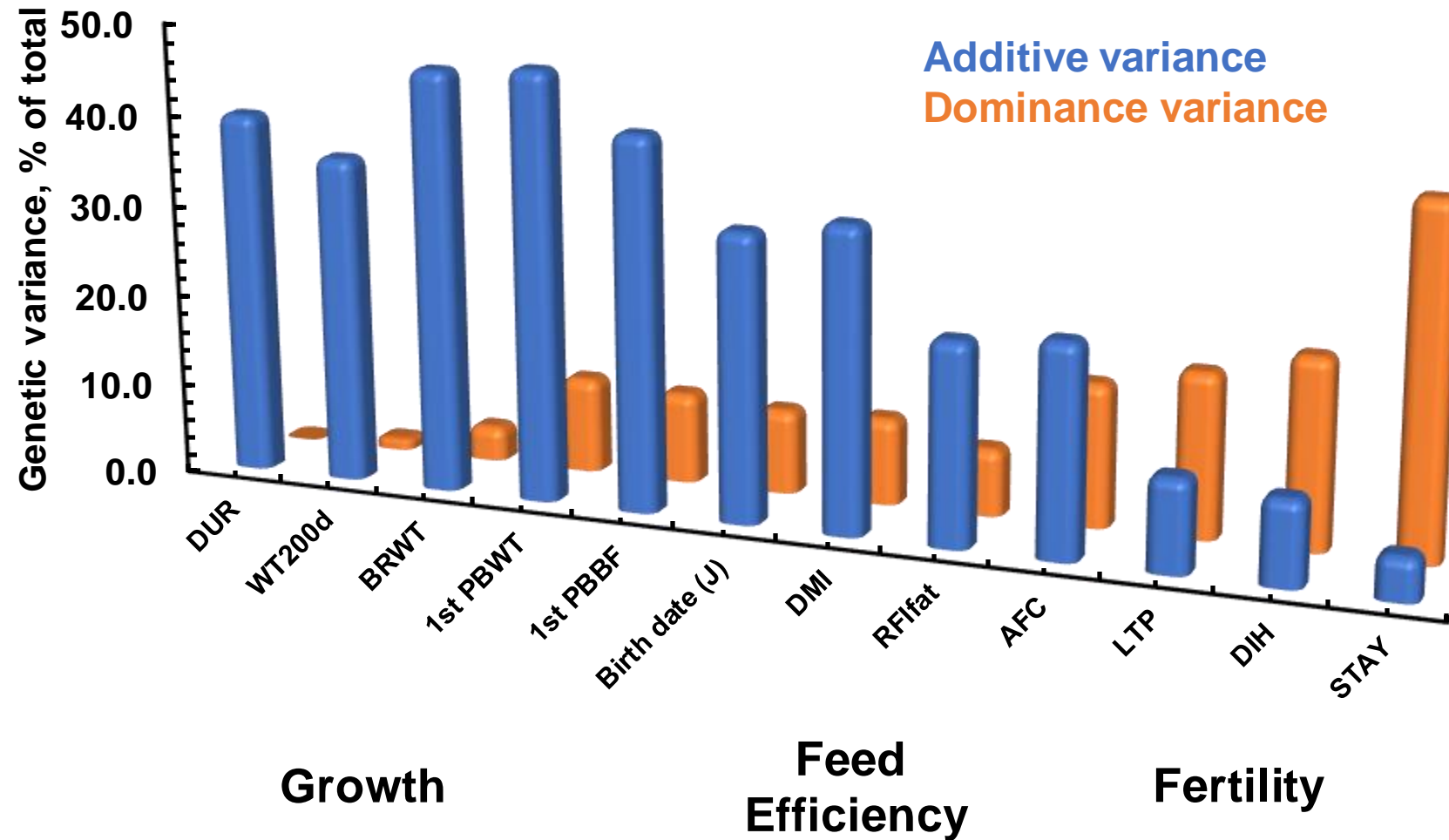
Valente et al. 2023

Variance as a percentage of total genetic variance

Additive variance
Dominance variance

Growth Feed Efficiency Fertility

Valente et al. 2023

Example: BIOLOGICAL MODEL OF HETEROSIS (dominance)
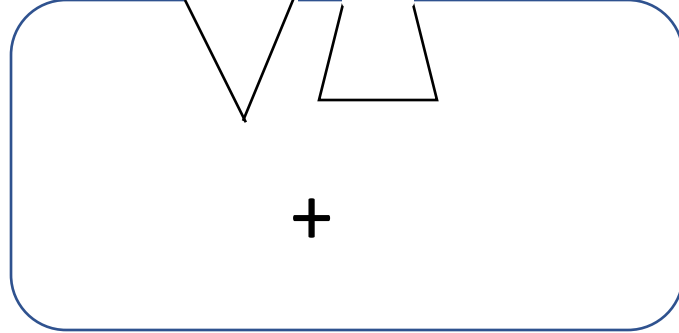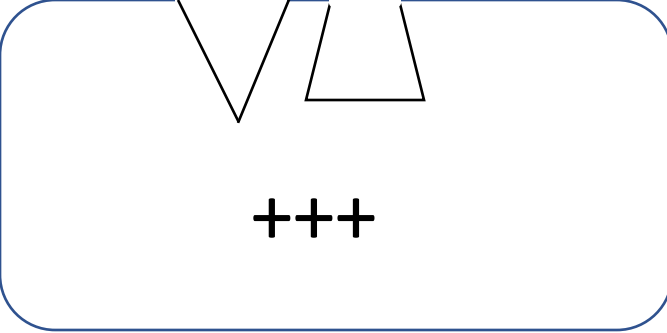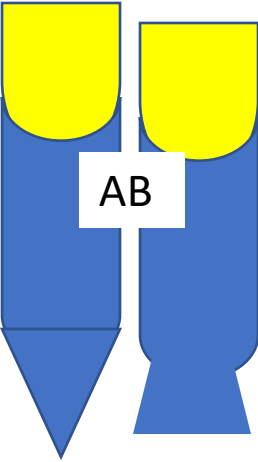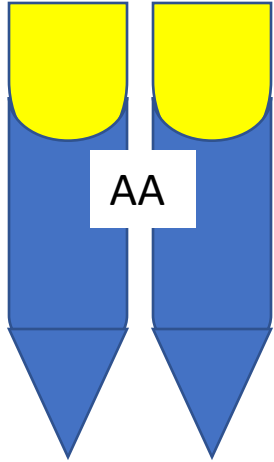
Phenotype = Genetic + Environment + Management

Genetic effect = additive + non-additive genetic effects (dominance and epistasis)

Additive genetic effect
- Traditional genetic evaluation models
- Cumulative or additive
- Stably inherited
- Major role growth, FE, carcass & maternal traits
- Predicts individual & offspring performance
- SNP coded as 0, 1 and 2

Non-additive genetic effect
- Useful for optimizing breeding schemes
- Within/across gene interaction
- Not stably inherited due to recombination
- Major role in fertility & fitness traits
- Predicts individual performance
- SNP coded as 0, 1 and 0

Examples of all-purpose (A) and maternal (M) indexes, and Replacement Heifer Index Scores (R)			
Breed Asc./company/orgs	System	Genetic effects for growth, feed efficiency, maternal & carcass traits	
		Additive	Non-additive
Angus-Canadian Balancer (CBI)	A	YES	NO
Red Angus - Herd Builder (HPI)	M	YES	NO
Simmental - All-purpose (API)	A	YES	NO
Hereford-Maternal Prod. (MPI)	M	YES	NO
Gelbvieh - $COW	M	YES	NO
Limousin - Elite & Super dams	M	YES	NO
Igenity® Beef, Igenity + Envigor	M	YES	YES
Gentec RHPI Score™	R	YES	YES

Replacement Heifer Profit Index Score™

A DNA based Selection Score for Commercial Cow-calf Producers

Breeding Goal: produce a calf every year, while improving calf wean weight, cow feed efficiency, fertility, and longevity.

Score = **Retained heterozygosity** + **RHP Index**
- (-) Birth weight
- (-) 200-day wean weight
- (-) Residual feed intake
- (-) Feeding event duration
- (-) Pre-breed weight
- (+) Pre-breed backfat
- (-) Age at first calving

Replacement Heifer Profit Index Score™

A DNA based Selection Index for Commercial Cow-calf Producers

**Grant Smith
Brush Hills Ranch**

Brush Hills Ranch

"A real world practical example of how genomics can help producers"

"So far the results have been truly mind blowing."

February 2023

Overall open rate = 19.4%

	RHPI Score™ (155 cows)	# open	All cows	2-yr old	3-yr old
Where did our culls come from?	Above 50%	7	23%	33%	17%
	Below 50%	23	77%	67%	83%
	Total	30			

Effect of the Replacement Heifer Profit Index Score™ on open rate

Open rate in crossbred beef heifers with BELOW vs ABOVE average RHPI Score™ (10 Alberta herds)			
Replacement heifers	BELOW average	ABOVE average	Total
# exposed to breeding	359	549	908
# calving	275	474	749
# open	84	75	159
Open rate, %	23.40	13.66	P=0.0002

Financial impact of the Replacement Heifer Profit Index Score™

Increased net Income from ABOVE average RHPI Score™ heifers

9 more calves per 100 replacement heifers

+ $14,175 from nine more calves

+ $8,550 from nine fewer replacements ($950/heifer)

- $3,000 to genotype 100 heifers
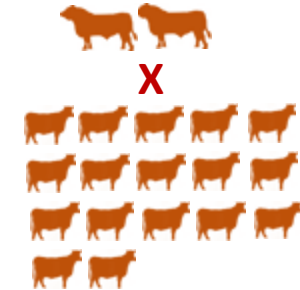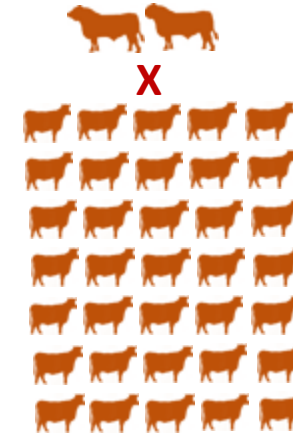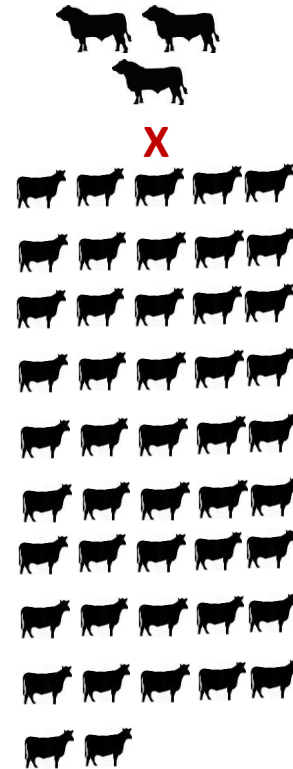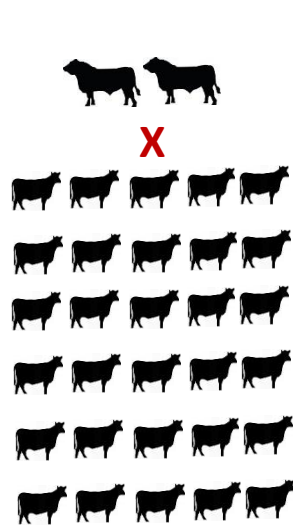
+ $19,725 net income

6 to 1 return on investment

$3.15/lb for 500 lb calves; Alberta Beef Producers Weekly Feeder Prices, April 12, 2023
The cost of $950/heifers accounts for all cost plus selling the cull replacement heifer

DNA pooling as a low-cost strategy for commercial cow-calf producers

Multi-sire Mating groups 2017 LRDC

Costs ($45/sample)
$6210
VS.
$567

Group characteristics

|				
Cow number	30 ANHE mature cows	47 ANHE mature cows	35 ARHE mature cows	17 ARHE mature cows
Color	black, blk-white face	black, blk-white face	red, red-white face	red, red-white face
Angus % (genomic)	AN 64%: HE 33%: SM 2%	AN 87%: HE 9%: SM 1%	AR 81%:HE 8%: CH 6%	AR 61%; HE 22%: CH 7%: SM 6%
Hybrid Vigour (genomic)	41%	22%	30%	52%
Open rate	13.3%	21.3%	8.6%	5.9%

Correlation between retained heterozygosity from individual and pooled genotypes.

A. Pool size (5, 10, 25, 50 , 100)
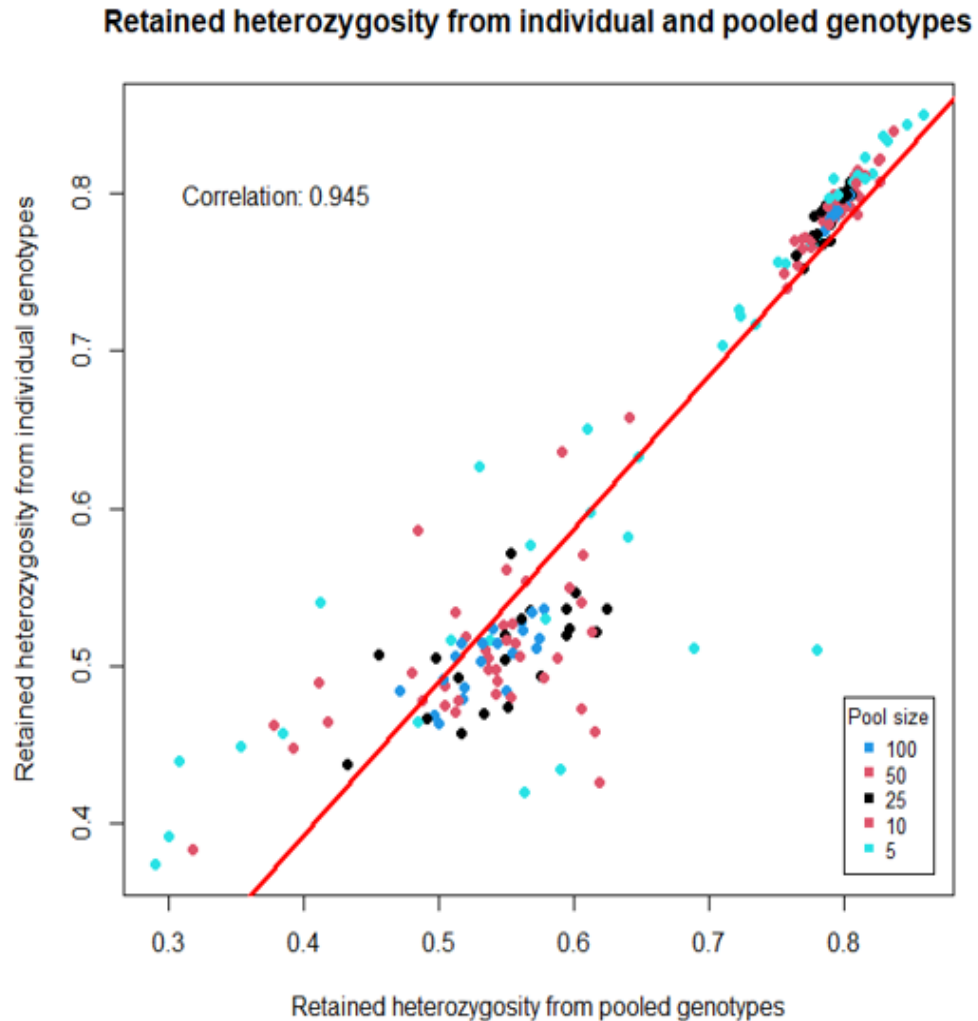
B. Herd (Kinsella, Lacombe)
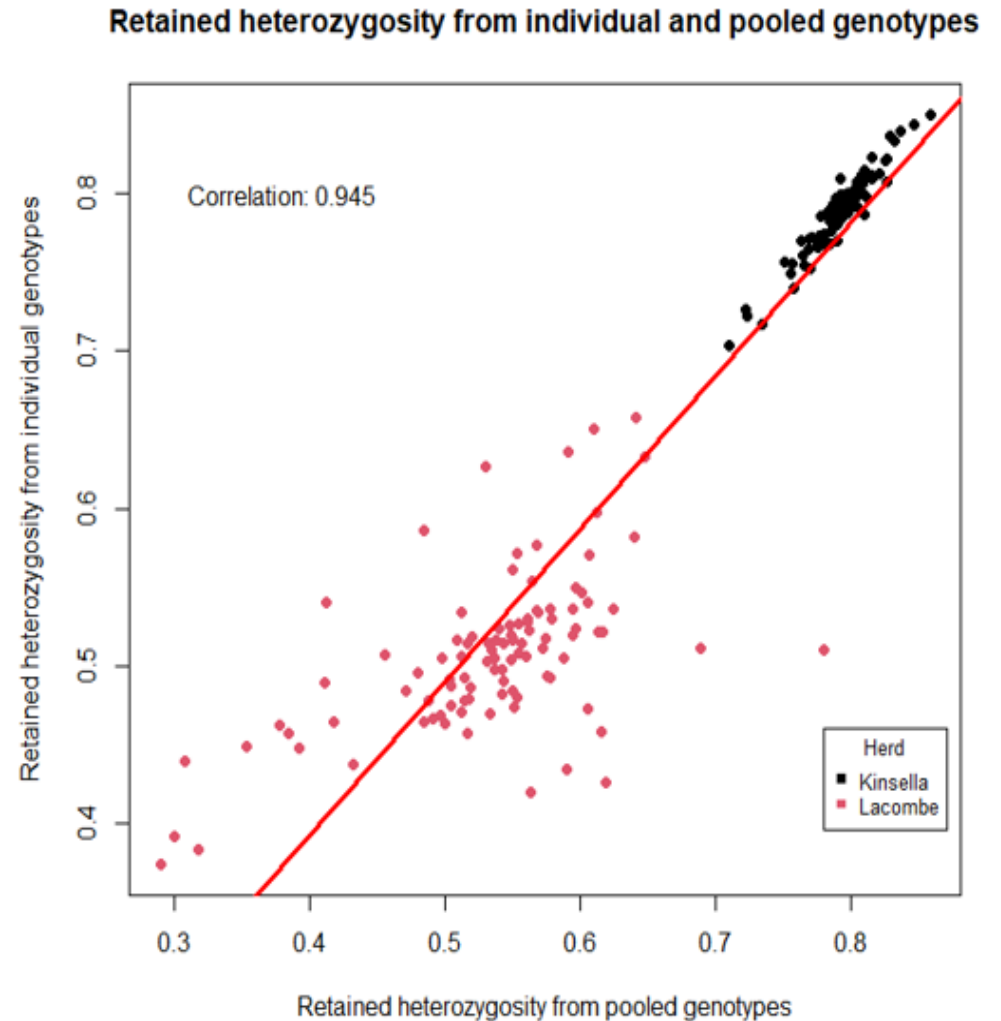
Conclusions

Genomic retained heterozygosity is a genomic indicator of heterosis

Retained heterozygosity is linearly related to female fertility and fitness traits

Non-additive genetic effects are due to dominance and epistasis

Dominance variance is a main source of phenotypic variation for

female longevity and stayability traits

Additive and dominance models can improve genomic prediction by 20-40%

Non-additive genetic effects are useful for breeding plans to increase longevity & LTP