

Limits to Selection in U.S. Dairy Cattle After Several Generations of Genomic Evaluation

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Topics

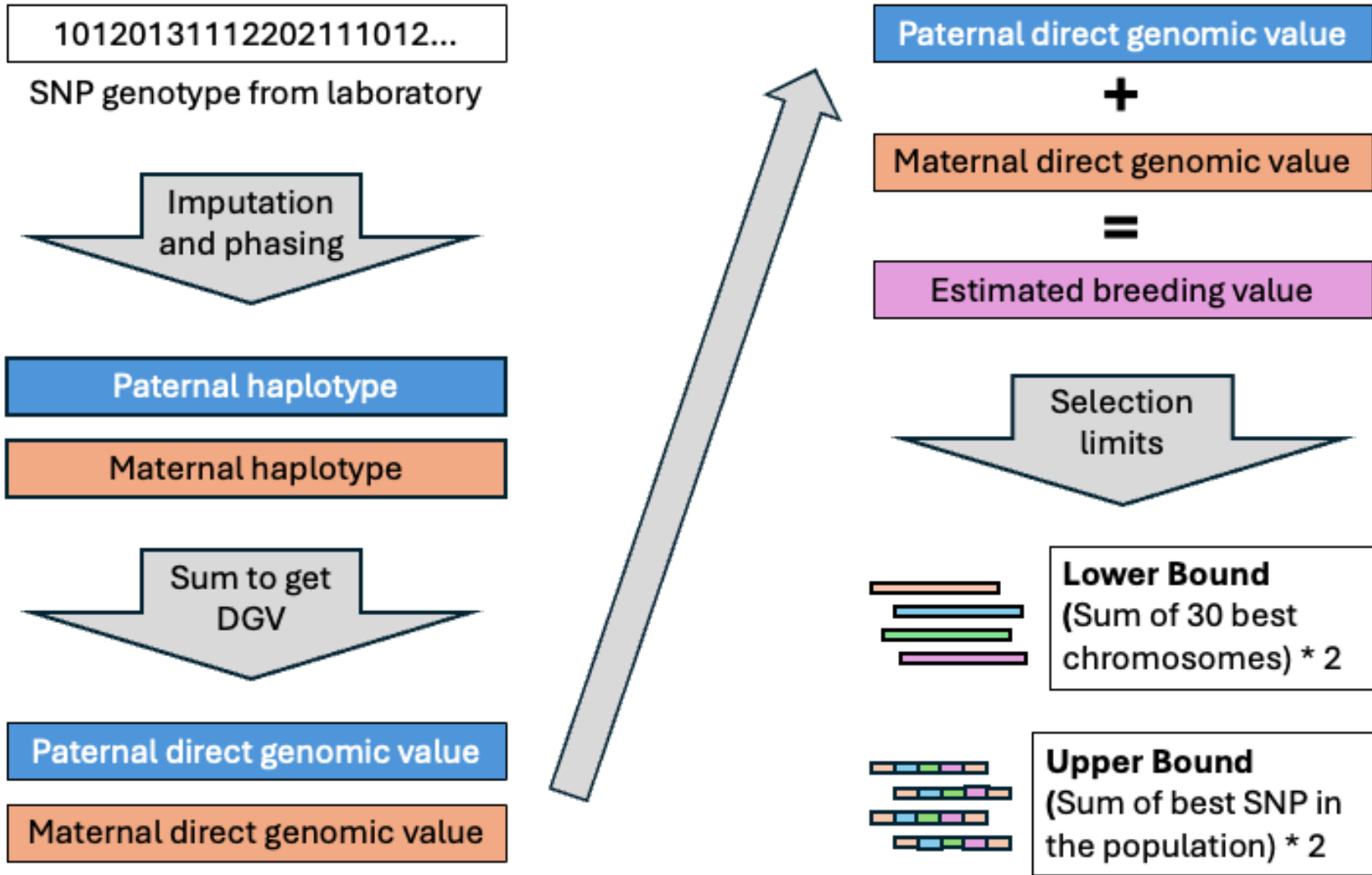
- ▶ Materials and methods
- ▶ Estimated selection limits
- ▶ What's the best animal we can make?
- ▶ Discussion and conclusions



Materials and methods


Animals and traits included

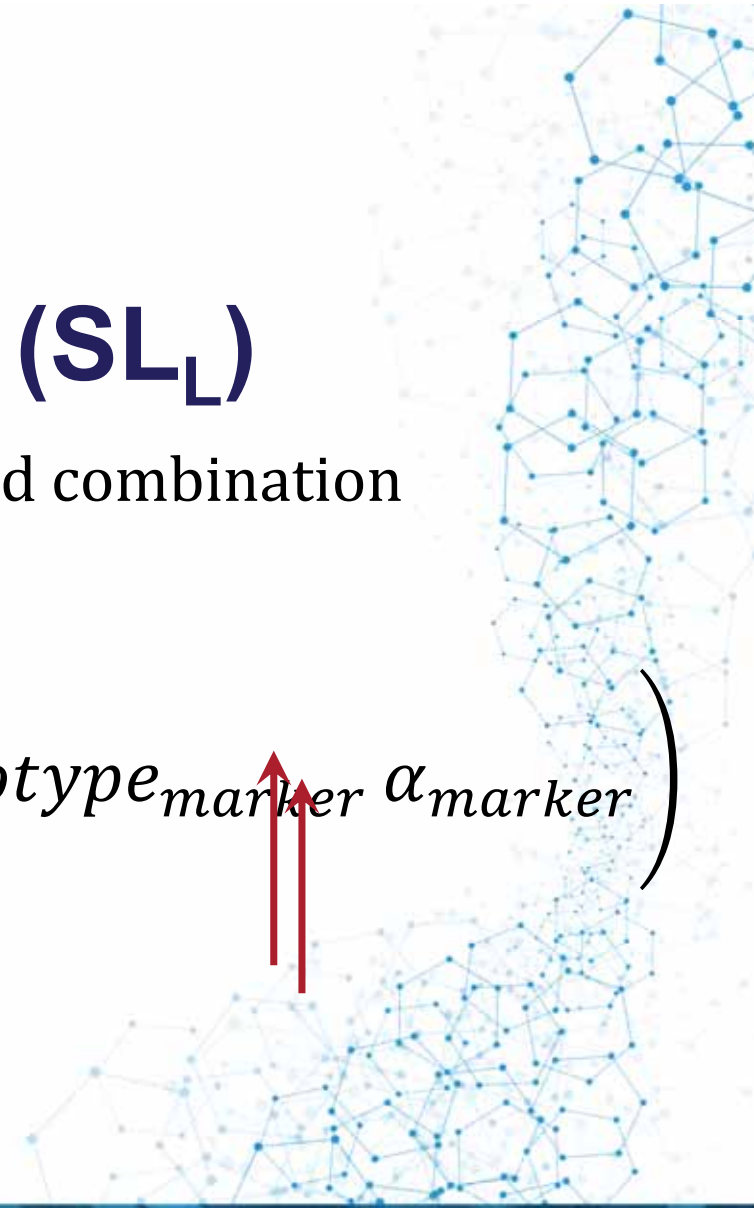
- Genotypes imputed to 69,200 SNP
 - Ayrshire (AY): 20,373
 - Brown Swiss (BS): 89,136
 - Guernsey (GU): 11,407
 - Holstein (HO): 9,119,871
 - Jersey (JE): 928,883
- Cole and VanRaden (2011)
 - Brown Swiss 1,455
 - Holstein 40,351
 - Jersey 4,064
- Milk, fat, and protein yields
- Productive Life (PL)
- Somatic Cell Score (SCS)
- Daughter Pregnancy Rate (DPR)
- Heifer & Cow Conception Rates (HCR & CCR);
- Heifer & Cow Livabilities (HLIV & LIV)
- Early First Calving (EFC)
- Gestation Length (GL)
- Health traits (BS, HO, and JE only): hypocalcemia (MFEV), displaced abomasum (DSAB), ketosis (KETO), clinical mastitis (MAST), metritis (METR), & retained placenta (RETP)
- Lifetime Net Merit (NM\$)



Lower bound selection limit (SL_L)

- Select the 30 best haplotypes for each trait-breed combination

$$SL_L = \sum_{chromosome=1}^{30} \max_{haplotype} \left(\sum_{marker=1}^{n_{markers}} genotype_{marker} \alpha_{marker} \right)$$




Upper bound selection limit (SL_U)

- Select the 69,200 best markers for each trait-breed combination

$$SL_U = \sum_{marker=1}^{69,200} \max_{loci} (genotype_{marker} \alpha_{marker})$$

Estimated selection limits

Summary of findings

- A subset of traits was chosen to represent phenotypes with differing heritabilities and varying amounts of available data.
- In all cases, DGV_{\max} is bounded by SL_L and SL_U , as expected.
- Ratios of SL_L to DGV_{\max} and SL_U to DGV_{\max} range from ~ 2.5 for protein and NM\$ in HO to ~ 16 for milk yield in JE and MAST in HO.
- Results are consistent with earlier findings of Cole and VanRaden (2011).



Production traits

Trait	Breed	SL _L	SL _U	DGV _{max}	SL _L to DGV _{max}	SL _U to DGV _{max}
Milk	AY	6,339.49	12,888.24	1,259.25	5.03	10.23
	BS	11,245.30	28,346.49	2,759.82	4.07	10.27
	GU	5,804.17	12,424.25	966.19	6.01	12.86
	HO	16,128.36	47,784.84	5,044.43	3.20	9.47
	JE	11,716.98	40,569.50	2,533.73	4.62	16.01
Protein	AY	167.89	338.86	167.89	3.65	7.36
	BS	304.34	744.82	304.34	3.35	8.20
	GU	157.80	340.24	157.80	4.76	10.27
	HO	375.20	1,215.64	375.20	2.55	8.27
	JE	306.90	1,130.18	306.90	3.50	12.89



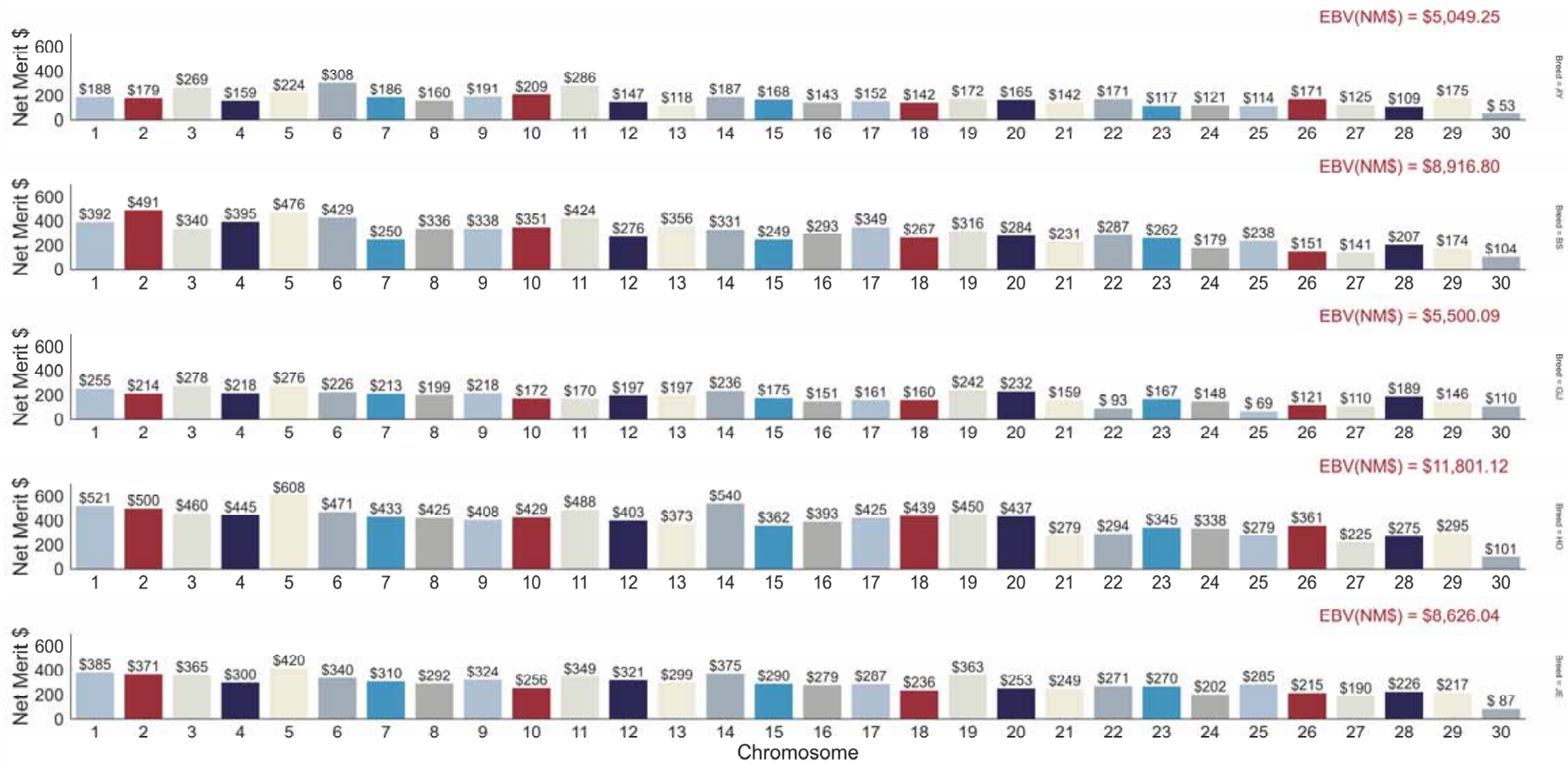
Lifetime profitability and longevity

Trait	Breed	SL _L	SL _U	DGV _{max}	SL _L to DGV _{max}	SL _U to DGV _{max}
NM\$	AY	4,144.15	8,393.45	908.88	4.56	9.23
	BS	8,085.39	18,124.87	2,086.48	3.88	8.69
	GU	4,187.75	8,318.17	744.13	5.63	11.18
	HO	11,704.89	39,902.78	4,728.14	2.48	8.44
	JE	8,175.53	26,400.41	2,766.43	2.96	9.54
PL	AY	42.60	80.19	12.92	3.30	6.21
	BS	90.38	207.06	22.35	4.04	9.26
	GU	46.95	80.71	15.96	2.94	5.06
	HO	98.48	357.82	31.62	3.11	11.32
	JE	94.35	253.13	30.43	3.10	8.32

Health traits

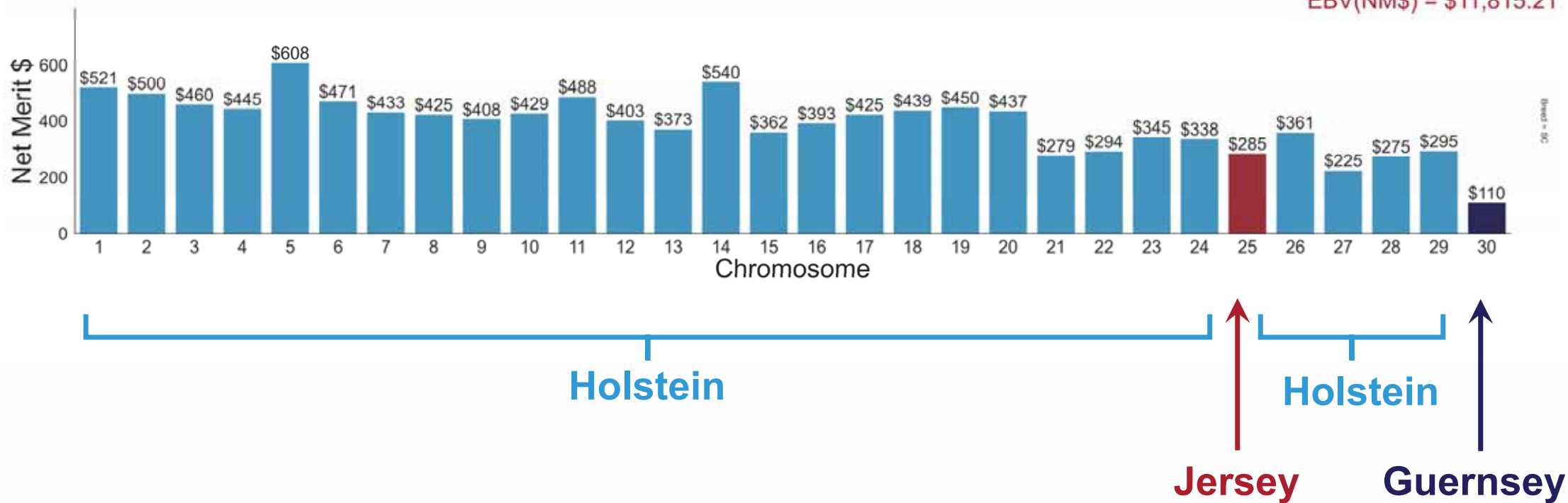
Trait	Breed	SL _L	SL _U	DGV _{max}	SL _L to DGV _{max}	SL _U to DGV _{max}
DSAB	BS	5.32	8.03	2.47	2.15	3.25
	HO	25.26	77.79	4.51	5.60	17.25
	JE	14.23	28.02	3.48	4.09	8.05
MAST	BS	45.96	83.90	11.45	4.01	7.33
	HO	97.44	276.77	17.61	5.53	15.72
	JE	66.04	137.95	14.94	4.42	9.23
METR	BS	4.33	8.73	0.07	61.86	124.71
	HO	42.73	100.09	9.83	4.35	10.18
	JE	23.69	39.64	8.35	2.84	4.75

What's the best animal we can make?



Holstein chromosomes aren't always best!

EBV(NM\$) = \$11,815.21



Breed = 50%

What's changed since 2010?

- Substantially more data are available.
- Chromosome 14 no longer dominates the others.
- Chromosome 5 is growing in importance.
- The pseudo-autosomal region accounts for much smaller effects, on average.

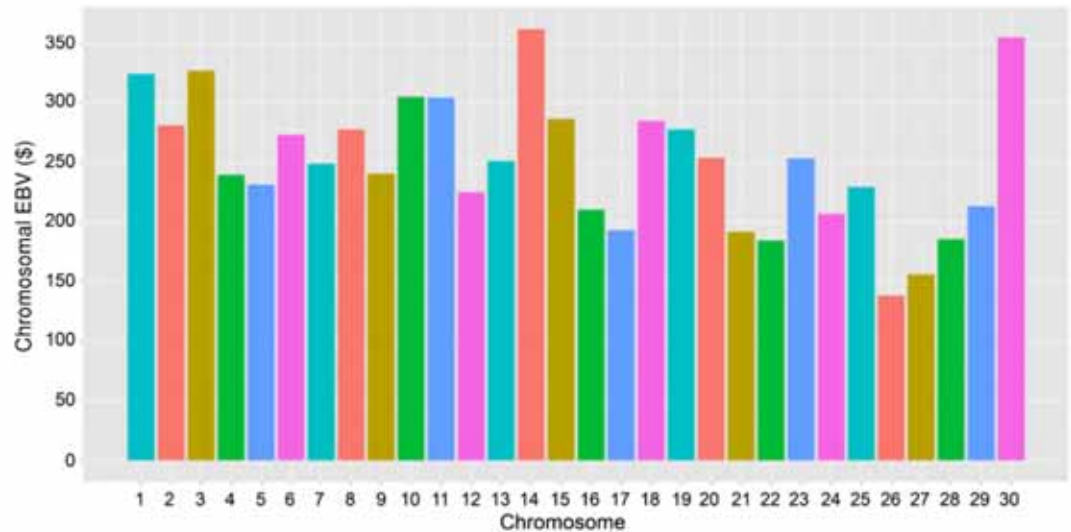


Figure 5 from Cole and VanRaden (2011) showing a Holstein with a potential EBV for NM\$ of \$7,515.

Discussion and conclusions

Discussion

- These results suggest substantial additional selection gains are achievable in all breeds with U.S. genomic evaluations.
- Gains may not be additive as populations approach selection limits.
- Physiological constraints may limit progress:
 - **Nutritional requirements** may exceed intake capacity or economically viable rations
 - **Homeostasis** may be disrupted, particularly capacity to maintain body temperature
 - Genetic and phenotypic correlations assume **linearity** which may not hold

“When the pure breeds finally reach equilibrium between the production of heterozygosis by mutations and the loss of heterozygosis because the effective number of animals in the breed is small, it is possible that the pure breed may support only a few scores of unfixed loci.”

J.L. Lush (1945)

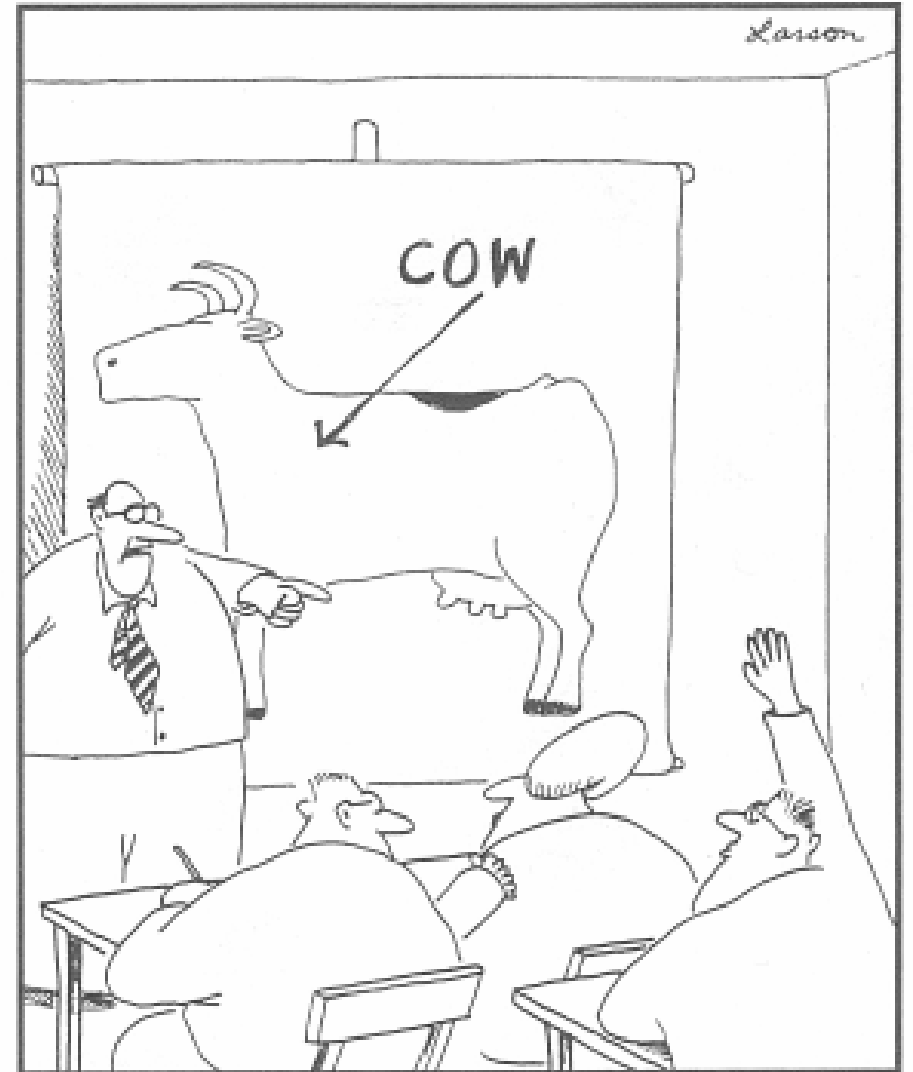
Conclusions

- Selection limits for BS, HO, and JE are similar to results of Cole and VanRaden (2011) .
- Selection limits for AY and GU reflect fewer segregations and reduced opportunities to create outlier haplotypes.
- Bounds on achievable EBV range from an average of 3.45 for SL_L to 7.44 for SL_U .
- Substantial opportunity for genetic progress remains in the US dairy cattle population.

Questions?

Thank you for your attention!

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"Yes ... I believe there's a question there in the back."