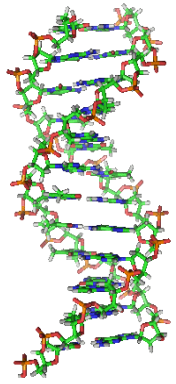
RightMate: Precision Breeding by Genomic Mating

RightMate powered by TOP GENOMICS

RightChoice powered by TOP GENOMICS



July 5, 2023

Mahdi Saatchi[1,2,3]

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[3]Iowa State University, USA.

ALLIED GENETIC RESOURCES

TOP GENOMICS Improving Beef Through Genomics

ABS

Breeding Decisions: Customer Needs and priorities

- Balanced Trait Mating?
- Terminal Mating?
- Heifer Mating?
- Multiply Priorities?
- Genetic Improvement, Genetic Diversity & Uniformity?

Complexity of Animal Breeding:

ORIGINAL ARTICLE

WILEY Journal of Animal Breeding and Genetics

Complexity of animal breeding choice making

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Abstract

The last decades of developments in animal breeding, genetics, genomics and data recording technologies have allowed the evaluation of larger numbers of animal and animal traits than ever before. This should help make animal breeding choices more informed, but it also makes them far more complex. This complexity may be overwhelming farmers, thus compromising realization of potential genetic gain in livestock industries. However, the effect of complexity of animal breeding choices on farmers' selection of animals has received very little theoretical consideration to date. This paper reviews the theoretical principles of complex decisions, contextualizes the findings to the field of animal breeding, and analyses how farmers and the animal breeding industry are currently dealing with complexity. According to the findings of the analyses of complex decisions in other fields, the complexity of animal breeding choices is likely to lead to farmers using conscious or unconscious simplifying strategies (heuristics) to handle such complexity. When these heuristics are ineffective, poor selection decisions and a potential loss of genetic progress can be expected. Further, studies using survey experiments to understand farmer behaviour and selection preferences may be compromised by the complexity of the survey´s

Complexity of Animal Breeding:

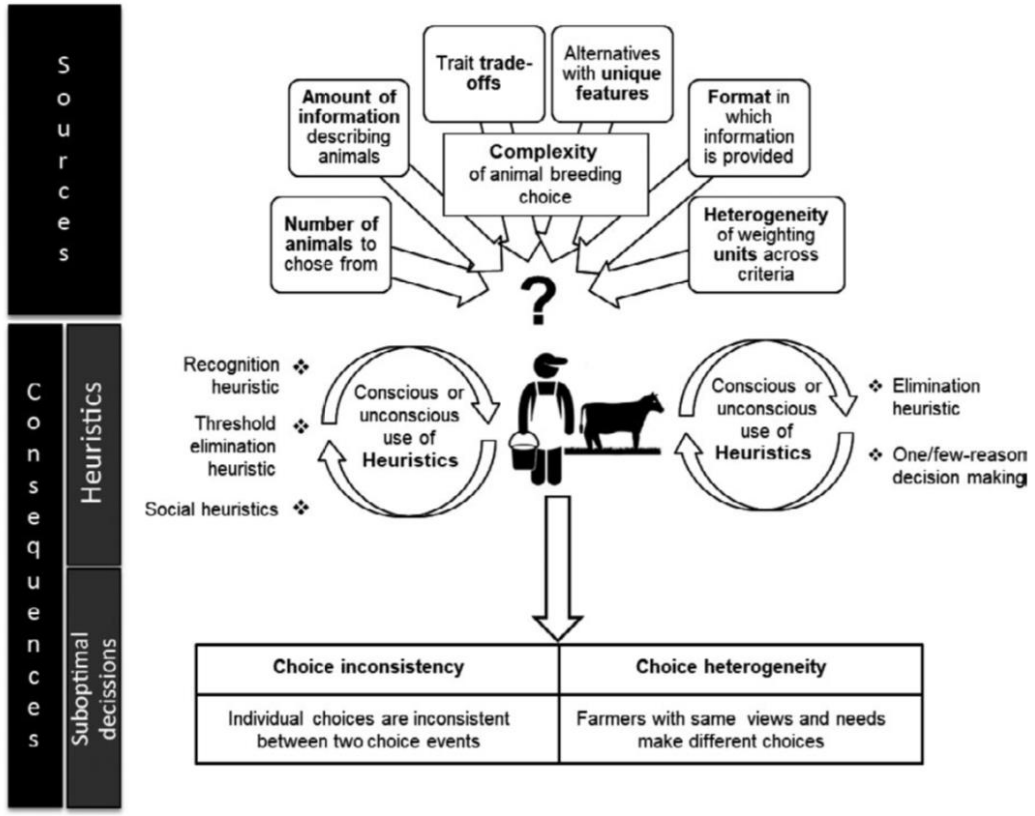


FIGURE 1 Description of how complexity might be affecting animal breeding choices made by individual farmers according to the theoretical principles of complex decisions. Key sources of complexity, potential heuristics used by farmers to simplify the decisions, and types of suboptimal decisions which may occur due to that complexity

So…What is RightMate?

- Genomic based Precision Breeding Tool.
- Primarily Designed for Seedstock Providers.
- Generations of Improvement per Mating Cycle.
- More Uniform Calf Crops.
- Optimized genetic diversity/Improvement with customized breeding objectives by integrating into MateSel software.
- Uses both EPDs and the Power of High Impact Genes.

Segelke *et al. Genetics Selection Evolution* 2014, **46**:42
http://www.gsejournal.org/content/46/1/42

RESEARCH Open Access

Prediction of expected genetic variation within groups of offspring for innovative mating schemes

Dierck Segelke[1,2*], Friedrich Reinhardt[1], Zengting Liu[1] and Georg Thaller[2]

Abstract

Background: Experience from progeny-testing indicates that the mating of popular bull sires that have high estimated breeding values with excellent dams does not guarantee the production of offspring with superior breeding values. This is explained partly by differences in the standard deviation of gamete breeding values (SDGBV) between animals at the haplotype level. The SDGBV depends on the variance of the true effects of single nucleotide polymorphisms (SNPs) and the degree of heterozygosity. Haplotypes of 58 035 Holstein animals were used to predict and investigate expected SDGBV for fat yield, protein yield, somatic cell score and the direct genetic effect for stillbirth.

Results: Differences in SDGBV between animals were detected, which means that the groups of offspring of parents with low SDGBV will be more homogeneous than those of parents with high SDGBV, although the expected mean breeding values of the progeny will be the same. SDGBV was negatively correlated with genomic and pedigree inbreeding coefficients and a small loss of SDGBV over time was observed. Sires that had relatively low mean gamete breeding values but high SDGBV had a higher probability of producing extremely positive offspring than sires that had a high mean gamete breeding value and low SDGBV.

Conclusions: An animal's SDGBV can be estimated based on genomic information and used to design specific genomic mating plans. Estimated SDGBV are an additional tool for mating programs, which allows breeders to identify and match mating partners using specific haplotype information.

Table 3 Correlations (r) between SDGBV with real progeny variations for different traits per minimum number of offspring per sire

Minimum number of offspring per sire	Number of sires	r_{FY}	r_{PY}	r_{SCS}	r_{SBd}
10	409	0.65	0.56	0.60	0.50
50	146	0.90	0.78	0.80	0.72
100	84	0.93	0.83	0.88	0.69
150	48	0.93	0.90	0.90	0.78
200	32	0.93	0.91	0.87	0.85
300	20	0.96	0.93	0.94	0.82
500	7	0.98	0.88	0.90	0.90

PY = protein yield; FY = fat yield; SCS = somatic cell score; SBd = the direct genetic effect for stillbirth.

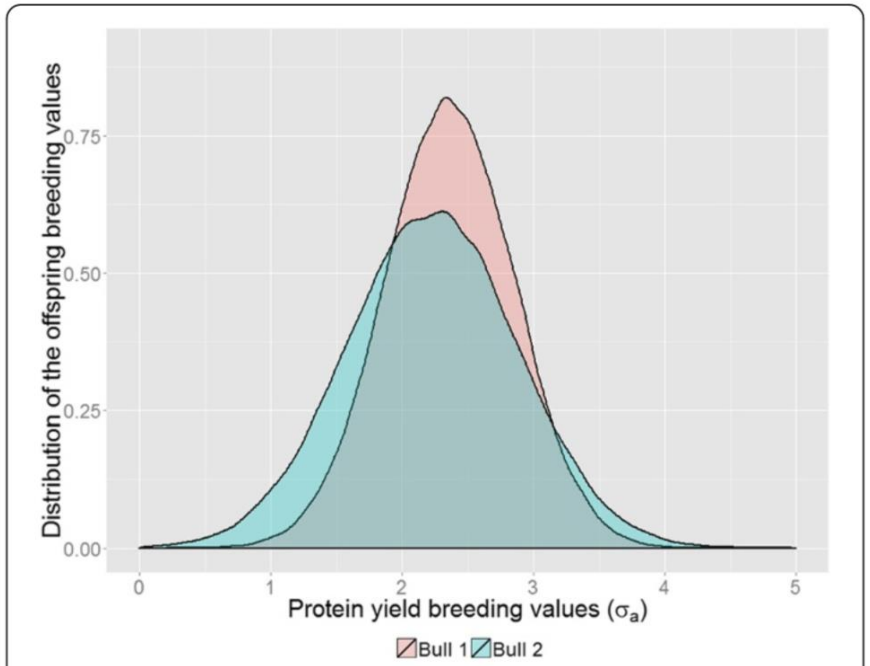


Figure 5 Distribution of the breeding values of offspring for protein yield. Two bulls (with MGBV equal to 1.81 σ_a and 1.68 σ_a and SDGBV equal to 0.29 σ_a and 0.52 σ_a, respectively) are mated with an average female of the population (MGBV equal to 0.55 σ_a, SDGBV equal to 0.39 σ_a).

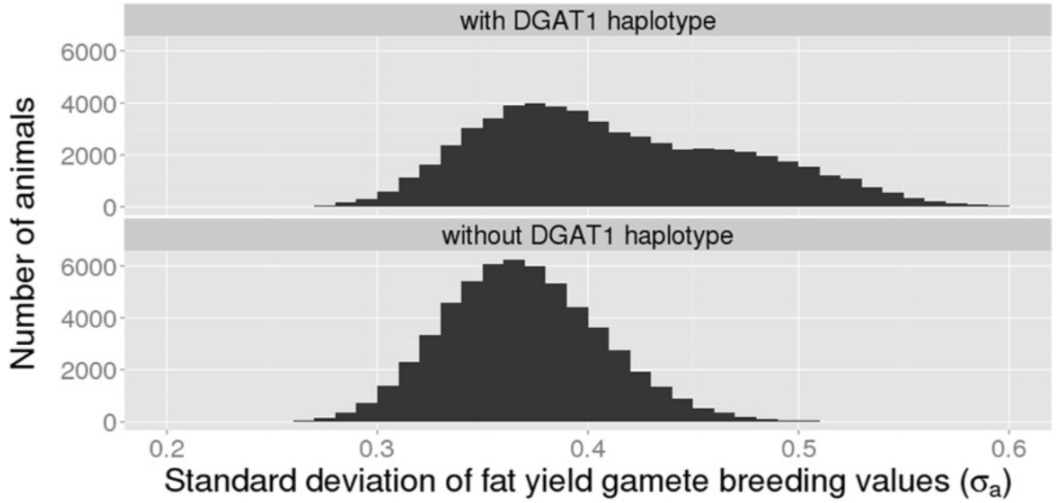


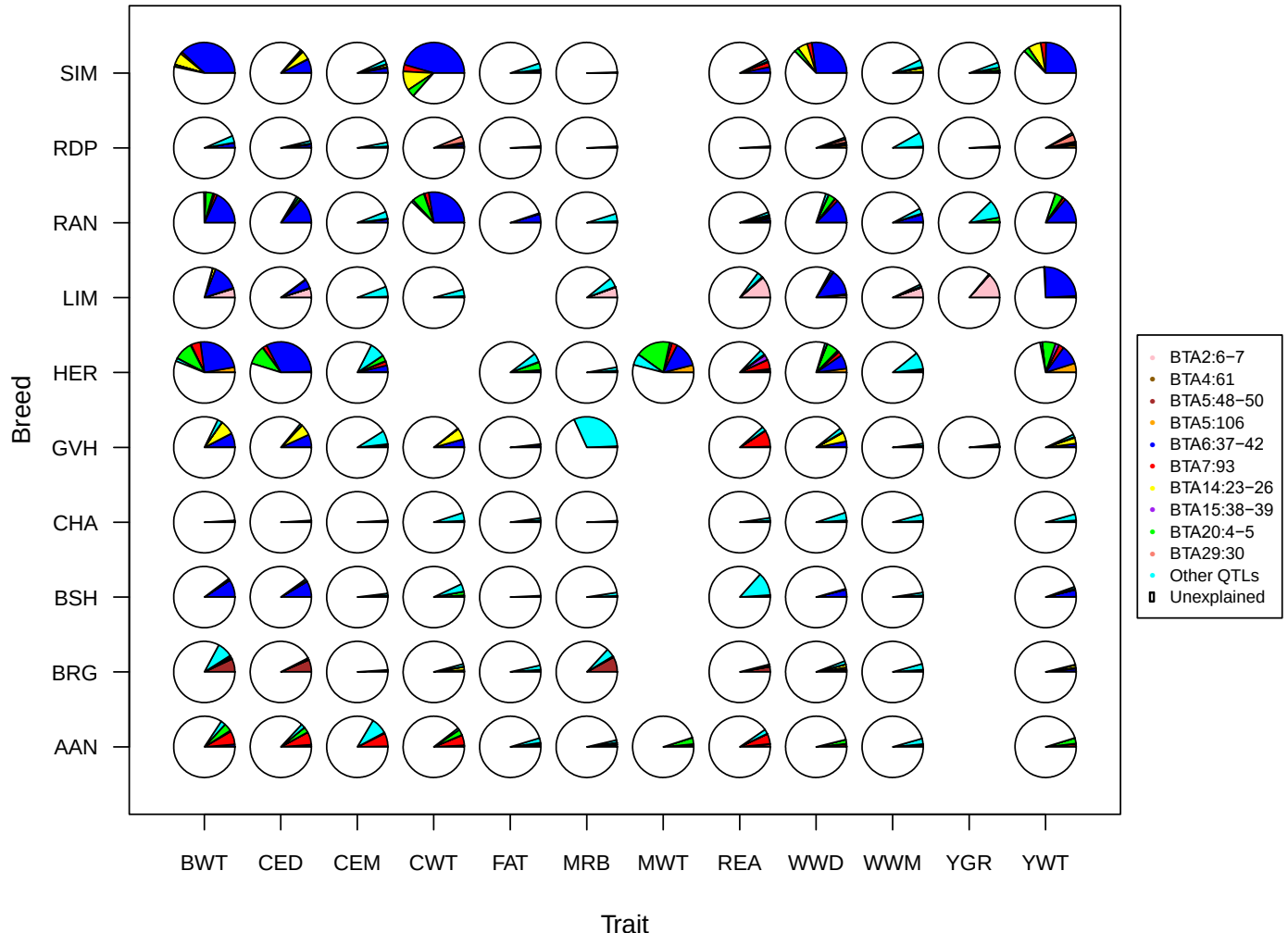
Figure 6 Distribution of SDGBV for fat yield with and without the *DGAT1* haplotype.

aatchi et al. BMC Genomics 2014, 15:442
ttp://www.biomedcentral.com/1471-2164/15/442

RESEARCH ARTICLE Open Access

Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds

Mahdi Saatchi[1], Robert D Schnabel[2], Jeremy F Taylor[2] and Dorian J Garrick[1,3*]



High Impact Genes (markers): USAMRC

Could functional variants be more effective?

Genetic correlations between birth weight and GPE-trained birth weight MBV

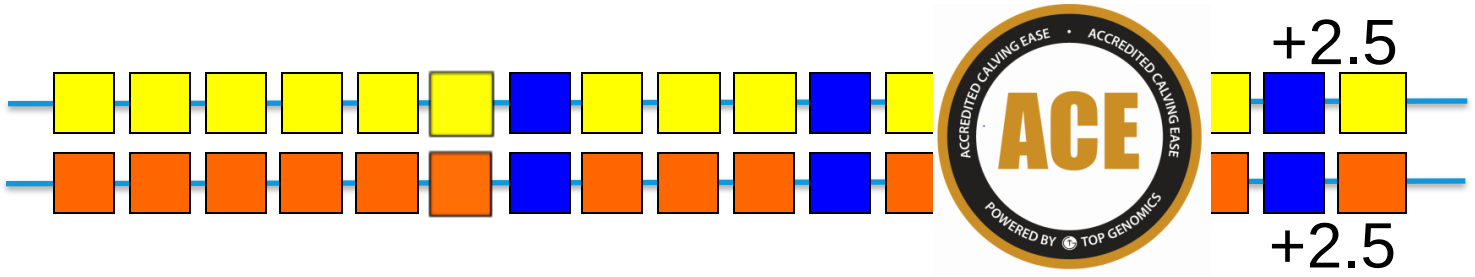
Marker set	size	GPE h^2	Evaluated population		
			SFA	Red Angus	Simmental
F250 shared with 50K	33,869	0.45	0.35	0.44	0.25
Significant GPE effects	279	0.34	0.44	0.43	0.25
LD reduced	12	0.30	0.49	0.47	0.28
NCAPG	1	0.06	0.31	0.32	0.22

- Small sets of functional variants can explain meaningful phenotypic variation within and across populations
  - depends on number and size of effects - difficult to identify variants causing sm effects, especially for traits influenced by many variants with small effects

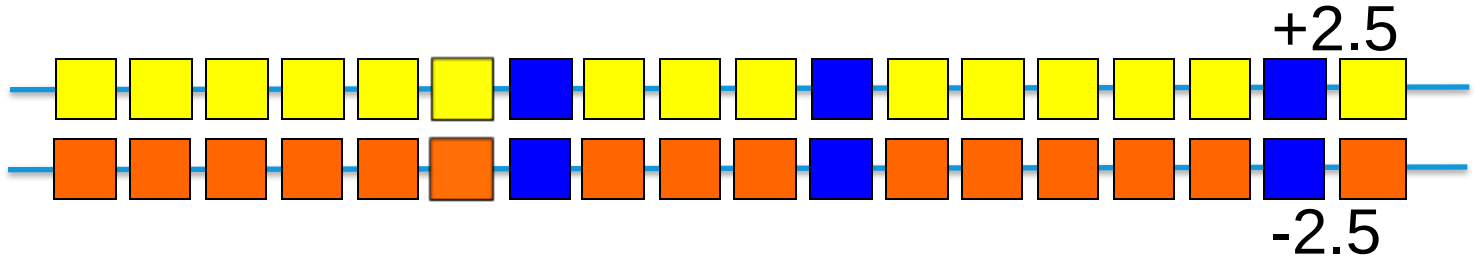
BeefImprovement.org/Symposium • #BIF2020

Larry Kuehn, Warren Snelling, Mark Thallman, BIF 2020.

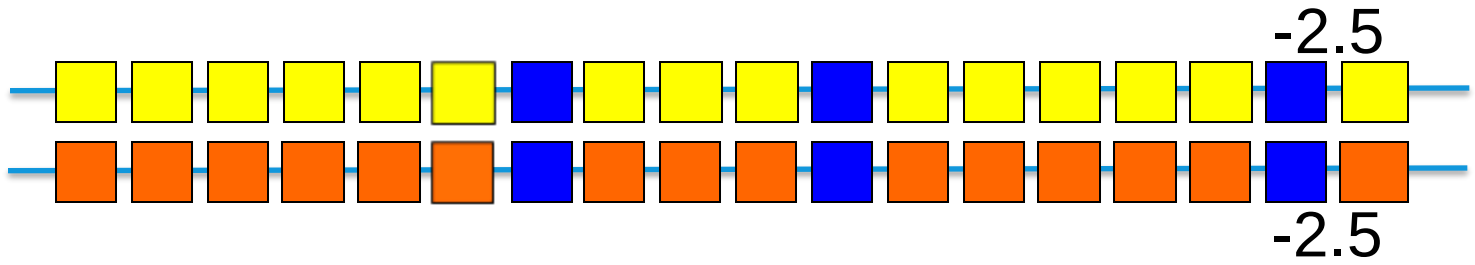
Which bull do you choose as a heifer bull?



CE EPD= 15



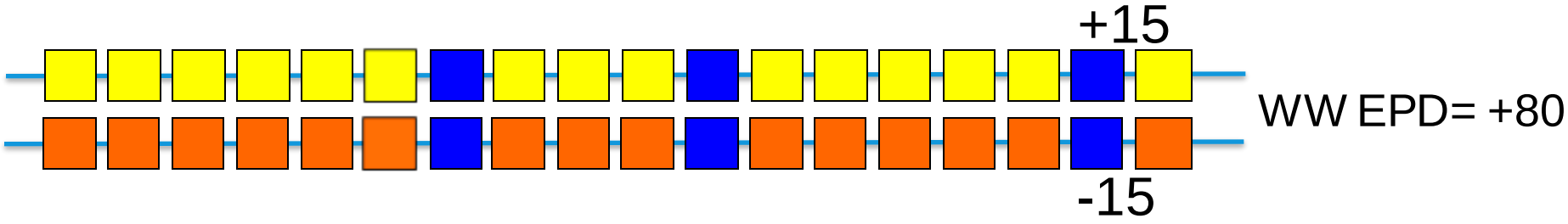
CE EPD= 15

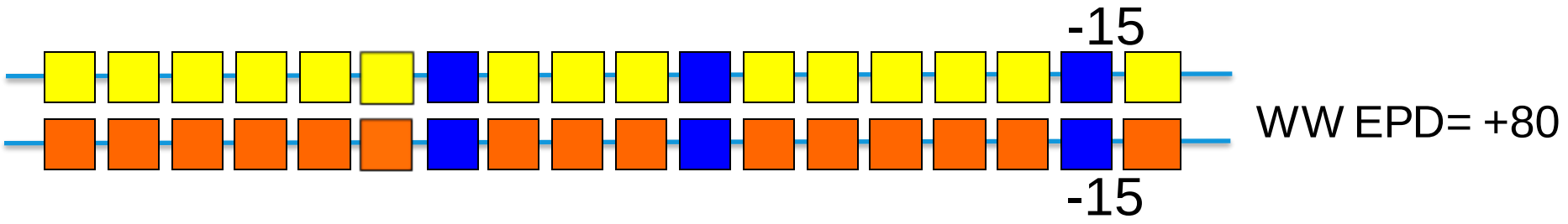


CE EPD= 15

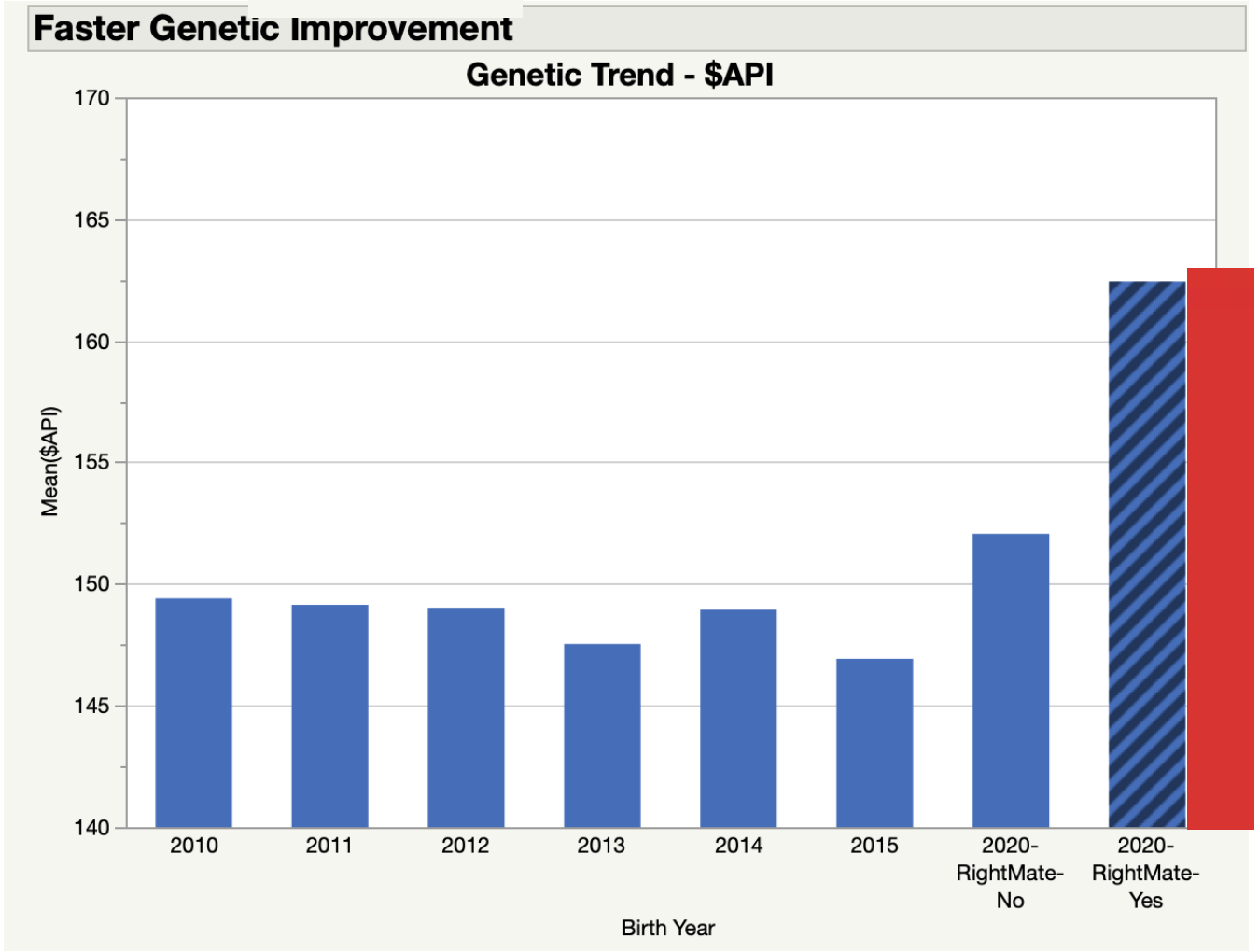
Which bull do you mate to a low growing cow?

That is a Precision Breeding!





Faster Genetic Improvement:

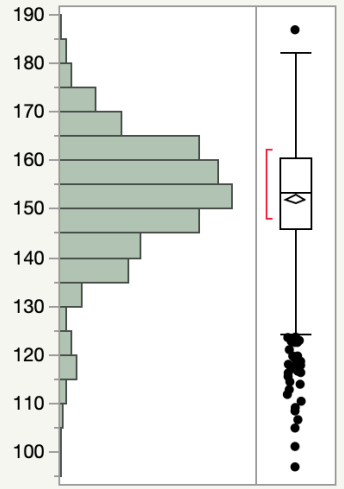


Projected

RightMate Validation: API

RightMate=No

API



Quantiles

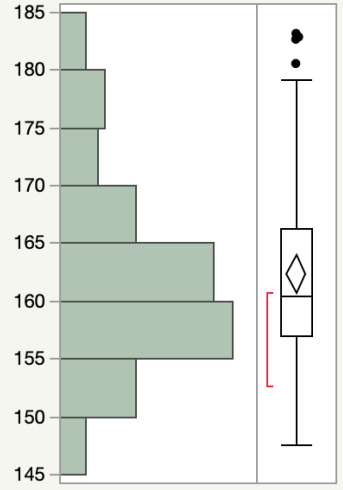
100.0%	maximum	186.7
99.5%		181.19
97.5%		173.55
90.0%		166.2
75.0%	quartile	160.4
50.0%	median	153.3
25.0%	quartile	145.7
10.0%		137.6
2.5%		117.8
0.5%		105.99
0.0%	minimum	96.8

Summary Statistics

Mean	152.05846
Std Dev	12.843435

RightMate=Yes

API



Quantiles

100.0%	maximum	183.1
99.5%		183.1
97.5%		182.715
90.0%		176.05
75.0%	quartile	166.275
50.0%	median	160.4
25.0%	quartile	156.925
10.0%		153.21
2.5%		149.1125
0.5%		147.5
0.0%	minimum	147.5

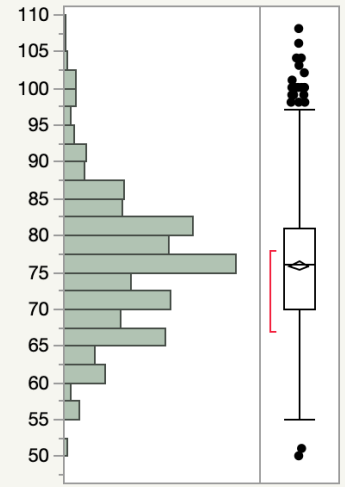
Summary Statistics

Mean	162.43125
Std Dev	8.2339133

RightMate Validation: Actual Birth Weight

RightMate=No

Actual BirthWt



Quantiles

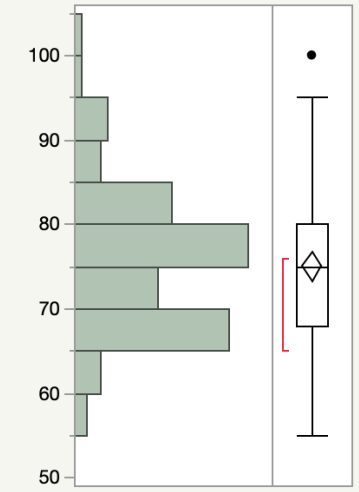
100.0%	maximum	108
99.5%		104
97.5%		98
90.0%		87
75.0%	quartile	81
50.0%	median	76
25.0%	quartile	70
10.0%		65
2.5%		59.55
0.5%		55
0.0%	minimum	50

Summary Statistics

Mean	75.905533
Std Dev	9.0881113

RightMate=Yes

Actual BirthWt



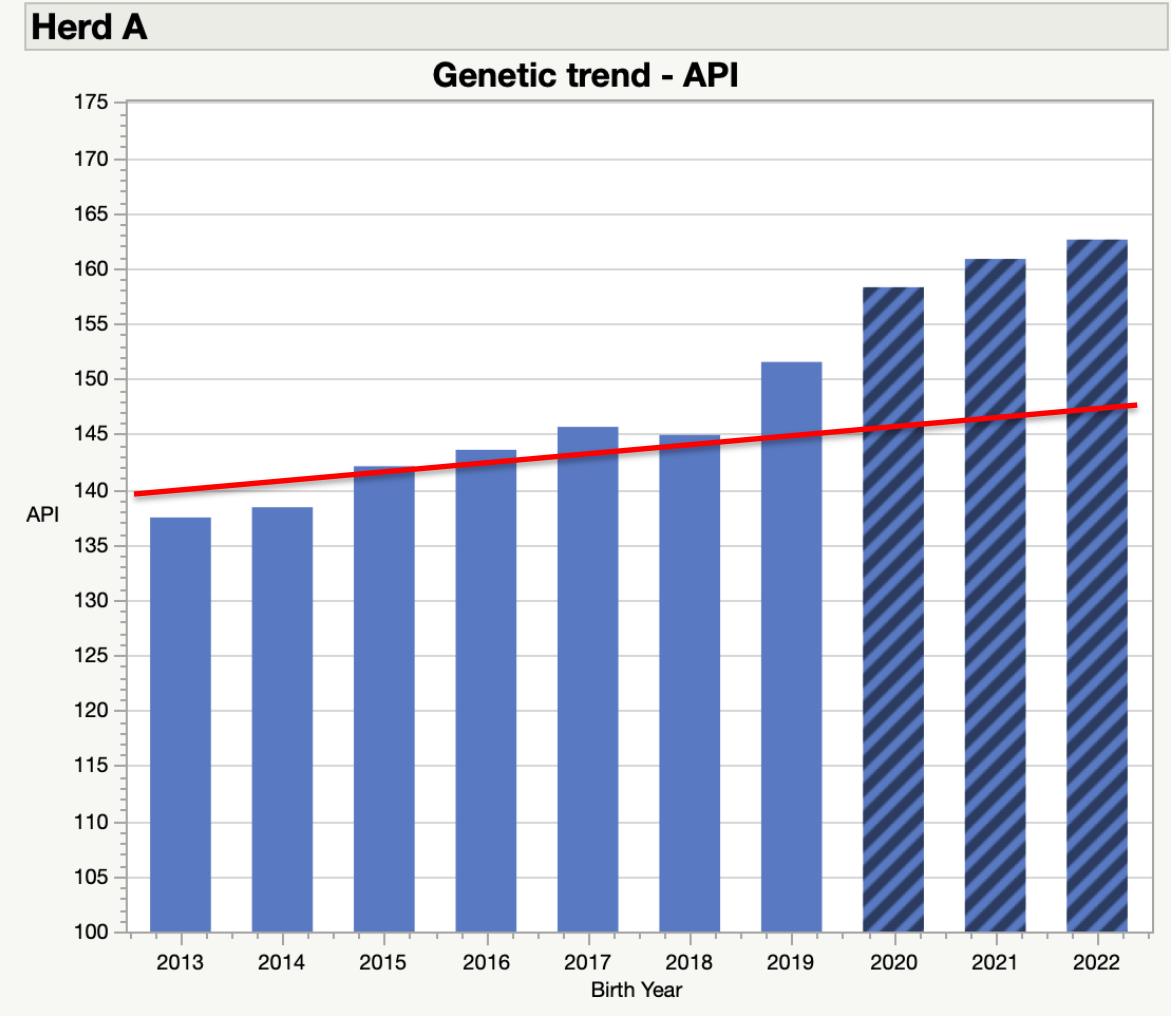
Quantiles

100.0%	maximum	100
99.5%		100
97.5%		94.575
90.0%		85.3
75.0%	quartile	80
50.0%	median	75
25.0%	quartile	68
10.0%		65
2.5%		59.7
0.5%		55
0.0%	minimum	55

Summary Statistics

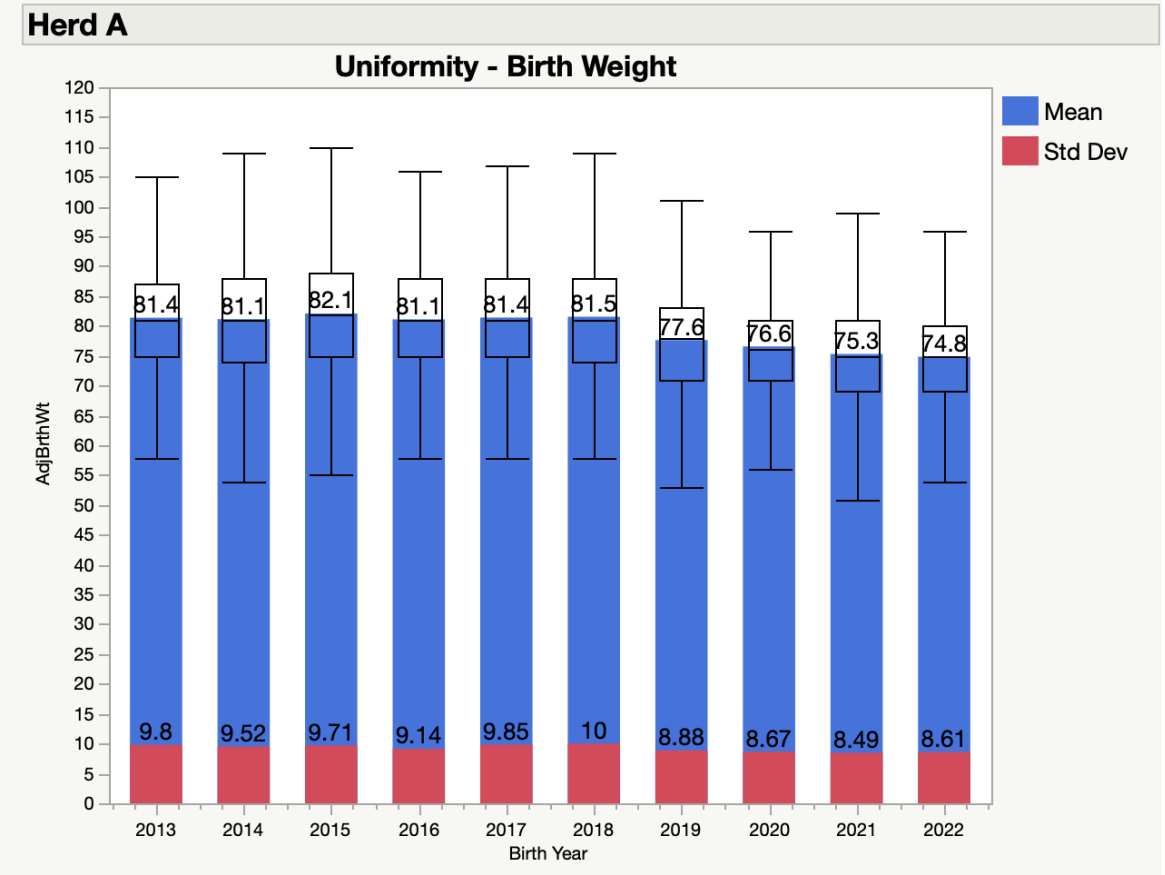
Mean	75.083333
Std Dev	8.4811452

Herd A - Genetic Improvement:

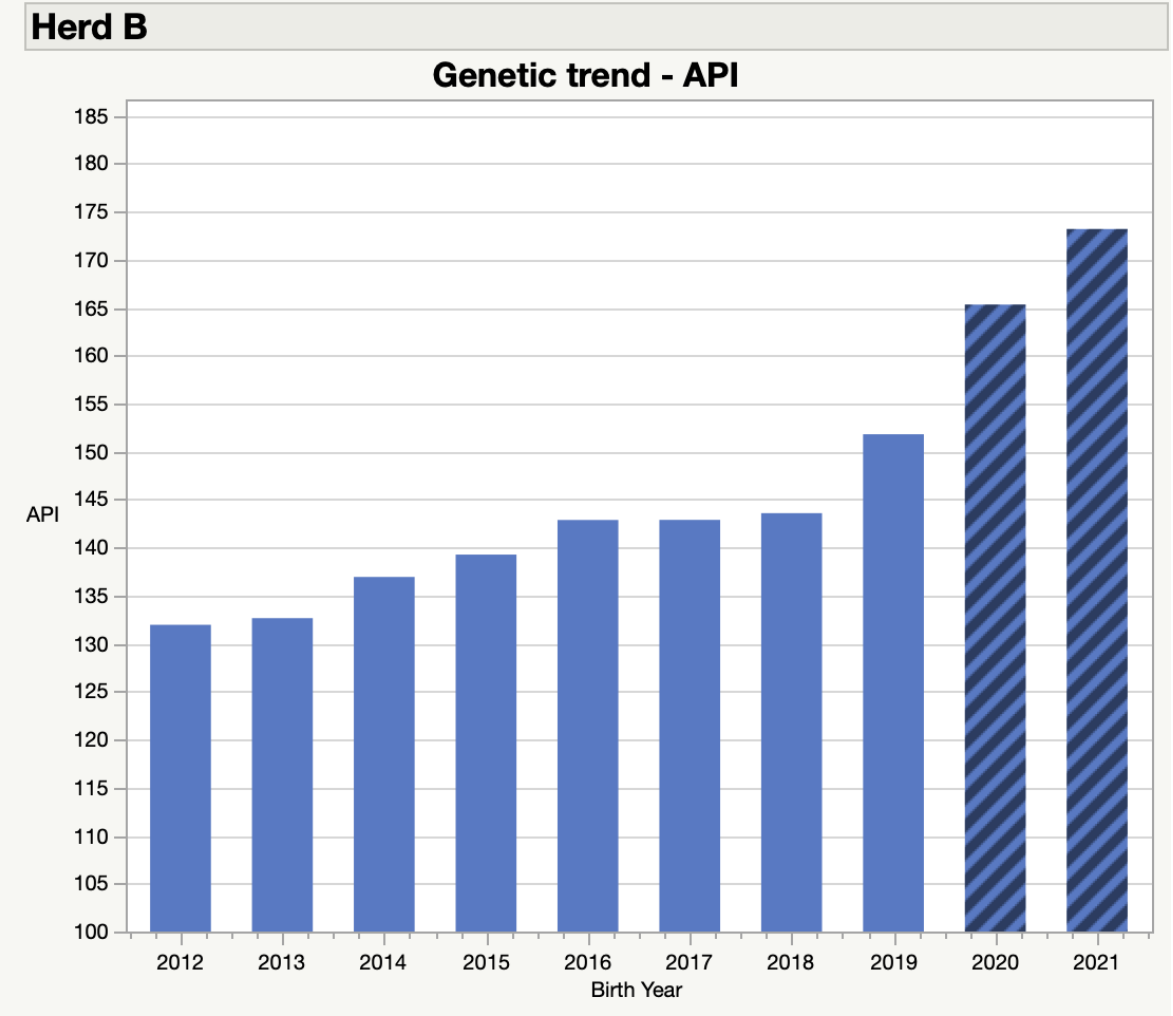


Before RM: +2.09/year
After RM: +3.60/year

Herd A - Uniformity:

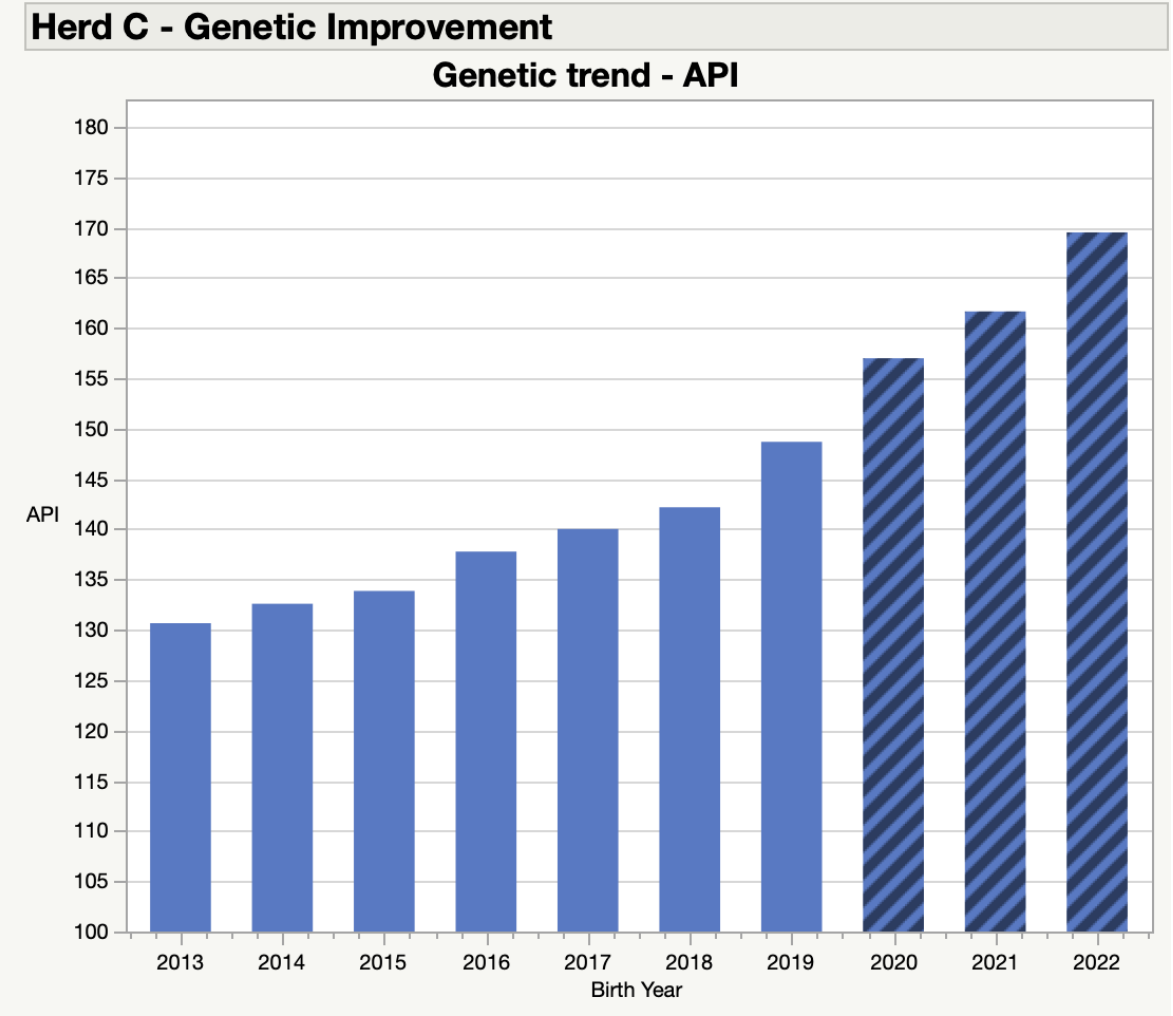


Herd B - Genetic Improvement:



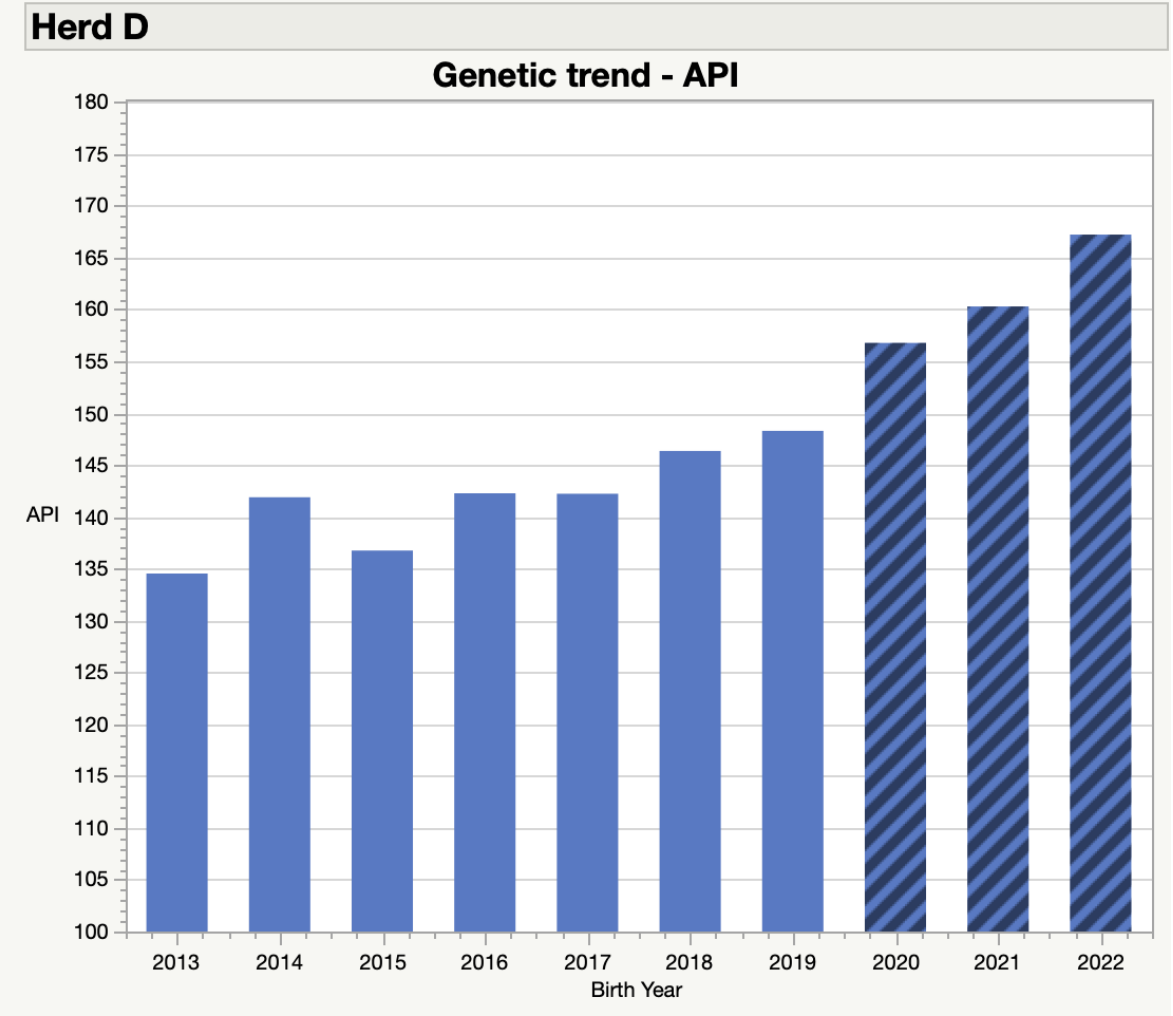
Before RM: +2.55/year
After RM: +11.2/year

Herd C - Genetic Improvement:



Before RM: +2.99/year
After RM: +6.67/year

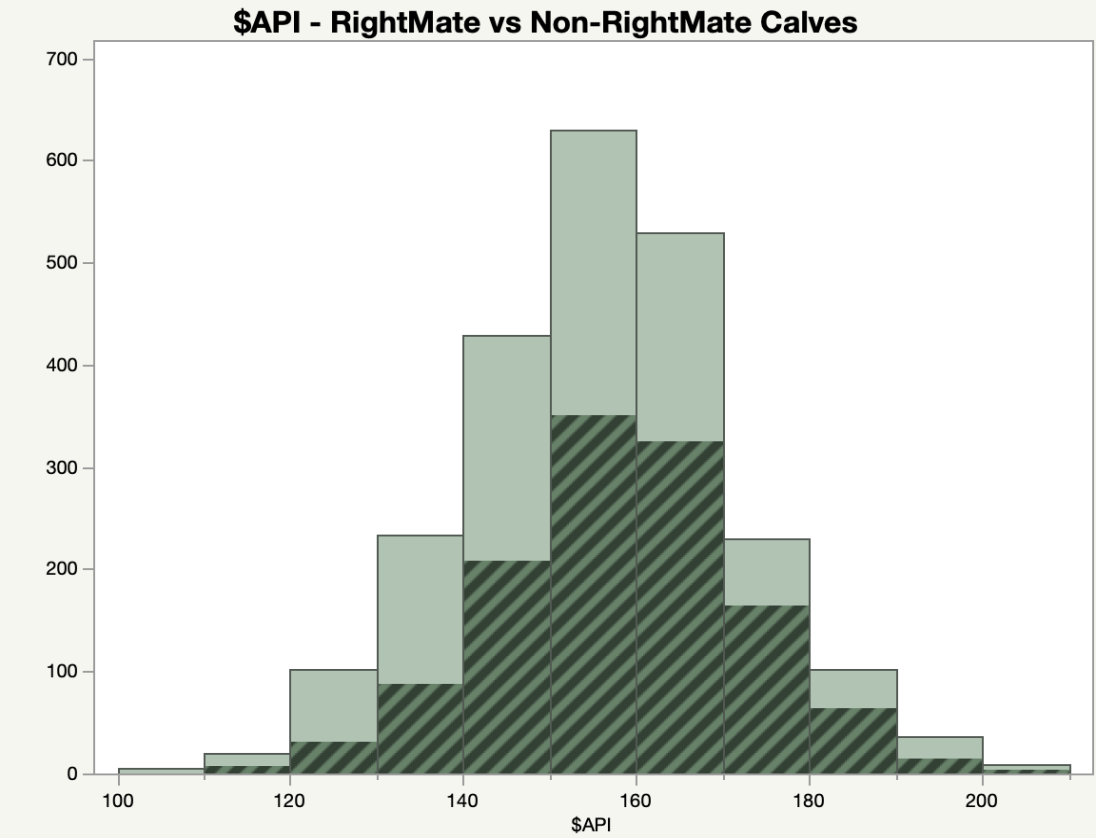
Herd D - Genetic Improvement:



Before RM: +2.05/year
After RM: +5.91/year

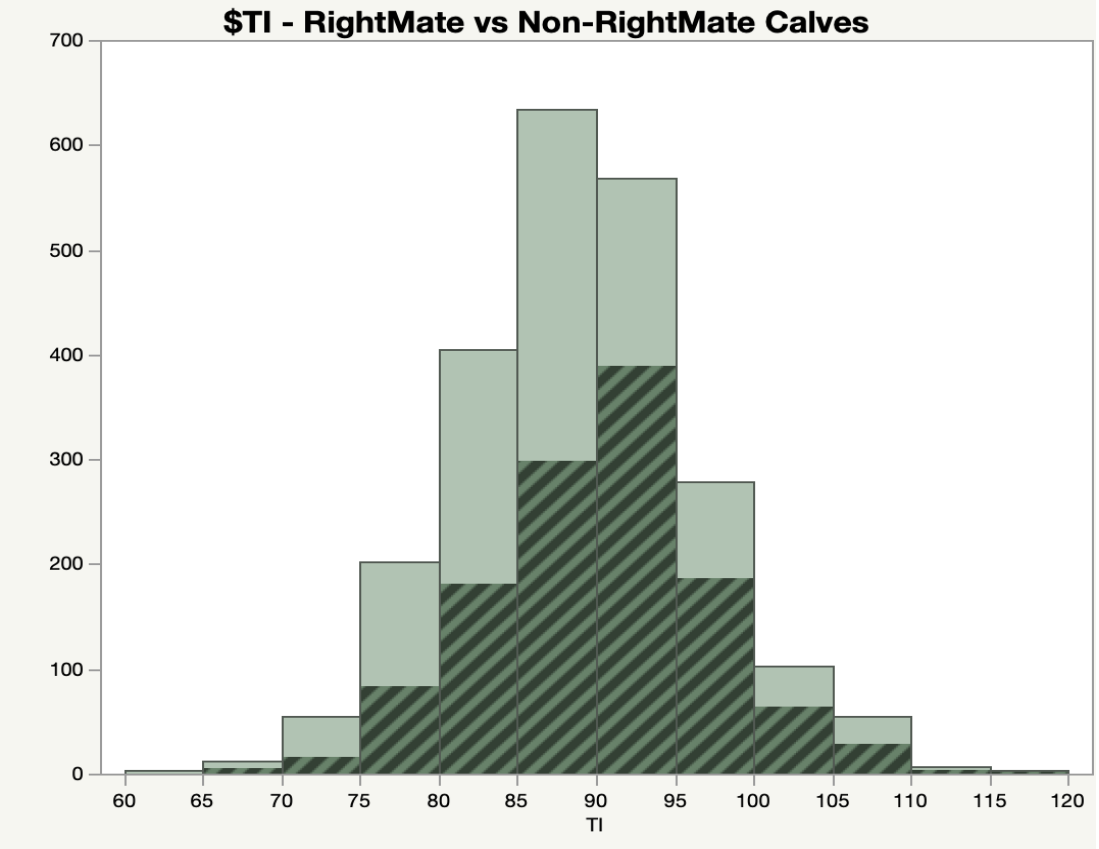
RightMate Results: 2021 Born Calves

Mate	N Calves	$API
Non-RightMate	1274	152.8
RightMate	1242	158.2



RightMate Results: 2021 Born Calves

Mate	N Calves	$TI
Non-RightMate	1274	87.4
RightMate	1242	90.2



RightMate Results: 2021 Born Calves

Traits	Non-RightMate	RightMate	Diff.
CE	13.6	14.2	+0.8
BW	-0.3	-0.6	-0.3
WW	80.2	81.7	+1.5
YW	125.6	128.3	+2.7
ADG	0.28	0.29	+0.01
MCE	7.8	8.1	+0.3
MILK	26.2	25.7	-0.5
MWW	66.3	66.5	+0.2

Traits	Non-RightMate	RightMate	Diff.
STAY	17.7	18.1	+0.4
CW	36.4	37.3	+0.9
YG	-0.26	-0.26	0
MRB	0.46	0.51	+0.05
BF	-0.05	-0.04	+0.01
REA	0.80	0.83	+0.03
SHR	-0.35	-0.37	-0.02

Commercial Application:

RightChoice powered by TOP GENOMICS

Simplify the decision making and reduce the risk

The 3 Accreditation Logos are designed to simplify bull selection and improve buyer confidence and reducing risk.

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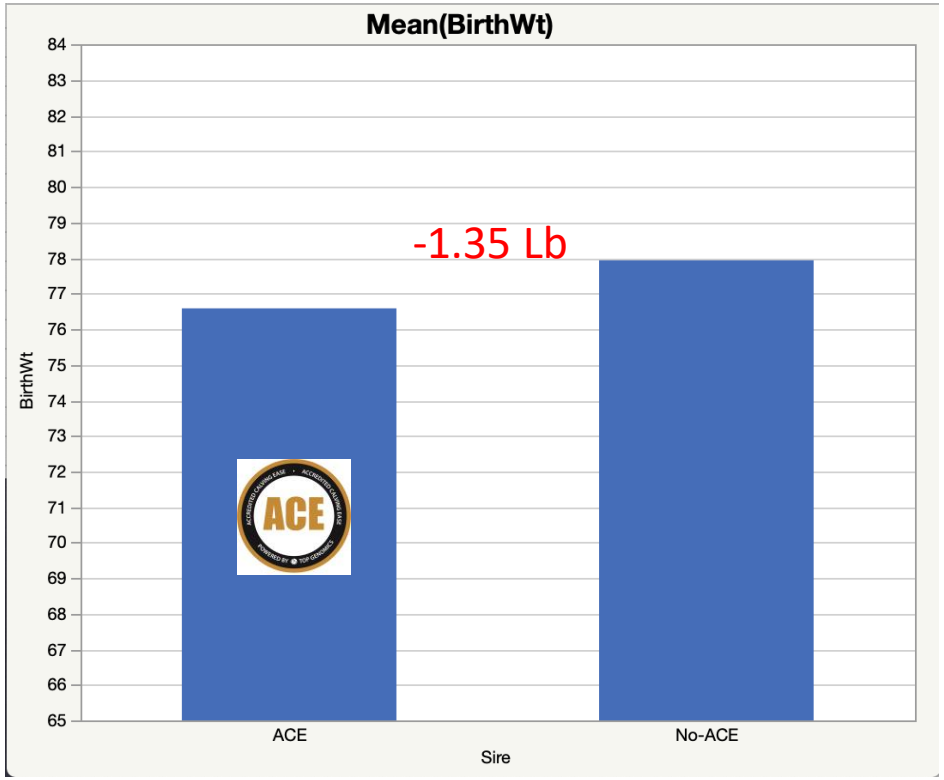

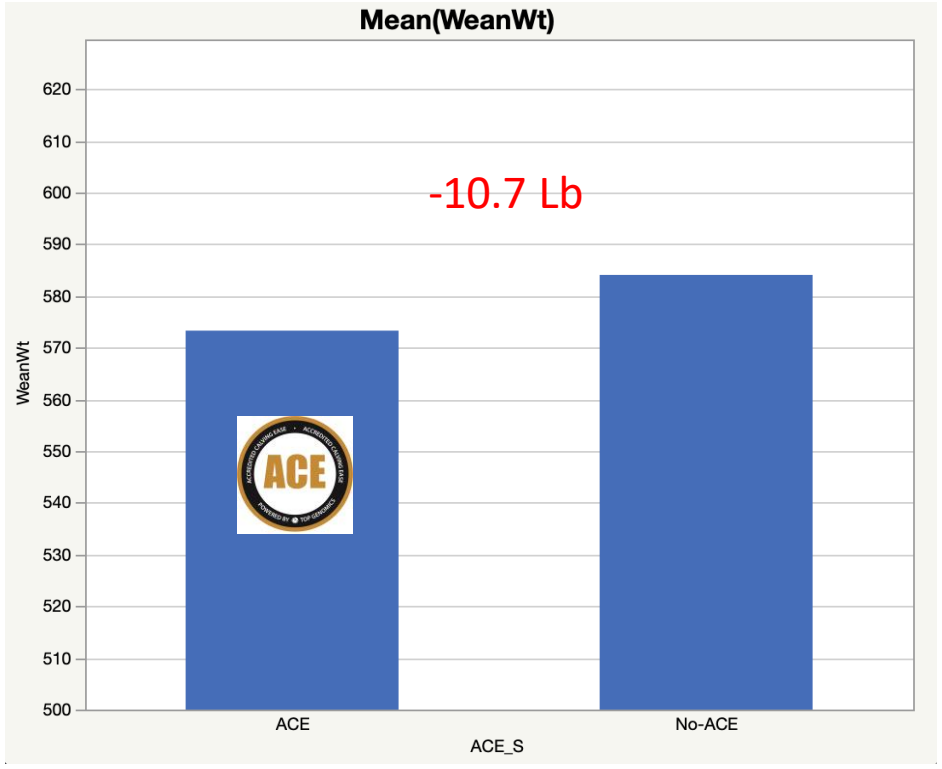

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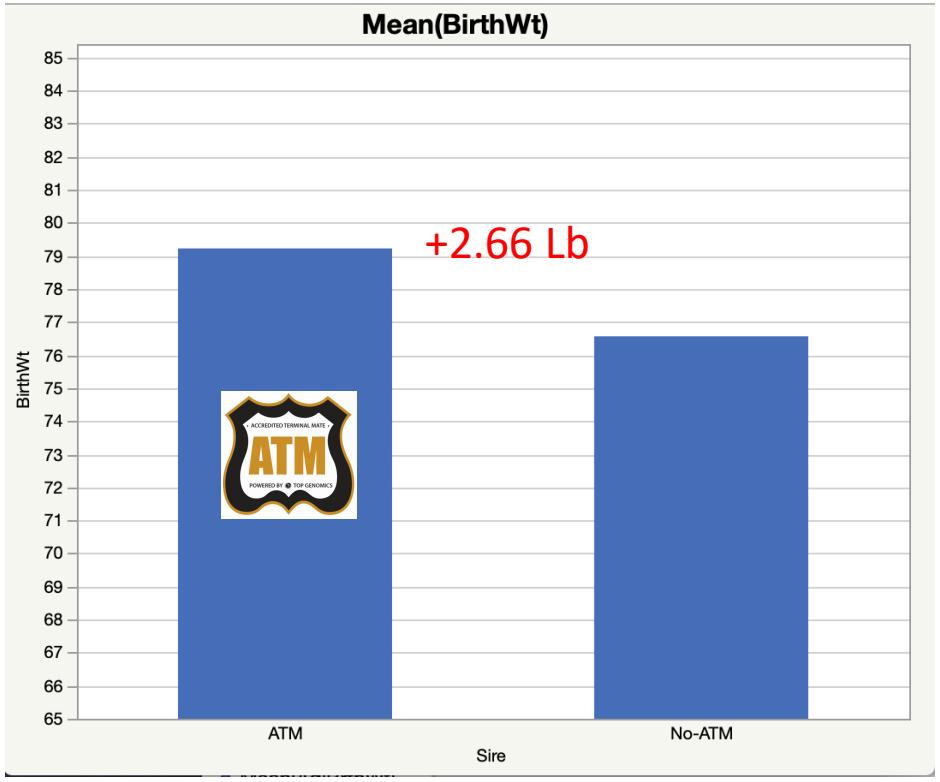

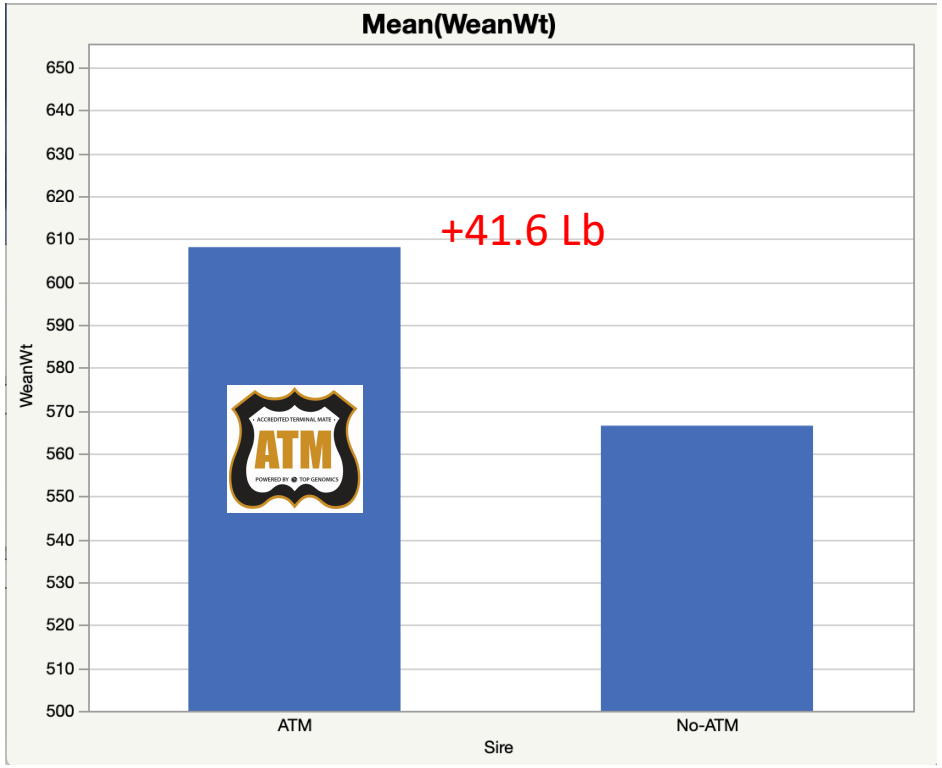

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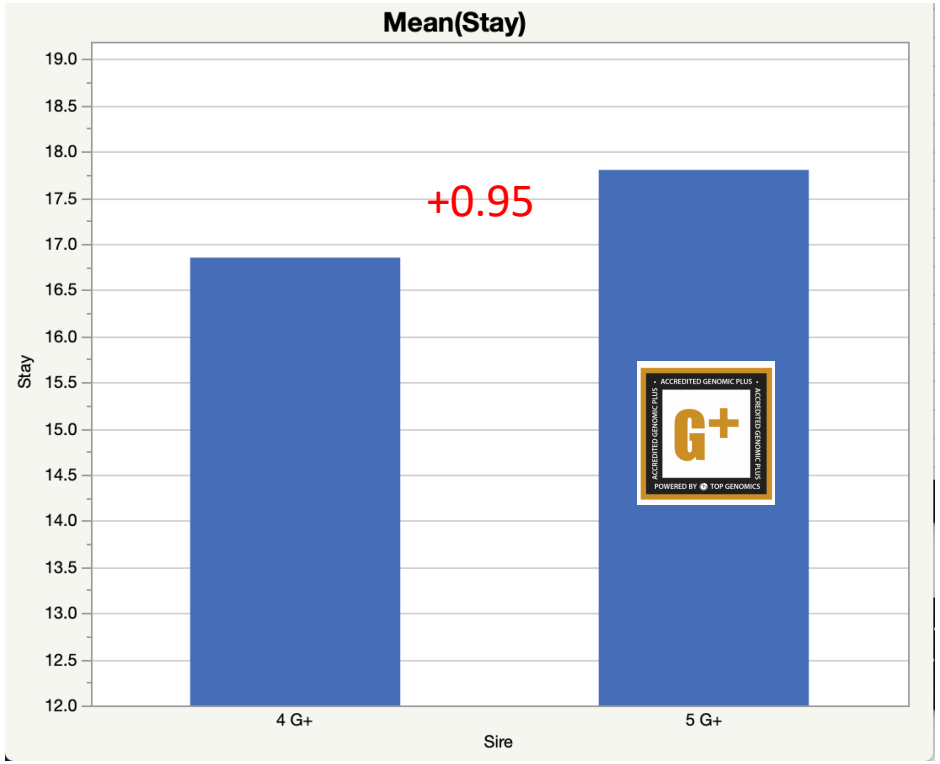

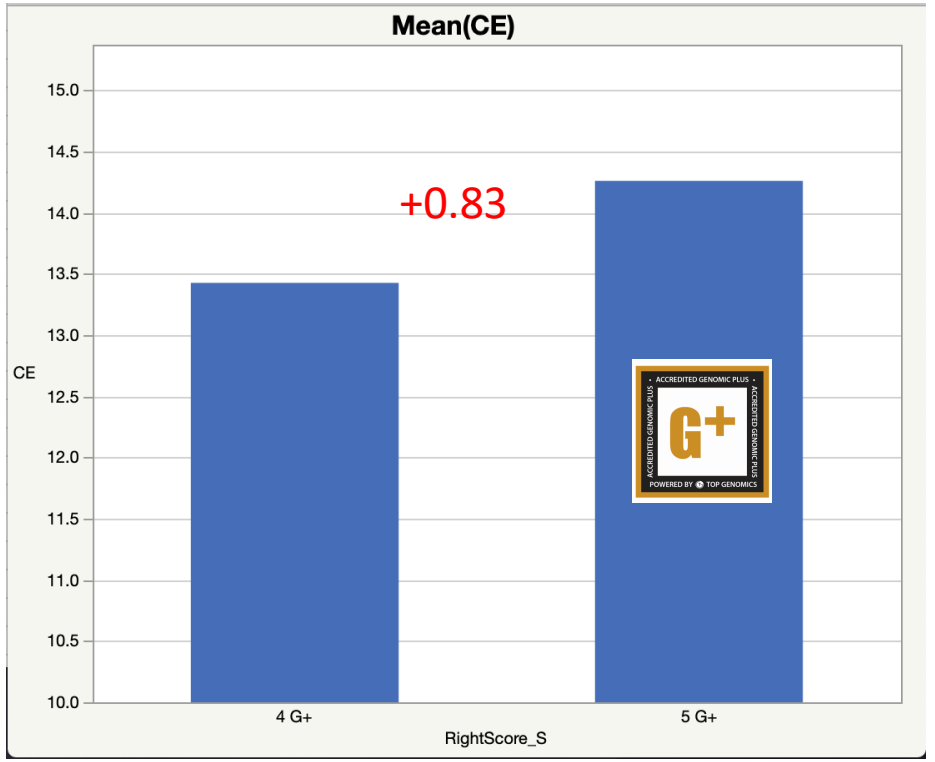

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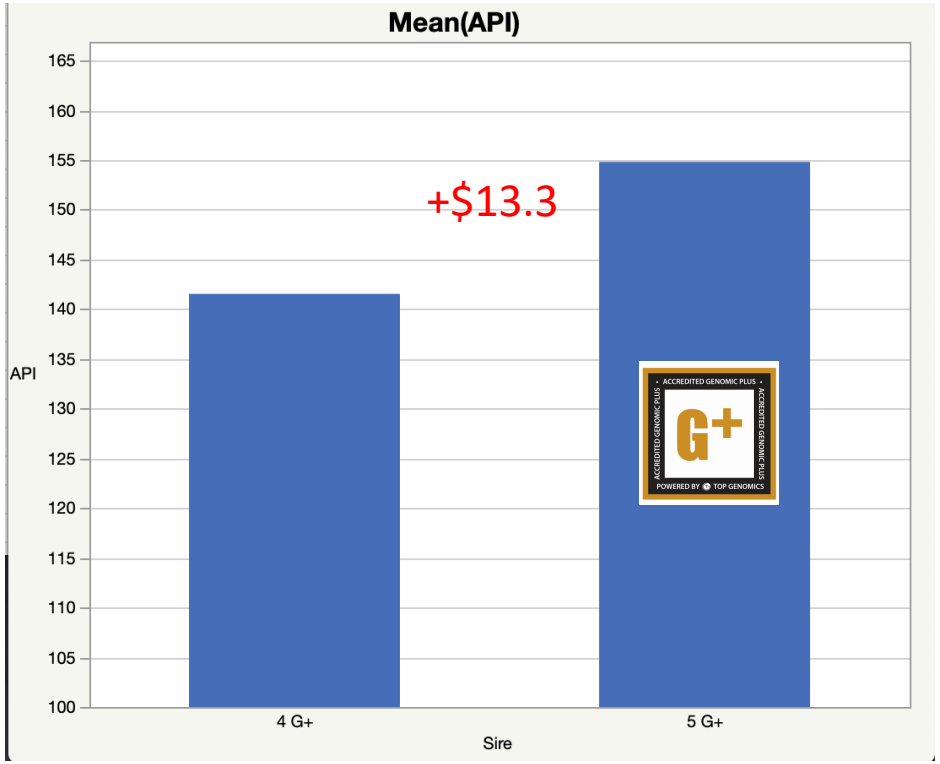

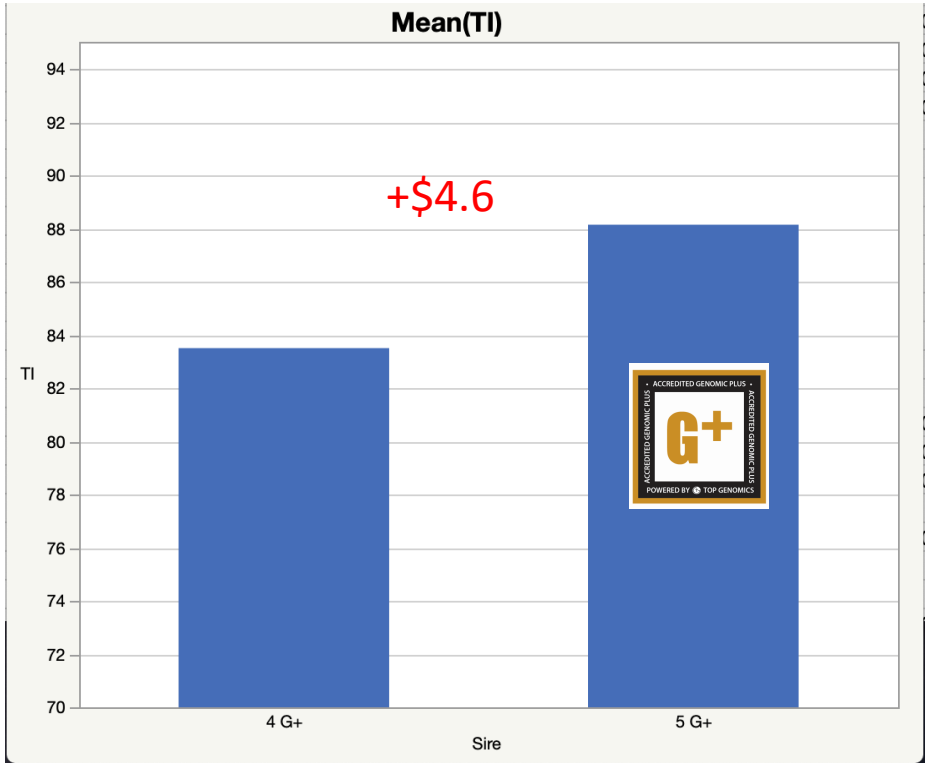

RightMate Benefits:

- **Precision Breeding using Genomics**
- **Avoid Wasted Mating to offer more Marketable Bulls and Heifers**
- **Reduce Variation and More Uniformity**
- **Genetic Improvement at a Higher Speed**
- **Managing Inbreeding, Genetic Diversity and Customized Breeding using MateSel**

2023 RightMate Statistics (So far):

- ✓ **>11,681** Cows RightMated from **>75** Herds

- ✓ **> 4,400** Bulls/Cows RightChoice evaluated from **>62** Herds

RightMate Added-Value for Beef Industry:

- ✓ >10,000 Cows RightMated
- ✓ >5,000 RightMate Calves
- ✓ >2,000 RightMate Bull Calves goes to Commercial Herds
- ✓ ~100 calves per commercial herd bull.
- ✓ >$5 extra genetic improvement ($API)
- ✓ > $1,000,000/year RightMate added-value in commercial beef sector.
- ✓ Much more $ added value for replacement heifers, Seed-stock and AI bulls!

Acknowledgments:

Marty Ropp and all Allied Genetic Resources Staff

Corey Wilkins, Rocky Forseth, Clint Berry, Jared and Jullie Murnin

Thank you!

Genomics wins!

www.topgenomics.com

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