

Modelling different forms of selection for linear type traits in a single-step GBLUP analysis.

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Outline

- Results from **two time periods**
- **Single-step genomic BLUP**, APY, 15,000 random core animals
 - Multiple trait animal model
- Discuss impact of adding
 - **Inbreeding for a Common Ancestor by Year-of-Birth in A^{-1}**
 - **Unknown Parent Groups in A^{-1} and A_{22}^{-1}**
- US Holsteins Linear Type Traits
 - **Different selection intensities and mating practices**

Two time periods

2010 data to predict **2014** GEBVs
2014 data to predict **2018** GEBVs

2010 data

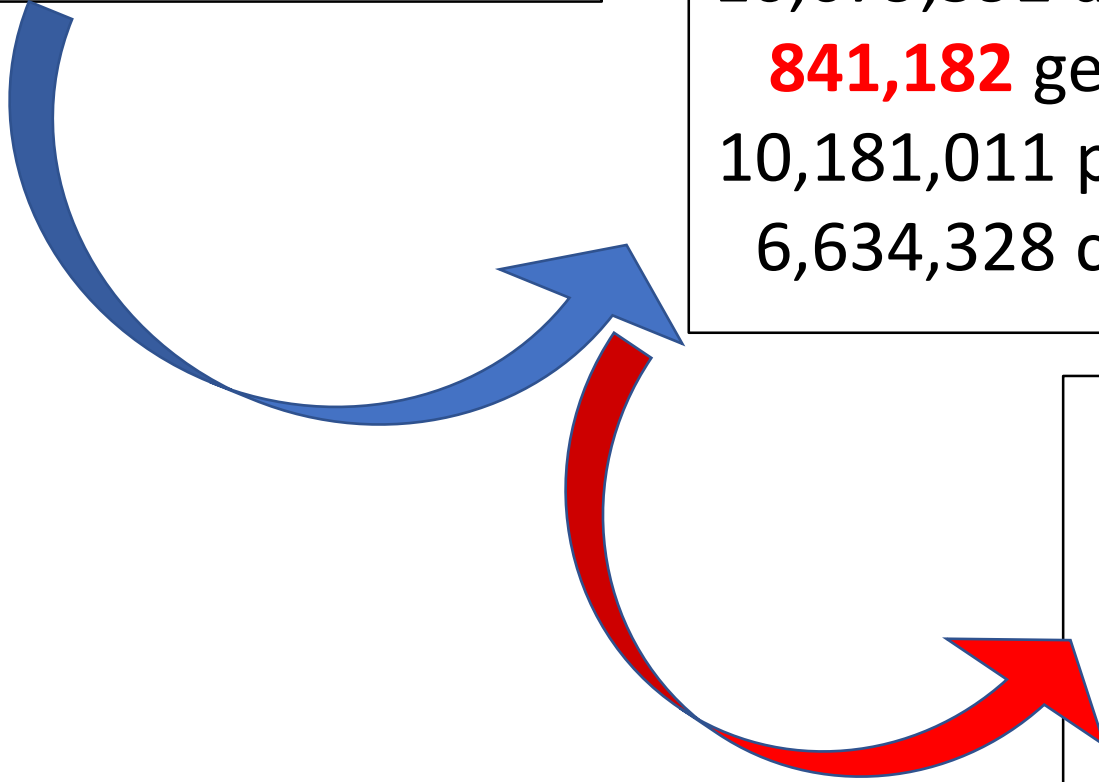
8,642,407 animals in pedigree
150,287 genotyped animals
9,235,328 phenotypic records
5,932,679 cows with records

2014 data

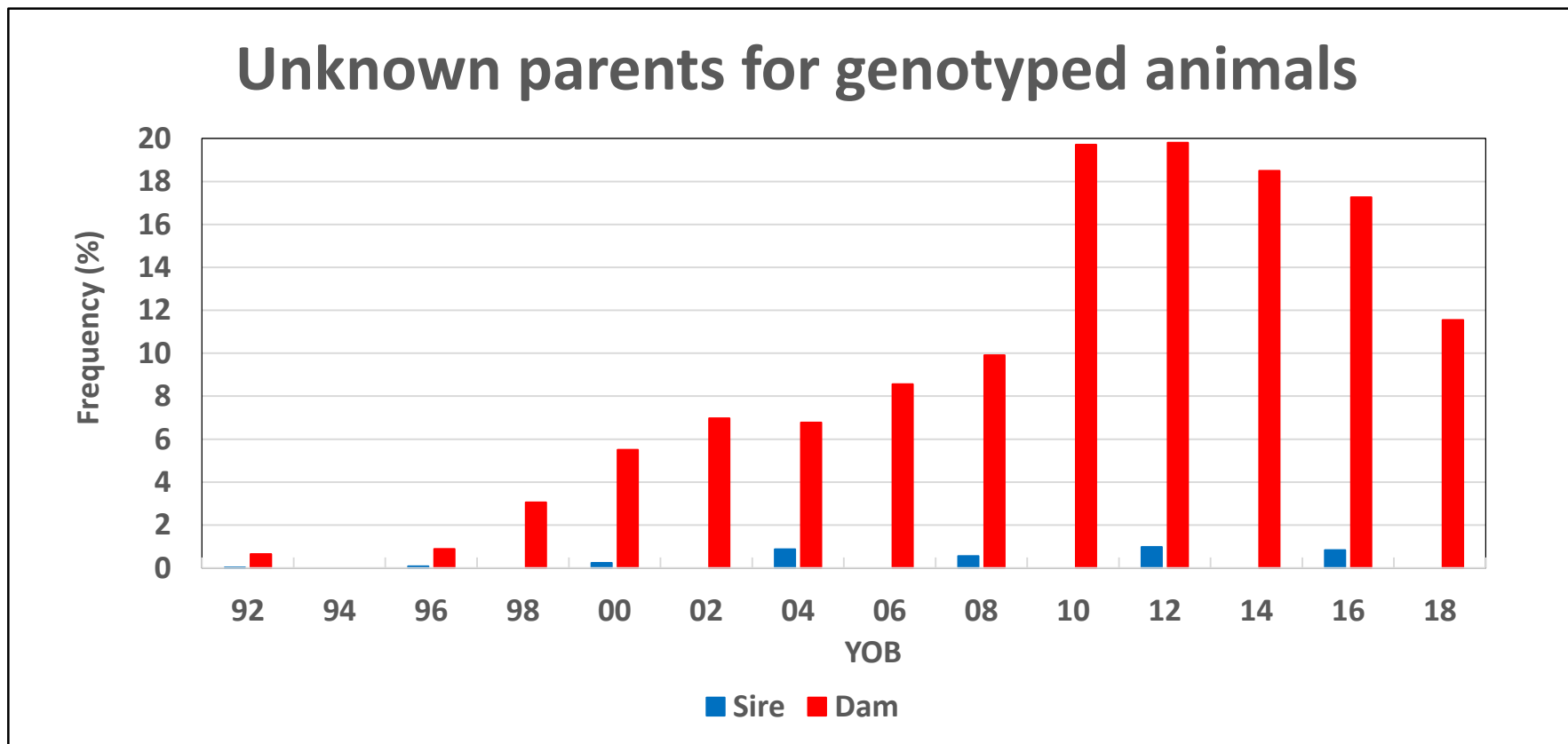
10,679,592 animals in pedigree
841,182 genotyped animals
10,181,011 phenotypic records
6,634,328 cows with records

2018 data

13,591,145 animals in pedigree
2,334,951 genotyped animals
10,946,264 phenotypic records
7,216,767 cows with records



Missing Ancestors



Proper modeling allows for better accounting of these missing ancestors

- **Inbreeding** of a Common Ancestor by Year-of-Birth in A^{-1} (already in A_{22}^{-1})
- **U**nknown **P**arent **G**roups in A^{-1} and A_{22}^{-1}

These MODEL additions should reduce bias

Accounting for inbreeding of missing ancestors results in a decrease in the Additive Genetic Variance.

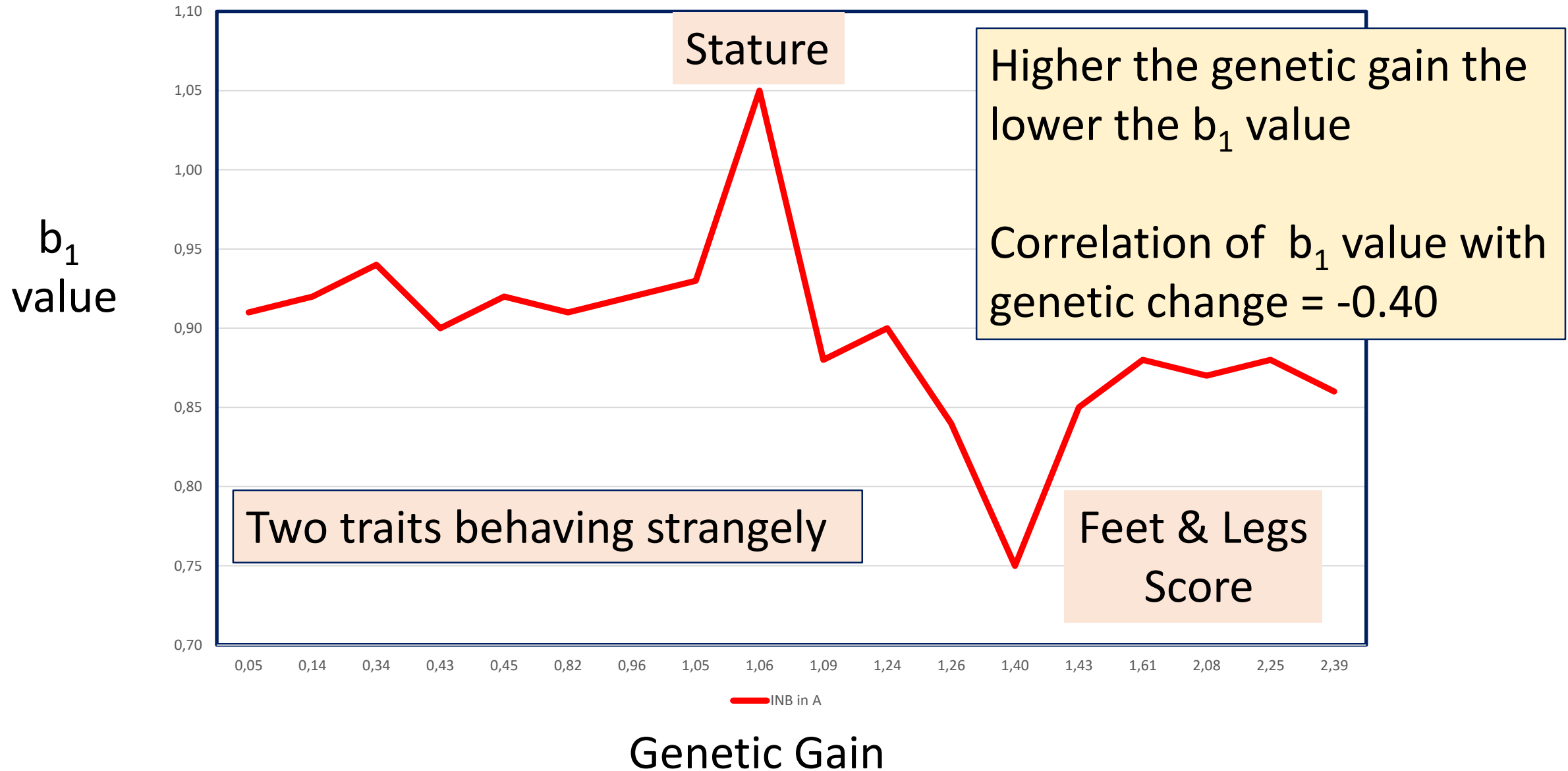
Lowering the Additive Genetic Variance or lowering the Heritability reduces overprediction of GEBVs.

UPG allows for the proper modelling of genetic trend

Results

| Different Models | Average b_1 |
|---|---------------|
| Inbreeding for a Common Ancestors by Year-of-Birth in A^{-1} AND UPG in A^{-1} and A_{22}^{-1} | 1.07 |
| Inbreeding for a Common Ancestor by Year-of-Birth in A^{-1} | 0.90 |
| Parent Average | 0.78 |

Adding Inbreeding to A^{-1}

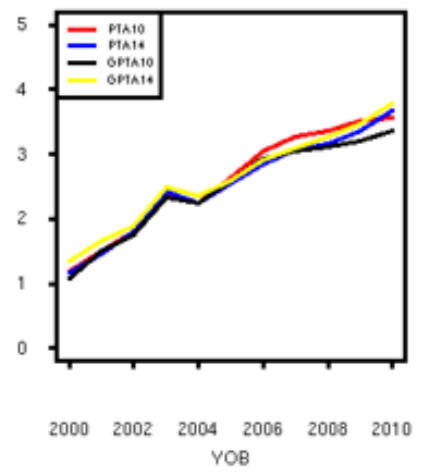


Directional selection

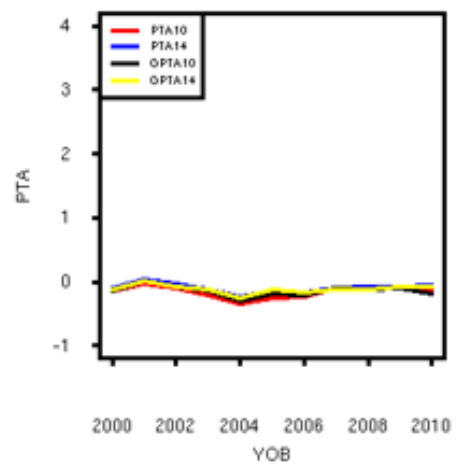
Intermediate optimum

New Trait

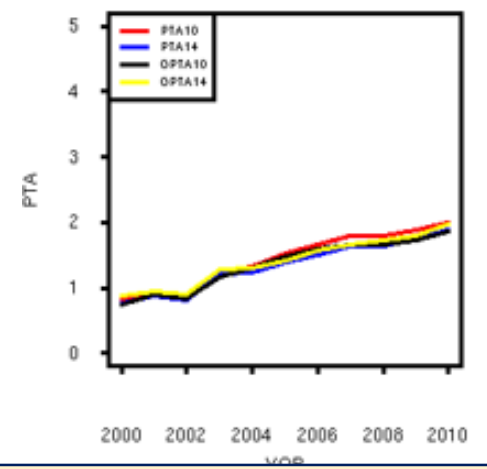
TRAIT 10



TRAIT 7

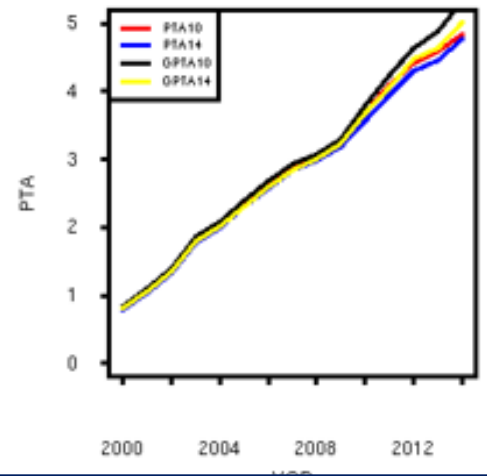


TRAIT 17

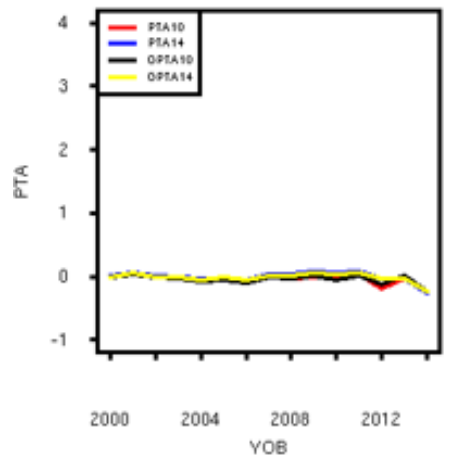


Genotyped bulls: Data up to **2010**

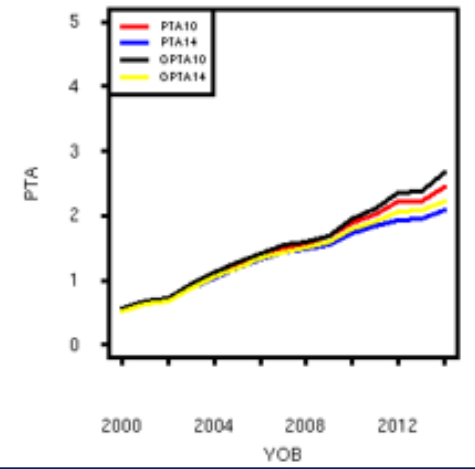
TRAIT 10



TRAIT 7



TRAIT 17



Genotyped bulls: Data up to **2018**

Directional – Score of 50 is ideal

REAR UDDER, HEIGHT - UH

Primary Trait



1-5 pts.
Extremely low



25 pts.
Intermediate height



45-50 pts.
Extremely high

REAR UDDER, WIDTH - UW

Primary Trait



1-5 pts.
Narrow rear udder



25 pts.
Intermediate width



45-50 pts.
Extremely wide rear udder

Higher Height and Wider Width of the udder is related to Higher Milk Yield

Directional – Score of 50 is ideal

REAR LEGS, REAR VIEW - RL

Primary Trait



1-5 pts.
Severe toe-out



45-50 pts.
No toe-out

Higher score
Is Better

Cows with Feet pointing STRAIGHT have better Locomotion

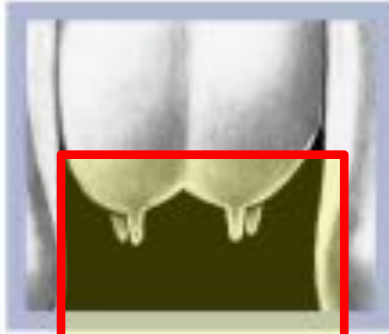
Intermediate optimum – Score of **25** is ideal

FRONT TEAT PLACEMENT - TP

Primary Trait



1-5 pts.
Extremely wide placement
on outside of quarter



25 pts.
Centrally placed
on quarter



45-50 pts.
Base of teats on
extreme inside of quarter

REAR TEAT PLACEMENT - RT

Primary Trait



1-5 pts.
Extremely wide placement
on outside of quarter



25 pts.
Centrally placed
on quarter



45-50 pts.
Base of teats on
extreme inside of quarter

RUMP ANGLE - RA

Primary Trait



1-5 pts.
Pins clearly higher
than hooks



25 pts.
Slight slope from
hooks to pins



45-50 pts.
Extremely sloped from
hooks to pins

REAR LEGS, SIDE VIEW - LS

Primary Trait



1-5 pts.
Posty and straight

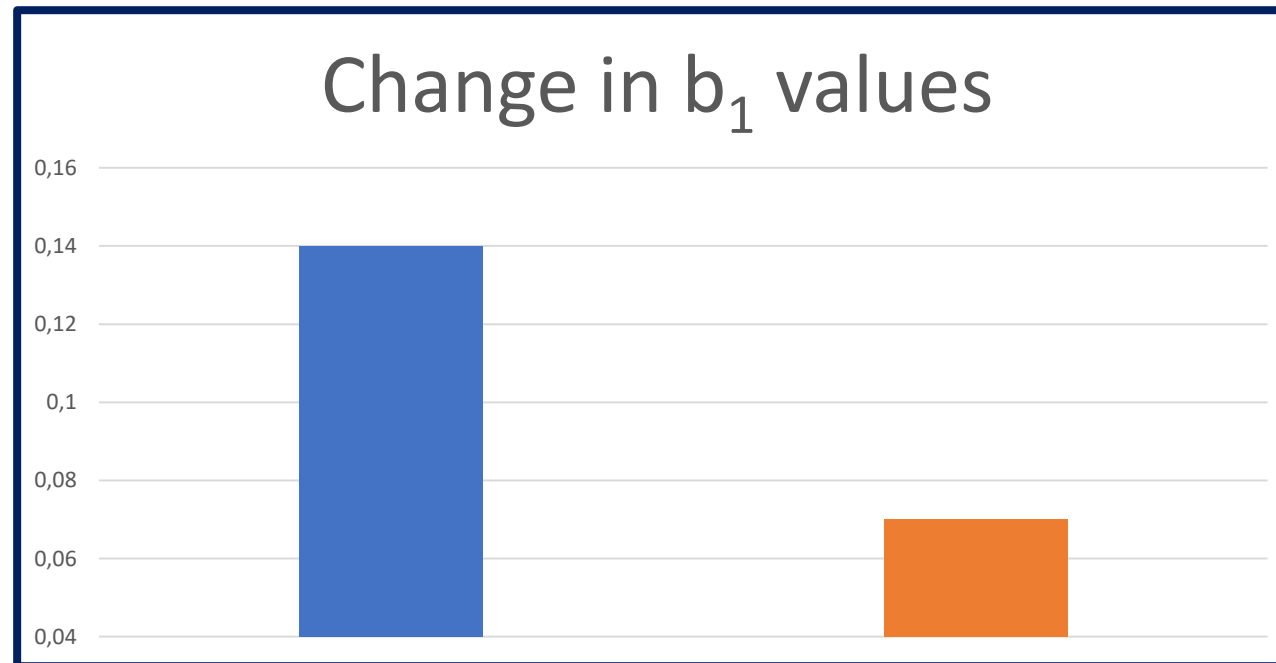


25 pts.
Intermediate set in hock



45-50 pts.
Extremely sickled

Adding Inbreeding values for a Common Ancestor by Year-of-Birth in A^{-1}



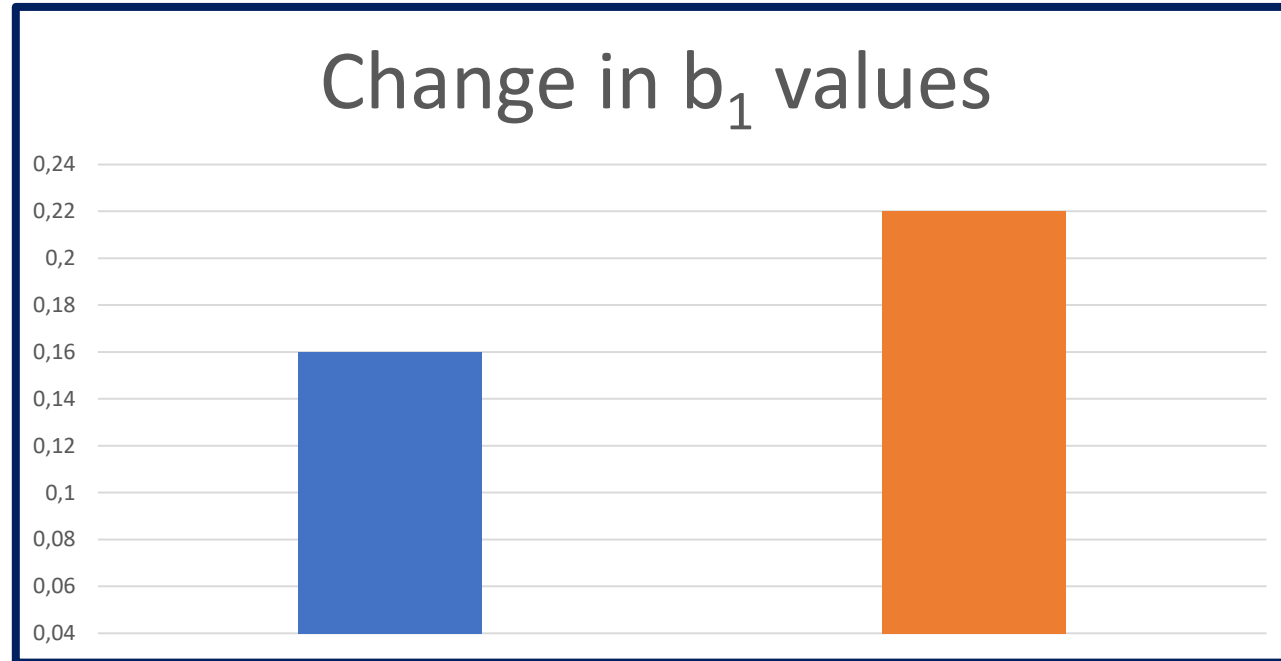
Random or
Positive Assortative Mating

b_1 changed from **0.76** to **0.89**

Negative
Assortative Mating

b_1 changed from **0.84** to **0.91**

Unknown Parent Groups in A^{-1} and A_{22}^{-1}



Random or
Positive Assortative Mating

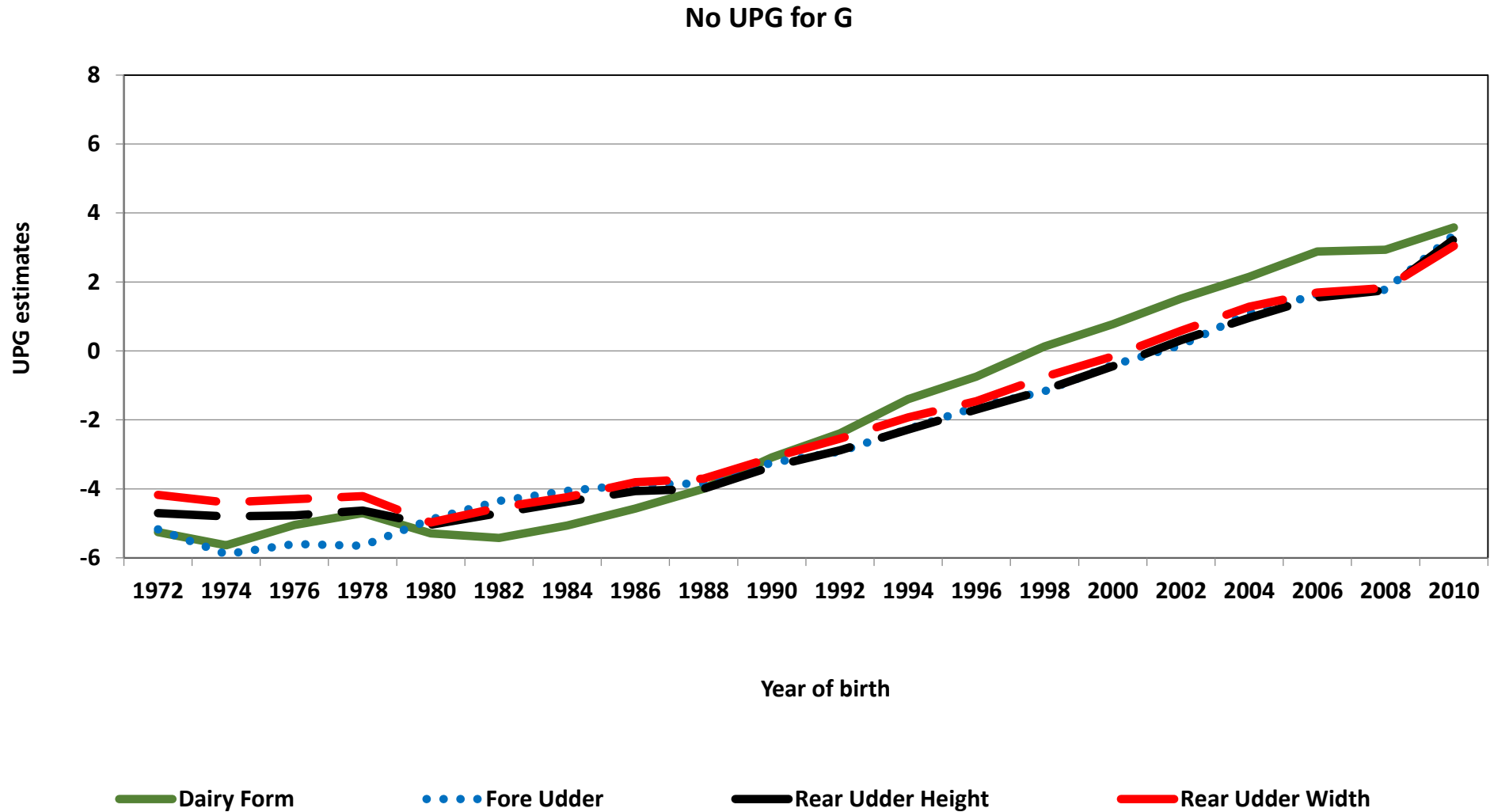
b_1 changed from **0.89** to **1.05**

**Negative
Assortative Mating**

b_1 changed from **0.91** to **1.13**

Under-prediction $b_1 = 1.13$ for traits with **Negative Assortative Mating**

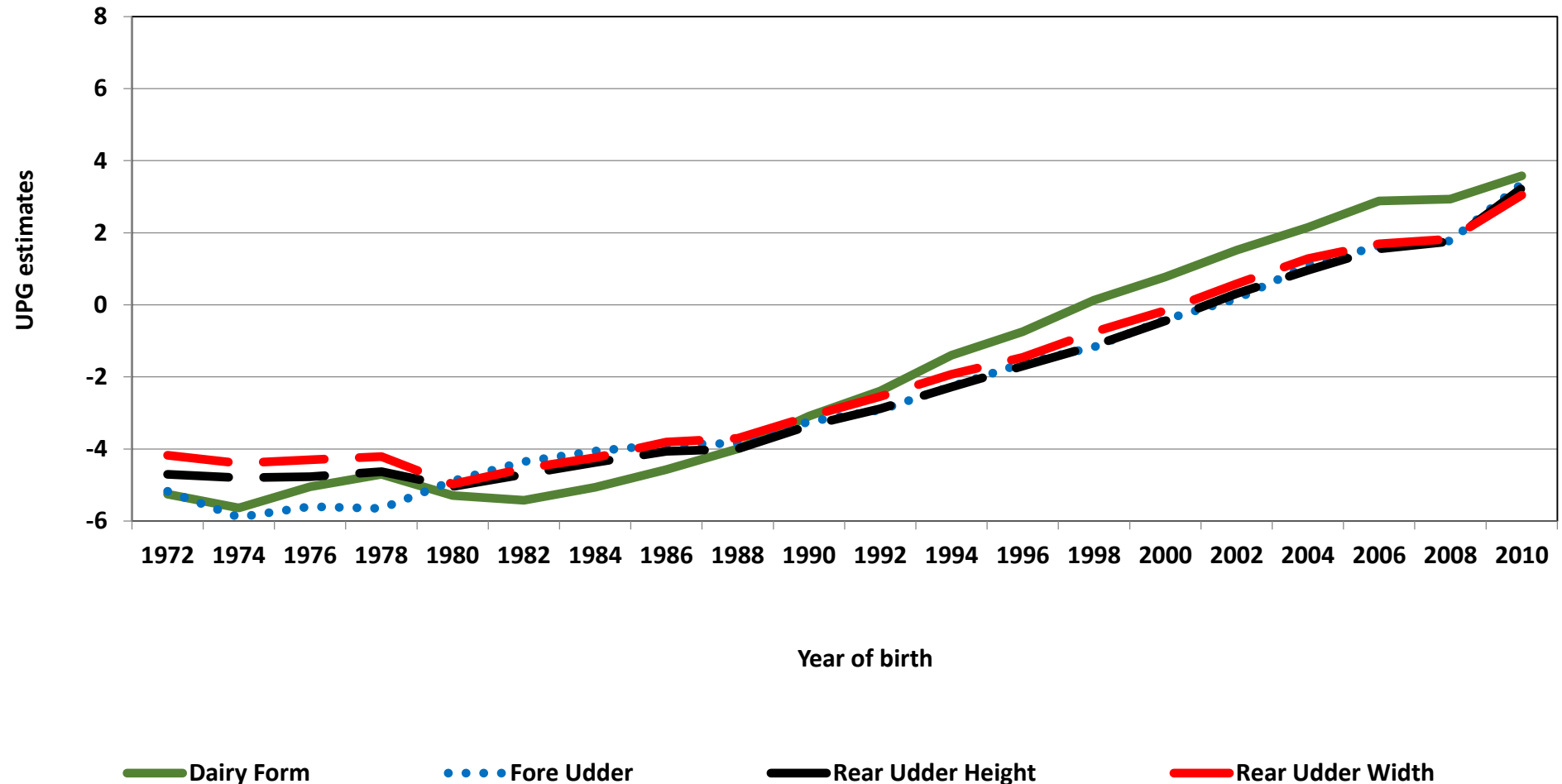
UPG solutions for Directional Selection Traits



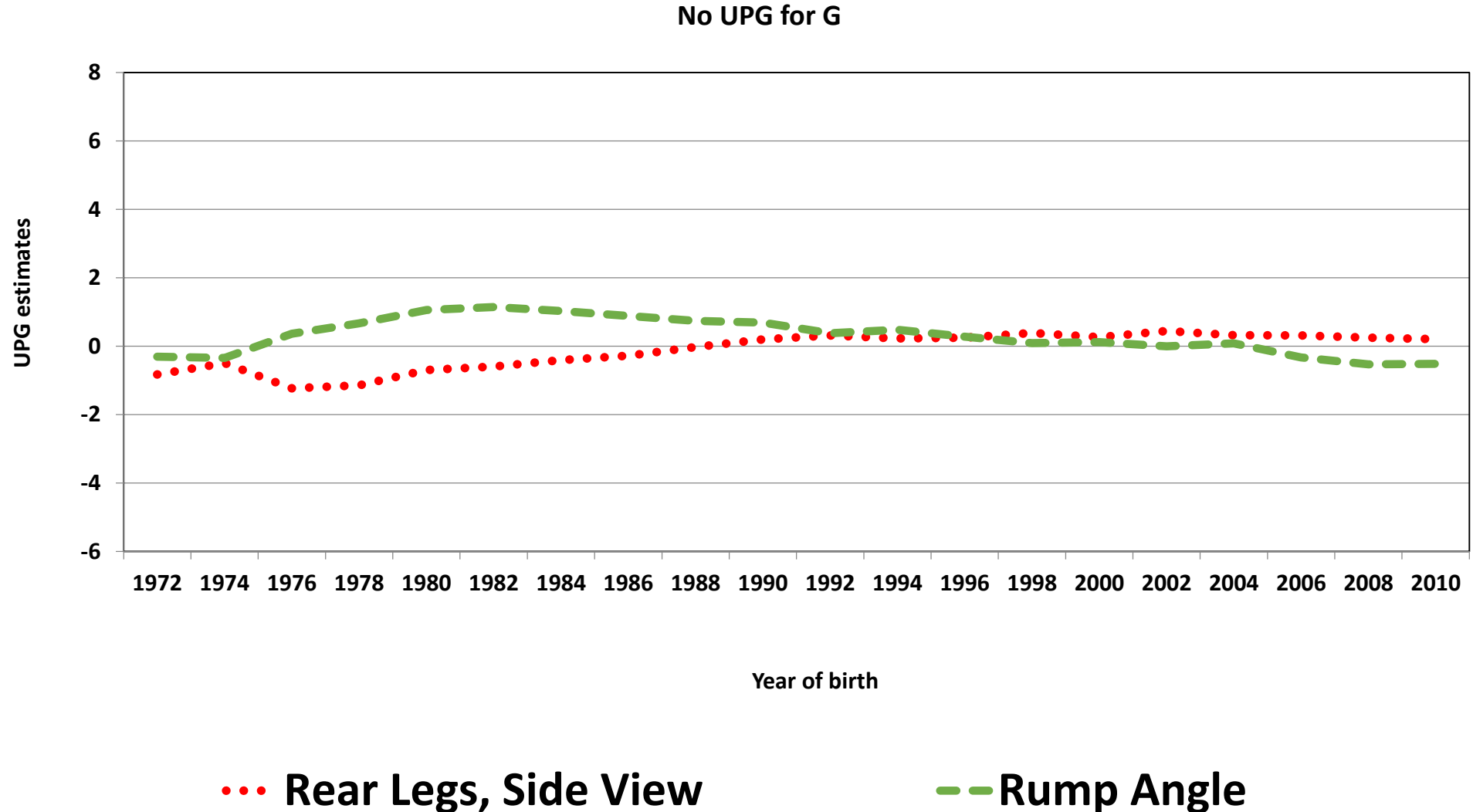
UPG solutions for Directional Selection Traits

Higher EBV

for Unknown Mate in more recent years



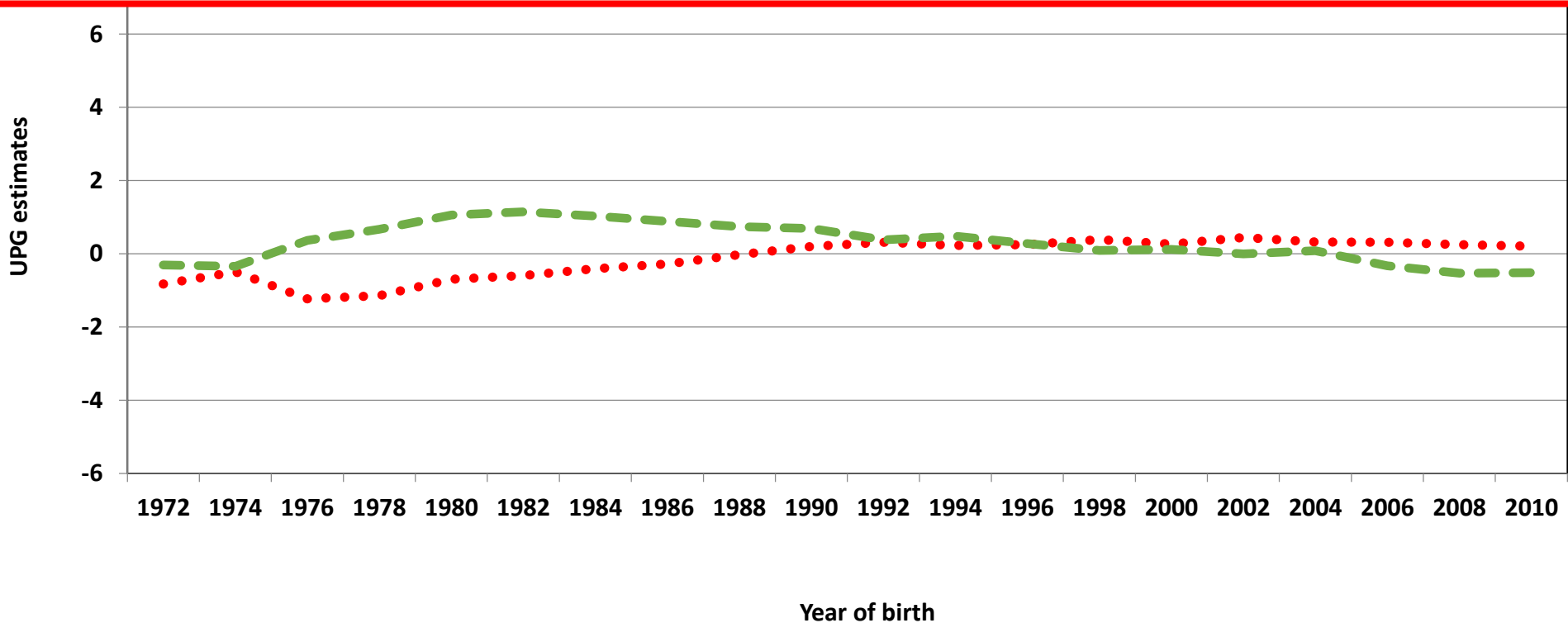
UPG solutions for Intermediate Optimum



UPG solutions for Intermediate Optimum

EBV = 0

Is **NOT** a good assumption for an Unknown Mate
when Negative Assortative Mating is occurring

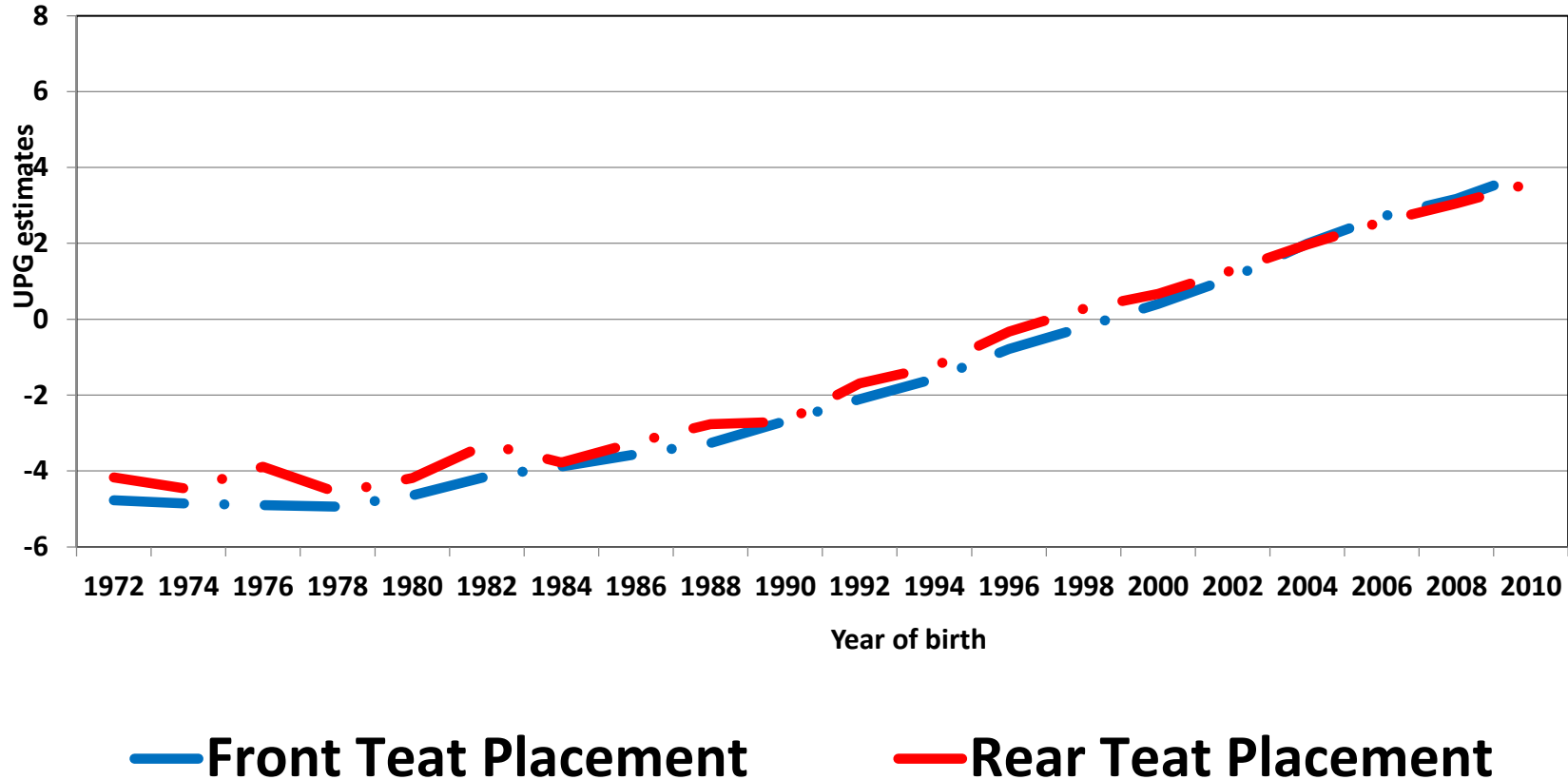


••• Rear Legs, Side View

--- Rump Angle

UPG solutions for Intermediate Optimum *

Does not take into account that High EBV would have a Low EBV mate



* Positive trend due to High genetic correlation with other UDDER traits

Changes in b_1
are associated with the changes in the trait's
Additive Genetic Variance

| | Category | Change in Heritability |
|-------------------------------|------------------------------|------------------------|
| Two traits behaving strangely | Feet & Legs Score | +2.0% |
| | Feet & Legs Score Stature | - 0.3% |
| | Directional | -1.6% |
| | Intermediate Optimum | -2.9% |

Two Goals Positive Assortative Mating

Stature and Body Depth

Size = Height and Width

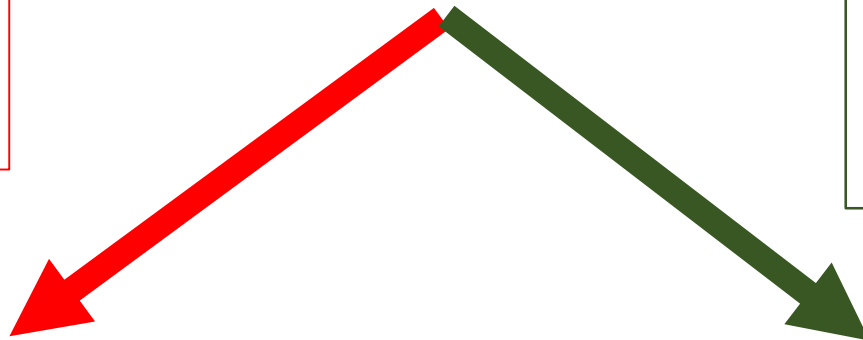
Moderate
with
Moderate

Big
with
Big



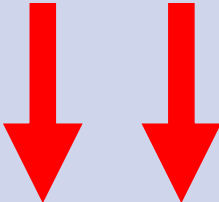
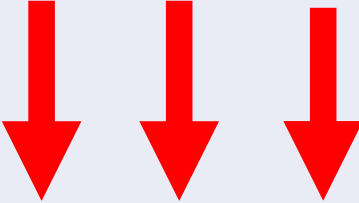
1 10 **20** 30 40 **50**

Moderate Size
More Feed Efficient

Big Cows
Show Winner



Alternative Forms of Selection and Mating

| Category | Mating | Variance |
|----------------------|----------------------|--|
| New Trait | Random |  Increase |
| Two Goals | Positive Assortative |  Small Decline |
| Directional | Random |  Decrease |
| Intermediate Optimum | Negative Assortative |  Large Decrease |

**2018
results
from
complete
model**

| | | | |
|-----------------------|------|-----|--------------------------------------|
| Feet & Leg Score | 0.75 | * | New Trait - increase in heritability |
| Strength | 0.93 | | |
| Stature | 0.95 | ** | Positive assortment mating |
| Rear Udder Width | 0.96 | | |
| Foot Angle | 0.98 | | |
| Body Depth | 0.98 | | |
| Udder Cleft | 0.98 | | |
| Rump Width | 0.99 | | |
| Rear Udder Height | 1.01 | | |
| Fore Udder Attachment | 1.02 | | |
| Udder Depth | 1.02 | | |
| Teat Length | 1.02 | | |
| Rear Legs – Rear View | 1.05 | | |
| Dairy Form | 1.05 | | |
| Rump Angle | 1.12 | *** | Negative assortative mating |
| Front Teat Placement | 1.13 | *** | Negative assortative mating |
| Rear Legs – Side View | 1.13 | *** | Negative assortative mating |
| Rear Teat Placement | 1.24 | *** | Negative assortative mating |

Conclusions

- Genetic evaluation models will need to be fine tuned for:
 - Differences in genetic progress.
 - Differences in changes in heritability.
 - Differences in types of assortative mating.
- Current UPG causes problems for traits with Negative Assortative Mating
- More genotyping improves performance of ssGBLUP

Acknowledgements

