HF update
stability and connection to reference

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BACKGROUND

- Conducted several runs
- Changes were:
  - number of bulls in reference
  - weighted analysis
  - import bulls
  - Bulls change from candidates to reference
- Large changes when sires of candidates are included in reference
- Markers capture genetic relationships (Habier et al., 2007)

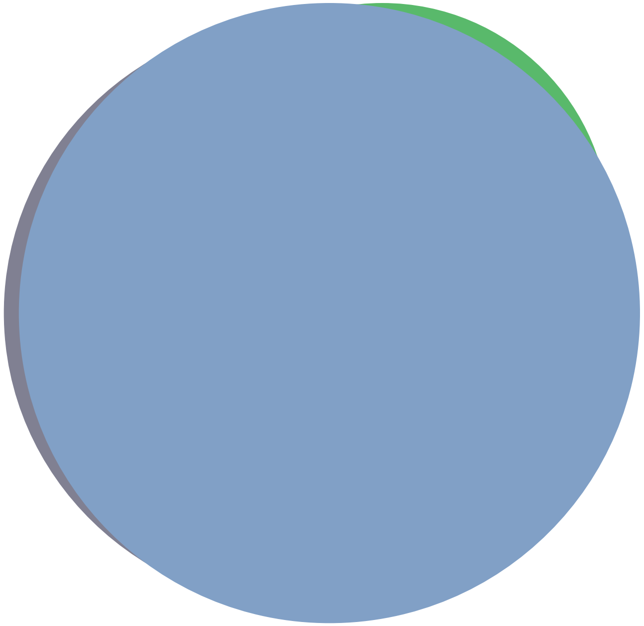
HYPOTHESES

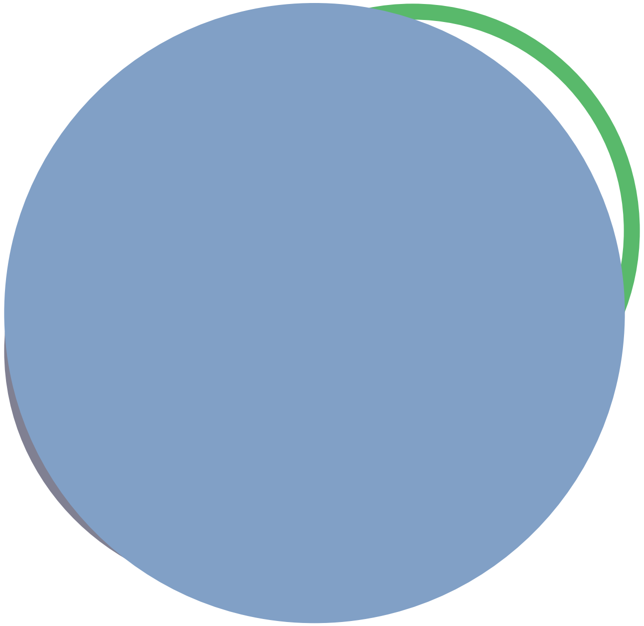
- When the sire is included in the reference population:

1. Reliability of DGV is higher
2. Correlation between DGV and parent average is higher
3. Reliability of blended GEBV is unaffected

HYPOTHESES

When the sire is included in the reference population:





› In reference

outside reference

DATA

- Cross validation with and without sire in the reference
- 3330 Nordic Holstein sires in 258 halfsib groups
- Illumina SNP50 Beadchip
- 38134 SNPs after data editing
- Response variables (EBVs):
  - Protein yield
  - Udder health
  - Female fertility

RESULTS

Data	Trait	$R^2_{DGV,EBV}$
Sire in reference	Fertility	0.41
	Protein	0.41
	Udder health	0.44
Sire NOT in reference	Fertility	0.33
	Protein	0.36
	Udder health	0.34

RESULTS

Data	Trait	$R^2_{DGV,EBV}$	Model reliability
Sire in reference	Fertility	0.41	0.57
	Protein	0.41	0.53
	Udder health	0.44	0.56
Sire NOT in reference	Fertility	0.33	0.49
	Protein	0.36	0.49
	Udder health	0.34	0.49

RESULTS

Data	Trait	$R^2_{DGV,EBV}$	Model reliability	$r_{DGV,PA}$
Sire in reference	Fertility	0.41	0.57	0.71
	Protein	0.41	0.53	0.58
	Udder health	0.44	0.56	0.70
Sire NOT in reference	Fertility	0.33	0.49	0.54
	Protein	0.36	0.49	0.47
	Udder health	0.34	0.49	0.50

RESULTS

Data	Trait	$R^2_{DGV,EBV}$	Model reliability	$r_{DGV,PA}$	$R^2_{GEBV,EBV}$
Sire in reference	Fertility	0.41	0.57	0.71	0.45
	Protein	0.41	0.53	0.58	0.49
	Udder health	0.44	0.56	0.70	0.47
Sire NOT in reference	Fertility	0.33	0.49	0.54	0.45
	Protein	0.36	0.49	0.47	0.50
	Udder health	0.34	0.49	0.50	0.47

RESULTS

Data	Trait	$R^2_{DGV,EBV}$	Model reliability	$r_{DGV,PA}$	$R^2_{GEBV,EBV}$	Model reliability
Sire in reference	Fertility	0.41	0.57	0.71	0.45	0.57
	Protein	0.41	0.53	0.58	0.49	0.57
	Udder health	0.44	0.56	0.70	0.47	0.56
Sire NOT in reference	Fertility	0.33	0.49	0.54	0.45	0.55
	Protein	0.36	0.49	0.47	0.50	0.58
	Udder health	0.34	0.49	0.50	0.47	0.56

SUMMARY

- When the sire of a candidate is in the reference:

1. R^2 between DGV and EBV is higher
2. Correlation between DGV and parent average is higher
3. Differences in R^2 for blended index (GEBV) are small

Conclusions:

Blended index should be used

Index should take account of different correlations

Last update showed stable results

- 300 new bulls in reference
- Correlation between predictions were over 95% on average

European collaboration

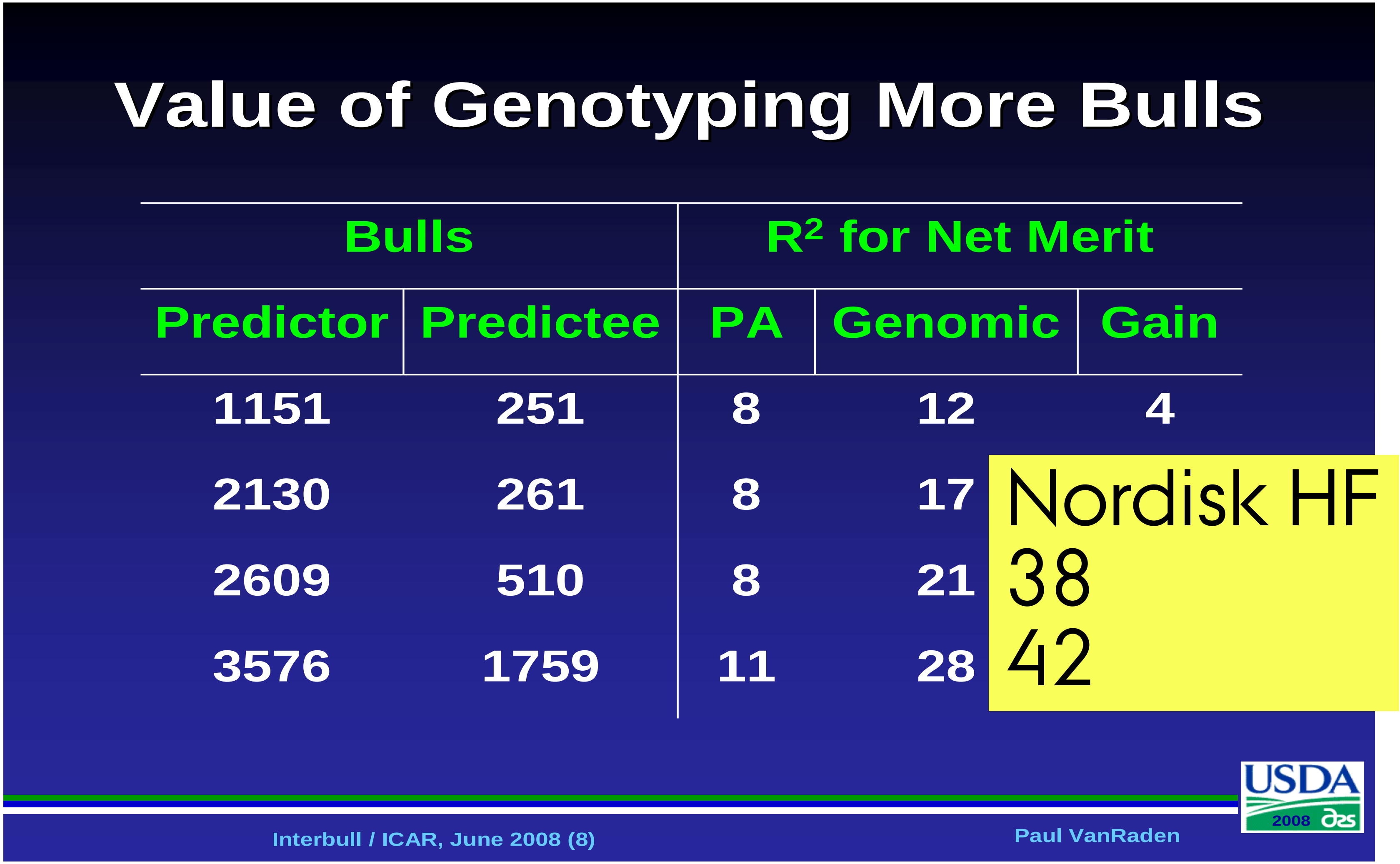
- Reliability of GEBVs increase with reference size
- Exchange of genotypes – first 2000 then 4000 -> ref=16000
- Imputation – transform from CRV SNP chip to USDA SNP chip
  - 50K -> 90K
- Use international EBVs on national scale

Value of Genotyping More SNP

9,604 (10K), 19,208 (20K), and 38,416 (40K) SNP

Trait	R^2 of PA	Genomic R^2		
		10K	20K	40K
Net Merit $	11	25	26	28
Milk yield	28	45	47	49
Fat yield	15	41	43	44
Protein yield	27	45	46	47
Longevity	17	24	25	27
SCS	23	34	36	38
Fertility	20	27	28	29

Reliability increase with reference size



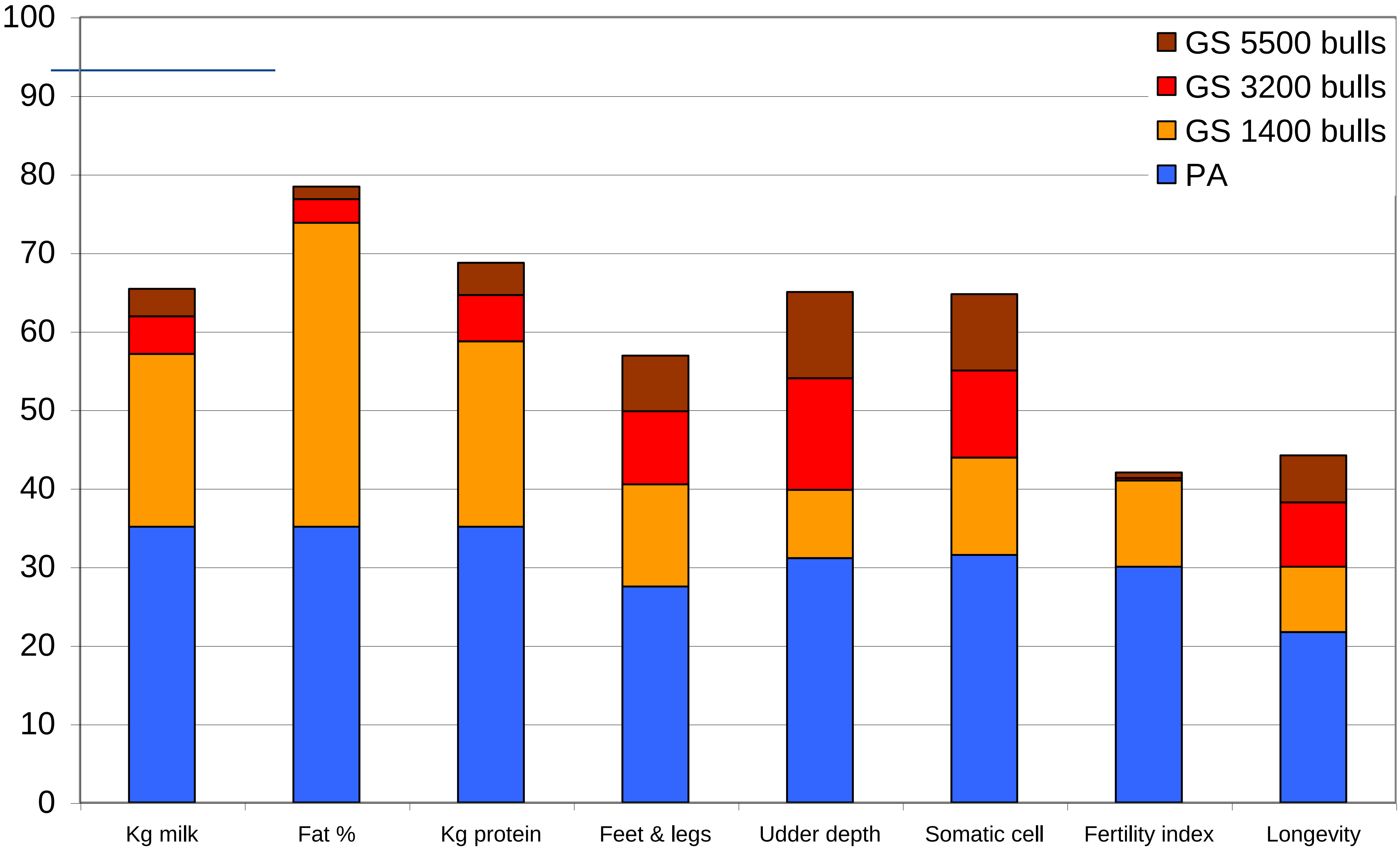
Value of Genotyping More Bulls

Bulls		R² for Net Merit		
Predictor	Predictee	PA	Genomic	Gain
1151	251	8	12	4
2130	261	8	17	
2609	510	8	21	
3576	1759	11	28	

Nordisk HF
38
42

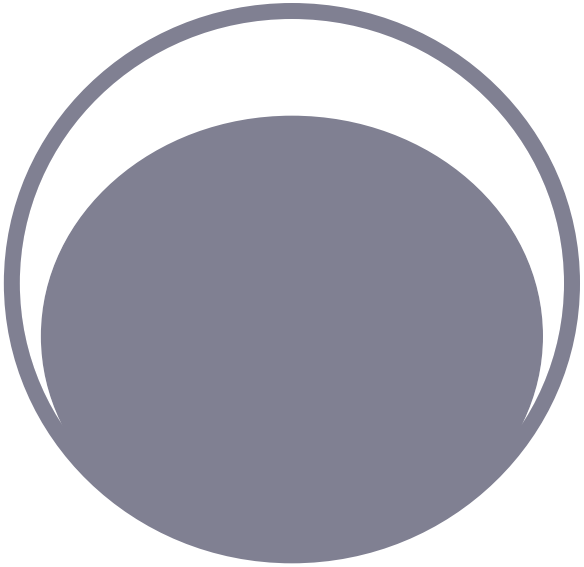
Interbull / ICAR, June 2008 (8)

Paul VanRaden

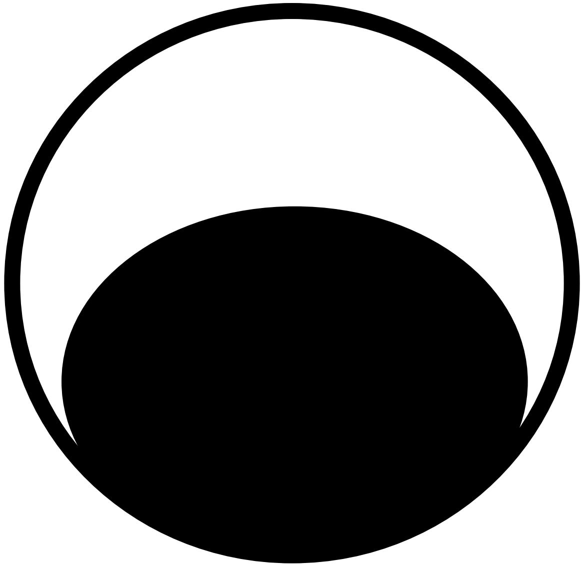

100
90
80
70
60
50
40
30
20
10
0
GS 5500 bulls
GS 3200 bulls
GS 1400 bulls
PA
Kg milk
Fat %
Kg protein
Feet & legs
Udder depth
Somatic cell
Fertility index
Longevity

Production

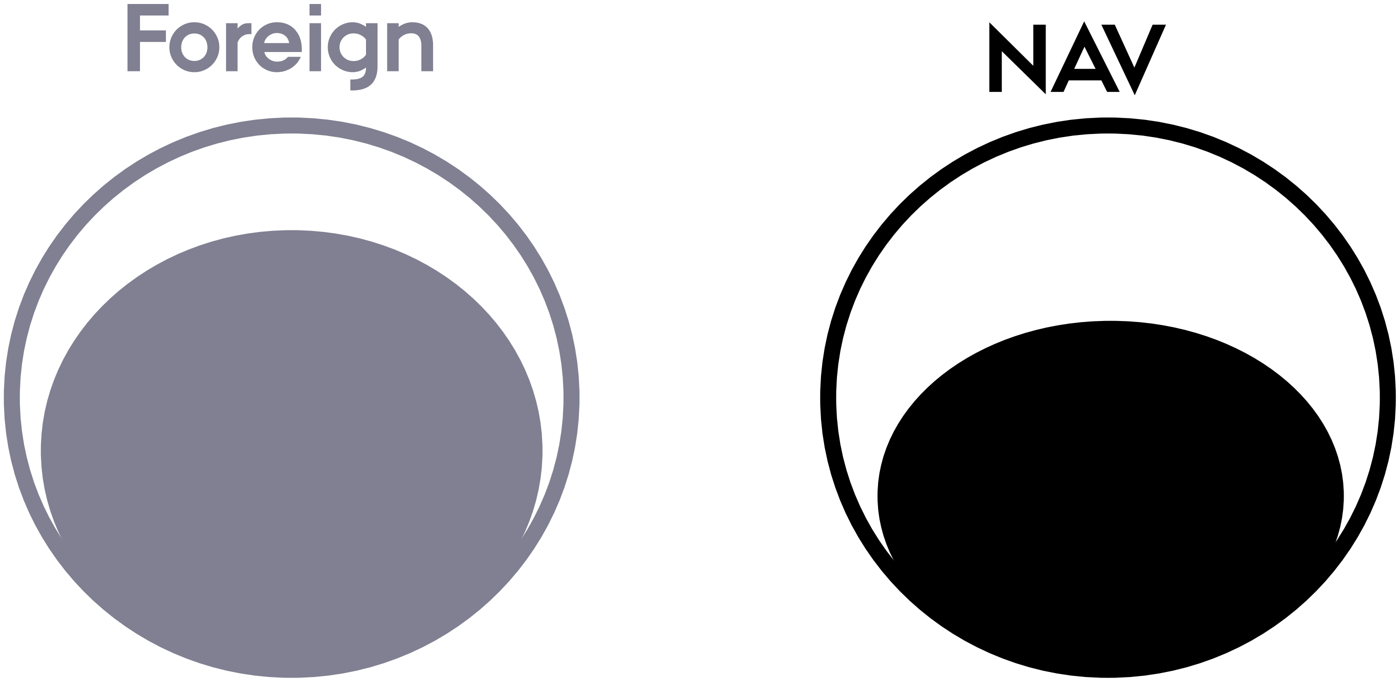
Foreign



NAV



Udder health



We expect

- Slightly higher reliabilities due to more SNPs used
- Relatively high increases due to much larger reference
- Highest increase production
- Lower increase for Udder health
- Results will be published jointly