

# Validation of genomic and genetic evaluations

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# Validation of genetic/genomic evaluations

1. Development of genetic evaluations  
(Repeatability and bias of estimated breeding values for dairy bulls and bull dams calculated from animal model evaluations. *Uimari & Mäntysaari; Animal Production 1993*)
2. Continuous quality control for national evaluations
3. Monitor the reliability of EBVs as MACE input
4. Provide international (and EU) standards for GEBVs

# Validation of genetic/genomic evaluations

Interbull validation tests I, II and III are all testing the genetic trend

(Three methods to validate the estimation of genetic trend for dairy cattle. Boichard, et al.. J Dairy Sci, 1995)

- Actually, they are testing estimated environmental trend
- Tests rely on repeated records (daughters) for sires over time
- Will become unusable as soon as all sires are young
  - Need for alternative tests

GEBV validation test is cross validation test based on forward prediction

- Designed at the time when multi-step genomic evaluation was standard

# GEBV validation test

Model I

$$\text{DYD} = b_0 + b_1 \text{GEBV} + e$$

Model II

$$\text{DYD} = b_0 + b_1 \text{EBV} + e \quad \% \text{ i.e. EBV is parent average}$$

- EBV and GEBV are estimated using truncated (-4 years) data
  - DYD (or DRP) are estimated using full data
- 
- ✓ Regression  $b_1 = 1.00$   
if the evaluations and DYD are consistent
  - ✓ GEBV should explain more of DYD than the EBV

(Interbull validation test for genomic evaluations. Mäntysaari, Liu, and VanRaden, 2010; Interbull Bull, 41).

# GEBV validation test problems

- DYD (or DRP) for the estimation of GEBV (or PA) are from the full data
  - Most GEBV are based on MACE proofs, no truncated data MACE available
- Full data DYD or DRP are difficult to define when:
  - Test day models,
  - maternal effect models,
  - multi-lactation multi-trait

# GEBV validation test problems (ssGBLUP)

- Generally badly suited for testing genomic animal models (**single-step GBLUP**)
  - Validation bulls should not have daughters, but the daughters might be essential part of genomic reference population
  - Validation can be done by predicting cow phenotypes (not cure to above)
- Generally young bulls highly selected according to GEBVs
  - Eventually the bull based validation  $R^2$  start to decrease

# GEBV validation test problems (ssGBLUP)

- In our single-step test day model development:  
Interbull GEBV validation test results not satisfying  
(see e.g. Koivula et al. 2016 EAAP, Belfast)
  - Too low  $b_1$  (and  $R^2$ )
  - Also the parent average validation is poor**Is this a problem of model or test ?**

The aim in this presentation is to take a better look on accuracy and stability of our evaluations (normal and genomic)

# Nordic RDC Data

- Protein TD observations were used to derive 305d yields
  - single trait repeatability model for protein only  
 $h^2 = 0.37$  and  $r = 0.55$
- 1. Animal model EBVs
- 2. Genomic animal model: single-step GEBVs.

The ss-GBLUP calculated

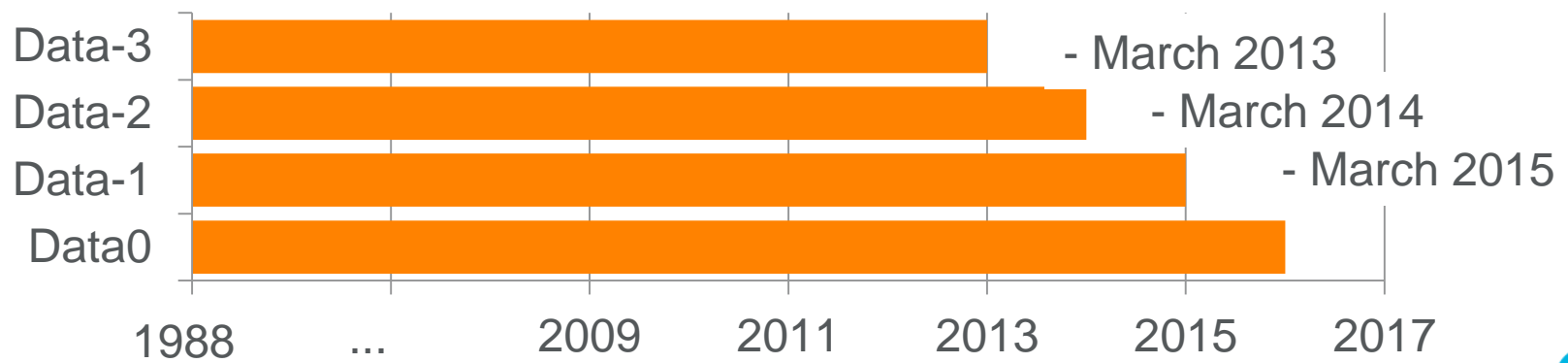
- with standard  $G_w$ -matrix,  $w = 0.10$
- full QT-transformation (Matilainen et al. 2016, Interbull, Chile)
- always applied for all the genotypes existing in whole data.



# Nordic RDC

## Data reduced data sets

- Full data Data0
  - Calvings up to March 2016
  - 3.5M cows with 7M observations
  - Pedigree 5.4M animals, 33,321 genotyped
- Reduced data sets:



# Model validation statistics

## Interbull GEBV validation test

### Reliability

Correlation(EBV1,EBV2) and regression EBV2 on EBV1  
(SireType == Proven sires)

### (G)EBV Stability

$$(EBV2-EBV1) = C\text{-Year} + Parity + SireType + \begin{matrix} C\text{-year} \\ * \\ Parity \\ * \\ SireType \end{matrix}$$

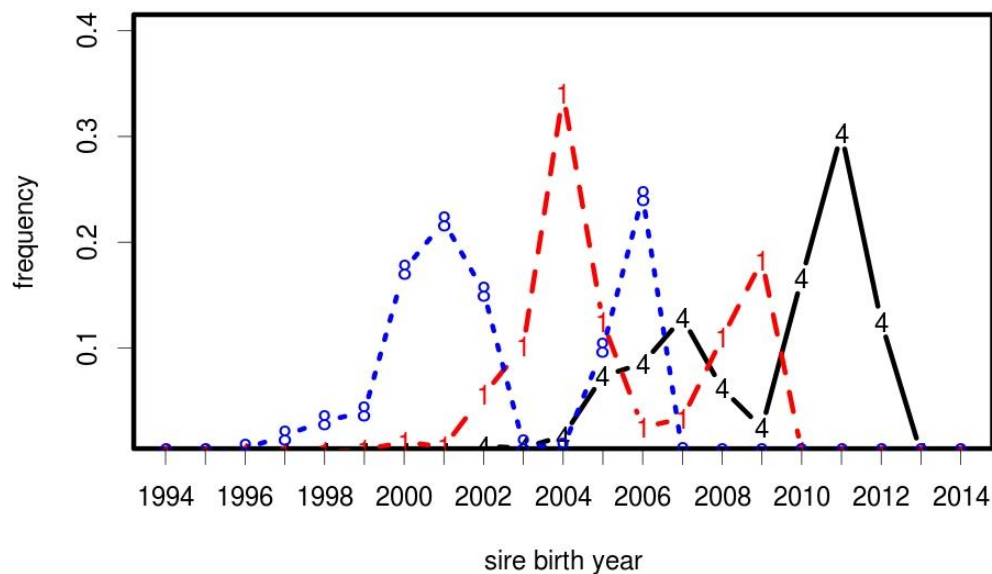
EBV1 is always the evaluation with less information, and  
EBV2 the following, next evaluation, with +1 record

# Siretypes of cows by first year of calving (% of all used sires)

Sire type	2010	2011	2012	2013	2014
No daughters			30	37	44
Progeny-tested			70	63	56
- Inseminations :	61	54	49	42	16

3

Distribution of sire age classes for cows born 2008, 2011, and 2014



# GEBV validation test results bulls, n=462

Regression of  $DYD_{data0}$  on  $PA_{data-3}$  or  $GEBV_{data-3}$

	PA		GEBV	
	$b_1$	$R^2$	$b_1$	$R^2$
Protein	0.75	0.20	0.57	0.28

$$R^2_{\text{validation}} = \frac{R^2_{\text{model}}}{r^2_{DYD}}$$

# GEBV validation test results genotyped cows

Regression of YD to GEBV or EBV (PA)

ProdYear	PA		GEBV	
	$b_1$	$R^2$	$b_1$	$R^2$
2012	0.95	0.22	0.70	0.23
2013	1.07	0.43	0.83	0.55
2014	1.01	0.38	0.85	0.53

$$R^2_{\text{validation}} = \frac{R^2_{\text{model}}}{r^2_{\text{YD}}}$$

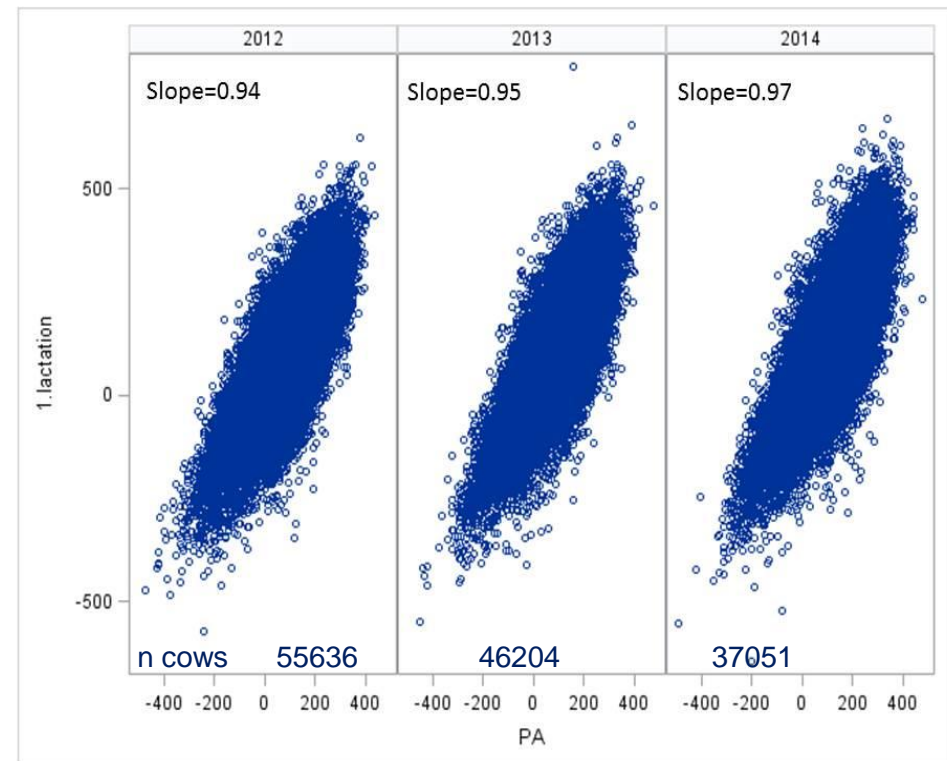
Note: Reference population in 2014 is much larger than in 2012

# Correlation between parent average (PA) and first lactation EBV

## Correlation of PA to 1. lactation EBV

Prod year	EBV	mean	std	$r_{PA,1.Lact}$
2012	PA	127	89	0.78
	1.Lact EBV	130	109	
2013	PA	130	92	0.79
	1.Lact EBV	135	112	
2014	PA	150	97	0.81
	1.Lact EBV	156	120	

## PA versus 1. lactation EBV by evaluation year of the PA



Correlation for cows with SireType == "progeny-tested sire"

Let EBV1 include all information ( $\sim ERC1$ ) in EBV2

Then

$$R_{EBV2}^2 = \frac{ERC1 + ERC2}{ERC1 + ERC2 + \lambda}$$

where  $\lambda$  is the variance ratio

Because

$$r_{EBV1,EBV2}^2 = \frac{R_{EBV1}^2}{R_{EBV2}^2}$$

Reverter, A., et al. Technical note:  
detection of bias in genetic predictions.  
Journal Animal Sci 72 (1994): 34-37.

If you assume constant  $ERC2$ , e.g.  $\sim 0.9$ ,

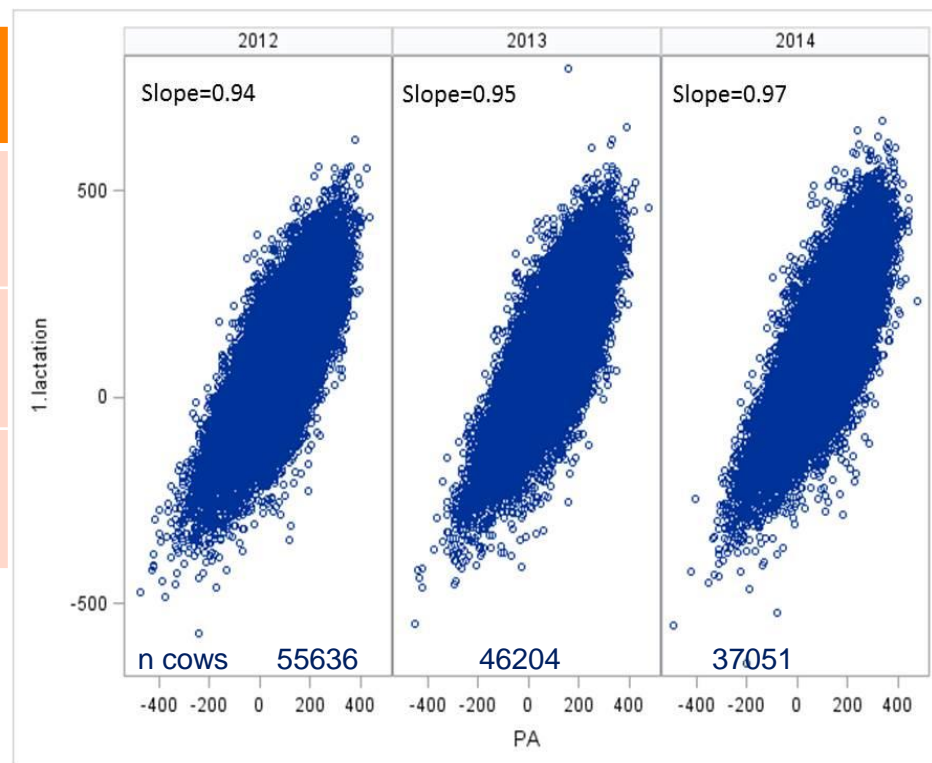
it is possible to solve  $ERC1$  and thereafter  $R_{EBV1}^2$

# Correlation between parent average (PA) and first lactation EBV

## Correlation of PA to 1. lactation EBV

Prod year	EBV	mean	std	$r_{PA,1}$	$R^2_{PA}$
2012	PA	127	89	0.78	0.31
	1.Lact EBV	130	109		
2013	PA	130	92	0.79	0.32
	1.Lact EBV	135	112		
2014	PA	150	97	0.81	0.34
	1.Lact EBV	156	120		

## PA versus 1. lactation EBV by evaluation year of the PA



Theoretically sire having 150 daughters and dam  $N_{rec}=2$ ,  $R^2_{PA} \sim 0.37$

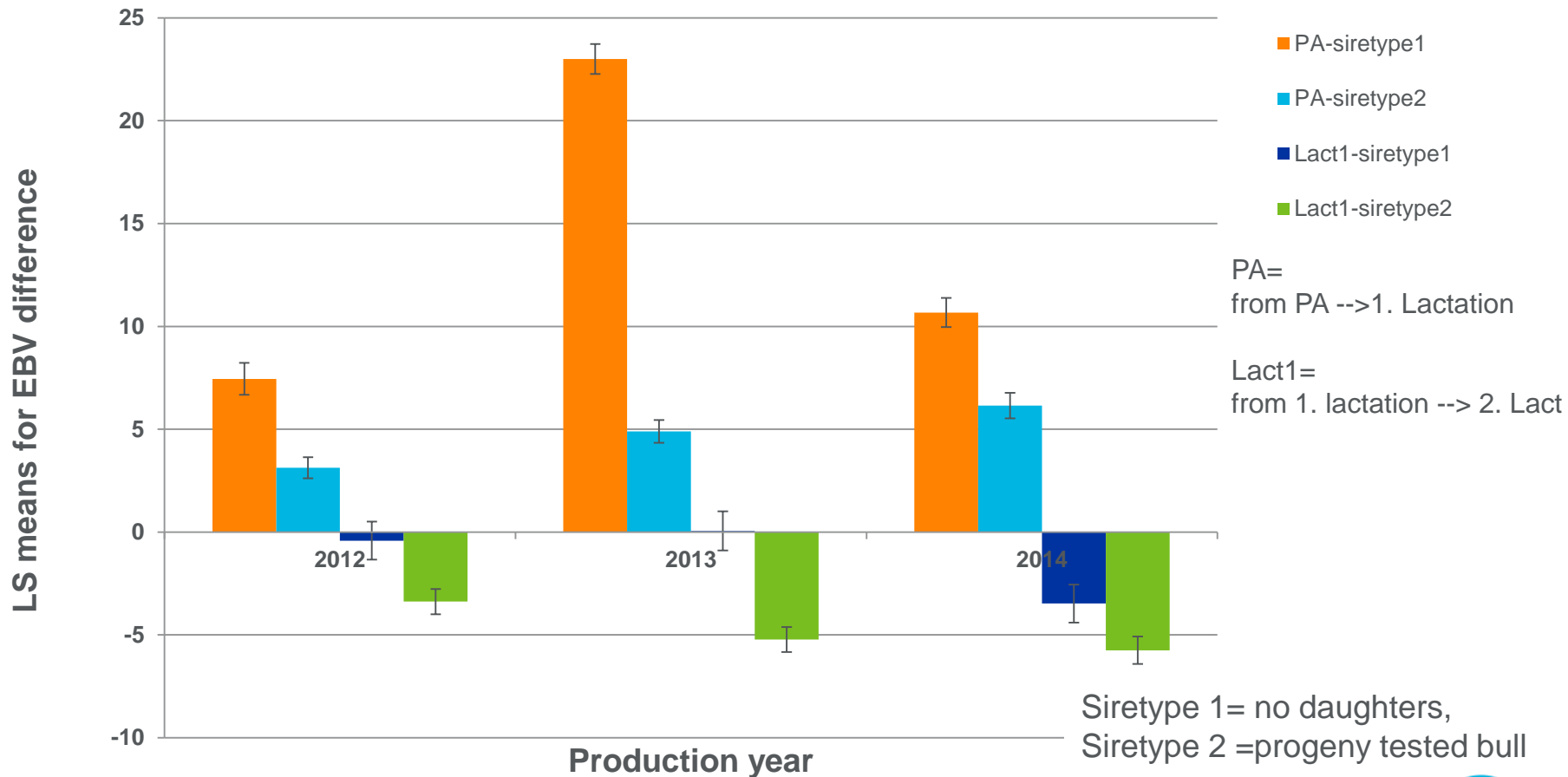


# Correlation between 1. lactation EBV and 2. lactation EBV within each production year

Prodyear	EBV	mean	std	Corr
2012	EBV1	122	104	0.93
	EBV2	109	104	
2013	EBV1	133	106	0.93
	EBV2	128	107	
2014	EBV1	140	109	0.94
	EBV2	134	110	

Correlation for cows with SireType == "progeny-tested sire"

# LS means for EBV difference by lactation, siretype and production year ( $\pm$ 95%CL)



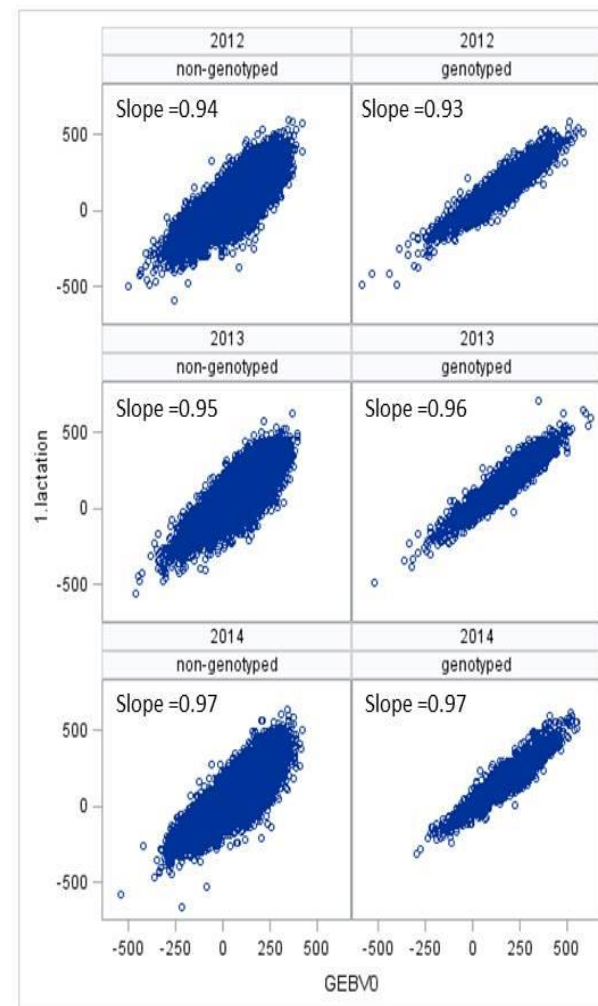
EBV difference= EBV2 – EBV1, change from evaluation to another

# Correlation with **GEBV0** and first lactation **GEBV**

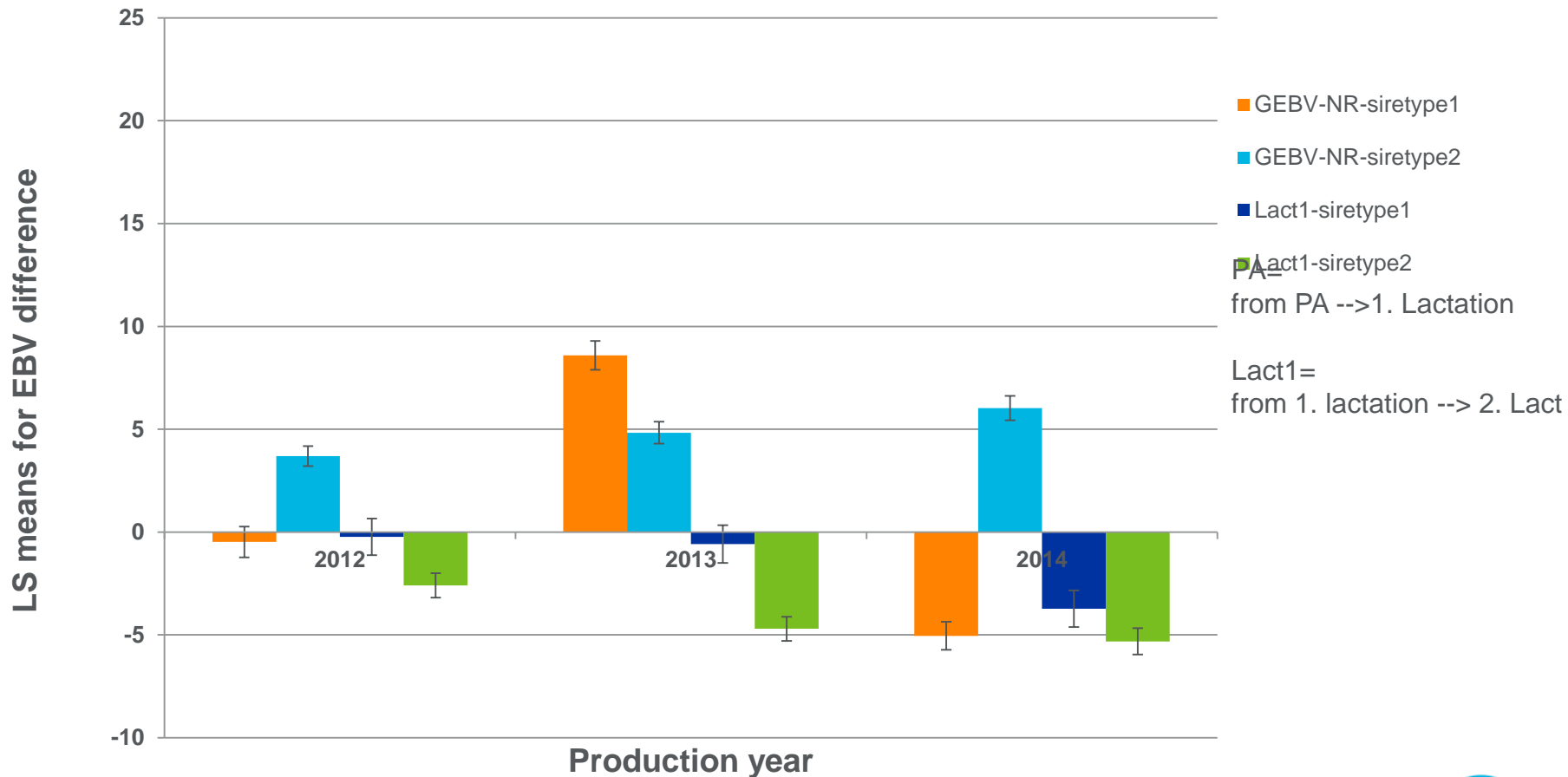
## Correlation of GEBV0 to 1. lactation

Prodyear	GEBV	mean	std	$r_{PA,1.Lact}$	$R^2_{PA}$
<b>Non-genotyped cows</b>					
2012	GEBV0	100	88.83	0.78	0.31
	1.Lact	104	108		
2013	GEBV0	105	85	0.72	0.24
	1.Lact	114	110		
2014	GEBV0	122	96	0.81	0.34
	1.Lact	129	112		
<b>Genotyped cows</b>					
2012	GEBV0	157	127	0.93	0.56
	1.Lact	153	126		
2013	GEBV0	172	116	0.90	0.49
	1.Lact	176	124		
2014	GEBV0	192	122	0.93	0.56
	1.Lact	189	129		

## GEBV-0 versus 1. lactation GEBV by evaluation year of the GEBV-0

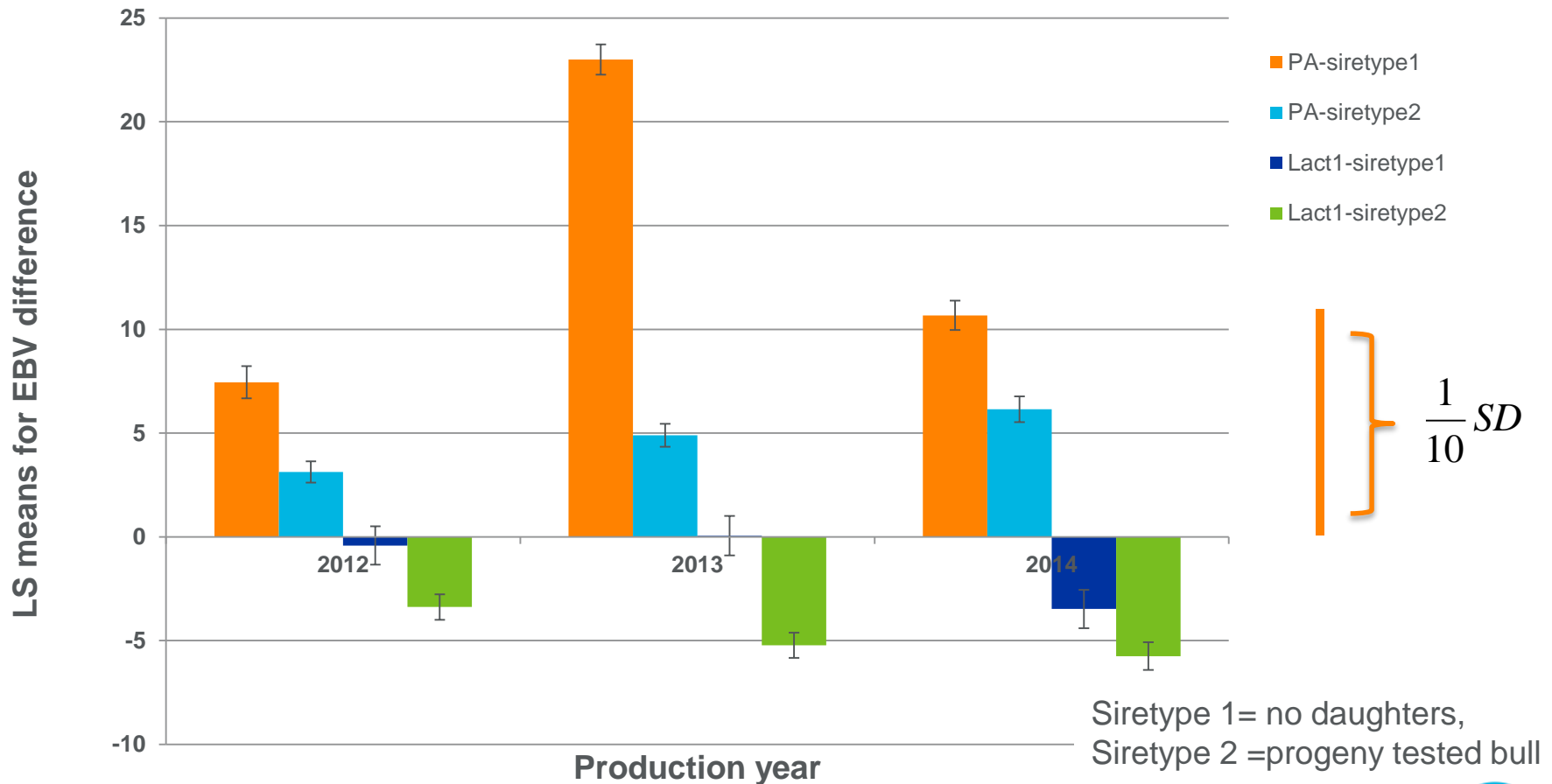


# LS means for difference GEBV2-GEBV1 by lactation, siretype and production year ( $\pm$ 95% CL)



GEBV difference= GEBV2 – GEBV1, change from evaluation to another

# LS means for difference EBV2-EBV1 by lactation, siretype and production year ( $\pm 95\%CL$ )



EBV difference = EBV2 - EBV1, change from evaluation to another

# Conclusions - use (G)EBV stability validation

Changes during consecutive evaluations with one year added can illustrate the stability of the evaluations

- Especially useful when trait measured yearly at each animal

Use of females as validation group

- Instead of one test (bulls) you can do yearly tests
- Straight copy of current GEBV validation test has a weakness that the environmental effects (used to attain the DYD) are from the EBV model

Correlations between consecutive (G)EBVs reflected the accuracy

- Correlation estimates consistent with expectations based on  $R^2$
- High correlation does not automatically mean high accuracy ??

# Conclusions – RDC 305 d test evaluations

With simple 305 d animal model:

- Validation results for EBVs were at the low side
- Validation results for ssGBLUP GEBVs were also low
- Genomic selection might have affected accuracy of DYD ?

Stability measured as year-to-year change was satisfactory

- Except for PA EBV, which increased --> EBV1 at the best 0.2 SD
- GEBV from ssGBLUP was much more stable
- General trend:
  - (G)EBV increases with 1<sup>st</sup> lactation record,
  - (G)EBV decreases with 2<sup>nd</sup> and 3<sup>rd</sup> lactation records,
- True effect of GS not yet visible: selection 2010 not strong

Thank you!

