

# Validation of genomic and genetic evaluations in 305d production traits of Nordic Holstein cattle

M. Koivula, I. Strandén, G. P. Aamand  
and E. A. Mäntysaari\*

Biometrical Genetics, Luke, Finland  
NAV, Denmark



27.8.2017

on, Estonia

© Natural Resources Institute Finland



# 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
- DRP (or DYD) 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 (ssGBLUP)

- Generally poorly suited for testing genomic animal models (**single-step GBLUP**)
  - Validation bulls are by definition young, and have no daughters. But their genotyped daughters might be essential part of genomic reference population
- Generally young bulls are (heavily) selected using GEBVs
  - Eventually the bull based validation  $R^2$  starts to decrease

- With our single-step test day model the GEBV validation results are often unsatisfactory (see e.g. Koivula et al. 2016 EAAP, Belfast)
  - Too low  $b_1$  and  $R^2$
  - Bit, also the parent average validations are poor**Is this a problem of model or test ?**

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

# Model validation alternatives

## 1. Interbull GEBV validation test

- **Problem 1 Validity of "golden standard"**

- After years of Genomic Selection the EBV model accuracy starts to deteriorate:  
WE CAN NOT FULLY TRUST THE DRPs (Deregressed genetic predictions)
- Solution: Start using DYDs and YDs from the ssGBLUP

- **Problem 2 Reduced reliability due selection**

- The validation bulls in 4 year reduced data are selected with GEBV values → correlation between GEBV and BV are reduced
- Assumption: the correlation of GEBV and DY will be closer to expected one in (unselected) genotyped cows.

# Model validation alternatives

## 1. Interbull GEBV validation test

- **Problem 1 Validity of "golden standard"**

- After years of Genomic Selection the EBV model accuracy starts to deteriorate:  
WE CAN NOT FULLY TRUST THE DRPs (Deregressed genetic predictions)
- Solution? Start using DYDs and YDs from the ssGBLUP

- **Problem 2 Reduced reliability due selection**

- The validation bulls in 4 year reduced data are selected with GEBV  
→ correlation between GEBV and BV are reduced

Solution? In (unselected) genotyped cows, the correlation of GEBV and YD will be closer to what we expect

# Model validation alternatives

## 2. Reliability

Correlation (EBV1,EBV2) and regression EBV2 on EBV1

## 3. (G)EBV Stability

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

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

# Evaluations tested

## Data set

- Nordic Holstein 305 d production data
  - 305d lactation records compiled from the data used in official nordic TD evaluations

## Analysis models

- Multitrait (lactations 1-3) model for protein
  - Variance parameters derived from national evaluations

	1st	2nd	3th
$h^2$	0.36	0.29	0.26

Model:

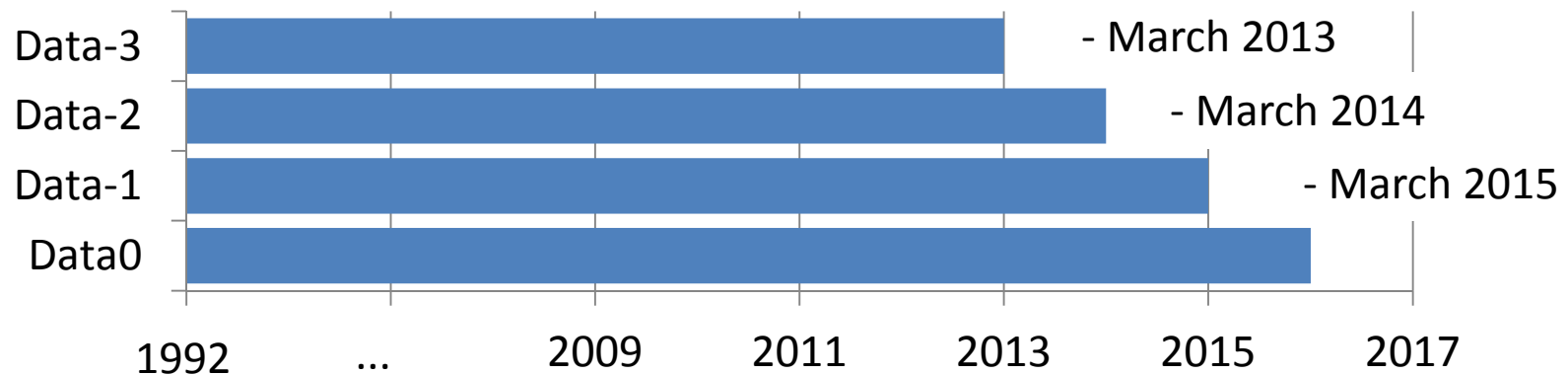
Protein=herd\_year+calving\_year\_season  
+calving\_age+animal+residual  
! Weights= (Number of TD)/10

- MT -animal model (**EBVs**)
- ssGBLUP (**GEBVs**)



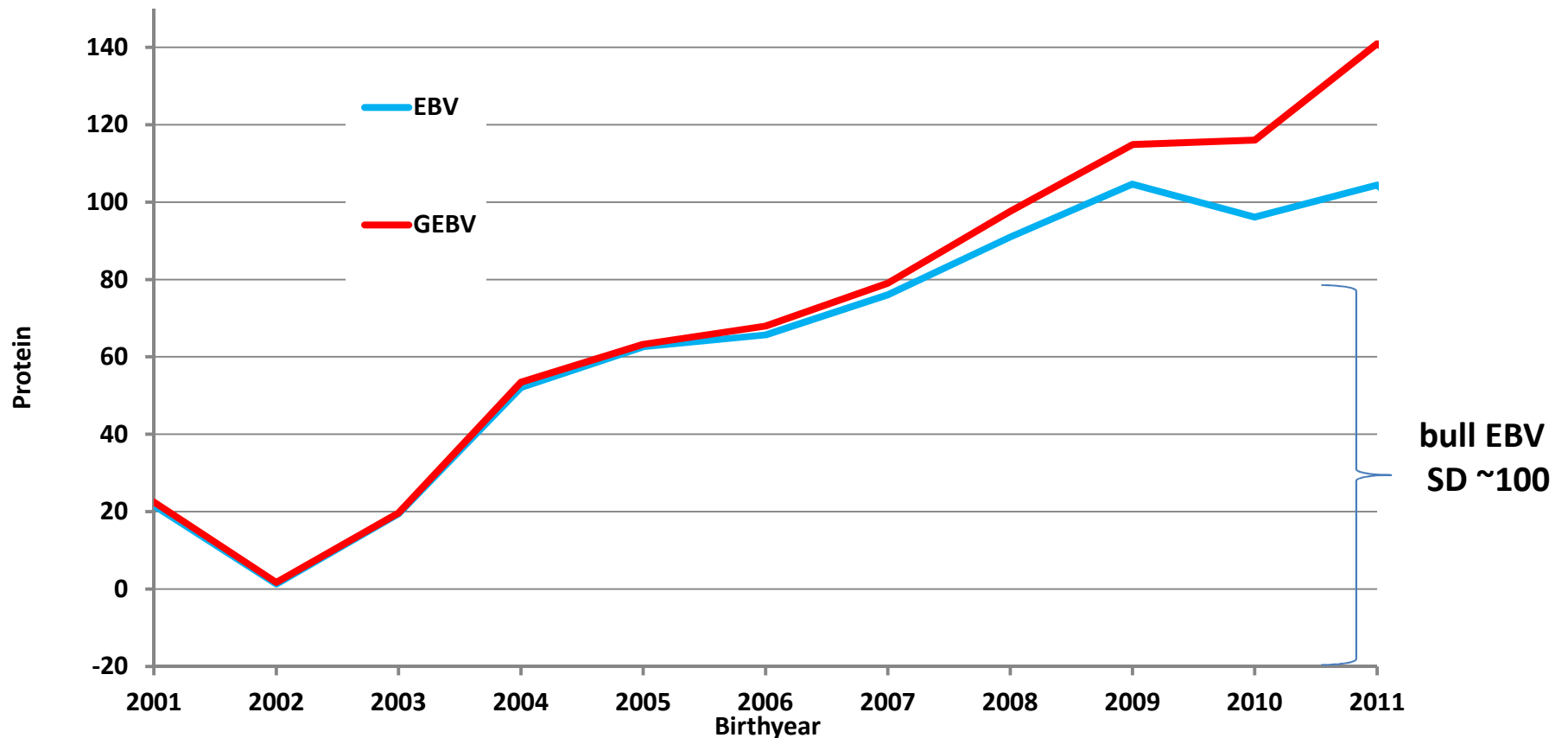
# Nordic HOL Data & reduced data sets

- Full data Data0
  - Calvings up to March 2016
  - 7.3 million cows with 15.6 million observations
  - Pedigree 9.9 million animals, 30056 genotyped
- Reduced data sets:



# Genetic Trends with different evaluations

## Protein (G)EBV; bulls with $\geq 50$ daughters



Year	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012
N	723	624	616	585	605	633	508	439	386	351	246	40

(G)EBV trend, combined and weighted over lactations 1-3

# GEBV validation test results for protein

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

	PA		GEBV	
Combined (G)EBV	$b_1$	$R^2$	$b_1$	$R^2$
<b>EBV_DYD</b>	<b>0.67</b>	<b>0.14</b>	0.75	0.36
<b>GEBV_DYD</b>			<b>0.77</b>	<b>0.39</b>
1. Lactation (G)EBV (783 bulls)				
<b>EBV1_DYD1</b>	<b>0.71</b>	<b>0.17</b>	0.74	0.40
<b>GEBV1_DYD1</b>			<b>0.78</b>	<b>0.44</b>

$$R_{GEBV}^2 = R_{model\ 1}^2 / \bar{w}$$

# GEBV validation test results for protein

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

	PA		GEBV	
Combined (G)EBV	$b_1$	$R^2$	$b_1$	$R^2$
<b>EBV_DYD</b>	<b>0.67</b>	<b>0.14</b>	0.75	0.36
<b>GEBV_DYD</b>			<b>0.77</b>	<b>0.39</b>
1. Lactation (G)EBV (783 bulls)				
<b>EBV1_DYD1</b>	<b>0.71</b>	<b>0.17</b>	0.74	0.40
<b>GEBV1_DYD1</b>			<b>0.78</b>	<b>0.44</b>

$$R_{GEBV}^2 = R_{model\ 1}^2 / \bar{w}$$

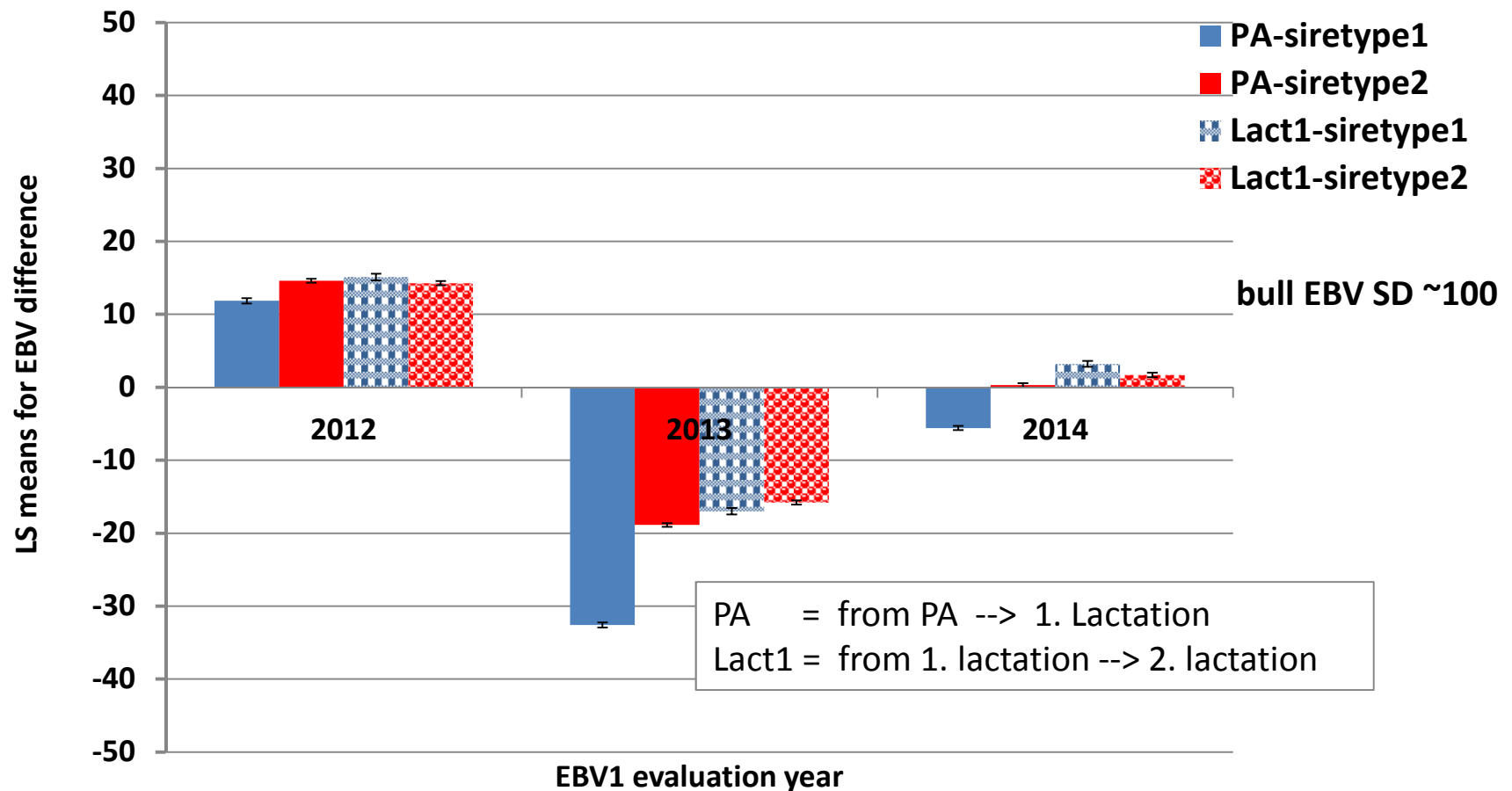
# GEV validation test results genotyped cows

Regression of YD to GEV or EBV (PA), 1. Lactation (G)EBV only

EBV_YD	PA1 <sup>st</sup>		GEV1 <sup>st</sup>	
Prod.year	b <sub>1</sub>	R <sup>2</sup>	b <sub>1</sub>	R <sup>2</sup>
2012 (n=2967)	<b>1.19</b>	<b>0.36</b>	1.00	0.57
2013 (n=4446)	<b>1.01</b>	<b>0.29</b>	1.01	0.57
2014 (n=8556)	<b>1.11</b>	<b>0.28</b>	1.04	0.56
GEV_YD	Note: Female reference population: 2012 n=4376; 2013 n=7342; 2014 n=11788			
2012 (n=2967)			<b>1.02</b>	<b>0.60</b>
2013 (n=4446)			<b>1.03</b>	<b>0.59</b>
2014 (n=8556)			<b>1.06</b>	<b>0.58</b>

$$R_{GEV}^2 = R_{model\ 1}^2 / \bar{w}$$

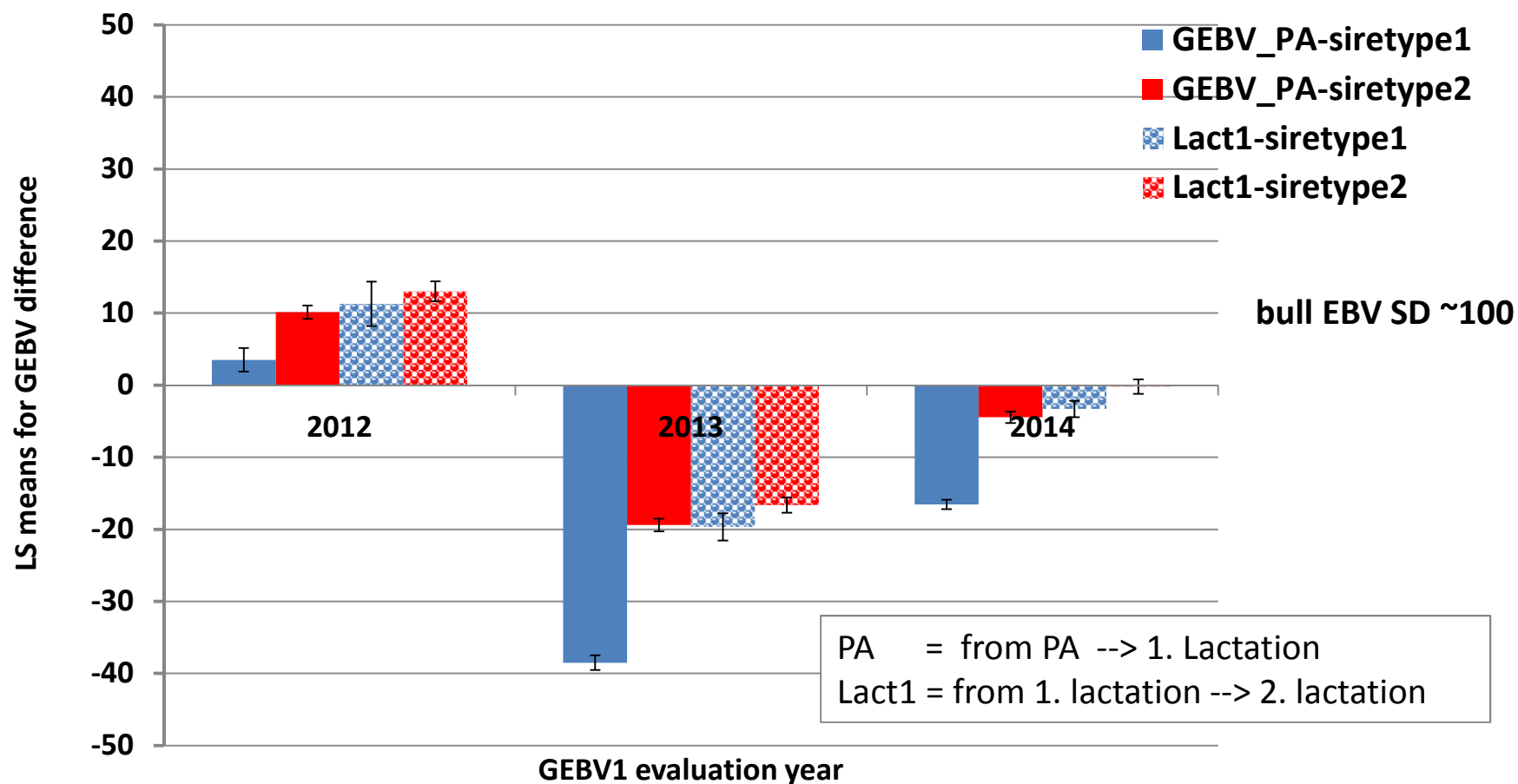
# LS means for difference EBV2-EBV1 by lactation, siretype and year of EBV1 evaluation ( $\pm 95\%CL$ )



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

Siretype 1= no daughters,  
Siretype 2 =progeny tested bull

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



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

Siretype 1= no daughters,  
Siretype 2 =progeny tested bull

# Conclusions

- Use of DYDs from animal model run will give lower validation reliability (0.36) than using DYD from ssGBLUP (0.39)
- Estimate of validation reliability using bull DYDs is lower (0.44) than using cow YD (0.60)
- In the stability test both the evaluations were equally good: No obvious pattern was found



Thank you!

