

NAV evaluation of udder linear and coordinate traits

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Why use robotic milking data?

- High genetic correlations (~ 0.90) between udder linear and AMS traits
- high heritabilities of AMS traits
 - → Increased EBVs accuracy
- Information from multiple lactations
 - → Accurate EBVs for 2nd and 3rd lactations
- It is possible to get information from more herds than those enrolled in linear classifications today and with a lower cost

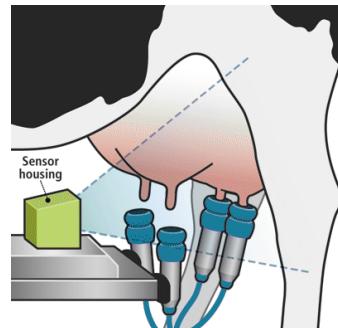
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Udder coordinates from Lely milking robots (AMS data)

- AMS data from Danish herds (HOL, RDM and JER)
- Multiple observations from udder traits are available:
 - Teat placement front = TPLF
 - Teat placement back = TPLB
 - Udder balance = UB
 - Udder depth = UD



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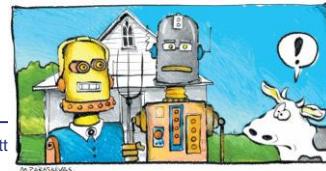
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Time span of linear and AMS traits

Linear
TPLF
UD (DNK)
~1985



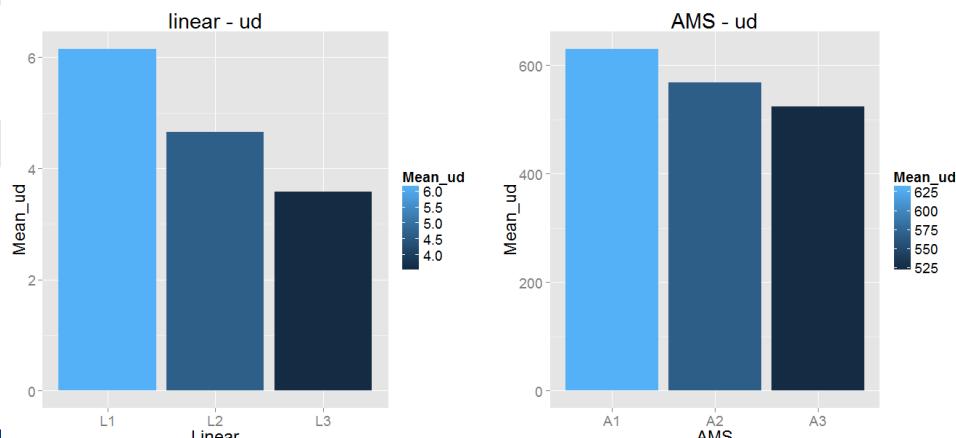
Linear +
TPLB
UB
AMS
(TPLF, TPLB,
UB and UD)
2016



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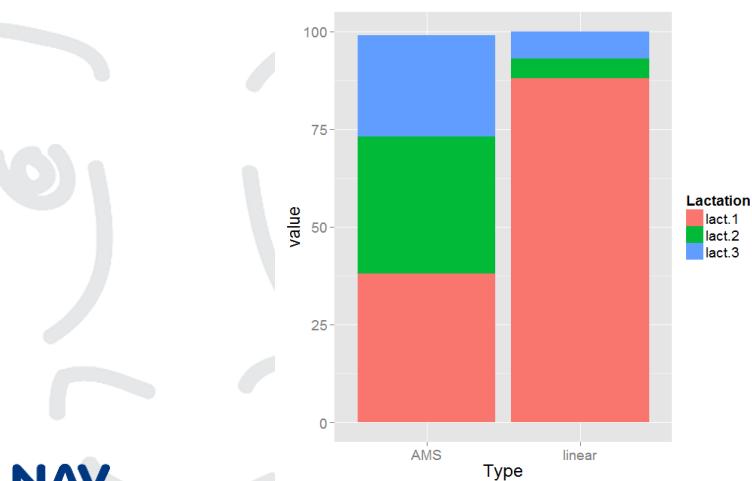
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Means of Udder Depth - Hol



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Traits by lactations

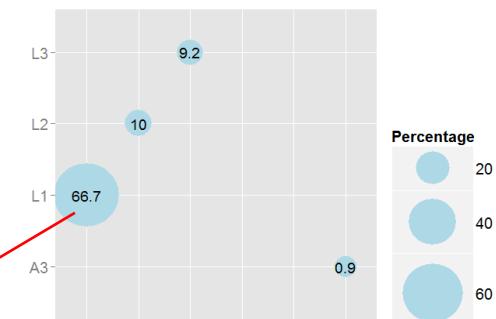


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- Overlapping number of observations in udder balance - between AMS and Linear traits

From the total of cows with AMS data 66.7% also have linear data

HOLSTEIN

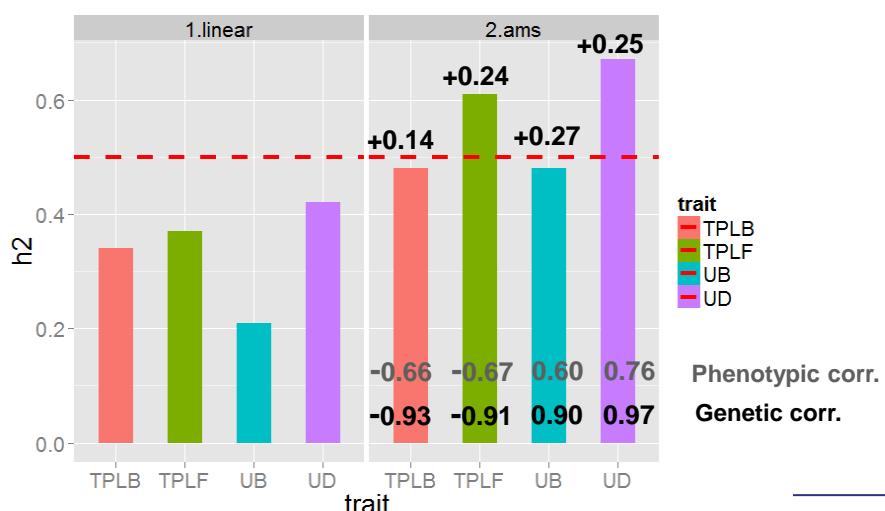


Breed	N		% of both AMS and linear					
	Linear	AMS	L1	L2	L3	A1	A2	A3
HOL	1,762,652	38,664	1,7	1,1	0,9	67	10	9
JER	164,490	3,595	0,6	0,6	0,2	60	4	3
RDM	853,678	3,693	0,2	0,1	0,2	77	9	24

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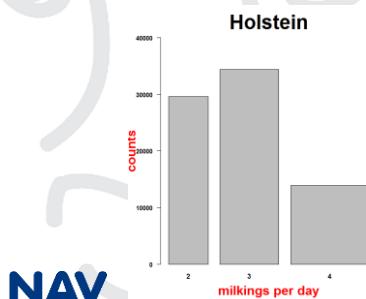
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Genetic parameters (lact.1)



Genetic model

- Udder linear traits model as in routine evaluation
- AMS data is included as a correlated trait
- **NEW:** number of milkings per day (AMS)



Photograph by Lely

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Holstein sires with AMS data

Description	Value
Number of AMS sires	1824
Average AMS daughters/sire	14.4
highest number of AMS dghters/sire	805
Sires with > 10 AMS dgthrs	15.4% (274)
Sires with > 50 AMS dgthrs	4.1%
Sires with > 100 AMS dgthrs	2.3%

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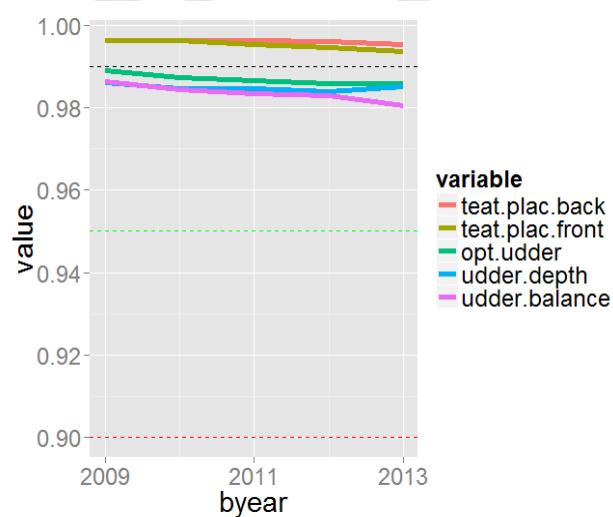
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HOLSTEIN - EBV correlations between current and new evalaution

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What are the changes in breeding values? Correlations between current evaluation and AMS evaluation - cows with linear traits

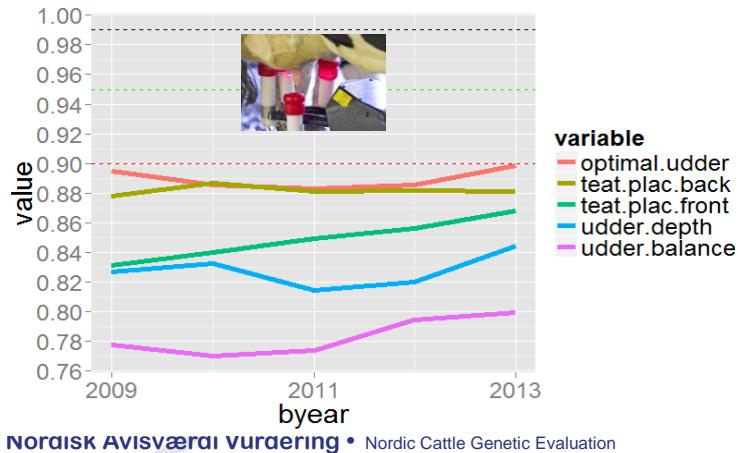


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Influence of AMS data on breeding value estimation

Correlations between current evaluation and AMS evaluation
- for cows with both AMS and linear traits

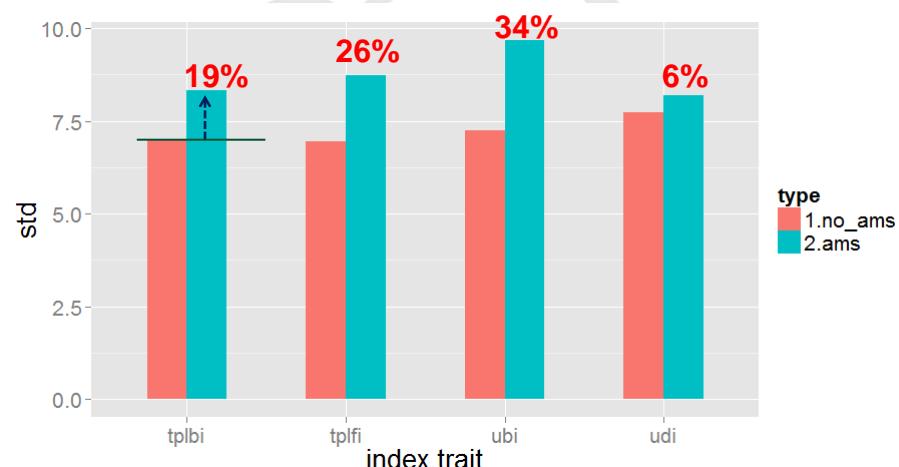


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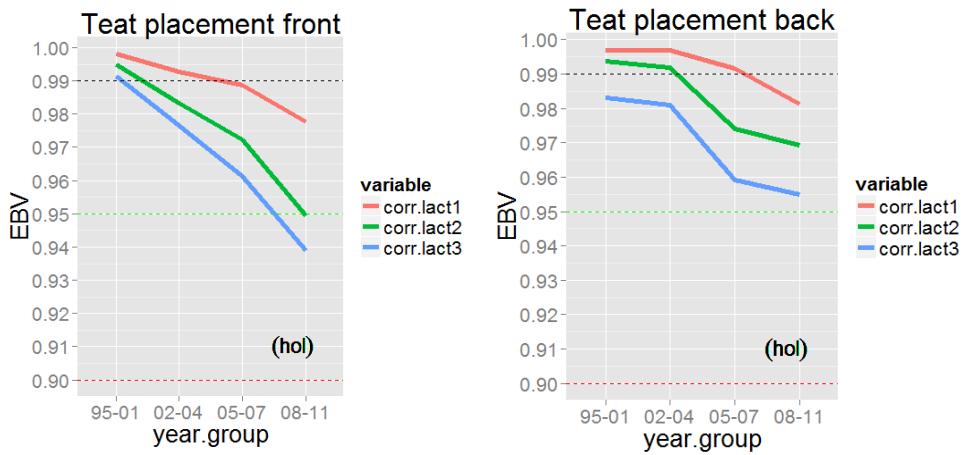
Standard deviation of EBVs - HOL cows



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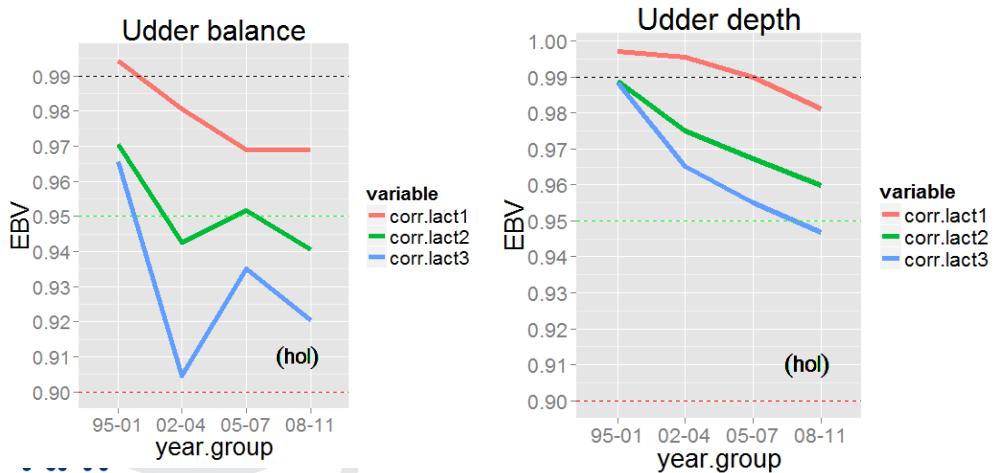
HOL- correlation old vs. new Sires with ams daughters



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HOL- correlation old vs. New Sires with ams daughters



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Final remarks

- MORE Data: #3 lactations
- High heritabilities for AMS
- Genetic correlations >90 = same trait
- No change on the genetic trends
- Higher reliability for sires (with AMS daughters) and cows (especially later lactations)
- Plan for implementation in routine (parallel runs in 2016)
- IB test September and implementation Nov'16



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