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# Development of breeding values for mastitis derived from SCS results

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## Motivation

- Udder health in Germany:
  - Breeding value on SCS
  - As relative EBV, RZS, 7% in total merit index (RZG)
  - Also important auxiliary trait of functional longevity
  - → real total weight of SCS in RZG is higher than 7%
  - SCS is an indirect trait to consider mastitis



## Motivation

- Use of SCS as measure for mastitis:
  - ,There is more useful information in SCS distributions than currently used in practice‘ (J. ten Napel, 2009)
  - Uninfected mammary gland has a low SCS
  - Mastitis influences the distribution of SCS
  - Several countries use SCS – test day results for the prediction of clinical and subclinical mastitis



## Motivation

- Use of SCS as measure for mastitis:
  - Heritabilities for mastitis are low (in general for health traits)
  - Estimates between 4% and 8% (Heringstadt, 2000 and 2008, Madsen et al., 2008, Govignon-Gion et al., Miglior et al., 2012)
  - Genetic correlations to SCS between .50 and .80 (see above)
  - Modified SCS-results are widely used to estimate mastitis → alternative traits



## Motivation

- Use of SCS as measure for mastitis:
  - Alternative traits:
  - Excessive values (>500.000 cells/ml)
  - Standard deviation of SCS
  - Genetic correlations were only little higher (.62-.82) to mastitis than direct measurements of SCS (Madsen et al., 2008; Miglior et al., 2012)

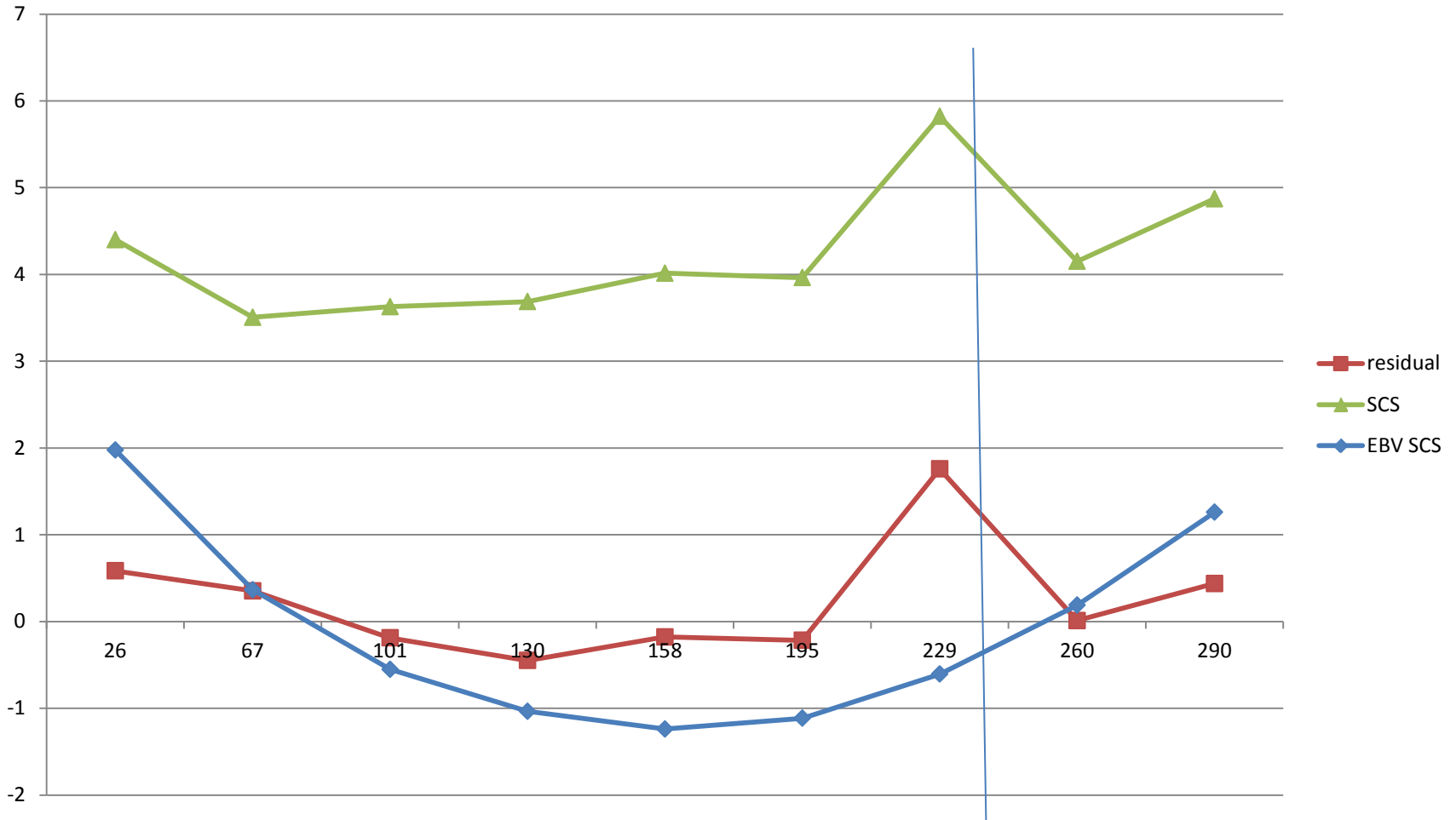


## Data analysis

- Udder health in Germany:
  - New projects help collecting mastitis results
  - GKuh and BHNP
  - Results give ,real' mastitis events during a lactation
  - Analysis of ,real' mastitis and influence on SCC



# Mastitis and SCS





## Data analysis

### ■ Genetic evaluation model:

$$y_{ijklo} = h_{il} + \sum_{m=1}^3 \beta_{jlm} f_{jlm} + \sum_{m=1}^3 b_{klm} a_{klm} + \sum_{m=1}^3 b_{klm} p_{klm} + e_{ijklo}$$

- Random-Regression Test-Day model
- phenotype = environmental effects + genetic effects + residual
- If single mastitis events are not covered in the genetic model
  - → residual effects contain useful information
  - What else than mastitis can it be?



## Data material

- Mastitis records from health trait recording:

Lactation	Mastitis event	No masitis	All
1	12017	14784	26801
2	11943	10757	22700
3	10375	6622	16997
All	32163	34335	66498



## Methods

### ■ Trait definition

- STD = deviation of residuals within a lactation
  - High deviation → one or more mastitis events as residual peak within lactation
- N\_RES = number of residual peaks in lactation (higher than 95% quantile)
- N\_SCS = number of Cell Score peaks (higher than 95% quantile)
- RZS = relative breeding value SCS



## Methods

- Means for analysed traits in lactations with different numbers of mastitis events(\*)

mastitis events within lactation	STD	N_SCS	N_RES	RZS
<b>0</b>	0.74	0.22	0.35	105.7
<b>1</b>	1.16	0.55	0.61	103.1
<b>2</b>	1.39	1.11	1.01	100.1

\*) all differences are statistically significant with  $p=0.001$



## Methods

### ■ Trait definition

- R<sup>2</sup>-analysis to determine influence on target trait
- Target trait = number of mastitis events within lactation

R-Square	STD	N_SCS	RZS	N_RES
0.1537	X			
0.2012	X	X		
0.2138	X	X	X	
0.2145	X	X	X	X

- Combination of: deviation of residuals and number of cell score peaks
- STD + N\_SCS



## Methods

- Genetic model

- $y = hy + \text{lact.nr.} + \text{sire} + e$
- Two-trait-model:
  - STD and N\_SCS
- Sire model for better convergence

- Genetic parameters estimated:

	<b>STD</b>	<b>N_SCS</b>
<b>STD</b>	0.09	0.76
<b>N_SCS</b>	0.22	0.04

(heritabilities on, r(g) above, r(p) below diagonal)



## Results

- Estimation of sire-EBVs for mastitis using alternative traits
- Validation of EBV with direct EBV from health recording
- Correlation between breeding values:

	<b>Direct mastitis</b>	<b>STD</b>	<b>N_SCS</b>
<b>Direct mastitis</b>	1	0.34	0.27
<b>STD</b>		1	0.72

- Number of bulls with mastitis recorded daughters is very low



## Results

- Mastitis recording currently available for a small fraction of cow population
- Definition of alternative traits for mastitis is useful
- Use of SCS-RRTDM evaluation gives phenotypes for all cows in population
- Using residuals is promising in detecting influences of mastitis not covered by SCS-evaluation
- Alternative traits have heritabilities in expected range
- Validation is difficult because of low number of bulls with reliable EBV for target trait (mastitis)





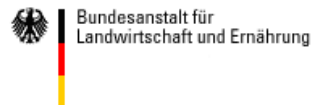
# Results

- More validation data is needed

If you are interested to support validation with your mastitis data, please contact me!

## Acknowledgements:

health data were generously provided by the innovation projects GKuh (Gesunde Kuh) and BHNP (Breed for Health NeoPartus)



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