

# Genetic variability of alternative SCC-traits and their relationship with clinical and subclinical mastitis

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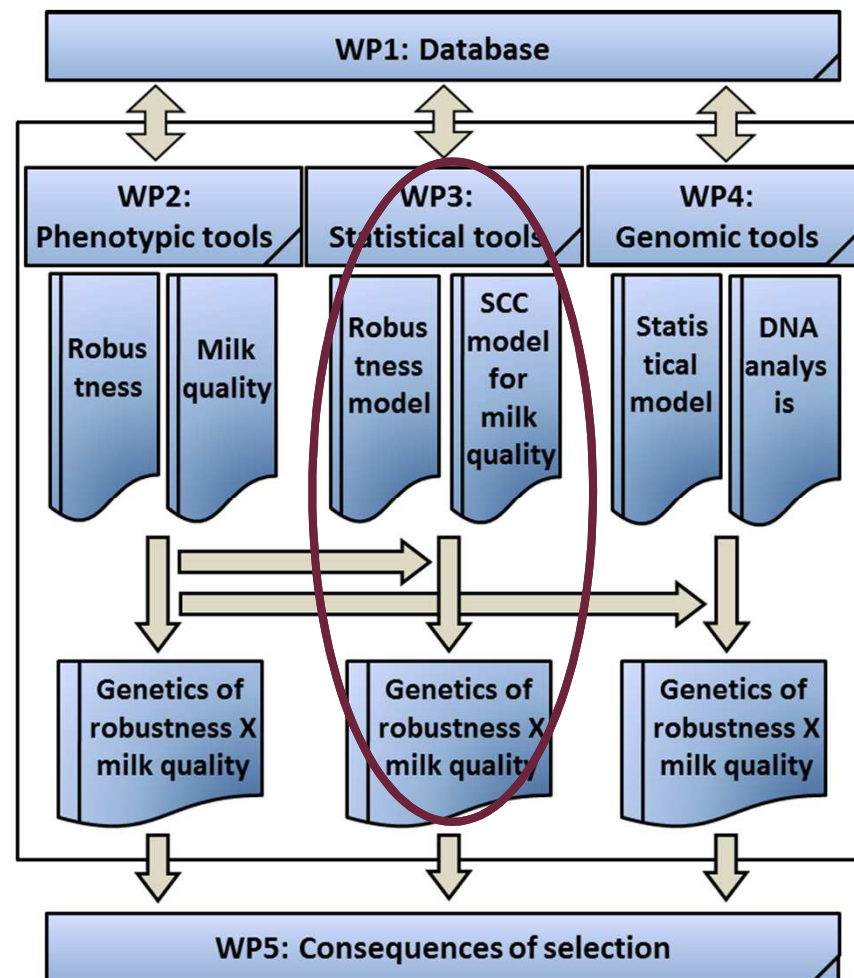
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# Introduction

- Mastitis is a common and costly disease in dairy cattle
- Additionally, both clinical and subclinical mastitis are of concern
- Recently, other SCC-derived traits have been proposed as alternatives for lactation average SCC

# Background

- In a previous study on experimental herd data with weekly (and mimicked monthly) SCC observations we found some traits to be interesting to continue to study in field data with monthly records
- Study was based on clustering approach and logistic regression to explain CM

# Objectives

- to estimate heritabilities of, and genetic correlations between, clinical mastitis, subclinical mastitis and alternative SCC-traits in the first 3 lactations of Swedish Holstein cows, and
- to estimate genetic correlations among these alternative SCC-traits.

# Traits

- **CM:** clinical mastitis; 1 if at least one veterinary-treated mastitis in lactation, 0 otherwise
- **SCM:** subclinical mastitis; number of months with  $SCC > 150,000$  but no clinical mastitis
- **SCC150D:** average somatic cell counts (SCC) in early lactation (5-150d);
- **SCCSD:** standard deviation of log of TD-SCC;
- **TD41-80:** at least one TD with  $41,000 < SCC < 80,000$
- **TD>500:** at least one TD  $SCC > 500,000$ ;
- **NPeaks:** number of peaks (at least one TD with SCC above 150,000) between two valleys;
- **ADSick:** average length of peak

**Posterior heritability and genetic correlation (standard deviation) estimates for clinical (CM) and subclinical (SCM) mastitis.**

**(CM using a Threshold model, SCM a linear model)**

	Parity 1		Parity 2		Parity 3	
	CM	SCM	CM	SCM	CM	SCM
$h^2$	0.08	0.17	0.08	0.16	0.07	0.12
$r_g$	0.74 (0.04)		0.72 (0.03)		0.62 (0.08)	

SD( $h^2$ )=0.01

# Posterior heritabilities and genetic correlations among SCC-traits in **first parity**

	SCC150D	SCCSD	TD>500	TD41-80	NPeak	ADSick
SCC150D	<b>0.13</b>					
SCCSD	0.90	<b>0.14</b>				
TD>500	0.94	0.94	<b>0.12</b>			
TD41-80	-0.37	-0.46	-0.49	<b>0.05</b>		
NPeak	0.96	0.96	0.93	-0.43	<b>0.10</b>	
ADSick	0.97	0.99	0.97	-0.50	0.98	<b>0.14</b>



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ADSick	0.97	0.99	0.97	<b>-0.50</b>	0.98	<b>0.14</b>

## Posterior heritabilities and genetic correlations among SCC-traits in 2<sup>nd</sup> parity

	SCC150D	SCCSD	TD>500	TD41-80	NPeak	ADSick
SCC150D	0.16					
SCCSD	0.98	0.16				
TD>500	0.96	0.99	0.17			
TD41-80	-0.81	-0.79	-0.80	0.09		
NPeak	0.93	0.92	0.89	-0.65	0.08	
ADSick	0.97	0.98	0.97	-0.79	0.95	0.15

# Posterior heritabilities and genetic correlations among SCC-traits in 3<sup>rd</sup> parity

	SCC150D	SCCSD	TD>500	TD41-80	NPeak	ADSick
SCC150D	0.13					
SCCSD	0.97	0.12				
TD>500	0.96	0.99	0.12			
TD41-80	-0.79	-0.56	-0.70	0.08		
NPeak	0.81	0.80	0.78	-0.46	0.06	
ADSick	0.94	0.94	0.94	-0.78	0.85	0.10

# Posterior genetic correlations of CM and SCM with alternative SCC-traits

	Parity 1		Parity 2		Parity 3	
	CM	SCM	CM	SCM	CM	SCM
SCC150D	0.82	0.96	0.81	0.96	0.76	0.94
SCCSD	0.82	0.97	0.79	0.97	0.74	0.94
TD>500	0.80	0.94	0.87	0.94	0.78	0.92
TD41-80	-0.22	-0.48	-0.50	-0.81	-0.26	-0.85
NPeak	0.79	0.96	0.74	0.94	0.67	0.84
ADSick	0.81	0.99	0.76	0.99	0.66	0.98

# Posterior genetic correlations of CM and SCM with alternative SCC-traits

	Parity 1		Parity 2		Parity 3	
	CM	SCM	CM	SCM	CM	SCM
SCC150D	0.82	<b>0.96</b>	0.81	<b>0.96</b>	0.76	<b>0.94</b>
SCCSD	0.82	<b>0.97</b>	0.79	<b>0.97</b>	0.74	<b>0.94</b>
TD>500	0.80	<b>0.94</b>	0.87	<b>0.94</b>	0.78	<b>0.92</b>
TD41-80	-0.22	-0.48	-0.50	-0.81	-0.26	-0.85
NPeak	0.79	<b>0.96</b>	0.74	<b>0.94</b>	0.67	0.84
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SCCSD	<b>0.82</b>	0.97	<b>0.79</b>	0.97	<b>0.74</b>	0.94
TD>500	<b>0.80</b>	0.94	<b>0.87</b>	0.94	<b>0.78</b>	0.92
TD41-80	-0.22	-0.48	-0.50	-0.81	-0.26	-0.85
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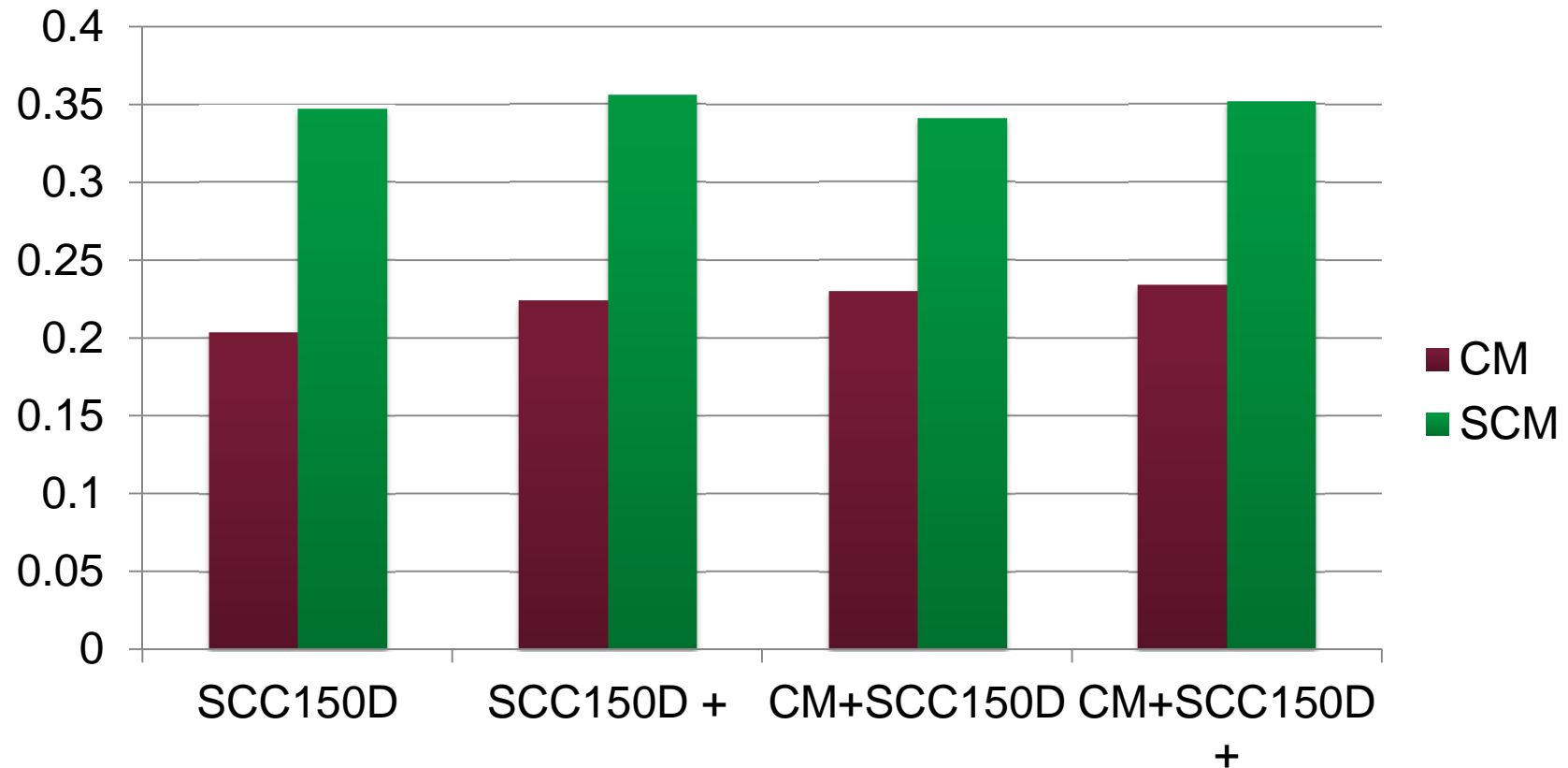
# Effect of adding two new SCC-traits to index, on the accuracy

Traits in index	Accuracy
SCC150D	0.848
SCC150D +SCCSD+TD41-80	0.893 (+5.4%)
CM+SCC150D	0.878
CM+SCC150D +SCCSD+TD41-80	0.900 (+2.5%)

Breeding goal: CM and SCM with equal weights  
per phenotypic SD

Sire selection based on 100 HS daughters

# Effect of adding two new SCC-traits to index, on genetic gain



# Conclusions

- Clinical and subclinical mastitis are distinct albeit correlated traits ( $r_g$  0.62-0.74)
- Alternative SCC traits show reasonable heritabilities, are closely associated to both CM and SCM (valuable indicator traits), but are generally highly inter-correlated (little new information)
- Exception TD41-80: less strongly correlated to other SCC-traits but reasonably correlated with SCM, especially in later lactations
- Using additional SCC-traits may improve accuracy
- Simple traits: standard linear models can be used for selection purposes