



# Genetic evaluation of differential somatic cell count in Italian Holstein

---

Galluzzo F<sup>1,2</sup>, Visentin G<sup>2</sup>, van Kaam JBCHM<sup>1</sup>, Finocchiaro R<sup>1</sup>,  
Marusi M<sup>1</sup>, Cassandro M<sup>1,3</sup>

*<sup>1</sup>ANAFIBJ, <sup>2</sup>University of Bologna, <sup>3</sup>University of Padova*

# Aims

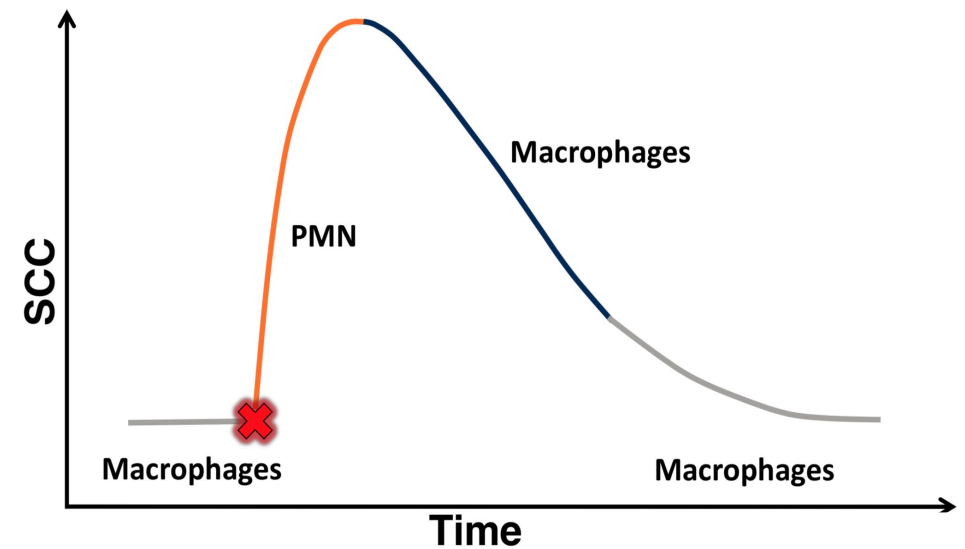
---

- Study genetic aspects of differential somatic cell count (DSCC) in the Italian Holstein breed in relation with somatic cell count (SCC): State of infection (SI)
- Develop and implement a routine genetic evaluation of SI in the Italian Holstein breed in order to indirectly identify the animals with the highest genetic potential for mastitis resistance
- Add females to training population for the studied trait

# What is DSCC?

4 macrogroups of somatic cells in milk:

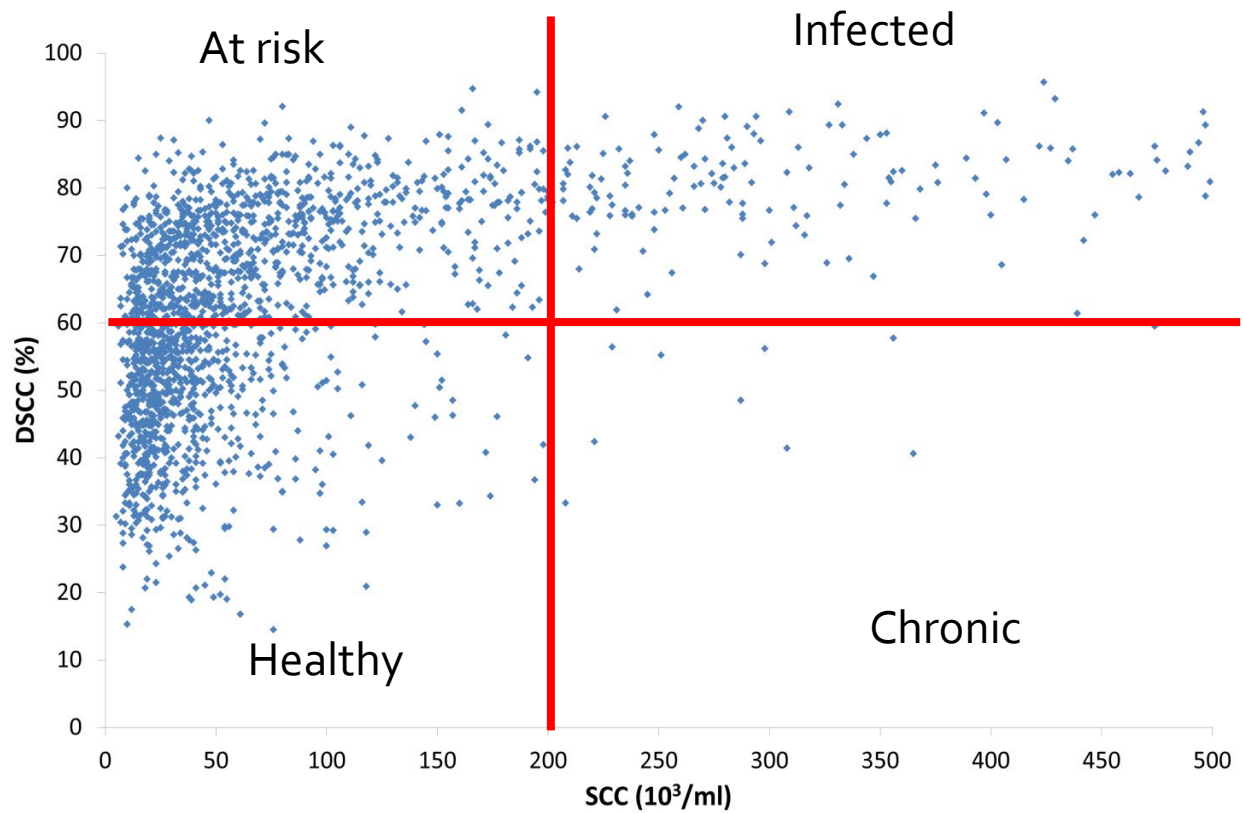
- Lymphocytes (LYM)
- Polymorphonuclear neutrophils (PMN)
- Macrophages
- Epithelial cells



$$DSCC = \frac{LYM + PMN}{SCC} * 100 [\%]$$

[Damm et al, 2017; Bobbo et al, 2019; Zecconi et al, 2020; Schwarz et al, 2020; +oth...]

# How can DSCC be used?



## Genetic analysis

- 1: Healthy
- 2: At risk
- 3: Infected
- 4: Chronic

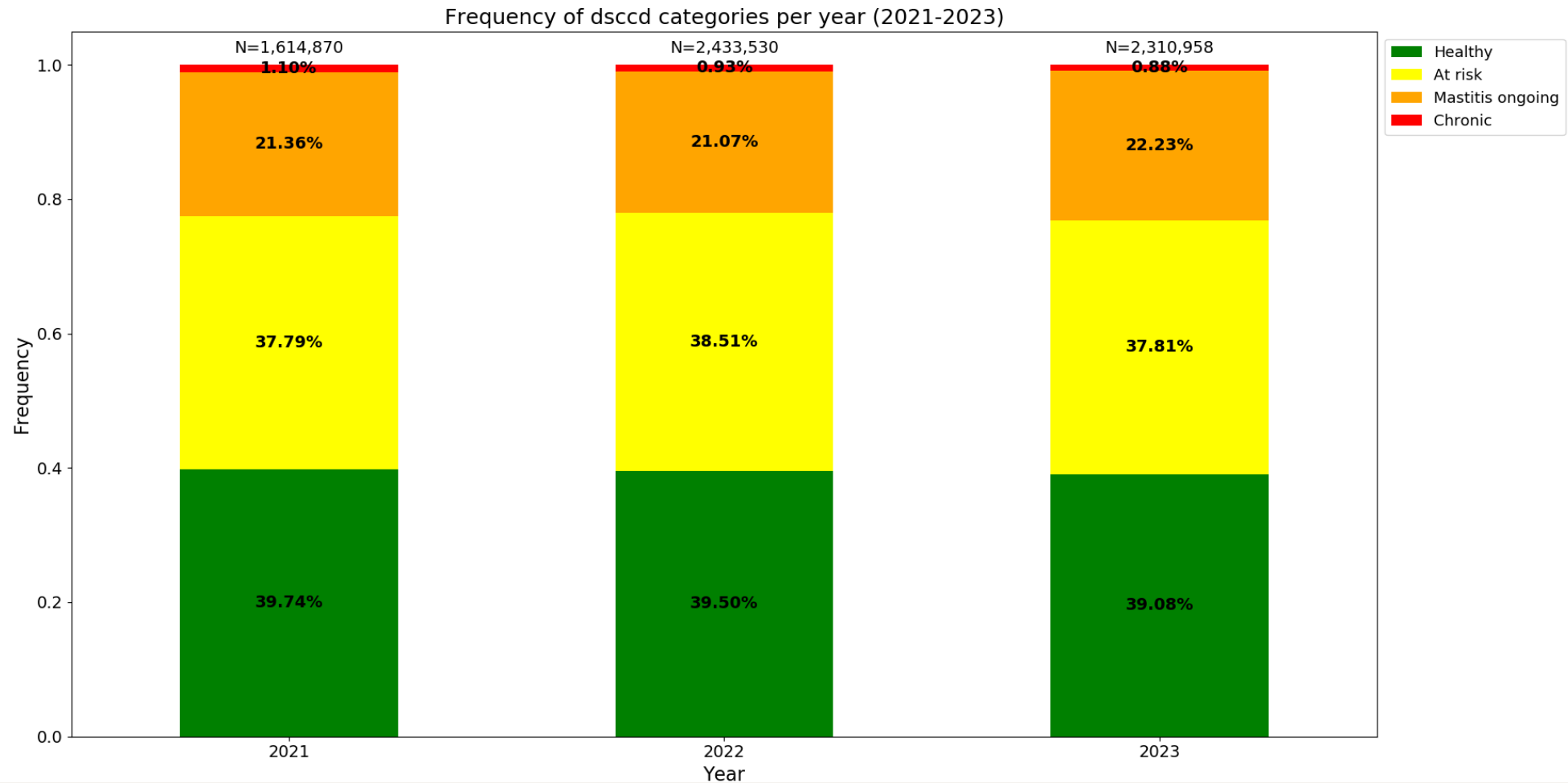
## Thresholds

1<sup>o</sup> parities: 60%; 100k cell/ml  
 Later parities: 65%; 200k cells/ml

From best (1) to worst (4)

*Thresholds from works of University of Padova research group (Cassandro et al, 2020)*

# Phenotypic situation



# Data editing criteria

*TD records from 2018 onwards (AIA, «LEO project», 2023)*

Developed in SQL+bash+python

- Max parity: 5
- DIM range: 5-405
- Maximum DIM at first test-day: 60
- Maximum distance between test-days: 70
- Range SCS (*Ali & Shook, 1980*): >0 – 9
- Range DSCC: 25-95%
- Min contemporaries: 5

**Observations after edits: ~8M**

# Descriptive statistics

	SCS	IS	DSCC
Mean	3.73	1.59	62.79
SD	1.83	1.11	16.50
CV	49.06	69.81	26.28
MIN	0.16	1	25
MAX	9	4	95

# Statistical model: MT repeatability linear animal model

$$P_{ijklmnopqrst} = S_k * Y_l + H_m + DIM_n * PARCo * Y_l + AGE_C\_PAR_p * Y_q + htdp_i + h ymp_j + a_r + pe_s + e_{ijklmnopqrst}$$

- $P_{ijklmnopqrst}$ : phenotypic observation (SCC or IS)
- $htdp_i$ : herd-test\_day-parity [R] – management+environment at test-day
- $h ymp_j$ : herd-year-month-parity of calving [R] – management+environment at calving
- $S_k * Y_l$ : year-season of recording [F] – time trends
- $H_m$ : herd of recording [F] – ‘better sires in better herds’
- $DIM_n$ : 10 classes of 40 days [F]
- $PARC_o$  (3 classes): 1, 2, 3+ [F]
- $AGE_C\_PAR_p$  (9 classes): 1 (<24mon), 1 (24-27mon), 1 (>27mon),  
2 (<36mon), 2 (36-40mon), 2 (>40mon), 3, 4, 5 [F]
- $a_r$ : animal additive genetic [R]
- $pe_s$ : permanent environment [R]



# Variance components

---

Software: THRGIBBS1F90 (*Misztal et al, 2014*)

Obs: 279,896 (200 herds)

Convergence: R package BOA (*Smith, 2007*)

Diagonal: PM (PSD)

Above diagonal: genetic correlations

SCS	SI
0.13 (0.01)	0.94
	0.09 (0.01)

# Genomic validation

Multi-step genomic evaluation (EDPs as pseudo-phenotypes)

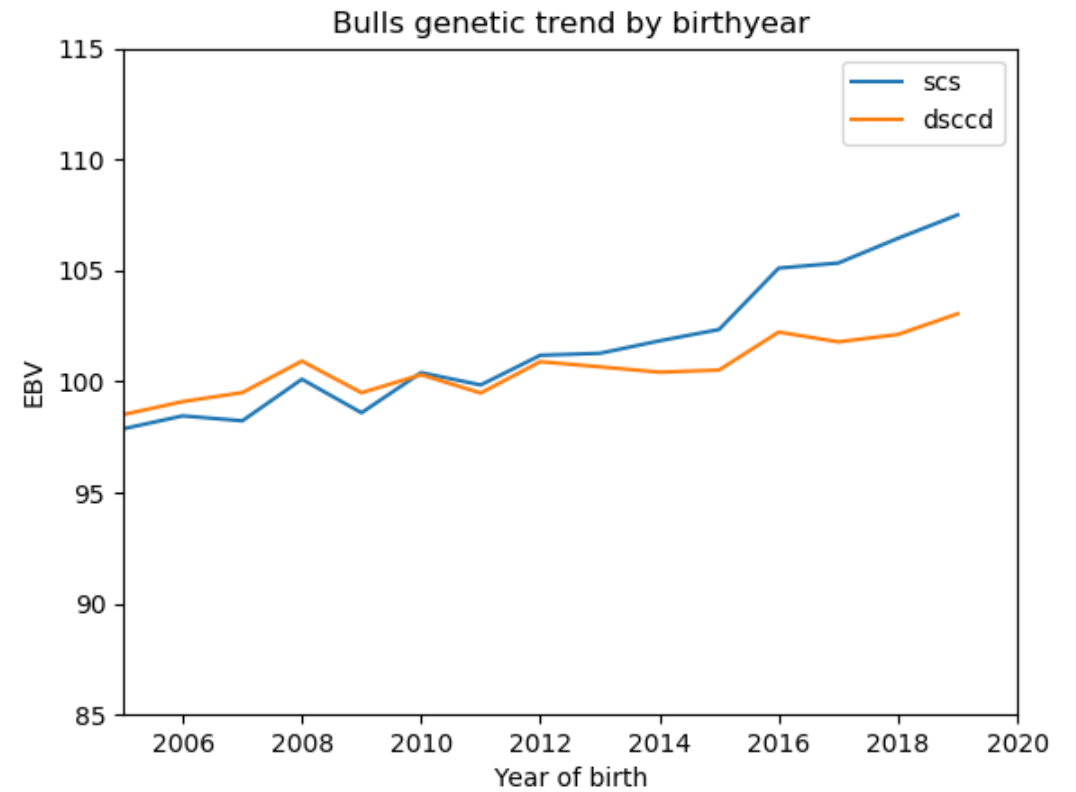
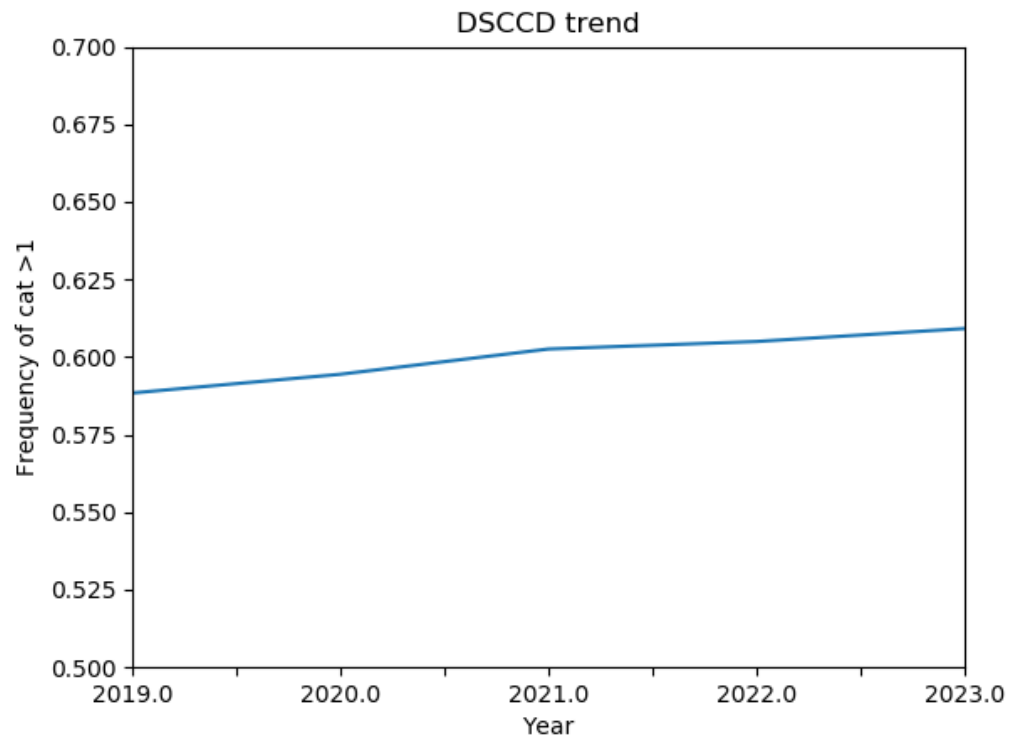
MiX99 (*MiX99 Development Team, 2022*) + GS3 (*Legarra et al, 2011*)

Full run and reduced run (YYYY-3)

$$EDP_{full} = a + bDGV_{red} + e$$

Trait	Training	N_training	b	r <sup>2</sup>
SI	Bulls	3,030	1,272	0,30
SI	Bulls+Cows	136,763	0.950	0,60

# Phenotypic and genetic trends



# Take home message(s)

---

- Selection for SI is feasible
- Indirect selection for SCS and MAS was effective
- The developed model is stable enough and suitable for routine genetic evaluation
- Adding females to training population is beneficial for SI

**This trait is planned to be part of the Italian Holstein routine genetic evaluation (after CTC approval)**

# Thank you



Ferdinando Galluzzo



ferdinandogalluzzo@anafib.it



[www.anafibj.it](http://www.anafibj.it)

