



Genetic evaluation of differential somatic cell count in Italian Holstein

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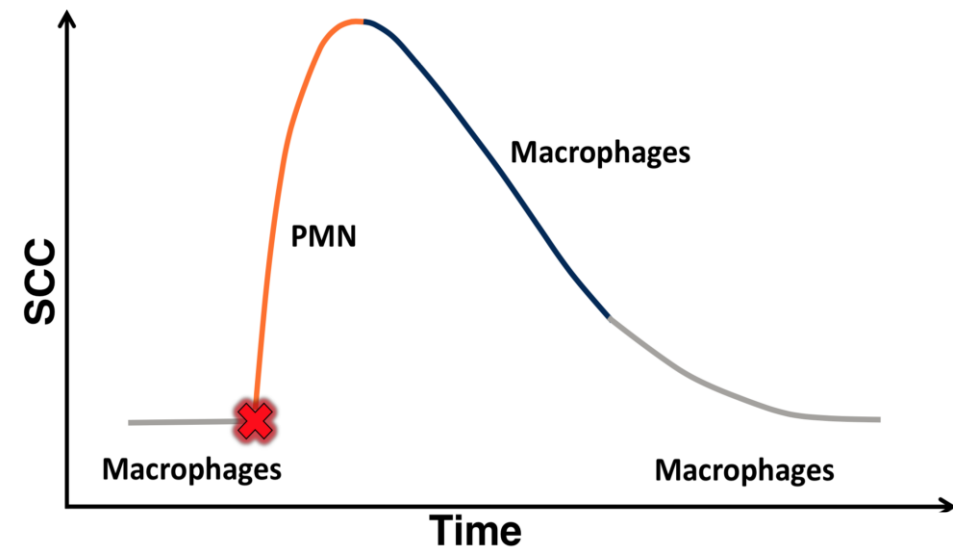
Aims

- 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:

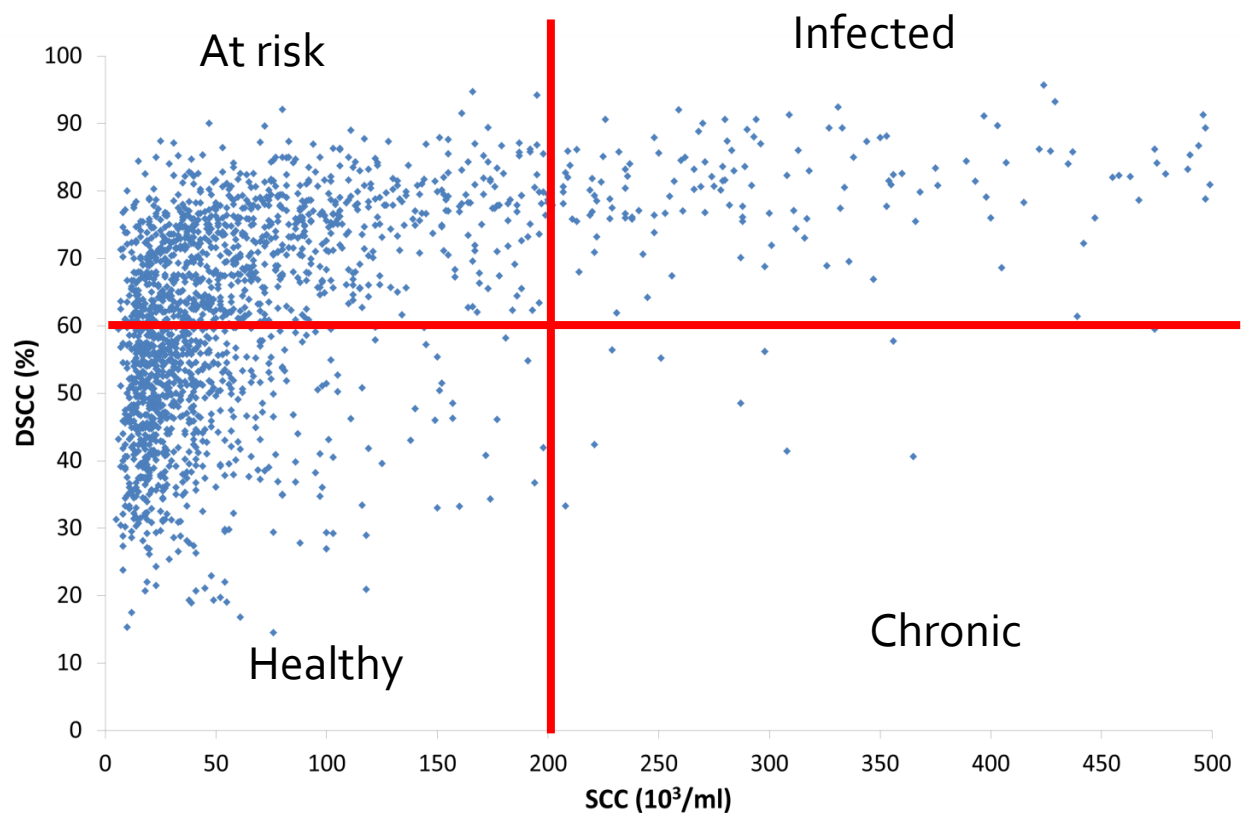
- Lymphocytes (LYM)
- Polymorphonuclear neutrophils (PMN)
- Macrophages
- Epithelial cells



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

[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

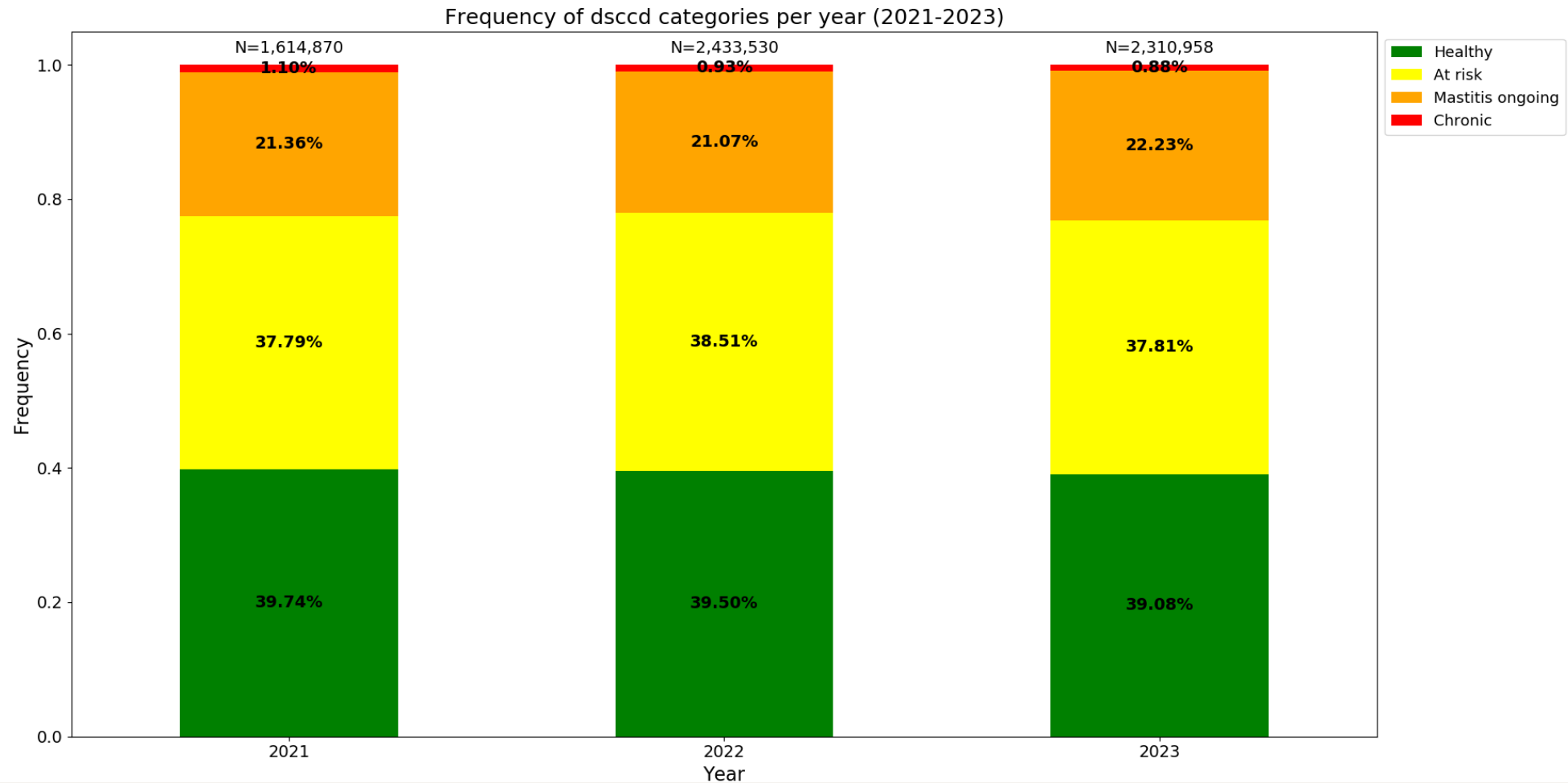
Thresholds

1^o 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

$$P_{ijklmnopqrst} = S_k * Y_l + H_m + DIM_n * PARCo * Y_l + AGE_C_PAR_p * Y_q + htdp_i + hymp_j + a_r + pe_s + e_{ijklmnopqrst}$$

- $P_{ijklmnopqrst}$: phenotypic observation (SCC or IS)
- $htdp_i$: herd-test_day-parity [R] – management+environment at test-day
- $hymp_j$: 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)

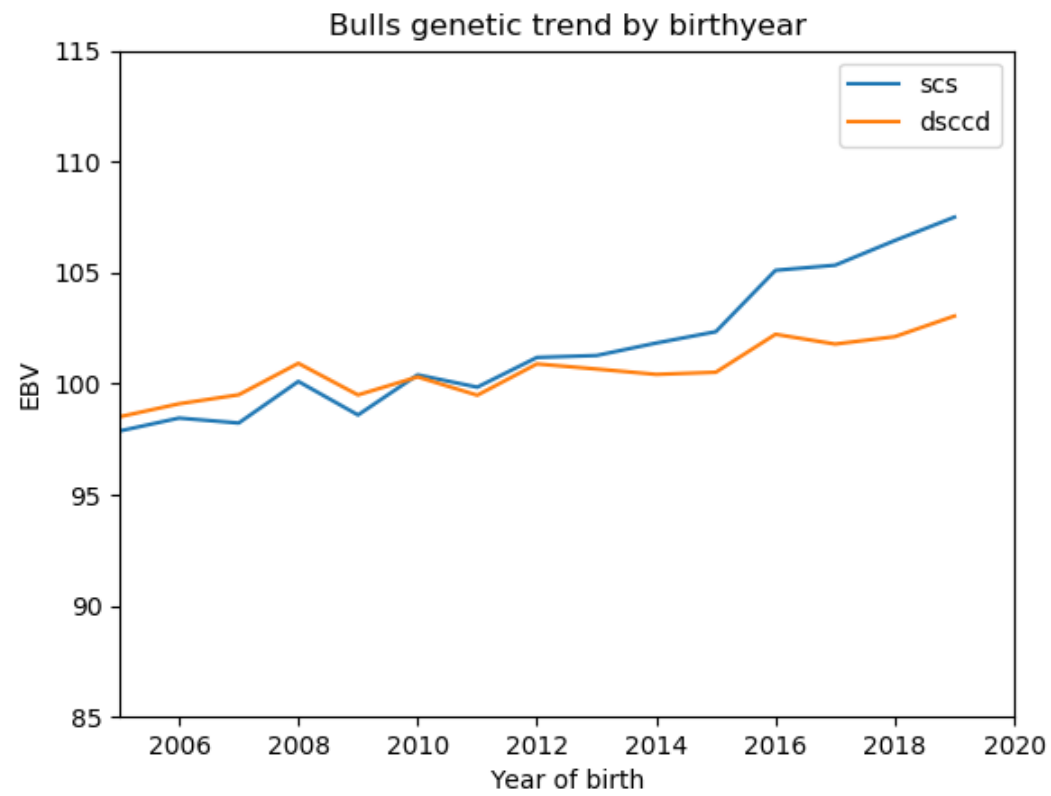
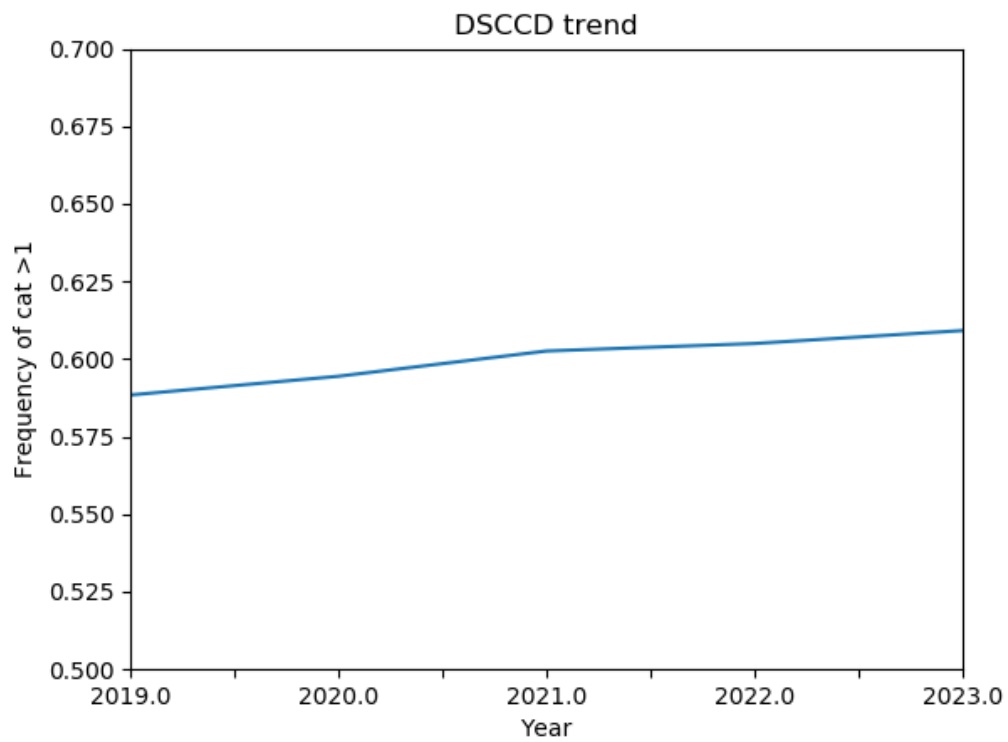
MiX99 (*MiX99 Development Team, 2022*) + GS3 (*Legarra et al, 2011*)

Full run and reduced run (YYYY-3)

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

Trait	Training	N_training	b	r ²
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



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