Response to a divergent selection based on somatic cell counts in Alpine dairy goats

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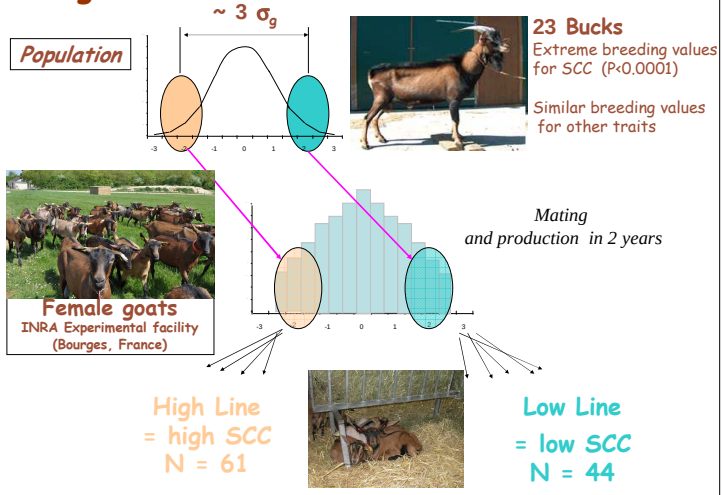
Milk somatic cell count (SCC) is routinely collected in French dairy goat populations (Alpine and Saanen breeds). The heritability of this trait has been estimated to be around 0.20 (Rupp *et al.*,2011). Accordingly, it is possible to consider improving mastitis resistance in goat by a selection on SCC. However, efficiency of such a selection raises some concerns, especially because non infectious factors of variation have a large effect on goat milk SCC. Our study therefore consisted in evaluating the consequences of SCC-based selection on intra-mammary infections.

Materials et methods

Divergent lines



Biological measures

- **Production traits** (Milk, Protein and Fat content)
- **Milk bacteriology half-udder** (negative vs positive; type; quantity)
- **SCC half-udder**

Kidding date and 8 monthly time points in first lactation ⟶ 1620 samples

Statistical Analyses

- Log transformation (base 2) of SCC ➔ SCS : Somatic Cells Score

- **Linear mixed models** (proc MIXED, SAS@) to evaluate the effect of line on the different repeated continuous traits (production traits, SCS from udder halves)

Model 1 : line + stage of lactation + year + bacteriological result
Model 2 : model 1 + bacterial type + bacterial quantity

- **Chi2-test** (proc FREQ, SAS@) to assess statistical differences on the total number of bacteria between lines

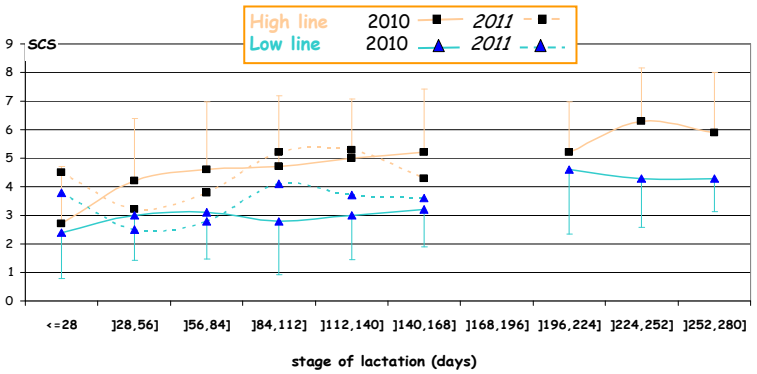
Discussion

Within the High line, the SCS of positive samples are significantly higher than in negative samples (+0.9 point of SCS), but not in the Low line (+0.4 point of SCS). This observation can be explained by a higher quantity of pathogens in the positive samples in the High line than in the Low line.

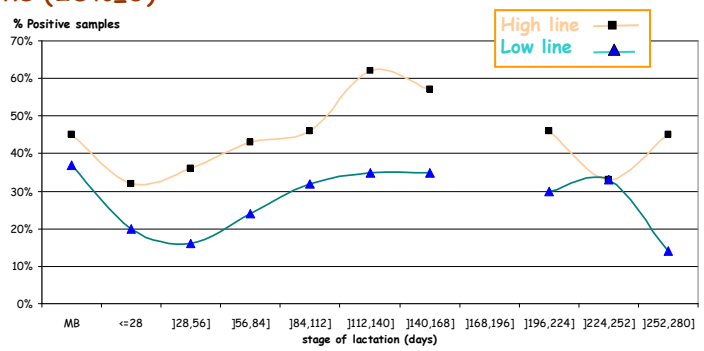
These results gave good evidence that ***SCS-based selection in goat will decrease the prevalence of intra-mammary infections*** *and the amount of bacteria within infected samples*

Results

- The **Low line goats have a significantly lower half-udder SCS** (3.4±0.2) than the High line (4.6±0.2)

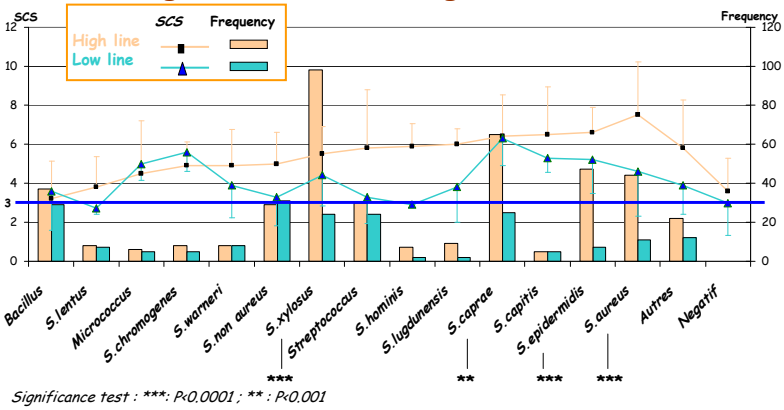


- **Frequency of positive samples is significantly higher in the High line** (46%±3) than in the Low line (28%±3)



- Main bacterial types found are **Coagulase Negative Staphylococci** (58.4%) and especially *S. xylosus* (19.7%)

- Milk SCS depends on Bacterial type : ***S.aureus*** (5.5±0.5), ***S.caprae*** (5.2±0.3) vs. *Bacillus* (4.0±0.3) and negative samples (3.6±0.1). Positive samples have higher SCS in the High than in the Low line.



*Significance test : ***: P<0.0001 ; ** : P<0.001*

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