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

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Longissimus muscle fatty acid profile of lambs fed a high-concentrate diet containing canola, sunflower or castor oil

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Lamb meat is a good protein source; however, it's high in saturated fatty acids. Thirty six Longissimus muscle of crossbred Dorper x Santa Inês lambs (BW at slaughter=36.7±1.5 kg and 120 d old) were used to determine the effects of diets with 3% of vegetable oil on meat fatty acid composition. Lambs were assigned to a randomized complete block design and fed the experimental diets during 8 weeks. The control (CON) diet contained 90% concentrate and 10% hay in a DM basis. In the remaining treatments, diets were added with 3% canola oil (CAN), 3% sunflower oil (SUN) or 3% castor oil (CAS). Total lipids were extracted, esterified and methylated. Methyl esters were separated by gas chromatography (Agilent/Model 7890) using a 100 m capillary column. Data were analyzed using the MIXED procedure of SAS and means were compared by Tukey Test. CON and CAS diets increased (P=0.01) proportions of C16:1. SUN diet increased concentrations of C18:1 trans (4.12, 4.00, 6.57, 3.88% for CON, CAN, SUN and CAS, respectively) and decreased (P=0.02) C18:1n9 compared to CAS (35.53, 39.99% for SUN and CAS, respectively). CAS decreased (P=0.02) C18:2 n-6 (7.68, 8.45, 9.03 and 6.33% for CON, CAN, SUN and CAS, respectively). CAN diet increased the concentration of C18:3 n-3 (0.21, 0.36, 0.21 and 0.20% for CON, CAN, SUN and CAS, respectively). The inclusion of vegetable oils did not affect MUFA:SFA ratio. However, CAN and SUN diets increased PUFA:SFA (0.34 and 0.35%, respectively) in comparison with CAS (0.25%). The C18:1-OH was present only in CAS (0.21%) diet because the composition of the castor oil. The proportion of C18:2 cis-9, trans-11 (CLA) was higher when CAN (0.59%) and SUN (0.44%) were included in the diet, in contrast with CON and CAS (0.31 and 0.33%, respectively). Canola and sunflower oils changed Longissimus muscle fatty acid composition of crossbred Dorper x Santa Inês lambs, showing a higher CLA content.

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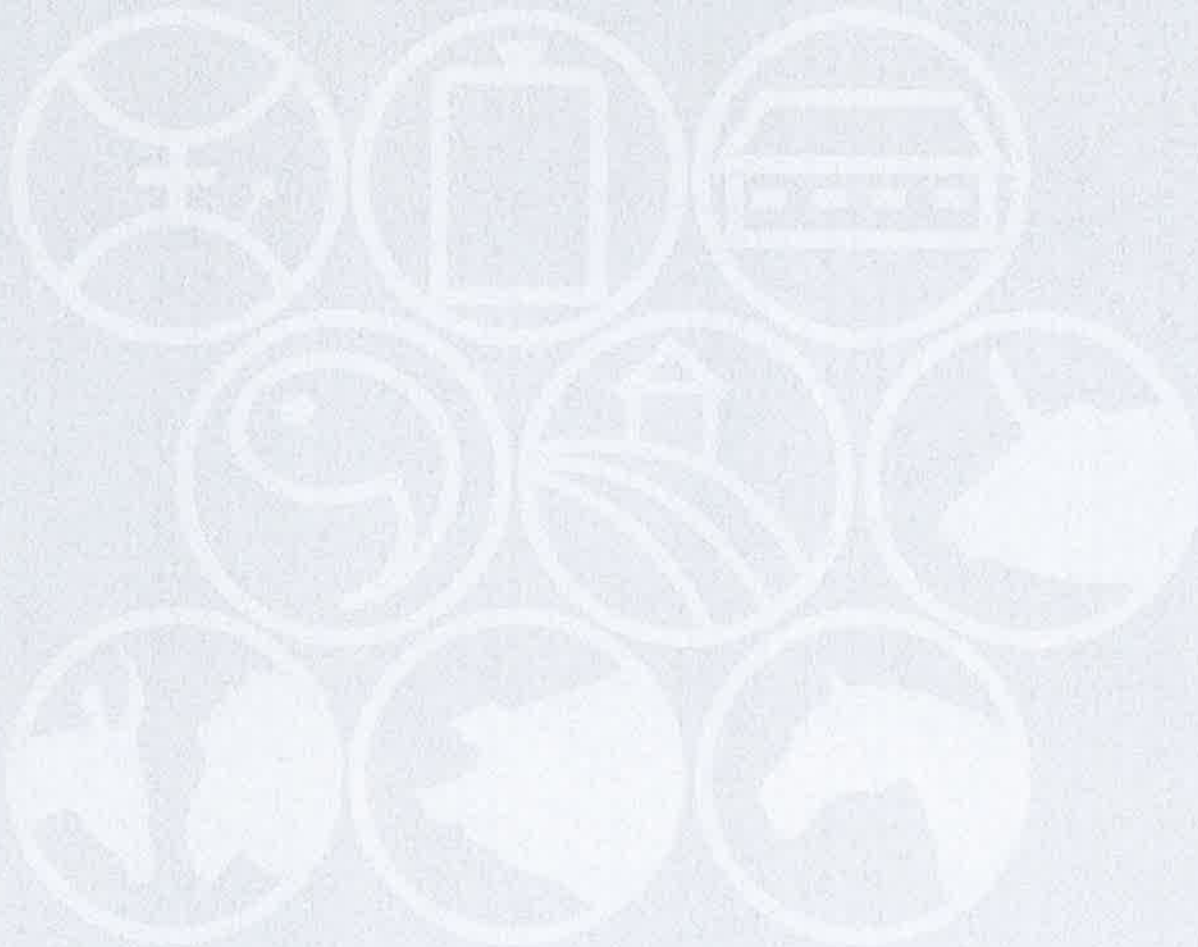
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Response to a divergent selection based on somatic cell counts in Alpine dairy goats

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Milk somatic cell count (SCC) is routinely collected in the French Alpine and Saanen dairy breeds and its heritability has been estimated to be around 0.20. Accordingly, it is possible to consider improving the mastitis resistance in goat by 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. Using 13 progeny-tested AI bucks selected for extreme breeding values for somatic cell scores (SCS), we created two groups of 28 High SCS and 25 Low SCS goats which were raised at the INRA experimental facility of Bourges. Milk bacteriological analyses and SCC of half-udders were performed at the kidding date and at 7 monthly points in first lactation. Milk production was similar in the 2 lines. The mean SCC was 1,709,000 cells/ml and 592,000 cells/ml for the High and Low SCS goats, respectively, with a significant (P<0.05) difference of 1.4 point in SCS. Regarding milk bacteriology results, 35% of samples were positive. The bacterial types found most frequently were Coagulase Negative Staphylococci (67%), *S. xylosum* being the most prevalent (19.5%). Frequency of positive samples was significantly higher in the High SCS (43%±2) than in the Low SCS line (25%±2). Additionally, the mean SCS was significantly higher for the positive than for negative milk samples (4.8±0.2 vs 3.8±0.1). This difference was also significant within the goat line. Preliminary results in the High and Low SCS lines therefore gave evidence that SCS-based selection in goat will lead to decreased intra-mammary infection prevalence and mean SCS.

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