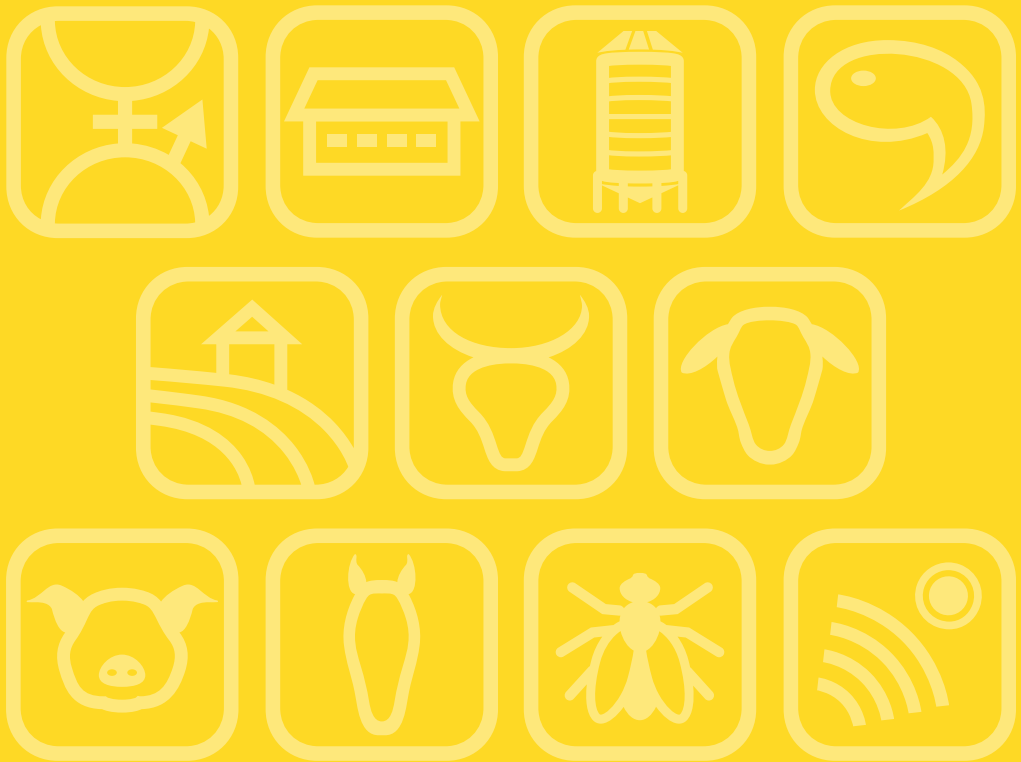


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Detailed protein fraction profile of goat milk of six breedsG. Secchi¹, N. Amalfitano¹, S. Pegolo¹, M.L. Dettori², M. Pazzola², G.M. Vacca² and G. Bittante¹¹University of Padova, Department of Agronomy, Food, Natural resources, Animals and Environment, Viale dell'Università, 16, 35020, Legnaro (PD), Italy; ²University of Sassari, Department of Veterinary Medicine, Via Vienna, 2, 07100, Sassari (SS), Italy; giorgia.secchi@phd.unipd.it

The protein profile of goat milk is very different from cow milk in terms of proportion of the different protein fractions and especially for its much higher genetic polymorphism. The aim of this study was to investigate breed effect on the detailed protein profile of goat milk. This research is part of the GOOD-MILK project which involved 1,272 goats from 6 different breeds reared in 35 farms located in Sardinia (Italy). The breeds are divided in two categories: the Alpine breeds (ALP: Camosciata delle Alpi and Saanen); and the Mediterranean breeds (MED: Murciano-Granadina, Maltese, Sarda, and Sarda Primitiva). A total of 1,090 individual milk samples from 23 farms (823 samples + 267 duplicates) were analysed for identification and quantification of milk protein fractions by RP-HPLC method. The data were analysed using a linear mixed model with the classes of days in milk (DIM), parity, and breed as fixed effects, while the flock effect was included as random. In a second model, the fixed effects of casein genotypes were also included. Breed affected all milk protein fractions, while DIM and parity had small effects. The main differences in protein profile among breeds were between ALP and MED types, being the former richer in whey proteins and lower in caseins than the latter; within MED, Sarda and Sarda Primitiva showed higher concentration in caseins than the other breeds, and no significant differences from each other. The inclusion of casein genotypes did not change relevantly the breed effect estimates but it decreased the residual variance, especially for α_{S1} - and β -caseins. Further investigation about the relationships between milk protein profile and milk quality and cheese-making ability in different goat breeds are envisaged.

Assessment of dairy sheep carcass composition with X-ray computed tomographyA. Argyriadou¹, M. Monziols², M. Patsikas¹ and G. Arsenos¹¹School of Veterinary Medicine, Aristotle University, University Campus, 54124 Thessaloniki, Greece, ²IFIP institut du porc, La Motte au Vicomte BP 35104, 35651 Le Rheu Cedex, France; argyrian@vet.auth.gr

The objective was to test a CT-acquisition protocol, with automated settings, for post-mortem assessment of dairy sheep carcasses using also two image analysis protocols (IAP). Twenty-six sheep of both sexes were used. After slaughter, hot carcass weight was recorded. Carcasses were chilled for 24h, then subjected to CT-scanning (Optima CT520, GE). The two CT-acquisition protocols (CT1, CT2) were tested on 4 carcasses. CT1 was automated and involved dose efficiency parameters, commonly used in medical practice (ranging field of view-FoV and tube current-TC, standard tube tension-TT of 120 kV). In CT2, parameters were manually set as defaults throughout scanning (Large FoV, TC: 80 mA, TT: 140 kV). Slice thickness was 0.625 mm in both CT1 and CT2. The remaining 22 carcasses were scanned only with CT1. Two IAPs were tested on CT1 images of all carcasses; different thresholds were used to allocate voxels to muscle (IAP1: 0-120 HU, IAP2: 0-200 HU) and bone tissue (IAP1: HU>120, IAP2: HU>200), whereas fat tissue thresholds were standard; -200 to -1 HU. Tissue volumes and weights were calculated based on voxel volume, number of tissue voxels and tissue densities. Bone weight was calculated by subtracting fat and muscle weight from carcass weight. Paired sample t-tests and Wilcoxon signed-rank tests were used to assess estimation differences between CT1 and CT2. Mann-Whitney U tests were used for tissue estimations of both IAPs with available dissection data from similar sheep of the same population (n=101). Differences between CT1 and CT2 were not statistically significant. Bone estimations of both IAPs and muscle content estimation of IAP1 significantly differed from dissection data (P<0.01). Both CT-protocols are suitable for post-mortem assessment of dairy sheep carcass composition; hence automated CT1 can replace CT2. IAP2 better estimates muscle tissue compared to IAP1. However, bone tissue estimations are more complex. Work was funded by GreQuM project (T1EDK-05479), co-financed by Greece and EU (EPAnEK 2014-2020, Partnership Agreement 2014-2020).