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of the European Federation of Animal Science**



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Book of Abstracts of the 76th Annual Meeting of The European Federation of Animal Science

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Date: Monday 25 August 2025; 15:45 - 17:45

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Impact of Birth Weight and Early Growth on Milk Yield in Ewes' First Lactation

L. Mačuhová¹, V. Tančin^{1,2}, J. Mačuhová³, M. Uhrinčat¹, J. Škopcová⁴, R. Búci⁴, M. Herko⁴¹ National Agricultural and Food Center, Research Institute for Animal Production Nitra, Hlohovecká 2, 95141 Lužianky, Slovakia, ² Slovak University of Agriculture in Nitra, Institute of Animal Breeding, Tr. A. Hlinku 2, 94901 Nitra, Slovakia, ³ Institute for Agricultural Engineering and Animal Husbandry, Vöttinger Str. 36, 85354 Freising, Germany, ⁴ Bukovina Sheep Farm, Bukovina 288, 966 01 Bzenica, Slovakia

The aim of this study was to evaluate the effect of birth weight and daily weight gains by life day 10, 20, and 30 on milk yield and somatic cell score (SCS) during the first lactation. Slovak dairy sheep (N=26) were divided into three groups based on birth weight (BW1: 2.5-3.5 kg; BW2: 3.5-4.5 kg; BW3: ≥ 4.5 kg) and average daily gains by life day 10, 20, and 30 (NDG: 0.01-0.20 kg; MDG: ≥ 0.2 -0.25 kg; HDG: ≥ 0.25 kg). Artificial rearing was carried out from the 3rd life day using a feeding machine, providing ad libitum access to a milk feeding mixture. From life day 10, animals received supplementary concentrate feed and hay. Animals were regularly weighed using a digital scale (accuracy 0.1 kg). Individual milk yield was recorded and milk samples were collected once a month from March to July. Data were analysed by ANOVA (post hoc: Tukey); the model included the fixed effects of birth weight and average daily gains by life day 10, 20, and 30. Significance was set at $P \leq 0.05$. The significant differences in milk yield during the first lactation were observed between BW1 and BW2, BW3 the birth weight groups ($P=0.0066$). Concerning daily weight gains, the highest milk yield (207.78, 223.77, 232.24 L) was observed in animals with NDG by life day 10, 20, and 30, resp., while the lowest yield (193.58, 166.36, 179.87 L) was recorded in animals with MDG by life day 10, 20, and 30. However, a significant difference was observed only between animals with NDG and MDG by life day 20 ($P=0.0007$). The only significant differences in SCS were observed by life day 10 between daily gain groups NDG (1.89) and MDG (2.32) ($P=0.0467$). In conclusion, only the birth weight and the weight gain by life day 20 influenced milk yield during the first lactations, while weight gain by life day 10 affected SCS. This publication was written as part of the APVV-21-0134 project.

Session 22

Poster 11

The Cathelicidin Gene Cluster in Goats (*Capra hircus*): Organization and DiversityS. González-Acosta^{1,2}, M. R. López¹, P. Asensio-Calavia^{1,2}, A. Otazo-Pérez^{1,2}, J. M. Pérez De La Lastra¹, A. Morales-Delanuez^{1,3}¹ Biotechnology of Macromolecules Research Group, Instituto de Productos Naturales y Agrobiología, Avda. Astrofísico Francisco Sánchez 3, 38206 San Cristóbal de la Laguna, Spain, ² Escuela de Doctorado y Estudios de Posgrado, Universidad de La Laguna, Avda. Astrofísico Francisco Sánchez, SN, 38200 San Cristóbal de La Laguna, Spain, ³ IUSA-ONEHEALTH 4 Animal Production and Biotechnology Group, Institute of Animal Health and Food Safety, Universidad de Las Palmas de Gran Canaria, Transmontaña s/n, 35413 Arucas, Spain

The innate immune system is the first line of defence against pathogens. Among these, host defence peptides play a crucial role as they have direct antimicrobial activity and modulate the immune response. Cathelicidins are a well-known HDP found in most vertebrates, including goats. These peptides contribute to the immune system by targeting a broad spectrum of microorganisms being involved in immune regulation. Cathelicidins are structurally diverse and are classified according to the secondary structure of their mature peptides, including α -helices, β -hairpin structures, and elongated forms rich in proline-arginine or tryptophan. Their genes are typically organised in genomic clusters, as seen in ruminants such as sheep and cows. The identification of several cathelicidin genes and their organisation is necessary to understand the organisation and diversity of these antimicrobial peptides in the goat genome. This information provides valuable insights into their role in immune defence and disease resistance. The aim of this study was to identify and characterise the goat cathelicidin cluster using bioinformatics tools and analysis of the reference goat genome. Our results show that all cathelicidin genes in the goat genome are grouped in a cluster on chromosome 22 spanning approximately 75 Kb. It was identified a total of seven cathelicidin genes and one potential pseudogene. The average gene size was 1719 bp and ranged from 1309 bp (CATH1) to 1956 bp (CATH3). The first gene of the cluster, MAP34B, encodes a mature peptide containing a CAP-18 domain, a characteristic LPS-binding domain in mammals. Three cathelicidins exhibited a proline-arginine-rich structure, while the other four adopted an α -helix conformation.