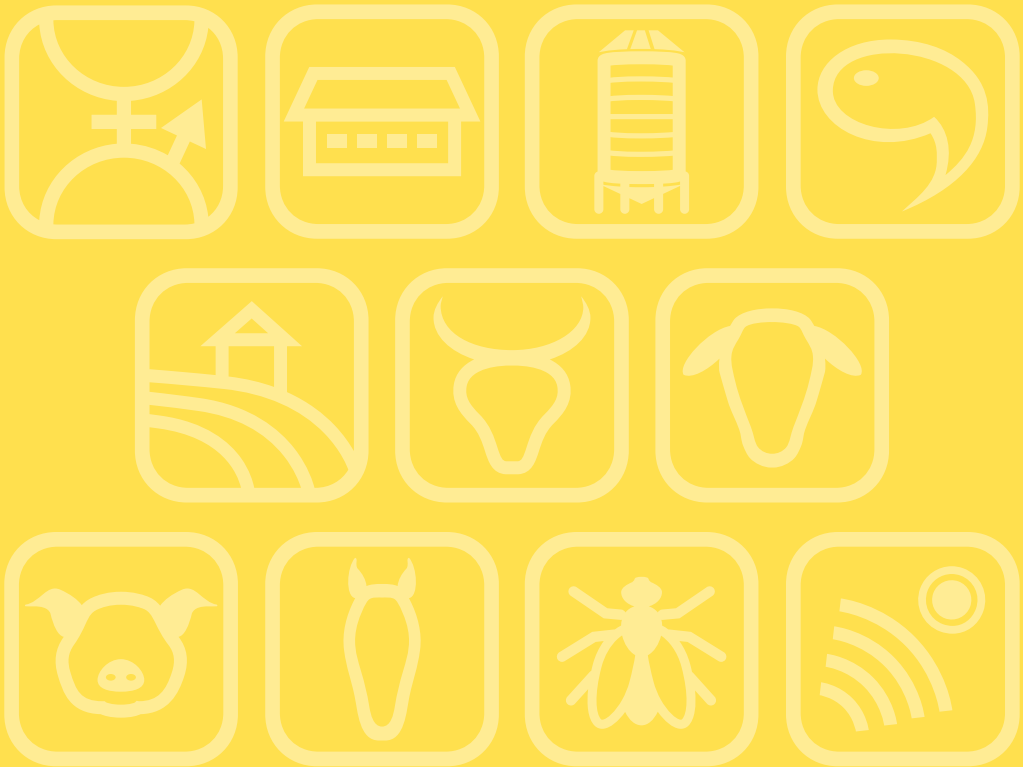


# Book of Abstracts of the 68<sup>th</sup> Annual Meeting of the European Federation of Animal Science



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**68<sup>th</sup>** ANNUAL MEETING OF  
THE EUROPEAN FEDERATION  
OF ANIMAL SCIENCE

28 August – 1 September 2017, Tallinn, Estonia

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European Federation of Animal Science**

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**Genetic parameters of medullation percentage in alpacas**A. Cruz<sup>1</sup>, R. Morante<sup>1</sup>, I. Cervantes<sup>2</sup>, A. Burgos<sup>1</sup> and J.P. Gutiérrez<sup>2</sup><sup>1</sup>INCA TOPS S.A, Miguel Forga 348, Arequipa, Peru, <sup>2</sup>Universidad Complutense de Madrid, Departamento de Producción Animal, Avda Puerta de Hierro s/n, 28040 Madrid, Spain; gutgar@vet.ucm.es

Alpaca fiber is one of the main natural textiles produced in Peru. The mean fiber diameter goes from 20 to 36  $\mu\text{m}$ , being highly appreciated some categories such as baby alpaca ( $<23 \mu\text{m}$ ), superbaby alpaca ( $<20 \mu\text{m}$ ) and royal alpaca ( $<18 \mu\text{m}$ ). However medullation of alpaca fiber is a usual disappointing feature that prevents being greatly estimated by the textile industry and the final consumer, given that it has been related to prickling. Therefore the present work aimed to estimate the genetic parameters of the percentage of medullation and its genetic correlations with other interesting traits. Data from 2000 to 2016 were obtained from PacoPro v5.4 software belonging to Pacamarca experimental farm, totaling 1,833 records of medullation percentage corresponding to 1,482 Huacaya (HU) and 351 Suri (SU) ecotypes. Fiber samples were taken from the mid side, and analyzed in an OFDA100 device, quantifying the percentage of continuously medullated fibers (PM). Genetic correlation was assessed between PM and other traits. Fiber diameter, standard deviation, coefficient of variation were analyzed concerning fiber traits; density, crimp in HU or lock structure in SU, head conformation, fiber coverage and general aspect were studied as morphological traits, and weaning weight (WW), age at first calving and calving interval as functional and secondary traits. PM ranged from 0.3 to 100% with an average of  $28.46 \pm 28.98\%$ . PM heritabilities resulted high (0.454) or very high (0.801) for HU and SU respectively. Genetic correlations were found to be moderate to high (0.269 to 0.584) between PM and other fiber traits in both ecotypes, being lower than 0.376 in absolute value between PM and the rest of traits, with only those with WW being unfavorable 0.232 for HU and 0.096 for SU ecotypes. The PM repeatabilities were found 0.746 and 0.840 for HU and SU ecotypes respectively. The genetic parameters and its economical importance make this trait valuable as selection criterion in the breeding program of the population. The high magnitude of the heritabilities suggest the possible existence of a segregating major gene.

**CSN2 and CSN3 gene polymorphisms and their effects of milk production in Latvian local breed cows**

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Latvian Brown (LBGR) and Latvian Blue (LZ) cow breeds that are named local in Latvia. The local breeds characterizes with lower milk yield than Holstein Black and White cows, but their milk has better composition. To preserve the valuable traits of local breeds we need to find out their genetic suitability for production of high quality milk. The purpose of our study was to investigate the genetic diversity of beta (*CSN2*) and kappa (*CSN3*) casein proteins in local Latvian dairy cattle breeds and their association with milk yield and composition traits. Genotypes of milk protein genes, *CSN2* and *CSN3* were detected in 102 cows of LBGR breed, and 86 cows of LZ breed. In the LBGR breed the allelic frequencies for *CSN2* were  $A_1=0.578$  and  $A_2=0.422$ , while for *CSN3*, they were  $A=0.750$ ,  $B=0.235$  and  $E=0.015$ . For LZ breed the allelic frequencies for *CSN2* were  $A_1=0.605$  and  $A_2=0.395$ , while for *CSN3*, they were  $A=0.512$ ,  $B=0.482$  and  $E=0.006$ . Analyzing the frequency of genotypes after *CSN2* gene found that in LBGR and LZ breeds a higher it was for cows with heterozygous genotype  $A_1A_2$ , respectively 0.549 and 0.558, but the lowest – for  $A_2A_2$  genotype (0.147 and 0.116). For both analyzed breeds by *CSN3* gene were observed four genotypes. Largest amount of LBGR breed cows had AA genotype, but LZ breed cows – AB genotype (respectively 0.539 and 0.558). Unfortunately in both analyzed breeds there were few cows with the optimal genotype for milk processing – BB which for LBGR breed cows had 0.039 frequency, but for LZ breed cows – 0.198. Both LBGR and LZ breeds had a few amount of cows whose genotype had unwanted E allele. Analyzed LBGR breed cows didn't have preferred gene combination ( $A_2A_2BB$ ), but in LZ breed group with this combination there was only three cows (3.50%). First lactation LBGR breed cows with genotype  $A_2A_2AB$  had the highest milk yield in closed standard lactation ( $5,278.3 \pm 466.25$  kg) and highest protein content in milk ( $3.43 \pm 0.09\%$ ), but for LZ breed cows it was higher obtained from cows with genotype  $A_2A_2BB$  ( $5,028 \pm 82.40$  kg and  $3.38 \pm 0.15\%$ ). The research is supported by State Research Program AgroBioRes 3 project (LIVESTOCK).