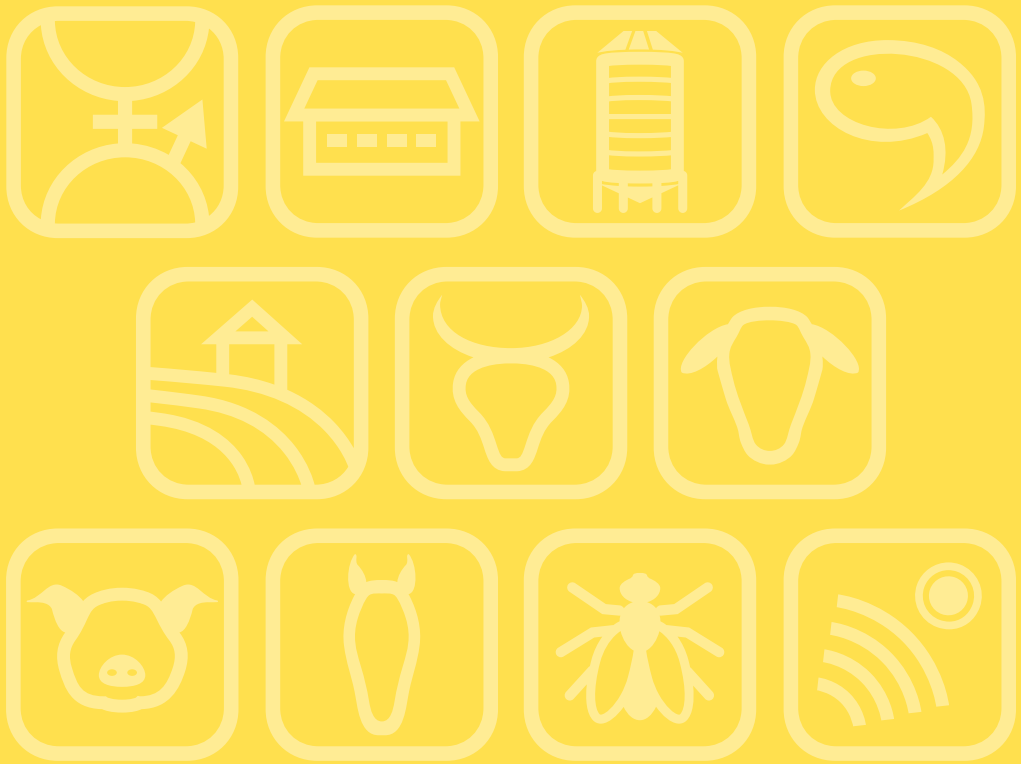


# Book of Abstracts of the 72<sup>nd</sup> Annual Meeting of the European Federation of Animal Science



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# Book of Abstracts of the 72<sup>nd</sup> Annual Meeting of the European Federation of Animal Science

Davos, Switzerland, 30<sup>th</sup> August – 3<sup>rd</sup> September, 2021



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**Influence of intensity of selection on the accuracy of genomic breeding values – a simulation study***S. Andonov and D.J. De Koning**Swedish University of Agriculture, Ulls Vag 26, 750 07, Sweden; andonov.sreten@slu.se*

One requirement for unbiased genetic estimation is the unselected population, which is not the case in livestock breeding programs. With genomics available, many approaches in breeding values (BV) estimation can be applied. The aim was to test modalities in genomic BV estimations in the simulated population under no selection, moderate selection, and intensive selection. Three dairy cattle populations were simulated in 10 replicates, consisting of 3,000 males and 25,000 females for 20 generations. The trait was milk yield with  $h^2=0.30$ . For the last 5 generations for 29 chromosomes, 45,000 SNPs were simulated. It was assumed that the trait is affected by 450 QTLs equally distributed over the genome. Accuracy of predicted breeding values for young animals in the last generation were calculated using BLUP, single-step genomic BLUP (ssGBLUP), and SNP-BLUP. In the evaluations, the pedigree and SNPs for animals – parents of the young animals were restricted to the last 3 generations. In case of no selection in population, the predicted breeding values for young animals were unbiased with accuracy from 0.64 (BLUP) to 0.77 (ssGBLUP). In the scenario with moderate selection compared to the scenario without selection, the bias was slightly increased while the accuracy of predicting young animals' performance was decreased. The accuracies of prediction with BLUP, SNP-BLUP, and ssGBLUP were 0.50, 0.65, and 0.70, respectively. In the scenario with intensive selection, estimates of predicted BV of young animals were even more biased than for the scenario with moderate selection. The accuracy of BV predictions with BLUP was low (0.16), while ssGBLUP and SNP-BLUP were remarkably higher (0.61). The ssGBLUP and SNP-BLUP performed similarly only in the scenario with intensive selection.

**Efficiency of genomic selection for fibre traits in alpacas***B. Mancisidor<sup>1</sup>, A. Cruz<sup>1</sup>, G. Gutiérrez<sup>1</sup>, A. Burgos<sup>2</sup>, J. Moron<sup>1</sup>, M. Wurzinger<sup>1</sup> and J.P. Gutiérrez<sup>3</sup>**<sup>1</sup>Universidad Nacional Agraria La Molina, Av. La Molina s/n, Lima, Peru, <sup>2</sup>Fundo Pacamarca, – Inca Tops S.A, Miguel Forga 348, Arequipa, Peru, <sup>3</sup>University Complutense de Madrid, Avda. Puerta de Hierro s/n, 28035 Madrid, Spain; gutgar@vet.ucm.es*

Alpaca breeding is of great economic importance in the Peruvian High Andes. To satisfy the textile industry's demand, the improvement of fibre quality is the main breeding goal. A recently developed SNP chip for alpacas could potentially be used to implement genomic selection and accelerate genetic progress. Therefore, this study aimed to compare the increase in prediction accuracy of three important fibre characteristics: fibre diameter (FD), its standard deviation (SD), and percentage of medullation (PM) in Huacaya type alpacas. Pedigree information and phenotypic data were obtained from the PacoPro v5.10 software from the Pacamarca Scientific Research Experimental Station. Genotyping data from the SNP chip for alpacas with 69,685 SNPs were used. The reference population size was 431 alpacas. Prediction accuracy of breeding values was compared between a classical BLUP prediction and a single-step Genomic BLUP (ss-GBLUP) prediction. Deregressed phenotypes were predicted with both methodologies. The accuracy of the genetic and genomic values was obtained by the correlation coefficient between the predicted breeding values and the deregressed value of 100 random animals for the cross-validation process under both methods. Ten replicates were done. The BLUPF90 family programs were used. The heritability estimates were 0.243, 0.357, and 0.155 for FD, SD, and PM, respectively. Accuracies with ss-GBLUP improved by  $9.8\pm 3.5$ ,  $29.8\pm 10.8$  and  $29.1\pm 6.2\%$ , on average, for FD, SD, and PM respectively compared to the BLUP method. The increase in accuracy was relevant even when the number of genotyped animals was limited, suggesting that adding genomic data in prediction models could be beneficial for alpaca breeding programs.