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**External and genetic factors influencing fertility in Latxa dairy sheep breed**

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Pregnancy rate at artificial insemination (AI) is largely variable and dependent on genetic and non-genetic factors. In Latxa breed, herds within the breeding program make use of high genetic value rams to inseminate their ewes once per year. Despite the relevance of the success of AI on the breed's genetic progress and on farms' productivity, this trait has not been up to now explored in this sheep population. To this aim, 135,351 edited AI records from 63,480 Latxa Cara Negra from Euskadi ewes, collected between 2000 and 2021, were used. The outcome of an AI event was treated as a binary response of either success or failure in becoming pregnant. To identify the environmental variables influencing the AI outcome, a multiple logistic regression was first calculated. After that, using the relevant factors identified in the previous step, a threshold model was used to estimate the genetic components of the trait in females and males. Results show that the AI success is higher in ewes having their first parturition at 1 year of age than at 2 or 3 year of age (Odd Ratio [OR] 1.04 and 1.08, respectively), in those with high prolificacy in the lambing previous to the AI event (OR 1.04 and 1.13 by having 2 or 3 lambs, respectively, vs 1 lamb), in those with a larger lambing-AI interval (OR 1.07 and 1.35 for intervals between six months or more, respectively, vs three months interval), as well as in those who had the previous parturition from an AI event compared to natural mating (OR 1.39). In counterpart, the higher the milk produced in the nearest milking AI date, the poorer the AI results (OR 0.92 when producing more than 450 ml vs producing up to 300 ml). Moreover, ewes older than five years and six lambings have less AI success with respect to younger ewes (OR 0.78). Regarding genetic parameters, the heritability and repeatability were  $0.090 \pm 0.007$  and  $0.200 \pm 0.007$  in females and  $0.013 \pm 0.006$  and  $0.025 \pm 0.002$ , respectively, in males. These results indicate that there are extensive and diverse external factors influencing the AI success, while the additive component is low. Although the trait shows genetic variability susceptible of selection under the breeding scheme, the genetic progress would be slow.

**Single-step genome-wide association for milk urea concentration in Walloon Holstein**H. Atashi<sup>1,2</sup>, Y. Chen<sup>2</sup>, C. Bastin<sup>3</sup>, S. Vanderick<sup>2</sup>, X. Hubin<sup>3</sup> and N. Gengler<sup>2</sup><sup>1</sup>Shiraz University, Department of Animal Science, Shiraz, 7144113131 Shiraz, Iran, <sup>2</sup>University of Liège, GxABT, Pass. des Déportés 2, 5030 Gembloux, Belgium, <sup>3</sup>Elevéo asbl Awé Group, Ciney, 5590 Ciney, Belgium; hadi.atashi@uliege.be

Milk urea (MU), a normal non-protein nitrogen component in milk, is a by-product of the protein metabolism. It has been shown that MU is correlated with milk production, milk composition, cheese-making properties, nitrogen utilization efficiency and reproductive performance in dairy cattle. Therefore, selection for reducing MU can result in reducing N pollution, improving feed efficiency and animal health, and increasing milk quality and reproductive performance. The aims of this study were to estimate genetic parameters for MU and to conduct a single-step genome-wide association (ssGWAS) to identify candidate genes associated with MU in Walloon Holstein. The used MU data have been collected from 2014 to 2020 on 78,073 first-parity (485,218 test-day records), and 48,766 second-parity (284,942 test-day records) Holstein cows distributed in 671 herds in the Walloon Region of Belgium. Data of 730,539 single nucleotide polymorphisms (SNP), located on 29 *Bos taurus* autosomes (BTA) of 6,617 animals (1,712 males) were used. The proportion of the total additive genetic variance explained by windows of 50 consecutive SNPs (with an average size of ~ 216 Kb) was calculated, and the top-three genomic regions explaining the largest rate of the total additive genetic variance were considered promising regions and used to identify potential candidate genes. Mean (standard deviation) MU was 25.38 (8.02) mg/dl and 25.03 (8.06) mg/dl in the first and second lactation, respectively. Mean heritability estimates for daily MU were 0.21 and 0.23 for the first and second lactation, respectively. The top-3 regions combined explained 1.22 and 1.04% of the total additive genetic variance of MU in the first and second lactations, respectively. The identified regions were located from 80.61 to 80.74 Mb on BTA6, 103.26 to 103.41 Mb on BTA11, and 1.59 to 2.15 on BTA14. Genes including *PAEP*, *SOHLH1*, *GLT6D1*, *LCN9*, *DGATI*, *CYHR1*, *CPSF1*, *SCX*, *SCRT1*, and *SPATC1* were identified as positional candidate genes for the MU. The findings of this study provide a better understanding of the genomic architecture underlying MU in Holstein cattle.