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The development of a single-step genomic evaluation system for dairy cattle in the Walloon Region of Belgium

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For several years, the Walloon Region of Belgium provides dairy cattle breeders with locally estimated breeding values for important traits. These evaluations allow Wallonia to participate in the international MACE evaluations performed by INTERBULL. In current genomic evaluations, genomic and pedigree information is then combined with this external information (international EBV from MACE, "MACE_EBV") in a pseudo-single-step genomic evaluation, resulting in genomically enhanced EBV (GEBV). However, these pseudo-single-step evaluations result in potential biases. Therefore, the aim of this study was to implement a single-step genomic BLUP (ssGBLUP) that combines simultaneously all available national information with MACE information, and to validate it using milk production traits. Briefly, the new strategy first consists in defining "pseudo-traits", reflecting MACE-traits that are 305-day across the first three lactation averages for milk, fat, protein yields. MACE information is therefore converted into adjusted pseudo-phenotypes and deregressed effective contributions, avoiding double-counting of Walloon information contained in MACE_EBV. Second, the variance-covariance matrices of the national test-day random regression model was adapted to include the 3 MACE pseudo-traits as traits correlated to the different Legendre polynomials. Finally, an ssGBLUP is performed to analyze simultaneously test-day records and MACE pseudo-phenotypes. This integration of MACE information followed the strategy developed for integrating international EBV and associated REL in beef Italian Limousin evaluation. Validation of pedigree and ssGBLUP were conducted using data from official Walloon genetic evaluations of April 2022. Pearson correlations among MACE EBV and (G)EBVs with integration were close to 1 (0.95 – 0.97) in all cases, demonstrating the robustness of this new method. Next a linear regression validation approach will be used to perform a cross validation on the calculated values.

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Poster 16

Maturity is associated with casein alpha S1 region in Saanen and Alpine goats

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Maturity, defined as the ratio of milk yield (MY) in first parity to subsequent parities (e.g., MY in first parity divided by MY in second parity), is a trait linked to functional longevity in French dairy goats. The genetic correlation between maturity estimated breeding values (EBV) and longevity EBV is -0.5, highlighting its potential in selection objectives for Alpine and Saanen breeds. This study aimed to identify genomic regions associated with maturity. The dataset included MY records from 175,572 Saanen and 246,504 Alpine goats collected in France between 1990 and 2023. The goat *as1* casein gene is a complex gene: alleles A, B, C associated with increased levels of *as1* casein were coded as « strong effect (S) », allele E as « intermediate effect (I) », allele F were coded as « reduced effect (R) ». Genomic evaluation was performed using BLUPF90+, and the variance explained by 1 Mb windows was calculated with POSTGSF90 software following ssGBLUP. A 1 Mb region on chromosome 6 demonstrated the strongest association with maturity, explaining 3% of the total variance in Saanen and 1% in Alpine. One of the top SNP (snp59427-scaffold980-309132) at position 85,994,216 is located within the CSN1S1 gene. Genotypic frequencies among Saanen AI bucks (N=467) was 15% AA, 55% AG and 30% GG, while in Alpine (N=613), it was 53% AA, 41% AG, and 6% GG. The alpha S1 casein allele associated with each genotype at the significant SNP were in Saanen: AA to homozygote S (75%), AG to heterozygote S-I (87%), and GG to homozygote I-I (94%). Maturity EBVs were highest for AA genotypes, intermediate for AG, and lowest for GG in both breeds. While longevity EBVs did not vary significantly among genotypes, bucks with AA genotype had higher EBVs for fat and protein contents compared to AG and GG genotypes. Notably, GG bucks exhibited higher MY EBVs in both first and sixth parities, with greater differences observed in later parities. This study underscores the genomic influence on maturity and provides insights for integrating this trait into breeding programs to enhance longevity and production efficiency in dairy goats.