SHEEP GENOMICS
COMMUNICATION

JANUARY 2026

PROJECT STATUT AND TIMELINE

The genomic project led in partnership by the SEMRPQ, CEPOQ, and Université Laval is progressing well and remains ongoing. A no-cost extension was requested and granted, extending the project timeline to June 30, 2027. This extension was required to address delays encountered during the development of the custom SNP chip, which was modified to include mutations associated with known genetic defects, coat colour determination, and disease resistance.

These delays arose primarily from manufacturing issues affecting the first version of the custom chip. Several probes failed to function as expected, notably those required to accurately assess resistance to Maedi-Visna. Given the critical importance of this trait, the production of a second chip version was necessary. No-cost extensions are a standard mechanism within the granting program and are typically awarded when projects are progressing satisfactorily.

ACTIVITY 1: DEVELOPMENT OF THE GENOTYPIC DATABASE

The genotypic database currently contains data from 3,393 animals, with an additional 384 samples in processing. To date, animals representing 22 breeds have been genotyped. The program has expanded to a national scale, with 235 collection kits distributed to breeders in Ontario and Alberta; 74 samples from these regions have already been successfully genotyped. Four additional samples from the United States were also processed. These international samples fall outside the scope of project support; however, participating breeders receive comprehensive genotyping reports for their animals.

The reporting system is being automated, allowing breeders to customize the certificates accompanying each animal. All genotyping is conducted at the Centre d'expertise et de services (CES) of Génome Québec using the Illumina SNP Chip platform, which provides highly reliable genotype data. However, both the USDA and the CFIA require genotyping laboratories to hold ISO/IEC 17025 accreditation. Meetings held in December with CES personnel confirmed that the accreditation process is underway.

ACTIVITY 2: GENOMIC SELECTION

Genotypic data were transferred to CEPOQ in April and December 2025. CEPOQ now oversees genomic-assisted breeding value evaluations (GEBVs) using MixBLUP, in collaboration with the Centre for Genetic Improvement of Livestock (CGIL) at the University of Guelph, which has released the first GEBV-related outputs.

SEMRPQ breeders expressed concerns regarding the sharing and dissemination of sensitive genomic information, particularly data related to genetic defects and disease resistance. To address these concerns, such sensitive data were excluded from the datasets used for genomic evaluations, and marker identifiers were anonymized. This approach is consistent with international best practices for commercial genomic partnerships, as confirmed by the MixBLUP development team in Wageningen, The Netherlands.

Improvements in accuracy associated with genomic selection are most pronounced in large datasets (>1,000 animals), which is currently achievable for the Rideau-Arcott and Romanov breeds. Preliminary analyses of young genotyped animals indicate accuracy gains of up to 15% and 53% for growth and carcass traits, and up to 110% and 181% for reproductive traits in the Rideau-Arcott and Romanov breeds, respectively. The highest average accuracies were observed in genotyped animals with existing performance records. In these animals, genomic information further increased accuracy by up to 3% and 4% for growth and carcass traits, and by 38% and 57% for reproductive traits in Rideau-Arcott and Romanov breeds, respectively.

An important remaining question concerns the value of genomic evaluation for breeds with small population sizes. Data pooling across breeds for mixed-breed analyses remains debatable. Breed-specific analyses may be preferable, even when sample sizes are insufficient to substantially increase accuracy. While gains may be limited, such analyses remain as precise as traditional genetic evaluations and better account for breed-specific characteristics.

ACTIVITY 3: GENETIC DIVERSITY

The project continues to develop a genomic-based metric for assessing genetic diversity. Preliminary results indicate a limited correlation with traditional pedigree-based estimates, likely reflecting allelic fixation that occurred during breed formation. While some breeds retain phenotypic variation, others appear more genetically uniform.

Genetic diversity assessment is closely linked to parentage verification, an area where genomic tools offer unparalleled precision. Both parents can be reliably validated, and in cases of misidentification, true parentage can often be established when parents or close relatives have been genotyped. Currently, approximately 7% of genotyped animals exhibit discrepancies between recorded and genomic pedigrees. In response, the Canadian Sheep Breeders Association has initiated a pilot project for genomic parentage verification and has approved the use of SNP chip data as an alternative to microsatellite-based testing.

ACTIVITY 4: GENETIC AND CHROMOSOMAL DEFECTS AND QUALITIES

An allele responsible for more imposing musculature has recently been reported in two breeds, and its effect has been confirmed in one of them. Additional analyses are planned to validate its effect in the second breed and to better define its impact on the phenotype.

In addition, a novel polymorphism in a gene linked to disease resistance has been identified. This previously unreported deletion causes a frameshift and introduces a premature stop codon. Ongoing investigations are correlating herd infection status with allelic frequencies to assess its functional relevance.

ACTIVITY 5: GENOME-WIDE ASSOCIATION STUDIES

Several GWAS bioinformatic tools have been tested to enable analyses across multiple available polygenic traits, including carcass and prolificacy traits. In parallel, sample collection is ongoing for apparently causal defects such as “curved legs,” “elf ears,” and jaw deformities. The combined phenotypic and genotypic datasets are expected to provide sufficient material to validate the GWAS pipeline and potentially identify causal mutations. In addition, a collaboration with a Swiss research team has emerged from this project, as they are investigating a genetic defect previously reported by Canadian breeders. Canadian breeders voluntarily submitted samples to Switzerland in December, and analyses are currently underway to confirm potential mutations.

CONCLUSION

Overall, the project is progressing very well, with substantial advances achieved across all activities. All objectives and milestones are expected to be met by the end of the extended project period. The SEMRPQ serves as the custodian of the genotypic data and manages all access requests. Upon project completion, SEMRPQ will be fully autonomous in continuing genotyping and genomic activities. Canadian sheep breeders nationwide are invited to submit samples for genotyping and to contact SEMRPQ for further information or collaboration.

INFORMATION

All the necessary tools are available on our website: request forms for tubes, sample return, and information requests

WWW.SEMRPQ.NET