Abstract: High-throughput technologies are available to aid producers in efficiently and sustainably raising many animals, including automated sensory technologies for phenotype measurement and genomic data. However, uptake of genetic selection by the beef cattle sector has been limited by segmentation of the industry. Therefore, easy to use genetic evaluation systems (GES) that can convert ‘big data’ into real-time and comprehensive results are needed, so that beef cattle producers can utilize the technologies that are becoming available to make accurate breeding decisions. The purpose of this study is to update a pre-existing purebred and crossbred beef cattle GES to become both flexible and efficient in its ability to evaluate high-throughput phenotypic data, and to assess the feasibility of including genotypes in a single-step genetic evaluation procedure (ssGBLUP). Firstly, computational operations required for the calculation of breeding values will be quantified and evaluated. A purebred and crossbred reference population will be assembled using data from Canadian beef breed associations purebred (n = 186,928) and commercial animals (n = 14,406). Multiple breeds will be considered (Angus, Charolais, Hereford, and Simmental), and multiple phenotypes analyzed (birth weight, weaning weight, yearling weight, and calving ease). Key component matrix operations with and without the use of Python Libraries (NumPy) will be evaluated. Computational performance of the different strategies will be compared, including CPU time, and memory allocation. Subsequently, a simulated ssGBLUP will be conducted using a population which mimics that observed in the preliminary analysis. Computational costs associated with the implementation of ssGBLUP will be compared to the existing GES. The results of this study will be directly applied to provide beef producers with the tools to improve the genetics of their own herds. This will facilitate the uptake of technology by the industry, thus increasing the economic value and sustainability of beef production.

Keywords: beef cattle, genomic selection