20. International genomic evaluations for beef cattle

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Reproductive technologies such as artificial insemination allow breeders to access the genetic material of elite sires worldwide. Both importers and exporters of sires' frozen semen seek a fair comparison of the genetic merit, i.e. the estimated breeding value (EBV), of foreign and national sires. To reach this goal, international evaluations compute an international EBV which takes into account pedigree and phenotypic data from different countries and allow breeders to compare sires across countries. In recent years beef cattle international evaluations led by Interbeef have undergone a period of rapid expansion and currently involve 15 countries worldwide for 3 traits and 5 breeds. In the last decade, individual-level genomic data revolutionized animal breeding and allowed to improve the accuracy of the EBV compared to the ones obtained from conventional sources of data (i.e. pedigree and phenotypic information). The genomic data used typically includes per individual observed genotypes at ~50,000 sites throughout the genome. To date, the so-called "single-step" genomic evaluations allow to efficiently combine conventional sources of data and genomic data. However, to reach good accuracies of EBV, genomic evaluations require a large and informative training dataset which is not always available or even cost-effective to build and maintain for single countries. Combining genomic data across countries in a single international training dataset is expected to be beneficial. However, current Interbeef evaluations only include pedigree and phenotypic data and the benefits of an international single-step genomic evaluation are unknown. Therefore, the aim of this study was to investigate the feasibility and the benefits of combining genomic data across countries in an international single-step genomic evaluation. Individual measurements on weaning weight of more than 330,000 Limousin male and female calves were available from seven countries. Genomic data were available for 17,607 animals from five countries. After defining the statistical model for the international genomic evaluations, we evaluated the accuracies of EBV from different scenarios representing national and international evaluations either with or without including genomic data. Results show that using genomic data in international evaluations will increase the accuracy of international EBV compared to those of current evaluations. Moreover, we showed that international single-step genomic evaluations are beneficial for countries regardless of the size of their national populations. Further results will be discussed at the conference.

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