International Genomic Cooperation

EuroGenomics significantly improves reliability of Genomic evaluations

Xavier David (UNCEIA), Alfred de Vries (CRV), Egbert Feddersen (DHV/vit),
Søren Borchersen (VikingGenetics)

EuroGenomics is an international project in genomic selection developed by the Cattle AI industry. It aims to improve the reliability of the Holstein genomic evaluation. This presentation describes the origins of the project, the field of this European cooperation and the first results.

At the end of 2008, thanks to a helpful context and a particular political vision, a new approach of collaboration in the European AI industry became a reality.

A Helpful Context in Science

At first scientific reasoning was very helpful. In 2008, scientists admitted that the quality of performances, the efficiency of methodology and the size of the reference population were the 3 key factors which contributed to the quality of genomic selection.

It has been demonstrated (Goddard & Hayes 2008) that the larger the size of the reference population, the more reliable the traits are, whatever the heritability.

A Helpful Context in the AI Industry

At the same time, the AI industry context also played an important role. In summer 2008, 2 players in Holstein genetics, the USA and Canada, decided to merge their reference population. This North American consortium enabled them to attain a reference population of 9 300 bulls with progeny results.

A Common Political Vision

In Europe at the beginning of 2009, 5 major competitors shared the same opinion: the need to merge their reference population in order to obtain better results in traits reliability in genomic selection. To reach this goal, they decided to start a new era of innovative cooperation to solve the technical problems related to genomic selection and new data exchanges.

Thanks to a French initiative, discussions started at the beginning of 2009 and some months later reached a common agreement: exchanges of genotypes of the reference population.

5 European Partners

The partners of EuroGenomics are CRV, DHV / vit, UNCEIA and VikingGenetics. They are in charge of Holstein breeding programs or representative of breeding companies respectively in the following countries: Netherlands/Belgium (CRV), Germany (DHV / vit), France (UNCEIA) and Denmark/Sweden/Finland (VikingGenetics). These 5 partners are breeder owned companies (cooperatives) and they work with the European organisation in terms of milk recording and animal identification. Furthermore, they share the same values, providing the most reliable genetics to their farmers.

Scientific Experts

EuroGenomics partners have developed this project together with their scientific partners. This capacity to add different scientific expertise to this project was very useful to reach the goal efficiently. The scientific partners that are taking part in this project are: INRA, University of Liege and University of Arrhus and Nordic Cattle Genetic Evaluation.

Exchanges

In the fall of 2009, EuroGenomics partners exchanged genomic SNP marker data (Illumina Bovine SNP50 BeadChip). Each partner contributed to the data with 4,000 proven bulls to further improve the reliability of genomic breeding values. A key point of EuroGenomics is the reciprocal win-win situation.

It was also necessary to develop imputation methodology to make the exchange of data between 2 different chips possible: on the one hand, the Illumina Bovine SNP50 BeadChip and on the other hand the CRV 60 K chip. This development was made by Tom Druet with a satisfactory error rate lower than 1%.

At the beginning of March 2010, all partners extended their reference population to a total of at least 16,000 bulls.

Results

All EuroGenomics partners use the same EuroGenomic reference population. Out of 19,4 million cows, daughters of EuroGenomics bulls, 14 million come from EuroGenomics countries and 5,4 million from other countries. The conventional daughter breeding values of the EuroGenomics bulls all resulted from sophisticated data collection systems and herdbook registration including comprehensive fertility data. Thus, data recording includes not only milk production traits but also functional traits.

The national genomic formulas are still individually country-based. Conventional (MACE) daughter proofs used for deriving national genomic formulas are different on the four country scales and the national indices reflect different breeding goals.

The new approach results in reliabilities that exceed current reliabilities of genomic proofs by about 10%. The range of average increase goes from 6% for protein to 15% for udder depth.

Conclusion

Firstly, these preliminary results which have been obtained in a short space of time are very promising. Due to a high level of cooperation and team work, these results prove that international collaboration to increase the reference population is beneficial.

Secondly, results are clearly better for traits with higher Interbull correlations. Consequently, Interbull must keep and reinforce its missions to promote collaboration and—harmonisation in order to improve correlations between countries for classical international evaluations.

To conclude, EuroGenomics common reference population is the largest reference population in the world. Furthermore, it is unique in its quality. All EuroGenomics partners run breeding programmes based on the best available Holstein genetics in Europe and North America. Therefore, the EuroGenomics reference population mirrors the full variation of international Holstein genetics perfectly. This will be certified by the next Interbull validation for national genomic evaluation systems once it is offered for official use.

This EuroGenomics project is also a good example for the effective cooperation of European countries setting new international standards for the benefit of dairy farmers.

Paris 3rd March 2010