Bulletin UASVM Animal Science and Biotechnologies, 66 (1-2)/2009 Print ISSN 1843-5262; Electronic ISSN 1843-536X

# Developing Advanced Management and Selection Tools for Dairy Cattle

## **Nicolas GENGLER**

Gembloux Agro-Bio Tech, University of Liège, B-5030 Gembloux, Belgium; gengler.n@fsagx.ac.be

**Abstract.** Developing advanced management and selection tools for dairy cattle is the current challenge our research group is facing. Based on existing, or new data, we have described the development of these tools. They will allow dairy farmers in the Walloon Region to reduce their costs and increase product quality.

Keywords: breeding, management, modeling, dairy cattle

## INTRODUCTION

In the next decencies, dairy production will be under even more pressure to provide healthy milk from well-managed and robust cows producing under economically and ecologically sustainable conditions. Performance recording has been for years linked to genetic improvement and to basic farm management. For yield traits, efforts to model, still in a genetic perspective, this type of longitudinal data focused on random regression, also called random coefficient, models. Other data from performance recording is available as linear data, body condition scores, health (i.e., somatic cell count), fertility and longevity data. In this presentation we will show how extensive data recording, combined with statistical modeling is the basis for the development of advanced management and selection tools for dairy cattle.

## MATERIALS AND METHODS

Research data is coming from milk recording schemes in Belgium, Luxembourg and potential other countries. Records include milk yields, fat, protein, lactose and urea content, as somatic cell counts. Recently we were able to add to this spectral data directly from the spectrometers used in the milk labs. Other data from performance recording is available as linear data, body condition scores, health (i.e., somatic cell count), fertility and longevity data. Pedigree records are available for most animals. For the moment, efforts are underway to add knowledge of genotypes for 50k SNP panel.

Research has been focusing on topics directly linked to dairy cattle production and that can be deducted from available field data. Data was fitted with adapted linear mixed models where fitted models allow interpretation. For selection tools, animal effects were linked through parentage based on pedigrees or based on genotypes. Management tools were based on similar models but modified to reflect different objectives. Research is done in close collaboration with breeders and producers associations as the Walloon Breeding Association (AWE) and the Luxembourg Breeding Association (CONVIS). Development of methodology is often done in an international or European framework.

#### **RESULTS AND DISCUSSION**

Genetic evaluations for the Walloon Region of Belgium were developed in 2002 after the Belgian genetic evaluation system was split. This system evaluates today milk production traits, linear type traits, somatic cell count, body condition score, fertility and longevity (http://www.elinfo.be). The Walloon evaluations participate in the INTERBULL international genetic evaluation system. Previously the genetic evaluation system for linear type traits of non-Holstein cattle in the USA was developed (e.g., Gengler et al., 1997), this is also the base of the current Walloon system). Currently research is done to address issues related to the development of genetic evaluations using dense SNP panels (e.g., Gengler and VanRaden, 2008).

Another direction of research for future genetic evaluation systems is based on new and advanced tools to select for milk quality and animal robustness based on milk spectral data used to calibrate new traits as fatty acid compositions (Soyeurt et al., 2006). This is the objective of a European project called RobustMilk. Additionally research is done on links between udder health and environmental footprints (e.g., methan emissions) and milk composition. Additional research is done on inbreeding, biodiversity, multinational genetic evaluation and breeding programs in dual purpose Belgian Blue cattle. Linked to this is research on new advanced methods to integrate molecular knowledge into genetic evaluation.

A last sub-topic in the field of genetic evaluation is the ongoing research to study GxE interaction in the data of Tunisia and Luxembourg and potentially other countries.

Based on the experience in dairy cattle genetic evaluation for swine are currently under development.

Research on alternative use of performance recording data for management tools started early. Intermediate results were reported by Mayeres et al (2004). This has led to the development of a new method to compute lactation yields by estimation daily production over the whole lactation. This method to compute is also called locally Vallait or Modified Best Prediction. Permanent research efforts are underway to improve the method and make it more robust to potential issues (e.g., abnormal lactations). Based on the excellent results from the Vallait project two follow-up projects were initiated (OptiVal and OptiVal+). Objective of this research was to create additional value for performance recording scheme through new tools for management purposes. This research is underway and considers fertility, body condition score, fertility and linear type traits.

#### CONCLUSIONS

Developing advanced management and selection tools for dairy cattle is in work at our group. Based on existing, or new data, new tools are development. They will allow dairy farmers in the Walloon Region to reduce their costs and increase product quality.

Acknowledgments. The author wants to acknowledge the support of the data providers and funding agencies in particular the National Fund for Scientific Research (FNRS); of which he is a research associate.

#### REFERENCES

1. Gengler, N., G. R. Wiggans, J. R. Wright, H. D. Norman, and C. W. Wolfe (1997). Application of canonical transformation with missing values to multitrait evaluation of Jersey type. J Dairy Sci 80: 2563-2571.

2. Gengler, N. and P.M. Van Raden (2008). Strategies to incorporate genomic prediction into populationwide genetic evaluations. J Dairy Sci 91(E-Suppl. 1):506(abstr. 523).

3. Mayeres, P., J. Stoll, J. Bormann, R. Reents, and N. Gengler (2004). Prediction of daily milk, fat, and protein production by a random regression test-day model. J Dairy Sci 87: 1925-1933.

4. Soyeurt, H., P. Dardenne, A. Gillon, C. Croquet, S. Vanderick, P. Mayeres, C. Bertozzi, and N. Gengler (2006). Variation in fatty acid contents of milk and milk fat within and across breeds. J Dairy Sci 89: 4858-4865.